Landes Bioscience

www.landesbioscience.com

Supplemental Material to:

Andrea D. McCue, Saivageethi Nuthikattu, R. Keith Slotkin

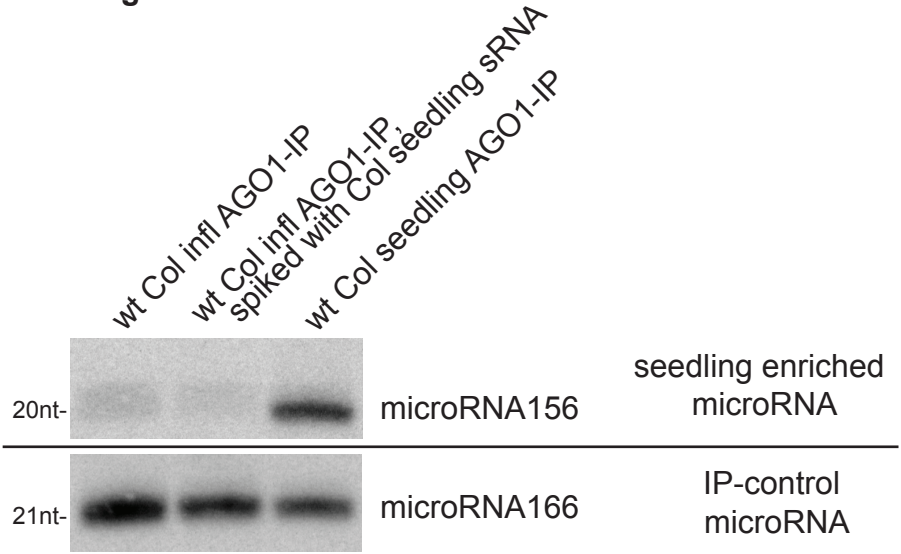
Genome-wide Identification of genes regulated in trans by transposable element small interfering RNAs

2012; 10(8)

http://dx.doi.org/10.4161/rna.25555

www.landesbioscience.com/journals/rnabiology/article/25555/

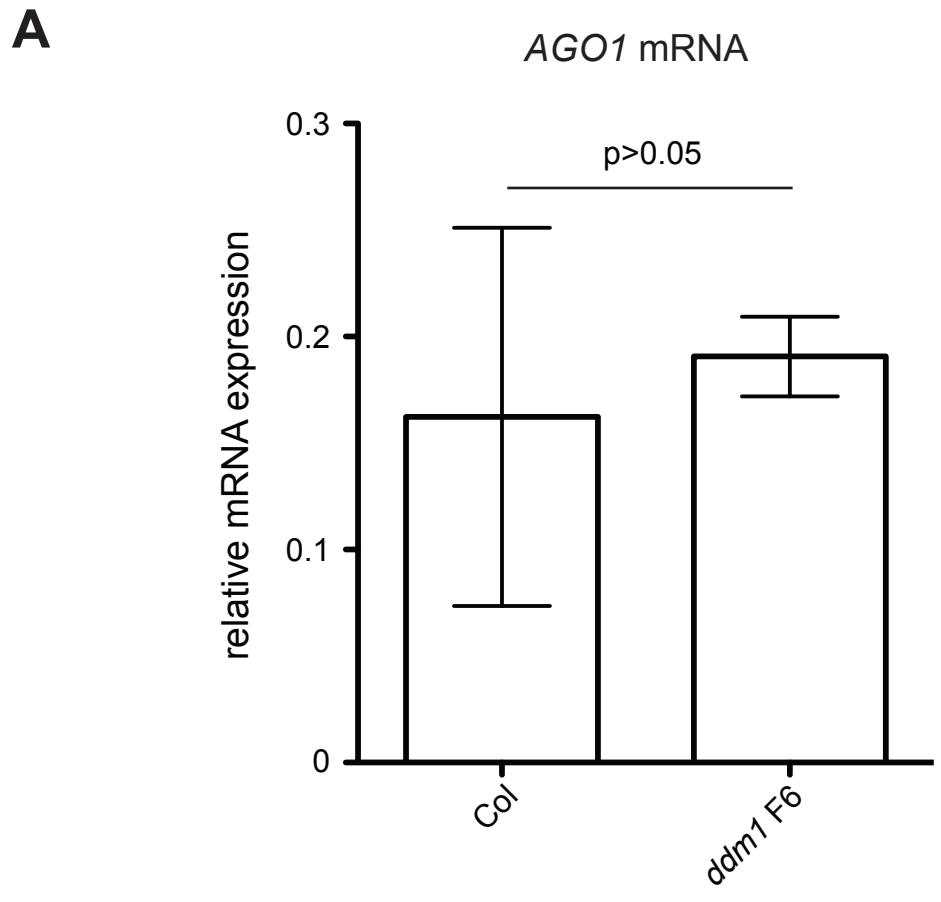
Supplemental Figure 1

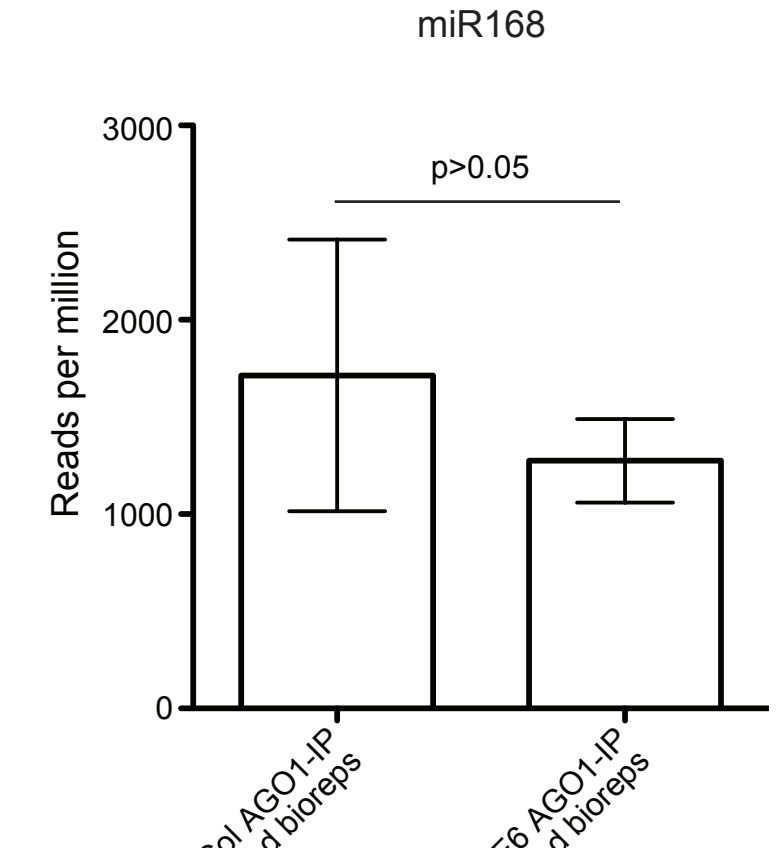


