Feltus_etal Supplemental Table I 384 Conserved Intron Scanning Primer (CISP) Sets

Sno	LOCUS_ID	FORWARD	REVERSE	TIGRv1_START	TIGRv1_STOP	AMPLICON_SIZE	CHR	TIGR_TU_ID	DESCRIPTION	PAN_GRASS_PRIMER	*Oryza*	*Sorghum*	*Zea*	*Pennisetum*	*Cynodon*	*Eragrostis*	*Triticum*	*Hordeum*	*Ananas*	Amplification Group
1	PRSC1_001	GCATAAGCAAGGCATCAAAG	TTCATTCCAACATCACGTCC	19081423	19081634	211	1	9629.t03158	unspliced-genomic 1 3-beta-glucan synthase component putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
2	PRSC1_002	GCATAAGCAAGGCATCAAAG	AGCTTTCACAAAGTGGCTCC	19080418	19081634	1216	1	9629.t03158	unspliced-genomic 1 3-beta-glucan synthase component putative	N	Y	Y	-	Y	N	-	-	-	-	-
3	PRSC1_003	CGTAGCTCATCAAAGAAGG	TTCCACAAGAGAATGCCTC	5771806	5772389	583	1	9629.t00991	unspliced-genomic Protein kinase domain	N	Y	Y	-	N	N	-	-	-	-	-
4	PRSC1_004	GGCATTCTCTTGTGGAAAATC	CCCCAACTATACTGAGTTC	5772373	5772613	240	1	9629.t00991	unspliced-genomic Protein kinase domain	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
5	PRSC1_005	CGTAGCTCATCAAAGAAGG	CCCCAACTATACTGAGTTC	5771806	5772613	807	1	9629.t00991	unspliced-genomic Protein kinase domain	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
6	PRSC1_006	ACTTGACCTCCAACCTCCAAC	TGGGGATACAGATGGCTGTAG	35420699	35420909	211	1	9629.t05807	unspliced-genomic serine carboxypeptidase II putative	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
7	PRSC1_007	CCATCAACAACTCGGTGATC	AACATAGGCGCCATTGGTGG	11725704	11725966	262	1	9629.t01927	unspliced-genomic 2-oxo acid dehydrogenases acyltransferase (cata	N	Y	Y	-	N	N	-	-	-	-	-
8	PRSC1_008	GTAGCCTGATGTAAGCAAAG	TCTATGAGGAGGAAGTGCGG	22631542	22632170	628	1	9629.t03719	unspliced-genomic ATP synthase (C/AC39) subunit	N	Y	Y	-	Y	N	-	-	-	-	-
9	PRSC1_009	CCGCAACAACGGCAAGAAG	GCAAGGCACTCAGCAATGG	24327	25056	729	1	9629.t00006	unspliced-genomic ribosomal protein S7	N	N	Y	-	N	N	-	-	-	-	-
10	PRSC1_010	TGTCAACTGCATGCATTTTGTG	ATGGAAGTGGATGAGGCAAC	7123089	7123231	142	1	9629.t01196	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	-	-	-	-	-
11	PRSC1_011	TGTTGGGGTTGTATGGAAGC	CTATGGTTAAATCAATGAGCCG	35333825	35334373	548	1	9629.t05794	unspliced-genomic hypothetical protein	N	N	N	-	N	N	-	-	-	-	-
12	PRSC1_012	GTGGTAGCATAATACAGTGG	CTATGGTTAAATCAATGAGCCG	35334070	35334373	303	1	9629.t05794	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
13	PRSC1_013	GCTTCACTGTTTGGGATGTC	TCTCTGGCCTCAACAACACG	34366706	34367010	304	1	9629.t05625	unspliced-genomic ADP-ribosylation factor family	N	Y	Y	-	Y	N	-	-	-	-	-
14	PRSC1_014	CAACTGCATGCATTTTGTGC	GCACCCAGCTGAAAGAAAAG	7123092	7124068	976	1	9629.t01196	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	D
15	PRSC1_015	GTTGCCTCATCCACTTCCAT	GCACCCAGCTGAAAGAAAAG	7123212	7124068	856	1	9629.t01196	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
16	PRSC1_016	CTGGGTCTTGCTCCTTATTC	ATGTGATGGAGCGATCAGTG	10018676	10020461	1785	1	9629.t01655	unspliced-genomic Adaptin N terminal region putative	N	N	Y	-	N	N	-	-	-	-	-
17	PRSC1_017	AGATGCTTAAGAGTATGACC	TCAGTTTGTTCCATGCATTG	42049181	42049652	471	1	9629.t06896	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
18	PRSC1_018	AGCTTCACTGTTTGGGATGTC	TCTCTGGCCTCAACAACACG	34366705	34367010	305	1	9629.t05625	unspliced-genomic ADP-ribosylation factor family	N	Y	Y	-	Y	N	-	-	-	-	-
19	PRSC1_019	ATTGAGCCCCAGCATTTGAG	TTTGCTGGGCTTCCAAGTC	32404973	32405216	243	1	9629.t05307	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
20	PRSC1_020	AAAACGTGGAAGGTTGCTTG	TCCATAATAAGGGCCCAAAG	32405139	32405830	691	1	9629.t05307	unspliced-genomic Protein kinase domain putative	N	N	N	-	N	N	-	-	-	-	-
21	PRSC1_021	ATTGAGCCCCAGCATTTGAG	TCCATAATAAGGGCCCAAAG	32404973	32405830	857	1	9629.t05307	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
22	PRSC1_022	TGTAGCAGATGCCAGACTTC	CCATTGCTCCATAATCCAATC	32405726	32405982	256	1	9629.t05307	unspliced-genomic Protein kinase domain putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	D
23	PRSC1_023	AAAACGTGGAAGGTTGCTTG	CCATTGCTCCATAATCCAATC	32405139	32405982	843	1	9629.t05307	unspliced-genomic Protein kinase domain putative	Y	Y	Y	N	Y	Y	Y	Y	N	-	D
24	PRSC1_024	CCGCAACAACGGCAAGAAG	CTGTTGGATGAGCCCTTGG	24327	25095	768	1	9629.t00006	unspliced-genomic ribosomal protein S7	N	Y	Y	-	Y	N	-	-	-	-	-
25	PRSC1_025	AAGGACGTGATGTTGGAATG	TTGCATGGCGCACAACAAAC	19080467	19081444	977	1	9629.t03158	unspliced-genomic 1 3-beta-glucan synthase component putative	N	Y	Y	-	N	N	-	-	-	-	-
26	PRSC1_026	GAGTTCAAGGAGGCCTTCAG	TGCCCCAGCGAACGCATG	9884524	9885396	872	1	9629.t01631	unspliced-genomic EF hand putative	N	Y	N	-	N	N	-	-	-	-	-
27	PRSC1_027	AGTGGAGCCCTGCTTTGAC	CGGTCCGTCTTGTACATGTG	34651106	34651618	512	1	9629.t05673	unspliced-genomic Ubiquitin-conjugating enzyme	N	N	N	-	N	N	-	-	-	-	-
28	PRSC1_028	CCTCGTACTTGACCTGGAAC	TGGTATCCAGGAGCACATTG	5767890	5768778	888	1	9629.t00989	unspliced-genomic ribosomal L5P family C-terminus putative	N	N	N	-	N	N	-	-	-	-	-
29	PRSC1_029	GGTGTATGTGACCATGTACC	GAATCCTCTTCAGGTTCTTC	9872437	9872915	478	1	9629.t01629	unspliced-genomic magnesium-protoporphyrin IX monomethyl ester	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
30	PRSC1_030	AGGAGGAGAAGCACCACAAG	TTCTTCTCGTGGTGCTCGTG	41917805	41918134	329	1	9629.t06873	unspliced-genomic ABA/WDS induced protein putative	N	Y	Y	-	Y	N	-	-	-	-	-
31	PRSC1_031	TGCCCCTCTTCCTCTACAAC	TGAGCTCCAGCCTGAACTTG	20375560	20376840	1280	1	9629.t03363	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
32	PRSC1_032	CACAGGATGCTGAACGAGG	ACAAGCAGCACAGCATCACG	34367018	34367406	388	1	9629.t05625	unspliced-genomic ADP-ribosylation factor family	N	N	N	-	N	Y	-	-	-	-	-
33	PRSC1_033	CACAGGATGCTGAACGAGG	ACAAGCACGACAGCATCACG	34024699	34025087	388	1	9629.t05625	unspliced-genomic ADP-ribosylation factor family	N	N	Y	-	N	N	-	-	-	-	-
34	PRSC1_034	GCATATGAGAACTATCGTCG	GCATATCCCAGAGTTGCACC	3133894	3134390	496	1	9629.t00570	unspliced-genomic Thiamine pyrophosphate enzyme central domain	N	Y	N	-	N	Y	-	-	-	-	-
35	PRSC1_035	ATACGCCGAAGAGCTGTCAG	AGCGTAATGGCAGTCATGTC	42200375	42201256	881	1	9629.t06929	unspliced-genomic uridylate kinase putative	Y	Y	Y	N	Y	Y	Y	Y	N	-	D
36	PRSC1_036	TCAGAGACTTCCTGCTCAAG	CCCATCCCAGATTTTGCTTG	20346957	20348458	1501	1	9629.t03360	unspliced-genomic expressed protein	N	N	N	-	N	N	-	-	-	-	-
37	PRSC1_037	GTTCCATCAGTACCAGGTGG	CACGGTACTCCTTGTACATG	27052014	27053189	1175	1	9629.t04399	unspliced-genomic Ribosomal L18ae protein family	N	N	N	-	N	N	-	-	-	-	-
38	PRSC1_038	AGCTCATGCAGAGCTTCAAG	CCCTAAAAGATGGCTGGAAC	42060639	42061463	824	1	9629.t06900	unspliced-genomic Plectin/S10 domain putative	N	N	N	-	N	N	-	-	-	-	-
39	PRSC1_039	TCCTCTCTCTTCTTCTTTTGC	TCTTCGTCGGCATCAACAAG	35816395	35817692	1297	1	9629.t05874	unspliced-genomic Ribosomal protein L36e	N	N	Y	-	N	Y	-	-	-	-	-
40	PRSC1_040	GCAATCTCAGGGACAAGAGG	AAGACAAAGGTCTTCCATCC	34672531	34673780	1249	1	9629.t05678	unspliced-genomic Ubiquitin-conjugating enzyme	N	N	N	-	N	N	-	-	-	-	-
41	PRSC1_041	TGCAGACCGTAATCTGATTG	CAGCAAAGGCGCTCATAACC	36802801	36803799	998	1	9629.t06026	unspliced-genomic G10 protein	N	Y	Y	-	N	N	-	-	-	-	-
42	PRSC1_042	AGCGCGTCAACGTCTACTAC	CCAAGGGAATGGCAAACTTG	10096900	10097898	998	1	9629.t01668	unspliced-genomic tubulin beta-5 chain (beta-5 tubulin)	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
43	PRSC1_043	AGCTCATGCAGAGCTTCAAG	CCCTAAAAGATGGCTGGAAC	42060639	42061463	824	1	9629.t06900	unspliced-genomic Plectin/S10 domain putative	N	N	Y	-	N	N	-	-	-	-	-
44	PRSC1_045	GTACCTCTCACCAAAGCTTG	TGTTCAGGAAGGATTACTGG	42867214	42868125	911	1	9629.t07049	unspliced-genomic cysteine synthase A putative	N	Y	Y	-	Y	N	-	-	-	-	-
45	PRSC1_046	GAATGGCAAACTTGGAAACC	CCCCAACTATACTGAGTTCC	10096906	10097774	868	1	9629.t01668	unspliced-genomic tubulin beta-5 chain (beta-5 tubulin)	N	N	N	-	N	N	-	-	-	-	-
46	PRSC1_047	AGCCGATCTTCCACGAGTTG	ATGGGACCCTCTGTGGTTC	27814091	27815067	976	1	9629.t04518	unspliced-genomic expressed protein	N	Y	Y	-	N	N	-	-	-	-	-
47	PRSC1_048	CAGCGCACATCATGTTCTTG	GTTGAGAATGCTGATGAGTG	33955114	33955856	742	1	9629.t05562	unspliced-genomic beta-tubulin R1623 - rice	N	N	Y	-	N	N	-	-	-	-	-
48	PRSC1_049	GTCACCATCAGGTTGCCATC	ATCCATCGTGACATGAGACC	23506835	23507295	460	1	9629.t03861	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	N	Y	-	-	-	-	-
49	PRSC10_065	TGAAGATTGGAAGCCTGTTC	TGGTTCAACGGATCCTCATC	5904239	5905468	1229	10	9638.t00988	unspliced-genomic putative ubiquitin-conjugating enzyme	N	Y	Y	-	N	Y	-	-	-	-	-
50	PRSC10_066	ATGGACACCACCAGCCTTTG	TGCTGGTGGCCTTTTGGAATC	21460508	21460899	391	10	9638.t03665	unspliced-genomic putative arm repeat protein	Y	Y	Y	N	Y	Y	Y	Y	Y	N	D
51	PRSC10_067	GGCTATGAGATTGTGCAAAC	TGACGCTGCCTTGCAATACC	16349249	16349687	438	10	9638.t02792	unspliced-genomic putative hypersensitive-induced response protein	N	Y	Y	-	N	Y	-	-	-	-	-
52	PRSC10_068	CTGGTGGAATGTCAAGCATG	CCAGAACCTTCTCGAAGCTC	17145321	17147312	1991	10	9638.t02905	unspliced-genomic cytoplasmic malate dehydrogenase	N	N	N	-	N	N	-	-	-	-	-
53	PRSC10_069	TATCCATCTCCAAGAGGATG	AGGACTGGTGTGAAGCTTTC	18851049	18851762	713	10	9638.t03194	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	-	-	-	-	-
54	PRSC10_070	TTGAACCTACGGCAATGTAC	GTGAAGCTTTGGGATCTTCG	16435384	16436058	674	10	9638.t02810	unspliced-genomic putative WD-repeat containing protein	Y	Y	Y	Y	Y	Y	N	N	N	-	-
55	PRSC10_071	GCAGATATCCCATATCCAAAG	CATGCAAGACAATGGTGCTG	21463822	21464542	720	10	9638.t03666	unspliced-genomic putative WD40 protein	N	N	N	-	N	N	-	-	-	-	-
56	PRSC10_072	CTCTAGAGAAAGACTCAGAG	GAGTCTTCCTCTGAGTCTTC	10226929	10227261	332	10	9638.t01742	unspliced-genomic DNA-directed RNA polymerase beta subunit puta	N	N	N	-	N	N	-	-	-	-	-
57	PRSC4_050	ATGGCATCCTGTTTGACAAC	TGAAGAGCACAGTCACAAAG	19024791	19025335	544	4	9632.t03118	unspliced-genomic Calreticulin family putative	N	Y	Y	-	N	N	-	-	-	-	-
58	PRSC4_051	TCCTGAAGGAGTTGAAGGAC	CAATGAAACATGTCCTCACC	33070536	33071614	1078	4	9632.t05410	unspliced-genomic Ubiquitin-conjugating enzyme	N	N	N	-	N	N	-	-	-	-	-
59	PRSC4_052	GGGACTGTCATATTTCAAGG	GAGGAGAGAATGCCTTGTGC	23507823	23508492	669	4	9632.t03858	unspliced-genomic Nucleotide-sugar transporter putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
60	PRSC4_053	TGATCTCGCAGAAGCAGAAG	AGCATACTTCCTCATGGGGA	17479765	17480950	1185	4	9632.t02894	unspliced-genomic ribosomal protein L29 putative	N	N	Y	-	N	N	-	-	-	-	-
61	PRSC4_054	GCAGACTGAGAAGGCTTTCC	TGCTCTTCCAGAAGCGGTTG	30091794	30091984	190	4	9635.t03679	unspliced-genomic ribosomal protein S17 putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
62	PRSC4_055	ACCGCAATGAGATCTGCAAG	TGAAGCTCTGCATGAGCTTG	20388638	20389213	575	4	9632.t03332	unspliced-genomic Plectin/S10 domain putative	N	Y	N	-	N	N	-	-	-	-	-
63	PRSC4_056	CAAGATGGTGAAGTTCACGG	CGGAGCACAGTTTCAGTTTG	1013354	1014657	1303	4	9632.t00185	unspliced-genomic Elongation factor G domain IV putative	N	N	N	-	N	N	-	-	-	-	-
64	PRSC4_057	ACCGCAATGAGATCTGCAAG	CCAGGATTGTAGTCCTTCTTG	20388638	20389153	515	4	9632.t03332	unspliced-genomic Plectin/S10 domain putative	N	N	N	-	N	N	-	-	-	-	-
65	PRSC4_058	GCGCTGCCCATCTACAACAC	ACCTGGTGGTGGATGGCAG	27035680	27036343	663	4	9632.t04444	unspliced-genomic MIP family channel proteins putative	N	N	N	-	N	N	-	-	-	-	-
66	PRSC4_059	GGGGATTTGGCTGCAGATG	TTCTCAGACTGAGCTCCTTG	30807464	30809174	1710	4	9632.t05032	unspliced-genomic salt tolerance protein 6	N	N	N	-	N	N	-	-	-	-	-
67	PRSC4_060	AACGACCCCTTCATCACCAC	GAATCTCCTCAGGGTTCCTG	23296423	23297212	789	4	9632.t03821	unspliced-genomic glyceraldehyde-3-phosphate dehydrogenase type	N	Y	Y	-	N	Y	-	-	-	-	-
68	PRSC4_061	CTGAATGGAACGAGACCTTC	CTGCTGGAGTGAAGGTGAG	33808135	33808600	465	4	9632.t05546	unspliced-genomic C2 domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
69	PRSC4_062	CCGTAACTTGTAAGAGGAGAG	TGGAACTTCTTTGCAGTGAG	20575653	20576471	818	4	9632.t03362	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	-	-	-	-	-
70	PRSC4_063	TGAATGGAGTGTCCTTCCG	GATCAAGAAATGCTTCTCAAC	29951919	29952316	397	4	9632.t04899	unspliced-genomic coproporphyrinogen III oxidase aerobic putative	Y	Y	Y	Y	Y	Y	N	N	N	-	S
71	PRSC4_064	GACGCCTTCATCGTCAGC	GAAGCGGTACCTGACGTC	30279311	30280365	1054	4	9632.t04915	unspliced-genomic cinnamyl alcohol dehydrogenase	N	Y	N	-	N	N	-	-	-	-	-
72	SRSC1_001	GCCAAGTATCTGTACACATTTG	CTTCCTCCAGTTGATGAGAAG	15057943	15058571	628	1	9629.t02485	unspliced-genomic Putative cullin	N	Y	Y	-	Y	N	-	-	-	-	-
73	SRSC1_002	CGTAGTAGTCGGCGTACATG	GGGGAAACGACTACAACTAC	6316976	6317408	432	1	9629.t01078	unspliced-genomic GDSL-like Lipase/Acylhydrolase	N	N	Y	-	N	N	-	-	-	-	-
74	SRSC1_003	TTTGGCTGGCAGGGAAGTTG	TTGGCAAGGTTCCATGCCTC	15547458	15547925	467	1	9629.t02566	unspliced-genomic Cyclin N-terminal domain putative	Y	Y	Y	Y	Y	Y	N	N	N	-	D
75	SRSC1_004	TGACCCTTCTCATGAGAGAG	TCTGACAGCTTCATGTGACC	4624781	4625286	505	1	9629.t00825	unspliced-genomic Protein kinase domain putative	Y	Y	Y	N	Y	Y	Y	N	N	-	D
76	SRSC1_005	GGAGAGCTTCTTTACATCTG	CAGGGTTCTTGGGGTTATTG	7477598	7478088	490	1	9629.t01253	unspliced-genomic expressed protein	N	Y	Y	-	N	Y	-	-	-	-	-
77	SRSC1_006	GAGTAGTTTCTGGTGTACAG	CACGGACATGAGACTGTACA	30858601	30859543	942	1	9629.t05046	unspliced-genomic tryptophanyl-tRNA synthetase	N	N	Y	-	N	N	-	-	-	-	-
78	SRSC1_007	TTGAACCATATGCTCGCTTG	ACCAGCTCTCATTGACATTG	4330164	4330620	456	1	9629.t00775	unspliced-genomic gigantea-like protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
79	SRSC1_008	GAGCATTGCTCACACATCTG	GCATCTTCACGATCACCAAC	21944997	21945497	500	1	9629.t03609	unspliced-genomic DENN (AEX-3) domain putative	Y	Y	Y	N	Y	Y	Y	Y	Y	N	S
80	SRSC10_001	CTTCCATGGTCCACCCTAC	AGCTGGAATAGACACCTCAG	20709559	20710330	771	10	9638.t03540	unspliced-genomic putative UDP-N-acetylmuramoylananyl-D-glutama	N	N	Y	-	N	N	-	-	-	-	-
81	SRSC10_002	CATCCGCCTCTTCGTCAAC	TCAAGTGGGATGATACTGTC	22416768	22418102	1334	10	9638.t03833	unspliced-genomic putative Clp protease	N	N	Y	-	N	N	-	-	-	-	-
82	SRSC10_003	CTTCCTGGTTCTGGCAATG	GTTCATTGATGTCCCTGAAG	10698700	10699633	933	10	9638.t01815	unspliced-genomic expressed protein	N	N	Y	-	N	Y	-	-	-	-	-
83	SRSC10_004	TGCTTCAGCTGGATATGGAG	CACCCATAGATTGACCAAAC	2187961	2189038	1077	10	9638.t00366	unspliced-genomic lipase putative	Y	Y	Y	Y	Y	Y	N	N	N	-	D
84	SRSC10_005	CGCAACAGAATTTTGTCGAG	TTACGCTGTTGCCAAGTTG	20525385	20525961	576	10	9638.t03507	unspliced-genomic putative CorA-like Mg2+ transporter protein	Y	Y	Y	N	Y	Y	Y	N	N	-	D
85	SRSC10_006	CTTCAGGTCGTTCTGGTAC	CTTCCACTACTGGGCATTG	18016211	18016870	659	10	9638.t03042	unspliced-genomic putative ABC transporter	N	N	Y	-	N	Y	-	-	-	-	-
86	SRSC10_007	TGCTCCATAATTGATACCATC	TGCTGATGGATTGGCTTTTG	7108521	7109211	690	10	9638.t01212	unspliced-genomic putative membrane protein	N	Y	Y	-	N	N	-	-	-	-	-
87	SRSC10_008	GGACTCCATGAATATCCATC	CAAGGACTTTACTCTCCTTG	4441251	4442273	1022	10	9638.t00742	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
88	SRSC10_009	ACAAGGACTTGTGCTTCAAC	GCCAAAACTCCTCTTATTCG	17768700	17769371	671	10	9638.t02996	unspliced-genomic putative myosin	N	Y	N	-	N	N	-	-	-	-	-
89	SRSC10_010	GATGTCAGTGGTTCTGAGG	GGAATATCTGATTGCCCTGC	21538356	21539102	746	10	9638.t03681	unspliced-genomic putative casein kinase II beta subunit	N	Y	Y	-	N	N	-	-	-	-	-
90	SRSC10_011	CCTGCTTGGATAGGAACTTG	CATCAAGAACTGTACGAAGC	17027326	17028062	736	10	9638.t02897	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	N	N	N	-	D
91	SRSC10_012	GCCCAAATGAAGGGATATGC	GGGCACTCATAAGCCATGTG	20538276	20538702	426	10	9638.t03510	unspliced-genomic putative zinc finger protein	N	N	N	-	Y	N	-	-	-	-	-
92	SRSC10_013	GACACTGCTGACTCTTATGG	CCATGCTCAGTAGTGAGAAC	19225547	19226543	996	10	9638.t03258	unspliced-genomic putative aldo/keto reductase	N	N	N	-	N	N	-	-	-	-	-
93	SRSC10_014	GGTGTTGACAAGTCTGCAAG	GGTTCCCGGAGATATGGTAC	18233124	18234094	970	10	9638.t03079	unspliced-genomic putative epoxide hydrolase	N	N	Y	-	Y	N	N	-	-	-	-
94	SRSC10_015	CAACATCGGGATGATGGACG	GGATCATCTCGTACTCCGTC	18262737	18263077	340	10	9638.t03083	unspliced-genomic putative microtubule-associated protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
95	SRSC10_016	CGTTTCAAGCCACATGTTCTC	AAGGCCTACACCTTCGACAC	16489923	16491098	1175	10	9638.t02819	unspliced-genomic cap-binding protein p28	N	Y	Y	-	N	N	-	-	-	-	-
96	SRSC10_017	CCGGTTTTCACATGCACAG	CTGCTCCTGCTCATCATTG	17335616	17336665	1049	10	9638.t02922	unspliced-genomic putative extensin	Y	Y	Y	Y	Y	Y	N	Y	Y	-	D
97	SRSC10_018	CTTGTGGGCCATGTACTGTT	CAGGTTGAGAACCATCAGC	5289998	5290683	685	10	9638.t00884	unspliced-genomic alanyl-tRNA synthetase	N	N	Y	-	Y	Y	N	-	-	-	-
98	SRSC10_019	GAAACGGCTAAACTCAAGGC	GAGCCACCTTTTCCTAGAAG	18042772	18043215	443	10	9638.t03046	unspliced-genomic putative RNA-binding protein	Y	Y	Y	N	Y	Y	N	N	N	-	-
99	SRSC10_020	CCCAAGTCGTCGATCATTCC	CAAGGAGGGTCATGCTTCTG	13101169	13101645	476	10	9638.t02235	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	N	N	N	-	-
100	SRSC10_021	GTCCACTGCTTTGTCCTCAG	CCTTTGAGTATGTGGATGGC	14159897	14160255	358	10	9638.t02390	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
101	SRSC10_022	GCAGTGCAATGGAGGTATTTG	ACGAGTTACAACAAGGTCCC	18782523	18783160	637	10	9638.t03181	unspliced-genomic expressed protein	N	Y	Y	-	N	N	N	-	-	-	-
102	SRSC10_023	CAAATCAAGTGCAGTCCCAC	ACGACTCCATCATCATGCTC	21547503	21548442	939	10	9638.t03683	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	N	-	-	-	-
103	SRSC10_024	GATTCATCCCACACATCACC	AACGGTGTAAACTCTCAGGG	16993864	16994161	297	10	9638.t02893	unspliced-genomic putative protein phosphatase 2A regulatory subur	Y	Y	Y	Y	Y	Y	N	Y	N	-	D
104	SRSC11_001	TGACTGTCTCCATGGTTGTC	TTCGACTCATCCATGGCAAG	3502899	3503638	739	11	9639.t00612	unspliced-genomic Fructose-bisphosphate aldolase class-I	N	N	Y	-	N	N	-	-	-	-	-
105	SRSC11_002	AGTACAGGTCCTTGAACTTC	ATGTCCGCATGGTGATATTC	5266635	5267298	663	11	9639.t00919	unspliced-genomic G-protein alpha subunit putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
106	SRSC11_003	TGGAGGGAGCTGCAACAAG	AAAGGATCCTGCAAGCCTTC	23579748	23580275	527	11	9639.t04177	unspliced-genomic Glycosyl hydrolase family 1 putative	N	Y	Y	-	N	N	-	-	-	-	-
107	SRSC11_004	AGATTGATCCGTTTGGGCAC	CACGGTCTTGGTAATCAATC	15420440	15420847	407	11	9639.t02873	unspliced-genomic alpha-mannosidase	N	Y	Y	-	Y	N	-	-	-	-	-
108	SRSC11_005	TGTGCGGATAAGGTCCTTTG	AGATCAAGAAGGTGGCCAAG	24631098	24631768	670	11	9639.t04377	unspliced-genomic SNF7 family putative	N	Y	Y	-	N	N	-	-	-	-	-
109	SRSC11_006	AGCTCCTCACTTCCAGAAAG	GCCACCTGTTCTCTCAATAG	11603748	11604608	860	11	9639.t02119	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	-	-	-	-	-
110	SRSC11_007	CTGCTGAATCTATAGCGGAC	CTGGGAGGCAAGAATATGAC	17590714	17591138	424	11	9639.t03221	unspliced-genomic BRCA1 C Terminus (BRCT) domain putative	Y	Y	Y	Y	Y	Y	N	N	Y	-	D
111	SRSC11_008	TTGCCATGGTCAAGAGCAAC	CTGTTGTCATTCCTCGTCTG	2235161	2235764	603	11	9639.t00416	unspliced-genomic pyruvate kinase	N	N	Y	-	N	N	-	-	-	-	-
112	SRSC11_009	GTGTGGCCAAAGTCATAATC	CATTCAGGAATACAAGGGCC	4910843	4911154	311	11	9639.t00852	unspliced-genomic protein disulfide isomerase 3 precursor	N	Y	Y	-	N	Y	-	-	-	-	-
113	SRSC11_010	TCCAGATTCTCTGAATGAGC	GGATTTGGGCTTGATGATTCC	8185248	8185950	702	11	9639.t01455	unspliced-genomic Ntg1	N	Y	Y	-	Y	N	N	-	-	-	-

114	SRSC11_011	CGATCATGTAGAGGTTCCAG	TACCTCTTCGGCCACTTCAG	16025193	16025556	363	11	9639.t02971	unspliced-genomic xyloglucan endotransglycosylase XET2	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
115	SRSC11_012	AGGCGCTCAACGACAACATC	GGCATGTCCATTTGCTCAAC	18986389	18987750	1361	11	9639.t03451	unspliced-genomic Similar to AY088091 ATP-dependent RNA helicas	N	Y	Y	-	N	N	-	-	-	-	-
116	SRSC11_013	GATTGGTGATGGCAAATCACG	GTAGTTGCCGAAGAAGGTTC	5592380	5593387	1007	11	9639.t00959	unspliced-genomic alcohol dehydrogenase 1	N	N	N	-	N	Y	-	-	-	-	-
117	SRSC11_014	CCTCAAGTACAAAATGGTGG	GGTGGTGTTGGTGGTATTGC	17630393	17630990	597	11	9639.t03226	unspliced-genomic Similar to carotenoid isomerase	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
118	SRSC11_015	GGTATGTCTTTGCTGTTGCC	GGGCTCTATCCATAAGTTGC	5351096	5351877	781	11	9639.t00924	unspliced-genomic similar to mitogen-activated protein kinases	N	N	N	-	Y	Y	-	-	-	-	-
119	SRSC11_016	GTGATGAACTTCTCCACCTC	GAACCTTCTTCGGCAACTAC	5592147	5592399	252	11	9639.t00959	unspliced-genomic alcohol dehydrogenase 1	N	Y	Y	-	N	Y	-	-	-	-	-
120	SRSC11_017	CAGATGAAGGCTTGATTGGA	GATCTGTGAGATTCTTGCAC	21382091	21383126	1035	11	9639.t03812	unspliced-genomic F-box protein family AtFBL4	Y	Y	Y	N	Y	Y	N	Y	N	-	-
121	SRSC11_018	TCATCTTGGGCTGCTCGAAC	GAACAACCAGATGGTGAACG	24778945	24779467	522	11	9639.t04402	unspliced-genomic RuBisCO activase small isoform precursor	N	Y	Y	-	N	Y	N	-	-	-	-
122	SRSC11_019	GTTATCGAGGCAGAGTGATG	CTTCTCTTTGCGGCTGTCC	22494308	22494847	539	11	9639.t03998	unspliced-genomic hypothetical protein	N	Y	N	-	N	Y	N	-	-	-	-
123	SRSC11_020	CATGTTGCCATAAGTTACGC	CGACGAGTGCAAGAACATC	2838249	2839513	1264	11	9639.t00498	unspliced-genomic Similar to timing of CAB expression 1-like protein	N	N	Y	-	Y	N	N	-	-	-	-
124	SRSC11_021	CTCATGGTCGTCCACAGTTC	TTTCCAGACGCTCCATCATC	17623595	17624284	689	11	9639.t03225	unspliced-genomic Zinc finger C3HC4 type (RING finger) putative	N	Y	Y	-	Y	N	N	-	-	-	-
125	SRSC11_022	CCCTGATATCAATGAGGAGAG	TTCGCTGCAGCAACAGCTTG	21524025	21524413	388	11	9639.t03838	unspliced-genomic Similar to AT3g14120/MAG2_7	N	Y	N	-	Y	N	Y	-	-	-	-
126	SRSC11_023	CACCAAGCTTGCCCAAGTG	CATCATTGTCCTTGCTGAGG	11968250	11968553	303	11	9639.t02344	unspliced-genomic adenosylhomocysteinase	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
127	SRSC11_024	GCTACTCTCCTCAAGTCATC	CTCATCCATGGCAAGGATAC	3502904	3503717	813	11	9639.t00612	unspliced-genomic Fructose-bisphosphate aldolase class-I	Y	Y	Y	N	Y	Y	N	N	N	-	-
128	SRSC12_001	TTGCCAGATGTGTACAGAAC	GGTTCTTCAGAAGATGATGG	2514552	2515040	488	12	9640.t00460	unspliced-genomic hydrolase alpha/beta fold family putative	N	Y	Y	-	N	N	-	-	-	-	-
129	SRSC12_002	CGAATACCAACACCACTAGC	ACAAGCATGAGGAGAACCAC	7362899	7363429	530	12	9640.t01253	unspliced-genomic aspartyl aminopeptidase-like protein	N	Y	Y	-	N	N	-	-	-	-	-
130	SRSC12_003	CTTTAGCTGCTGGTGTTAAC	GCATAACCAACGAAGGGAG	11110746	11111275	529	12	9640.t01861	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
131	SRSC12_004	GACCACATTGAGGGCTTTG	TGGATACATGACAGTCTCAC	14588026	14588961	935	12	9640.t02397	unspliced-genomic prolyl-tRNA synthetase	N	Y	Y	-	N	N	-	-	-	-	-
132	SRSC12_005	ACACGAACCTTCCGATGTTG	GCACCTTATGTCATGTGGTG	22452095	22452499	404	12	9640.t03571	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	N	Y	Y	N	D
133	SRSC12_006	TGCTGCTGTTTCTGCTATTG	AGCTTCATGCCTGACCATTG	26141972	26142576	604	12	9640.t04131	unspliced-genomic expressed protein	N	N	Y	-	Y	Y	-	-	-	-	-
134	SRSC12_007	CAAGCCAATACACCCAAAAC	TGTAGGACTCGGAAGAATTG	4197176	4197915	739	12	9640.t00730	unspliced-genomic 3'(2') 5'-bisphosphate nucleotidase	N	Y	Y	-	N	N	-	-	-	-	-
135	SRSC12_008	CACCATTGCACTCTGCATTC	CTCCACAGTTCATTCCCTG	6638282	6638847	565	12	9640.t01135	unspliced-genomic AY062655 diacylglycerol kinase	N	Y	Y	-	N	Y	-	-	-	-	-
136	SRSC12_009	GATCCTTCACGTGTTCCTG	TCCCAATGGAATGGCCAAC	3239342	3239865	523	12	9640.t00580	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
137	SRSC12_010	GCAGGCTCTATATCATGAGG	TATCTCAGAGGAGGCAGTTG	3307932	3308739	807	12	9640.t00591	unspliced-genomic Nrap protein putative	N	N	Y	-	N	Y	-	-	-	-	-
138	SRSC12_011	GAACAAGCTGTTGATGGAGG	GATTCCAATGGAATCCGGAC	25305403	25306013	610	12	9640.t04006	unspliced-genomic homeodomain transcription factor (ATHB-14) [imp	Y	Y	Y	Y	Y	Y	-	N	Y	-	S
139	SRSC12_012	CAGAAGATGATGGCAATGCC	CAGATGTGTACAGAACCCTC	2514559	2515035	476	12	9640.t00460	unspliced-genomic hydrolase alpha/beta fold family putative	N	N	Y	-	N	N	-	-	-	-	-
140	SRSC12_013	GTTTGATAGAACCTGTTCCC	CGGAAGCACAACTTCTATCC	3536338	3537700	1362	12	9640.t00632	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
141	SRSC12_014	CCAGCCAACAATGTTCAGTC	CCTTGCAAGGCTGCTTGTAG	26725071	26725635	564	12	9640.t04231	unspliced-genomic receptor-like protein kinase	N	N	Y	-	Y	Y	Y	-	-	-	-
142	SRSC12_015	TTCTTCAAGGGCGTGTCGAG	CTAGAGAAGTGCTGACTAAG	26411403	26412800	1397	12	9640.t04177	unspliced-genomic IBR domain putative	N	Y	N	-	Y	Y	-	-	-	-	-
143	SRSC12_016	CGATCTTCTCCCTGATGTTC	CCAGGATTTTGCTGCTGAAG	21073950	21074633	683	12	9640.t03378	unspliced-genomic Elongation factor TS putative	N	Y	Y	-	N	Y	-	-	-	-	-
144	SRSC12_017	CCTTTCCCACTATCAAGCTG	AAGACTAAGCCTGATCGAGG	17172137	17172771	634	12	9640.t02784	unspliced-genomic expressed protein	N	N	N	-	N	N	N	-	-	-	-
145	SRSC12_018	GACAATCTTCTTGGCACCAG	TTCAAGTCCCACACCCACC	22749451	22750637	1186	12	9640.t03617	unspliced-genomic 60s ribosomal protein l2 (l8) (ribosomal protein tl2	N	N	N	-	N	N	N	-	-	-	-
146	SRSC12_019	AGCACTTCTTTAACAGCCTC	GCGATGGTTCTATTCTGGTG	3429577	3429954	377	12	9640.t00611	unspliced-genomic probable acyl-CoA synthetase 62297-59022 [impo	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
147	SRSC12_020	TGCTCTCGTTCATGCCGTTC	GTTCAGCTCCTTCACCATTG	24691720	24692935	1215	12	9640.t03909	unspliced-genomic auxin-responsive protein IAA1	N	Y	Y	-	N	N	N	-	-	-	-
148	SRSC12_021	CGGTGCTCATGTACACATTC	TGATAGCCTGCTGCATGAAG	22649113	22649456	343	12	9640.t03601	unspliced-genomic HCO3- transporter family putative	N	Y	N	-	Y	Y	Y	-	-	-	-
149	SRSC12_022	TCCATAACCATGACAGGCTG	TGGTTTCCTCCAAGAACTCG	24960106	24961119	1013	12	9640.t03944	unspliced-genomic methylcrotonyl-coa carboxylase alpha chain mitoc	N	Y	Y	-	N	N	N	-	-	-	-
150	SRSC12_023	GCCATCCATCTGTATGTTCC	GAAGTTTGCAGTTGATGTATGC	3179276	3179677	401	12	9640.t00567	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	N	Y	Y	-	-	-	-
151	SRSC12_024	GGCAAACACAATCACCAACG	CAAAAGATCAACCTCACTGG	19000987	19001378	391	12	9640.t03067	unspliced-genomic Similar to zinc finger transcription factor WRKY1	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
152	SRSC2_001	TCAAGATCCTCTTCACCGCG	TGCACCTCAGTTACTCCTTC	34516106	34516948	842	2	9630.t05449	unspliced-genomic alcohol dehydrogenase class iii (ec 1.1.1.1) (gluta	N	Y	Y	-	N	N	-	-	-	-	-
153	SRSC2_002	AGCTGGCCGTCTTCTACG	AGTATCACGATCATCAGAGC	743194	744107	913	2	9630.t00130	unspliced-genomic serine carboxypeptidase iii precursor (ec 3.4.16.5	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
154	SRSC2_003	AGGCACTTAGGGCTGGAATG	TTCAGAACACACTGCAAAGC	35104395	35105052	657	2	9630.t05555	unspliced-genomic ABC transporter protein putative	N	N	Y	-	Y	Y	-	-	-	-	-
155	SRSC2_004	TGGTTGATACTGCAGAGGTG	CCACCAGAAGCTCCACAAAC	34927431	34927782	351	2	9630.t05522	unspliced-genomic growth-on protein GRO10	N	Y	Y	-	N	Y	-	-	-	-	-
156	SRSC2_005	AGTTCTCCTGCCCTTTCCTG	CTGGCACTCGATCATACAGC	17239222	17239806	584	2	9630.t02711	unspliced-genomic hypothetical protein	N	N	Y	-	Y	N	-	-	-	-	-
157	SRSC2_006	CAATGTTAAGGCAAGCCAAG	CCTTCCACCATGTTGAGAAC	10573960	10574384	424	2	9630.t01658	unspliced-genomic Elongation factor Tu GTP binding domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
158	SRSC2_007	TGCCTGTTCATGGAGAACTC	CTCCATGTGACTAAGTGGAC	19766147	19767311	1164	2	9630.t03084	unspliced-genomic metallo-beta-lactamase superfamily putative	Y	Y	Y	Y	Y	Y	Y	Y	N	-	D
159	SRSC2_009	GGACTGAAAAGGGAGTATTG	CACTGGATTTGGCAACATAG	10825010	10825757	747	2	9630.t01701	unspliced-genomic Suppressor Mra1 putative	N	N	N	-	N	N	-	-	-	-	-
160	SRSC2_010	GCGGATTCTCTGCAAAATAG	CCAGATGACACTGGTTTAGA	31929776	31930511	735	2	9630.t05021	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
161	SRSC2_011	GGTGACAAACAATGGGCGC	CGGAAAATAGGTCCACGCC	26594192	26594918	726	2	9630.t04149	unspliced-genomic Subtilase family putative	Y	Y	Y	Y	Y	Y	N	N	N	-	D
162	SRSC2_012	GGTGGCACTAGATTCAAGC	GCAAATGATCAGCTTCATCC	35087785	35088056	271	2	9630.t05551	unspliced-genomic DEAD/DEAH box helicase putative	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
163	SRSC2_013	CAACGGTAGTAGGCCATGTG	GCATGGGTCTTCTTCATCC	34221569	34222394	825	2	9630.t05398	unspliced-genomic expressed protein	N	N	N	-	N	N	-	-	-	-	-
164	SRSC2_014	GTCAAGATCCTCTTCACCG	GCACCTCAGTTACTCCTTC	34516105	34516968	863	2	9630.t05449	unspliced-genomic alcohol dehydrogenase class iii (ec 1.1.1.1) (gluta	N	N	N	-	Y	Y	Y	-	-	-	-
165	SRSC2_015	GTTGCCTGCCATTGCTTGTC	CAGGAGAAGGAAATGGCTTG	1320188	1320671	483	2	9630.t00218	unspliced-genomic hypothetical protein	N	Y	Y	-	Y	N	N	-	-	-	-
166	SRSC2_016	GACAATGCAACCCATGATAG	CTGCTGACCAGGAATTTGAG	23321313	23321817	504	2	9630.t03637	unspliced-genomic 1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate s	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
167	SRSC2_017	TACAAGCACAAGAAGACAGG	GGATAACATGTCCGATCTGG	31693153	31693555	402	2	9630.t04975	unspliced-genomic Peptidase M16 inactive domain putative	N	N	Y	-	Y	Y	-	-	-	-	-
168	SRSC2_018	AACAAGGGACCCAATATGCG	GGTGGCTTGCTGATAGTTC	30165911	30166278	367	2	9630.t04721	unspliced-genomic Similar to F26F24.8	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
169	SRSC2_019	GTGGTGAACGTCAAGTGCAG	CCTTCTTGACGTTGAGCATG	20755862	20757130	1268	2	9630.t03223	unspliced-genomic Similar to uridylyl transferases	N	Y	N	-	N	Y	-	-	-	-	-
170	SRSC2_020	ATGTGGCTCATCTTGTCGGC	CTTATTGAGAAGGCGAAGGC	3683066	3683806	740	2	9630.t00632	unspliced-genomic phosphoglycerate kinase	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
171	SRSC2_021	CAGAGTGGATGTTGACATTCC	CACCAATGCATGCAGTCCTG	908038	909142	1104	2	9630.t00158	unspliced-genomic expressed protein	N	Y	N	-	N	N	-	-	-	-	-
172	SRSC2_022	GAGGATGAAGGACAGCTTTG	CTTTTGGAACTCCATAGCCAG	34801283	34802113	830	2	9630.t05496	unspliced-genomic probable kinesin light chain [imported] - Arabidops	N	Y	Y	-	N	Y	-	-	-	-	-
173	SRSC2_023	CAGGTGCCAATTGCATCTAC	GGATTGCACATACAGAAGTC	1083700	1084130	430	2	9630.t00190	unspliced-genomic expressed protein	N	Y	Y	-	N	N	-	-	-	-	-
174	SRSC2_025	CAGGCTAAGCTGCAGGAATT	CTTCTTTGGAACTTCAACCC	29079098	29079958	860	2	9630.t04524	unspliced-genomic HSP protein putative	N	Y	Y	-	N	Y	N	-	-	-	-
175	SRSC2_026	TACATGCTCTCTCGGGCATC	CTGGCACTTGAGATCCATAG	29112556	29113051	495	2	9630.t04532	unspliced-genomic Similar to BT002727 At3g03380/T21P5_20	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
176	SRSC2_027	GCCAGTAGTGAAGGTCCTG	GATCCTCATTCAGCAGTGCG	29108270	29109360	1090	2	9630.t04532	unspliced-genomic Similar to BT002727 At3g03380/T21P5_20	N	Y	Y	-	N	Y	N	-	-	-	-
177	SRSC2_028	CAAGGCAACCAGAACTACTG	GCCTTGCTGATCATATGCAC	30061898	30062187	289	2	9630.t04702	unspliced-genomic Eukaryotic aspartyl protease putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
178	SRSC2_029	GCAGCCTTTTTCTTGCACAC	TTTGACAGCTATGGCCCATG	10578621	10578923	302	2	9630.t01658	unspliced-genomic Elongation factor Tu GTP binding domain putative	Y	Y	Y	Y	Y	Y	Y	Y	N	-	D
179	SRSC2_030	GGAAGAACTTGTTCAGGTTG	CACATCTGTTGCTGGTTATG	30671904	30672248	344	2	9630.t04805	unspliced-genomic Xanthine/uracil permeases family putative	Y	Y	Y	N	Y	Y	Y	Y	Y	N	D
180	SRSC2_031	ATCTGAGCGAGGTGGAGATC	CTGTTGCTACCAAGTTCAAG	7269065	7270058	993	2	9630.t01186	unspliced-genomic expressed protein	N	N	N	-	N	Y	N	-	-	-	-
181	SRSC2_032	GGCATTTGTCTCTGGAGATTG	GTGTAGATGCTCTACAAGCTC	10900010	10900408	398	2	9630.t01715	unspliced-genomic Similar to AY057493 At1g36320/F7F23_4	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
182	SRSC2_033	GCTTCAACTCCTCCATGGTG	GGTATCGGCATCTGATGCAG	22598735	22599416	681	2	9630.t03512	unspliced-genomic hypothetical protein	N	Y	N	-	N	N	N	-	-	-	-
183	SRSC2_034	TCGTACACCAGGTAGCAGTC	GAAGAAGATGAAGTGGGACG	27460492	27461974	1482	2	9630.t04277	unspliced-genomic Protein kinase domain putative	N	Y	N	-	N	Y	N	-	-	-	-
184	SRSC2_035	GATCAACAACTTGAAGAGGC	TCCAACATGTATCTCACTGC	30181261	30182166	905	2	9630.t04723	unspliced-genomic expressed protein	N	N	N	-	N	Y	N	-	-	-	-
185	SRSC2_036	TGCATATCAGCTGGGAGGG	GTGGAAGAGATCACATGGC	1936455	1936735	280	2	9630.t00339	unspliced-genomic AL132954 spliceosomal-like protein	N	Y	Y	-	N	N	Y	-	-	-	-
186	SRSC2_037	GATGGGAAGCTCACCTATTC	CACAAGCAAGCATGGCAATG	18971131	18971395	264	2	9630.t02971	unspliced-genomic acetyl-CoA synthetase putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
187	SRSC2_038	GAGAAACCTATTGGATGGGG	CTCAACCCAAGCAGCAGATG	3987474	3988053	579	2	9630.t00685	unspliced-genomic probable methyltransferase b0967 - Escherichia c	N	Y	Y	-	N	Y	N	-	-	-	-
188	SRSC2_039	GGTTTTGCAGCTGGGATTAC	TGCTACGCCATTGTAGTGGG	34197734	34198057	323	2	9630.t05395	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
189	SRSC3_001	ATGTCTAGTCCAGGCCCTTG	GCATCATTCCTTCCAACAAG	11965139	11965697	558	3	9631.t01961	unspliced-genomic expressed protein	N	N	Y	-	N	N	-	-	-	-	-
190	SRSC3_002	GGTCCAACACCAATGTAGTG	CTGGCTTGACATTGTTGCAC	3968841	3969398	557	3	9631.t00679	unspliced-genomic adenylosuccinate synthetase	N	N	Y	-	N	Y	-	-	-	-	-
191	SRSC3_003	ACCAGTTGTTGATCTGCTTC	TGCACTACAAATGGCCTTAC	28232892	28234059	1167	3	9631.t04798	unspliced-genomic homeobox 1 protein OSH1	N	Y	Y	-	N	N	-	-	-	-	-
192	SRSC3_004	TCATCATCACCAGATTGACG	TTGGCAAAGTGGCATAGGTC	21006924	21007577	653	3	9631.t03535	unspliced-genomic AY099551 lysyl-tRNA synthetase	N	N	Y	-	N	N	-	-	-	-	-
193	SRSC3_005	AGGAGAATTCAGCCGGTTTG	CAAACTTCACCTTCTCTGGC	4393242	4393615	373	3	9631.t00750	unspliced-genomic amine oxidase flavin-containing putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
194	SRSC3_006	GCTAAGCTTGCAAATATCCG	GAAGACCGTGCAGAAAATATAC	5308825	5310153	1328	3	9631.t00893	unspliced-genomic retrotransposon protein putative unclassified	N	Y	Y	-	N	Y	-	-	-	-	-
195	SRSC3_007	GCATCAGGTAGTGGTACTTG	CAGCATCCACTACCAGAGAC	29561403	29562550	1147	3	9631.t05029	unspliced-genomic putative strictosidine synthase	N	Y	Y	-	N	N	-	-	-	-	-
196	SRSC3_008	TCCATCCCGTATGACTATTG	GCTTTGCTGATGTTATCCAC	24117121	24117426	305	3	9631.t04077	unspliced-genomic DNA-directed RNA polymerase beta subunit puta	N	N	Y	-	N	N	-	-	-	-	-
197	SRSC3_009	GAAGAAGGTGCTGGAGACG	CCTCAGGAAGCATGACACA	6538113	6539174	1061	3	9631.t01092	unspliced-genomic expressed protein	N	Y	N	-	N	N	-	-	-	-	-
198	SRSC3_010	CTTCTAGATGCTGGTTGGAC	GCAGATCAAATTGCCTCCATC	29383074	29383935	861	3	9631.t04996	unspliced-genomic expressed protein	N	N	Y	-	N	Y	-	-	-	-	-
199	SRSC3_011	CTGCAAGGAGTACAATGCC	CTGGCAACTTCTCTTGAGC	1212351	1213702	1351	3	9631.t00200	unspliced-genomic ribosomal protein L11 putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
200	SRSC3_012	CTGACCCAATGCTGGTTTTG	CCTCTTCCTTCAGAATCTTG	27844469	27844918	449	3	9631.t04707	unspliced-genomic TGF beta receptor associated protein-like protein	Y	Y	Y	Y	Y	Y	N	N	N	-	D
201	SRSC3_013	GGAAACGAGCTTTCTCCAAC	GCAGCCTTCAAGATCTTGAG	6425349	6426494	1145	3	9631.t01076	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	N	-	-	-	-
202	SRSC3_014	CATCACACAAATCCTGTTGG	GCATGAATGAGCATGCTCAC	30771291	30772681	1390	3	9631.t05227	unspliced-genomic putative oxidoreductase	N	Y	Y	-	N	Y	-	-	-	-	-
203	SRSC3_015	GATGGCGTGGAACGTGTTC	CAATTTGGTGGAACAGAACC	32193908	32195224	1316	3	9631.t05492	unspliced-genomic putative zinc finger protein	N	Y	Y	-	N	Y	-	-	-	-	-
204	SRSC3_016	CTCAAGCAATGGTGGCAGC	GCCAGTCTCTTCAACAAGC	1324081	1324410	329	3	9631.t00215	unspliced-genomic ELK domain putative	N	Y	Y	-	Y	N	Y	-	-	-	-
205	SRSC3_017	GGTGGACAATTTGACCATGC	GCTGTACCGTAGAGGATGAG	29199813	29200972	1159	3	9631.t04960	unspliced-genomic putative beige protein	N	N	N	-	N	N	-	-	-	-	-
206	SRSC3_018	CAGGAAATCTCTACTGCTAGC	CTTACAGATCTCTGCCTGAG	5050566	5050949	383	3	9631.t00847	unspliced-genomic TFIIB-related protein	N	Y	Y	-	N	Y	-	-	-	-	-
207	SRSC3_019	GGACGATTACTCTAGTTCTCC	CTTGCAAGACCAGACATTGC	31956179	31956507	328	3	9631.t05448	unspliced-genomic putative GTP-binding protein	N	Y	Y	-	N	N	N	-	-	-	-
208	SRSC3_020	CGTGTACGAGATCAACGAGC	CGAAGTAGAAGCTGTAGATGG	17954950	17955270	320	3	9631.t02960	unspliced-genomic allene oxide cyclase	N	N	Y	-	Y	N	N	-	-	-	-
209	SRSC3_021	GGATGGTTGTCCATGGTGC	CTTTGCACCGCTTCCTATTC	31000028	31000513	485	3	9631.t05278	unspliced-genomic putative fatty acid hydroxylase	N	N	N	-	N	N	-	-	-	-	-
210	SRSC3_022	CAAGCAGCTGACGATGGTAC	GCTGAAAGAGCAGTATGCATG	31069979	31070404	425	3	9631.t05293	unspliced-genomic putative actin	N	N	Y	-	Y	N	Y	-	-	-	-
211	SRSC3_023	GAGTTGCTTGATGGAAGTCG	CCTCATTGCGCTCAAACAGC	13153380	13153639	259	3	9631.t02136	unspliced-genomic helicase putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
212	SRSC3_024	ATGGCTGAAGAACTCCCAAC	GGAAGCTGTTGAGATGTCAAG	6044867	6045226	359	3	9631.t01013	unspliced-genomic F14J16.13	N	N	Y	-	N	N	-	-	-	-	-
213	SRSC3_025	CTTCTTTGTGGATGGCGACG	CGGCGAATAACAGCATTTCC	34073850	34075009	1159	3	9631.t05857	unspliced-genomic expressed protein	N	N	N	-	Y	Y	N	-	-	-	-
214	SRSC3_026	CGACCTCGTCATCTGGAAG	GGAGCCATCGAATGACCAG	2559028	2559879	851	3	9631.t00427	unspliced-genomic lethal leaf-spot 1	N	Y	N	-	Y	Y	N	-	-	-	-
215	SRSC3_027	GGAGGAAATCCAGAAGAAAAC	GACACCGTCTCATACTGATG	21357799	21358617	818	3	9631.t03601	unspliced-genomic hypothetical protein	N	Y	N	-	Y	Y	N	-	-	-	-
216	SRSC3_028	CCTGCTAAGGAGGCAACTG	GAACTAGGAAGATCACTGCC	32465238	32465966	728	3	9631.t05542	unspliced-genomic hypothetical protein	N	Y	N	-	N	N	N	-	-	-	-
217	SRSC3_029	GATGTTCATCGAGAGCTTCC	CTTGCTGCACCTTGTCCTTG	4810257	4811211	954	3	9631.t00818	unspliced-genomic inositol-3-phosphate synthase (ec 5.5.1.4) (myo-i	N	Y	Y	-	Y	N	N	-	-	-	-
218	SRSC3_030	CTTACATCCAAGCCATTTGC	CAAAACCTCAGCAACAACTG	27734135	27735185	1050	3	9631.t04687	unspliced-genomic putative reductase	N	N	Y	-	Y	Y	N	-	-	-	-
219	SRSC3_031	CAATGGGAATTGGGATGAGG	GCTGTGTGATCTCCTTAAAC	8131906	8132209	303	3	9631.t01346	unspliced-genomic CTV.2	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	S
220	SRSC3_032	GGTACAAGAAGCTGTTCTGG	GCTGCAGAAGATGTTTGTCC	4922528	4923709	1181	3	9631.t00834	unspliced-genomic sulfate permease	N	N	Y	-	N	Y	N	-	-	-	-
221	SRSC3_033	GTTGGCGGATTTAAGATGCC	GGCATCCAGCAATTCAAAAC	17480971	17481322	351	3	9631.t02884	unspliced-genomic putative ubiquitin conjugation factor	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
222	SRSC3_034	CAGGTCCAACACCAATGTAG	CTGGCTTGACATTGTTGCAC	3968839	3969398	559	3	9631.t00679	unspliced-genomic adenylosuccinate synthetase	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
223	SRSC3_035	GTCGTGTCAATGCTATGCTG	CTTCTGACATCACGAAGATG	15066881	15068140	1259	3	9631.t02482	unspliced-genomic hypothetical protein	N	Y	Y	-	N	Y	N	-	-	-	-
224	SRSC3_036	CAATTGTTGAACCAGCACGC	GATAGTCTACTTCCTGGGCC	5289310	5289693	383	3	9631.t00888	unspliced-genomic hypothetical protein	N	Y	Y	-	Y	N	N	-	-	-	-
225	SRSC3_037	GCCATAGCTTCATCATCACC	GACCTGGATTGACTGAGAGG	21006915	21007555	640	3	9631.t03535	unspliced-genomic AY099551 lysyl-tRNA synthetase	N	Y	N	-	Y	Y	N	-	-	-	-
226	SRSC3_038	GAGCTTATCCCAACATACAG	GCAAACTTCACCTTCTCTGG	4393185	4393617	432	3	9631.t00750	unspliced-genomic amine oxidase flavin-containing putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
227	SRSC3_039	CTCGAAGAACAACAACGACC	CAGAATGCCTTCATGTTGCG	9512689	9513891	1202	3	9631.t01566	unspliced-genomic PsbP putative	N	Y	N	-	N	Y	N	-	-	-	-
228	SRSC3_040	ATCATGGACCACGAGAAGGG	CATCAGGAAGGTTCCTATCG	8665687	8666015	328	3	9631.t01427	unspliced-genomic anthranilate synthase component I	N	Y	N	-	Y	N	Y	-	-	-	-
229	SRSC4_001	GCAAAATCCATGGCTTCTTTC	TTTAATGCTGCTATGAAAACC	6154522	6154838	316	4	9632.t03939	unspliced-genomic Enhancer of rudimentary putative	N	N	N	-	N	N	-	-	-	-	-
230	SRSC4_002	GTTCGATGGGCACAACGG	GATCCCTCAGCTTCAAGGAC	21418025	21418467	442	4	9632.t03492	unspliced-genomic Protein phosphatase 2C putative	N	Y	Y	-	Y	N	-	-	-	-	-

231	SRSC4_003	TTTGCCCGCTCGGGTTAC	CCGTGTGAAGTCTTCAACAAG	21051842	21052299	457	4	9632.t03430	unspliced-genomic Similar to AY099856 cleft lip and palate associate	Y	Y	Y	Y	Y	Y	Y	Y	N	-	S
232	SRSC4_004	TTATGCAGATTCTTAGCTTTGG	TCCTCCAAATTGGCCTCCAG	17852595	17853076	481	4	9632.t02955	unspliced-genomic Exo70 exocyst complex subunit	N	Y	Y	-	Y	N	-	-	-	-	-
233	SRSC4_005	CCTGCTAAAGAACACTATCAG	TCTGAAGAGTCCTGATCCTC	23365379	23365612	233	4	9632.t03837	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
234	SRSC4_006	GAGCAGGGAATGTTGGCATG	AGGGATAAGTTCCCAGCTGC	23364976	23365255	279	4	9632.t03837	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
235	SRSC4_007	CCTGCTAAAGAACACTATCAG	AGGGATAAGTTCCCAGCTGC	23364976	23365612	636	4	9632.t03837	unspliced-genomic Protein kinase domain putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
236	SRSC4_008	GTGTCATACAGTGCTGTTTG	AGCTTTCCAACTGATGAGGG	17857961	17858571	610	4	9632.t02956	unspliced-genomic AKIN gamma	N	Y	Y	-	Y	N	-	-	-	-	-
237	SRSC4_009	TGCCTAAGTGGATGTTCCAA	AGTCTGCTGCTTACTCCAAC	6808747	6809105	358	4	9632.t04052	unspliced-genomic hypothetical protein	N	N	N	-	N	N	-	-	-	-	-
238	SRSC4_010	AGTCTGCTGCTTACTCCAAC	GTGAAGAACAGATTTGGGCG	23906927	23908305	1378	4	9632.t03934	unspliced-genomic Adenosylmethionine decarboxylase	N	N	N	-	N	N	-	-	-	-	-
239	SRSC4_011	GCGCTTCTTCAGTTCAAATG	GCAGCTTTAACAGCATCTTC	2018196	2018636	440	4	9632.t03234	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
240	SRSC4_012	AAGGATTTGTTGGCTGCTAG	GCAGCTTTAACAGCATCTTC	19768075	19768448	373	4	9632.t03234	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	-	-	-	-	-
241	SRSC4_013	TTTCGTGCAGCTGAGGCATG	GCAGCTTTAACAGCATCTTC	19768192	19768448	256	4	9632.t03234	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
242	SRSC4_014	AAGAGCTACCTCGTCAATGG	CAACCCTGCTTTATGAGCATC	22597983	22598760	777	4	9632.t03690	unspliced-genomic Glycerophosphoryl diester phosphodiesterase far	N	Y	Y	-	Y	N	-	-	-	-	-
243	SRSC4_015	GATGCAGATGGCGGCGAC	GTTTGCCTATTGCGGATAAC	21439657	21440995	1338	4	9632.t03495	unspliced-genomic RNA recognition motif. (a.k.a. RRM RBD or RNP	N	N	N	-	N	N	-	-	-	-	-
244	SRSC4_016	TGGGATCCTCAAAGATAATGAG	CTGGAGGAGGACCCTATTG	21196482	21196719	237	4	9632.t03446	unspliced-genomic PCI domain putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
245	SRSC4_017	ATGGCAATGGATCGTCATGAC	TGACTCCACTCTCAATATACTC	23126114	23126525	411	4	9632.t03793	unspliced-genomic MA3 domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
246	SRSC4_018	GGTGATCCCTGAAATGAAGG	CCTCCAAATTGGCCTCCAGA	17852690	17853075	385	4	9632.t02955	unspliced-genomic Exo70 exocyst complex subunit	N	Y	Y	-	N	Y	-	-	-	-	-
247	SRSC4_019	CTGGAGGCAAATTTGGAGG	TATCTGCCCAGAAAAGCACG	17853057	17853490	433	4	9632.t02955	unspliced-genomic Exo70 exocyst complex subunit	N	Y	Y	-	Y	N	-	-	-	-	-
248	SRSC4_020	GAGCAGATCACTTCTTTGTTG	CTGCATGTCCTCATAGTAGG	18803635	18804300	665	4	9632.t03090	unspliced-genomic Exostosin family putative	N	Y	Y	-	N	Y	-	-	-	-	-
249	SRSC4_021	AACGCACTGGACATTGTTTAC	TCTGAAGAGTCCTGATCCTC	23365379	23365826	447	4	9632.t03837	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	Y	N	-	-	-	-	-
250	SRSC4_022	AGGTTGGCTGTGGAGAAGTC	CACTTGTGCAACCTTGAAGC	23363251	23363776	525	4	9632.t03837	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	N	N	-	-	-	-	-
251	SRSC4_023	CCTCAGCAACCTTGGACTTG	AACAGCTTGTTCCAGGCATG	24185780	24187071	1291	4	9632.t03983	unspliced-genomic polyadenylate binding protein human types 1 2 3	N	Y	Y	-	N	N	-	-	-	-	-
252	SRSC4_024	ATCTCGACGGGGAAGTAGAC	TTCTACGAGCCTTTCTGGC	5743670	5744010	340	4	9632.t03861	unspliced-genomic Transmembrane amino acid transporter protein	N	Y	Y	-	Y	N	-	-	-	-	-
253	SRSC4_025	CGTCGTCCAGTTCTCGTAC	TTCTCCATGCCGGCGAAC	21872888	21873421	533	4	9632.t03572	unspliced-genomic gamma-glutamyltranspeptidase	N	N	Y	-	N	N	-	-	-	-	-
254	SRSC4_026	CGTAGCTGAAGTAGAGCAGG	TCTTCTGGTGCCTCTTCAAC	281116	281743	627	4	9632.t00053	unspliced-genomic expressed protein	N	N	Y	-	Y	Y	-	-	-	-	-
255	SRSC4_027	TCCTTGGTATTCAGGAGTTG	GATGTTGGACTTGGGAGAAC	33262452	33263576	1124	4	9632.t05450	unspliced-genomic auxin response factor 8	N	Y	Y	-	Y	N	-	-	-	-	-
256	SRSC4_028	ATCCGTTGACGAAGCTCTTG	TCTACGCCTACACCTACTTC	26695223	26695541	318	4	9632.t04397	unspliced-genomic BT000565 At5g47500/MNJ7_9	N	Y	Y	-	N	Y	-	-	-	-	-
257	SRSC4_029	CGTTCCTCAACAGCAACGTG	CGACGAGTAGTGGAACATGC	24296670	24296985	315	4	9632.t03999	unspliced-genomic Sialyltransferase family putative	N	N	Y	-	N	Y	-	-	-	-	-
258	SRSC4_030	AAGCTCTGGTAGATGAGGAG	AGTCTGCTGCTTACTCCAAC	23906927	23908254	1327	4	9632.t03934	unspliced-genomic Adenosylmethionine decarboxylase	N	N	Y	-	N	N	-	-	-	-	-
259	SRSC4_031	CGTCGAAGCAGTTCTGCTTG	ACATACCCATTGACATTGGC	27099518	27100121	603	4	9632.t04458	unspliced-genomic prolyl oligopeptidase family putative	Y	Y	Y	N	Y	Y	Y	N	N	-	D
260	SRSC4_032	GCATGGAGTTGATCTTGGTG	CCTTCGTCGTCTTCGACAAC	33677465	33677987	522	4	9632.t05516	unspliced-genomic hypothetical protein	N	N	Y	-	Y	Y	-	-	-	-	-
261	SRSC5_001	TTGAGGAAGCTAGCAGGATG	CATCACTTCCATGAATTGTCAG	7652206	7653436	1230	5	9633.t01218	unspliced-genomic Phosphatidylinositol 3- and 4-kinase putative	Y	Y	Y	Y	Y	Y	N	N	N	-	D
262	SRSC5_002	ACAAGATCCGGAGGCAGATC	CAGATTGGAAAGATCACGAAC	28177943	28178931	988	5	9633.t04682	unspliced-genomic V-ATPase subunit C putative	N	N	Y	-	N	N	-	-	-	-	-
263	SRSC5_003	TGCAGTGCAATATCCAGTGC	CCAGCTTCGTGCCAAAGC	24188205	24188555	350	5	9633.t03950	unspliced-genomic tubby-like protein 7	N	Y	Y	-	N	N	-	-	-	-	-
264	SRSC5_004	GATATGGTTCTGCCATTTGC	CAGCTACCAACACTTGAAAC	26427978	26428747	769	5	9633.t04370	unspliced-genomic expressed protein	N	Y	Y	-	N	N	-	-	-	-	-
265	SRSC5_005	CCTTGCTGGTGATGAATTTG	GAAGCAACAGCCAGATCAAC	27277366	27277794	428	5	9633.t04526	unspliced-genomic translation initiation factor IF-2 putative	N	Y	Y	-	N	Y	-	-	-	-	-
266	SRSC5_006	CTGATATGGTTCTGCCATTTGG	CAGCTACCAACACTTGAAAC	26427978	26428749	771	5	9633.t04370	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
267	SRSC5_007	GCTGCACAAGACATGGTTCG	GCATGTGACCTTGATGATTC	3041289	3041993	704	5	9633.t00517	unspliced-genomic kinesin-like protein	N	Y	Y	-	N	Y	-	-	-	-	-
268	SRSC5_008	GCTGGTGAAAGATAGCTATG	TCTCCAGAGCAAAGCTGAAC	237589	238896	1307	5	9633.t00049	unspliced-genomic S-adenosyl-L-methionine: L-methionine S-methylt	Y	Y	Y	Y	Y	Y	N	N	N	-	D
269	SRSC5_009	GAACCAATCCATCTGAGCAC	GAGCTTTCTTCTCAGACATC	4467700	4468086	386	5	9633.t00742	unspliced-genomic phosphatidylinositol 3-kinase root isoform (ec 2.7.	Y	Y	Y	N	Y	Y	Y	N	Y	-	D
270	SRSC5_010	GTCCCCTTGGTAATGTATGG	CAAACCAAGCTCCTGACATG	2026434	2026703	269	5	9633.t00358	unspliced-genomic probable protein kinase [imported] - Arabidopsis t	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
271	SRSC5_011	GCTTGGAACCAGATCAAAGTG	CACTCAAGATTTGCCTTGACC	429489	430057	568	5	9633.t00080	unspliced-genomic protein kinase	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
272	SRSC5_012	GCATGAGGCTCTTGAGGAAG	GCCATCACTTCCATGAATTG	7652195	7653438	1243	5	9633.t01218	unspliced-genomic Phosphatidylinositol 3- and 4-kinase putative	N	Y	N	-	Y	Y	Y	-	-	-	-
273	SRSC5_013	GAGATTGTGTTCAAAGCCCC	GGAATTACAGTGCCTTCAAG	18747283	18747577	294	5	9633.t03032	unspliced-genomic expressed protein	N	N	N	-	N	N	-	-	-	-	-
274	SRSC5_014	GTGGCAATGGTTGGATATCC	GGTATGCATCCAACAATGCG	241793	242424	631	5	9633.t00049	unspliced-genomic S-adenosyl-L-methionine: L-methionine S-methylt	N	Y	Y	-	Y	N	Y	-	-	-	-
275	SRSC5_015	GTCACCAAGAGATACTTCAC	GAGTACTTCAAGAACCACTC	21047224	21047443	219	5	9633.t03406	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	S
276	SRSC5_016	CAAGATCCGGAGGCAGATC	ACCAGATTGGAAAGATCACG	28177944	28178933	989	5	9633.t04682	unspliced-genomic V-ATPase subunit C putative	Y	Y	Y	Y	Y	Y	N	N	N	-	D
277	SRSC5_017	TGTGGCCACCAAGTGAAAGC	CGCTTGCCACCAGATATATC	25611693	25612041	348	5	9633.t04223	unspliced-genomic Leucine Rich Repeat putative	Y	Y	Y	Y	Y	Y	N	N	N	-	S
278	SRSC5_018	TGGGAGCTGGGTTGTGTTTG	CCTTTTGAGCCAGCAAAGG	13510236	13511020	784	5	9633.t02196	unspliced-genomic Similar to 37802-35617	N	N	N	-	Y	N	N	-	-	-	-
279	SRSC5_019	ACCTCAAGGACATGCCCAAG	CTTGATGGTGAACTCGGACG	15097569	15098082	513	5	9633.t02466	unspliced-genomic AF419595 AT3g51670/T18N14_50	N	Y	N	-	Y	Y	Y	-	-	-	-
280	SRSC5_020	CGTCAATGGCATATCTACAC	CCATACCAATGTCATTGAGC	11986437	11987617	1180	5	9633.t01955	unspliced-genomic acetyl-coenzyme A carboxylase	Y	Y	Y	N	Y	Y	Y	N	N	-	D
281	SRSC5_021	GACAACCTTGATGTTGCACG	GCAACAGCCAGATCAACATC	27277394	27277790	396	5	9633.t04526	unspliced-genomic translation initiation factor IF-2 putative	N	Y	N	-	Y	Y	Y	-	-	-	-
282	SRSC5_022	GGAGATCCAAATGATCCACG	CATTCGCAGCATAAAGGCTG	17666739	17667586	847	5	9633.t04768	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
283	SRSC5_023	GACTTGATAAATGAGGGTCG	CCAGCAGCAGCAAAATATTC	27066778	27067445	667	5	9633.t04485	unspliced-genomic Similar to AL049876 COP1 like protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
284	SRSC5_024	TTCTTGACCCCCAAATCTGG	GTGCTTGAGATAGCTCCTGC	3993102	3993575	473	5	9633.t00669	unspliced-genomic adenylate translocator brittle-1 homolog F8B4.100	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
285	SRSC6_001	TGAGGCTCACATGGAAGTTC	GCTTGCCATAGCACCAAATG	24212965	24214227	1262	6	9634.t03935	unspliced-genomic Similar to pitrilysin (EC 3.4.24.55) - garden pea	Y	Y	Y	Y	Y	Y	N	N	Y	-	D
286	SRSC6_002	GGATGTTCACTACATGCTTG	ACGCTCCATCAATCTCAATG	1792744	1793612	868	6	9634.t00325	unspliced-genomic 3-phosphoshikimate 1-carboxyvinyltransferase	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
287	SRSC6_003	CAGGTTTGAGGCTCACATG	GCTTGCCATAGCACCAAATG	24212965	24214233	1268	6	9634.t03935	unspliced-genomic Similar to pitrilysin (EC 3.4.24.55) - garden pea	N	N	Y	-	N	Y	-	-	-	-	-
288	SRSC6_004	GGATGTTCACTACATGCTTG	ACGCTCCATCAATCTCAATG	1792744	1793612	868	6	9634.t00325	unspliced-genomic 3-phosphoshikimate 1-carboxyvinyltransferase	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
289	SRSC6_005	CTTGTATTATACCAGAGGAAGG	CTTTAGCCCTCTCCTGAATAC	26095797	26096133	336	6	9634.t04222	unspliced-genomic actin filament bundling protein P-115-ABP	N	N	Y	-	N	N	-	-	-	-	-
290	SRSC6_006	TTGGGAATGTGGAAGCCTTC	TGTCCAAACTCTTGAAACCAAG	22600088	22601421	1333	6	9634.t03704	unspliced-genomic Similar to gb_AJ010025 unr-interacting protein fro	N	N	Y	-	N	N	-	-	-	-	-
291	SRSC6_007	GTTCAGGGCCTTGAAACAAC	GCCTTAGAAGCATCTGCAAC	191986	192727	741	6	9634.t00035	unspliced-genomic Acyl-CoA oxidase putative	Y	Y	Y	Y	Y	Y	N	N	N	-	D
292	SRSC6_008	GAGTAGAGCATCACATTTGAG	CATTGCAGGCCGTGAGAAAG	27421881	27422173	292	6	9634.t04427	unspliced-genomic ribosomal protein L24 putative	N	Y	Y	-	N	Y	-	-	-	-	-
293	SRSC6_009	GGAAGTCGTAGCAGAAGTTG	CAAGGTCTCCATCAACTGGC	24243715	24245026	1311	6	9634.t03940	unspliced-genomic K+ potassium transporter putative	N	Y	N	-	N	N	-	-	-	-	-
294	SRSC6_010	CTTGTTAACGCATCGGTAGG	CTTTGGTCTATCAAAGGAGG	9972267	9973030	763	6	9634.t01674	unspliced-genomic Similar to serine/threonine-specific protein kinase	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
295	SRSC6_011	GCAAGCACGATCATGGTTAC	CAAGGCACATTTCTCGTGAC	24638680	24639007	327	6	9634.t04004	unspliced-genomic Transmembrane amino acid transporter protein	N	Y	Y	-	Y	N	Y	-	-	-	-
296	SRSC6_012	GTACAACACTGCAGAAGGATG	GTCTTGAAGTTGCTTCCAGG	23812595	23813062	467	6	9634.t03873	unspliced-genomic Zinc finger C-x8-C-x5-C-x3-H type (and similar) p	N	N	Y	-	N	Y	-	-	-	-	-
297	SRSC6_013	AGCTTCAGTAGGTTGTCAAG	TCTGAGGGAAAATGGCATCC	26235187	26235721	534	6	9634.t04244	unspliced-genomic expressed protein	N	N	Y	-	N	N	-	-	-	-	-
298	SRSC6_014	GTGGGACCTCGACAACAAG	CCATGGCAACCAAATGTCAG	3283267	3283951	684	6	9634.t00603	unspliced-genomic Zinc finger C2H2 type putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	S
299	SRSC6_015	CAGCTGCAATCAAGACTGTG	AGCCCTCTCCTGAATACTTG	26095800	26096241	441	6	9634.t04222	unspliced-genomic actin filament bundling protein P-115-ABP	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
300	SRSC6_016	GACATATTGGACAAGCCCTC	AGTTTCTCGTAACCCCACAG	12096785	12097438	653	6	9634.t02020	unspliced-genomic Zinc finger C-x8-C-x5-C-x3-H type (and similar) p	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
301	SRSC6_017	GTCCATAGAAAAGAAGCCAC	CGCAAGTTCTCCTTCAAGC	5007583	5008588	1005	6	9634.t00915	unspliced-genomic expressed protein	N	N	Y	-	N	Y	N	-	-	-	-
302	SRSC6_018	GCACAAGCAGGTCTTGAATC	GCTGAAAGTGTCCTTCCAAT	23229357	23230155	798	6	9634.t03797	unspliced-genomic Zinc finger C3HC4 type (RING finger) putative	Y	Y	Y	Y	Y	Y	Y	N	Y	-	D
303	SRSC6_019	CTCAATCTGGAATGGTGAAG	TTTGGTGCACAAGAACCTGG	4288878	4289234	356	6	9634.t00775	unspliced-genomic glutathione peroxidase putative	N	Y	Y	-	N	Y	Y	-	-	-	-
304	SRSC6_020	GAGCTCCAGATGATGAACAC	CTTGCCATAGCACCAAATGG	24212966	24213508	542	6	9634.t03935	unspliced-genomic Similar to pitrilysin (EC 3.4.24.55) - garden pea	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
305	SRSC6_021	GCTGCTCAACGAGTTCATCG	CAGGGTTCTCCTTGAAGTAC	20509067	20510162	1095	6	9634.t03380	unspliced-genomic expressed protein	Y	Y	Y	Y	Y	Y	Y	Y	N	-	D
306	SRSC6_022	AGTTAAGCGTGTGGTGTTTC	GTGTCACCACGCTTCTTTTC	1967271	1967825	554	6	9634.t00357	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
307	SRSC6_023	TGGGCATGAAGTTCAATGAG	CTTTTCATGGCTATACGCCC	23271383	23271880	497	6	9634.t03804	unspliced-genomic EF hand putative	N	Y	Y	-	N	Y	Y	-	-	-	-
308	SRSC6_024	AGTAAGCTCTCCATCTCCTC	AGTTTGGCAAGGAGATGCTC	3469647	3470406	759	6	9634.t00633	unspliced-genomic Protein kinase domain putative	N	N	N	-	N	N	Y	-	-	-	-
309	SRSC7_001	ATCCTCAGCTCCATGTTTTC	ATTAGTCCATTGCTCAGGTG	29095211	29095686	475	7	9635.t04854	unspliced-genomic AMP deaminase putative	N	Y	Y	-	N	Y	-	-	-	-	-
310	SRSC7_002	TGTTCCACCACCATTTGCTG	GATGTCACCTGGCATGATTC	23057342	23057987	645	7	9635.t03801	unspliced-genomic succinyl-CoA ligase alpha subunit	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
311	SRSC7_003	CCACTGCTTCAGTCTGCTC	CCTGATCAATCCATGGGAAG	22955819	22956468	649	7	9635.t03780	unspliced-genomic expressed protein	N	N	Y	-	Y	N	-	-	-	-	-
312	SRSC7_004	TGCATTGCCCAGATTGCAAG	GAAATCTGGACAGGAGTAAC	14784529	14785211	682	7	9635.t02473	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
313	SRSC7_005	CATTTCGATGAGGCCTTCTC	GGTGTAGCTCATCTGGAATG	1764891	1765460	569	7	9635.t00342	unspliced-genomic hypothetical protein	N	Y	Y	-	Y	N	-	-	-	-	-
314	SRSC7_006	TTCTGCAGCAAGTGCATTTG	CAGTTGGATACTTGTAGCAG	26561496	26562328	832	7	9635.t04420	unspliced-genomic Phosphatidylinositol 3- and 4-kinase putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
315	SRSC7_007	GTAAGTCGATGTCTGCCTG	GTGGGCTGATACAATGAGTG	17974731	17975148	417	7	9635.t02963	unspliced-genomic Similar to AF395065 CSN complex subunit 7i	N	Y	Y	-	N	Y	-	-	-	-	-
316	SRSC7_008	CTTTCCAGACCATTCCATAG	GATGAGGAACCTTGAAGTTG	17131099	17131947	848	7	9635.t02833	unspliced-genomic Serine carboxypeptidase putative	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
317	SRSC7_009	CATGGTGTTATTGGACGTTG	GCGATATCACTTTGCTTAGC	23482409	23483828	1419	7	9635.t03875	unspliced-genomic amino-acid N-acetyltransferase	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
318	SRSC7_010	GTCATCGAGCTCGACATGTG	GTTGTTGCTCGCTCAAACTG	29132737	29133536	799	7	9635.t04861	unspliced-genomic phosphoinositide-specific phospholipase C	N	N	N	-	N	N	-	-	-	-	-
319	SRSC7_011	GGACCTTTCATTACCTCTCT	GGGAGATCTTTGGTTATAGC	22999002	23000039	1037	7	9635.t03789	unspliced-genomic hypothetical protein	N	N	N	-	N	Y	-	-	-	-	-
320	SRSC7_012	GTGTTGGTTCCATCTCAGG	CTGCCTCATGGTTATGATGG	29245330	29245913	583	7	9635.t04879	unspliced-genomic 2-oxoglutarate dehydrogenase E1 component	N	N	Y	-	N	N	-	-	-	-	-
321	SRSC7_013	GCCAGTCATGAAGCATTTCT	GGAGTTTGGAGTGTCTATGG	3380620	3381332	712	7	9635.t00636	unspliced-genomic prolyl-tRNA synthetase	N	N	N	-	N	N	-	-	-	-	-
322	SRSC7_014	CATAGCTTATCTTGCCATCC	CAAGTTCAAGAAGCATGCAC	22554174	22555071	897	7	9635.t03713	unspliced-genomic Protein kinase domain putative	N	N	N	-	N	N	-	-	-	-	-
323	SRSC7_015	GCTTCAGGTATTCGATGTCC	CTGATCCTCAACCAAACTGG	23228187	23229353	1166	7	9635.t03834	unspliced-genomic expressed protein	N	Y	N	-	N	Y	-	-	-	-	-
324	SRSC7_016	GATACTGCTGTAGCATCAGG	CTCTTGTTCCTGATCCTGAG	7053196	7054298	1102	7	9635.t01199	unspliced-genomic hypothetical protein	N	Y	Y	-	Y	N	Y	-	-	-	-
325	SRSC7_017	CAGGGAAAAGGAAATGCAGC	GCCTTTCCAGGCTTTTTCC	27292805	27293758	953	7	9635.t04557	unspliced-genomic ribosomal protein S9 putative	N	N	N	-	N	Y	N	-	-	-	-
326	SRSC7_018	CTCTTCCATGGAAGAACTGC	CCATGTGAGGAAGAACTTCC	21197569	21198465	896	7	9635.t03483	unspliced-genomic 28516 beta-amylase	N	Y	Y	-	N	Y	N	-	-	-	-
327	SRSC7_019	CTTGACCAAGCTCTTCATGG	CATCCGCAGTTTGCATCTTC	1762122	1762587	465	7	9635.t00342	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
328	SRSC7_020	CCATGTCCTTGTGGATTCTG	CACTTGAAGAGCTGGAAATC	25692510	25692833	323	7	9635.t04259	unspliced-genomic GTP1/OBG family putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
329	SRSC7_021	CATCGTGAACGTGAACTCG	GACGATGCCGATGTAGATG	7696069	7696567	498	7	9635.t01308	unspliced-genomic expressed protein	N	N	N	-	N	Y	N	-	-	-	-
330	SRSC7_022	GAACCTCATCCAACAATTCC	GCTGCTGATGTTGCTATTGC	3261983	3262413	430	7	9635.t00618	unspliced-genomic hypothetical protein	Y	Y	Y	N	Y	Y	Y	Y	Y	N	D
331	SRSC7_023	GCAACGTCAAGGAGTCCATC	CCAAAAGGCACAGTATCCTG	3496666	3497519	853	7	9635.t00656	unspliced-genomic NAD synthase putative	N	N	N	-	N	Y	N	-	-	-	-
332	SRSC7_024	AGCAGCTGATCAACGCTGTC	GAGAATCACTCCACATGACC	2562234	2562944	710	7	9635.t00490	unspliced-genomic AY035226 CBL-interacting protein kinase 23	Y	Y	Y	Y	Y	Y	N	Y	Y	N	D
333	SRSC8_001	CTCCACCGGATTGCAGATG	TGAGAGAAGCCTTTGCTGTG	950513	951422	909	8	9636.t00134	unspliced-genomic avr9 homolog F9L11.10 [imported] - Arabidopsis t	N	N	Y	-	N	N	-	-	-	-	-
334	SRSC8_002	CATGGCACCACTAGACATAG	GAAACTGACTTCATGATGGAG	3304488	3305142	654	8	9636.t00518	unspliced-genomic mitogen-activated protein kinase MMK2 (EC 2.7.1	N	Y	Y	-	Y	N	-	-	-	-	-
335	SRSC8_003	TTGCAGCTGAGAGGGAAATG	GTCCAGCTAAAATTTGGGTC	18312658	18312947	289	8	9636.t02997	unspliced-genomic ABC transporter protein putative	N	Y	Y	-	Y	N	-	-	-	-	-
336	SRSC8_004	ATGTGCCAAGGATGGCAATG	GCTGGTTGGCAAAAGGCTC	5135203	5135846	643	8	9636.t00806	unspliced-genomic glucose-6-phosphate/phosphate translocator	N	Y	Y	-	N	Y	-	-	-	-	-
337	SRSC8_005	TGATGGATCCCTCAGTATAC	GGGATCACCATTCTGCCAC	27131511	27132155	644	8	9636.t04376	unspliced-genomic protein-L-isoaspartate O-methyltransferase	N	Y	Y	-	N	N	-	-	-	-	-
338	SRSC8_006	TGTTGGAGAGCTTCTTGAAC	TATTTGCAAGCCTAGCTGTC	13183192	13184218	1026	8	9636.t02168	unspliced-genomic hypothetical protein	N	Y	Y	-	Y	N	-	-	-	-	-
339	SRSC8_007	AACTGCTGCCATGCATTCTG	GAACAGGCAGCAACATCTG	508504	509096	592	8	9636.t00083	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	-	-	-	-	-
340	SRSC8_008	GCGTGCTTGGTTCACATATC	ACAACTTCACTGAAGAGGAG	3124150	3124658	508	8	9636.t00495	unspliced-genomic Transaldolase putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
341	SRSC8_009	CAAGGGAAGTGGAAGGCTAC	CTGGAACAGGGCTCAATGTG	450361	450921	560	8	9636.t00074	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
342	SRSC8_010	CGATTATGTTGGTTCCTGGG	GTACAGCAGAGATGACCATC	25780534	25780820	286	8	9636.t04140	unspliced-genomic glutamate-1-semialdehyde-2 1-aminomutase	N	N	Y	-	N	Y	-	-	-	-	-
343	SRSC8_011	GCTCTTCAAATCATGGTGC	ACAAGCATGCTGGAGAAGG	3366783	3367338	555	8	9636.t00523	unspliced-genomic Similar to LHY protein	N	N	Y	-	N	N	-	-	-	-	-
344	SRSC8_012	GCCAATATTGCATCAGCACTC	CCTAATCCAATGCAGGAAGG	23935921	23937419	1498	8	9636.t03841	unspliced-genomic peroxisomal targeting signal 1 receptor	Y	Y	Y	Y	Y	Y	N	N	N	-	D
345	SRSC8_013	GGATGTCTGCATGAAGCCTG	TGTGGACCTCTCTTCTTGAC	3629209	3630489	1280	8	9636.t00561	unspliced-genomic ribosomal protein L13 putative	N	Y	Y	-	N	N	-	-	-	-	-
346	SRSC8_014	GTTGACTATGATGCTCCTGG	CATCTCCAGCAGCCAAGAAG	3666834	3667310	476	8	9636.t00562	unspliced-genomic expressed protein	N	Y	Y	-	Y	N	N	-	-	-	-
347	SRSC8_015	CCATGTTGTGCTGTTGGATTG	CTGCTGTGCAATCTGAAACC	7317095	7317606	511	8	9636.t01215	unspliced-genomic Similar to oxidosqualene cyclase	N	N	Y	-	N	N	-	-	-	-	-

348	SRSC8_016	CCATTCTGAAGACTCAGCG	CAGGGCCTGATGTTTGCATC	5474794	5475280	486	8	9636.t00850	unspliced-genomic hypothetical protein	N	Y	Y	-	Y	N	Y	-	-	-	-
349	SRSC8_017	TTCTTCCACCATTTGGCCTC	GAAGTGAAGTGGGCTCAGAG	15888064	15888410	346	8	9636.t02612	unspliced-genomic transposon protein putative mariner sub-class	N	N	Y	-	N	Y	N	-	-	-	-
350	SRSC8_018	CGAATCCTCTTGGTACCAAC	GATCGCTCTTCATGTGGTTC	3367868	3368475	607	8	9636.t00523	unspliced-genomic Similar to LHY protein	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D
351	SRSC8_019	AAGACGCTGCTGAAGCTGTC	ATGAGCTCGCAGAAGAGCTC	4379781	4380062	281	8	9636.t00697	unspliced-genomic expressed protein	N	N	Y	-	N	Y	N	-	-	-	-
352	SRSC8_020	CAAGTCCCTGATATCAGCTG	CGGTTTGATCATCACTGTCC	26000891	26001682	791	8	9636.t04181	unspliced-genomic DHHC zinc finger domain putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
353	SRSC8_021	AAGTGGCGGTGAAGCTCATC	GGAAGCAGACAAATAAGGTG	25107802	25108738	936	8	9636.t04025	unspliced-genomic oligouridylate binding protein putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
354	SRSC8_022	GTCAACTCCATCTACGTGC	GTGCCCTCAAGACGAAATG	8569621	8570708	1087	8	9636.t01421	unspliced-genomic hypothetical protein	N	N	N	-	Y	N	N	-	-	-	-
355	SRSC8_023	GAAATTGGCACACTAGATGG	CAATGTACTTACCACGAGC	8846006	8846419	413	8	9636.t01465	unspliced-genomic aspartate carbamoyltransferase	N	Y	Y	-	N	Y	Y	-	-	-	-
356	SRSC8_024	GGCGTCCACTTGAAGTGCA	GGCAAGGCTGACCCATTTG	12085981	12086992	1011	8	9636.t01974	unspliced-genomic C2 domain putative	N	Y	Y	-	N	Y	N	-	-	-	-
357	SRSC9_001	GGGAAGCTGATTGTGCTTG	CCTCTGTCCAACACTAATTG	17567499	17567899	400	9	9637.t02759	unspliced-genomic mitochondrial carrier protein putative	N	Y	Y	-	N	N	-	-	-	-	-
358	SRSC9_002	GCCCTCTCCAGCATGAAAG	CGTCACCTTGTACTGCTTC	10638395	10639054	659	9	9637.t01676	unspliced-genomic Heavy-metal-associated domain putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	D
359	SRSC9_003	AAGCTCTCCAGAACCCTTG	CTTGGGGTGGAAAAGTGAAG	19799646	19800110	464	9	9637.t03087	unspliced-genomic expressed protein	N	Y	Y	-	N	Y	-	-	-	-	-
360	SRSC9_004	AAAGGACCAGTCACGTGAAG	ATAGCCTGGCCATTTCCTC	12996461	12996968	507	9	9637.t02052	unspliced-genomic hypothetical protein	Y	Y	Y	Y	Y	Y	Y	Y	N	-	D
361	SRSC9_006	GCAACATCAGCTTACTGTGC	CCAGAACTATCCCAGCAAAC	375617	375968	351	9	9637.t00059	unspliced-genomic expressed protein	N	N	Y	-	N	N	-	-	-	-	-
362	SRSC9_007	GAATGGATGATGCAGATGAC	GGTAGTCCTTGTCACAGAAC	11098361	11098894	533	9	9637.t01744	unspliced-genomic AL357612 serine/threonine protein kinase	N	N	Y	-	Y	Y	-	-	-	-	-
363	SRSC9_008	TCTGTCCTCTCATCGATATC	TTTTGGAAGAGCAAGGCCTG	6033143	6033673	530	9	9637.t00968	unspliced-genomic Ubiquitin-conjugating enzyme putative	N	N	Y	-	N	Y	-	-	-	-	-
364	SRSC9_009	GAAGCAAAGGAGCTTGGATAC	CTGGTTGGAAGGAAATCCAAC	20876220	20876627	407	9	9637.t03296	unspliced-genomic Similar to WD repeat domain protein - Arabidopsi	N	Y	Y	Y	Y	Y	Y	Y	Y	N	D
365	SRSC9_010	TCGTAGAAGCAGGGCCTTG	TGTGGCCAGAATTAGAGCTC	15227543	15228849	1306	9	9637.t02375	unspliced-genomic formate--tetrahydrofolate ligase	N	Y	Y	Y	Y	Y	Y	N	N	-	S
366	SRSC9_011	GCTTTTGGAAGAAGGCACAG	CATACCATCACCAGCATCAG	11398168	11398912	744	9	9637.t01792	unspliced-genomic leucyl-tRNA synthetase	N	N	N	-	N	N	-	-	-	-	-
367	SRSC9_012	GCAACATCAGCTTACTGTGC	CCAGAACTATCCCAGCAAAC	375617	375968	351	9	9637.t00059	unspliced-genomic expressed protein	N	Y	Y	-	N	Y	-	-	-	-	-
368	SRSC9_013	GGTGTTCTTTATGGGTATCG	AGCTCTTTGGAAGCAGCCAC	16322179	16323051	872	9	9637.t02559	unspliced-genomic isoamylase-type starch debranching enzyme ISO	N	Y	Y	-	Y	N	Y	-	-	-	-
369	SRSC9_014	GTAGGCATGCTGATATAGGC	AGTGGTGAAAGTCCATGCTG	15327034	15327599	565	9	9637.t02388	unspliced-genomic potassium uptake protein	N	N	N	-	N	Y	-	-	-	-	-
370	SRSC9_015	GAAGGAACTTCTATGGCCAG	GAAAGGAGGTGGCAAAGAAC	20421848	20422489	641	9	9637.t03212	unspliced-genomic AY059162 AT4g30210/F9N11_60	N	N	Y	-	N	Y	-	-	-	-	-
371	SRSC9_016	TGAACGGCTGCTAACATAGC	CAAACATGGCCATGGACATG	17584935	17586141	1206	9	9637.t02761	unspliced-genomic expressed protein	N	N	Y	-	Y	Y	Y	-	-	-	-
372	SRSC9_017	TTGCGCCAAGAGATTCACAC	TGCCAACCCTTGTAGTTCAC	13450738	13451146	408	9	9637.t02115	unspliced-genomic expressed protein	N	Y	Y	-	N	Y	Y	-	-	-	-
373	SRSC9_018	GCAAGCAAGAGCAGATTCAC	CACAAGAGCTTCTTCAGGTG	18420396	18421253	857	9	9637.t02868	unspliced-genomic bromodomain protein 103	N	Y	Y	-	N	N	N	-	-	-	-
374	SRSC9_019	GTGAAAAAGGGTCCAAAGGG	GAAGCCCCAGTAAGTCTTC	18424763	18425244	481	9	9637.t02869	unspliced-genomic Proteasome A-type and B-type putative	Y	Y	Y	Y	Y	Y	Y	N	N	-	S
375	SRSC9_020	GAACGGCTGCTAACATAGC	CAAACATGGCCATGGACATG	17584935	17586140	1205	9	9637.t02761	unspliced-genomic expressed protein	Y	Y	Y	-	N	Y	N	-	-	-	-
376	SRSC9_021	CCACAAGTGCAGCAGTAAG	GACATGATGACTGACTTGAG	6993319	6994802	1483	9	9637.t01108	unspliced-genomic F9L1.2 protein - Arabidopsis thaliana	Y	Y	N	-	N	Y	N	-	-	-	-
377	SRSC9_022	GCTTTCCTTCATGAAGAAGC	GCCCTGACATCATCTCAAG	10453424	10454809	1385	9	9637.t01645	unspliced-genomic Protein kinase domain putative	N	Y	Y	-	N	Y	N	-	-	-	-
378	SRSC9_023	GTTCTCCCTGCAGATCTTC	GAAGGATGACGACTTCGAG	20575047	20575497	450	9	9637.t03247	unspliced-genomic potassium uptake protein	N	Y	Y	-	N	Y	Y	-	-	-	-
379	SRSC9_024	GGAAAGCTTTGCTTCTGCAG	GTGTAAACACAGTCCCCAC	2893285	2894000	715	9	9637.t00483	unspliced-genomic expressed protein	N	Y	Y	-	N	Y	N	-	-	-	-
380	PRSC1_044	TGTTCACCTGATCTATGTGG	GAGGACCTATTGAAGAACATC	9881092	9881695	603	1	Unknown	No hit	N	Y	Y	-	Y	N	-	-	-	-	-
381	SRSC2_008	GTTCACCTACGGAAACCTTG	GCGGCTTAATTTGACTCAAC	28343878	28344491	613	2	Unknown	18S small subunit ribosomal RNA	Y	Y	Y	Y	Y	Y	Y	Y	Y	Y	S
382	SRSC2_024	GCTGGTGTATCACAACCAGC	CAACCGTGCTCTAGCAAGAG	1279702	1280696	994	2	Unknown	No hit	N	N	Y	-	N	Y	Y	-	-	-	-
383	SRSC2_040	CCTTCTTCAAAGCCCCAATC	CTCGACAAGAACTCCAAGAC	23769899	23771064	1165	2	Unknown	No hit	Y	Y	Y	N	Y	Y	N	N	N	-	-
384	SRSC9_005	AACTCTTCATTCCTGCTGTC	CACCAACATGAACTCAATGC	789262	789935	673	9	Unknown	No hit	Y	Y	Y	Y	Y	Y	Y	Y	Y	N	D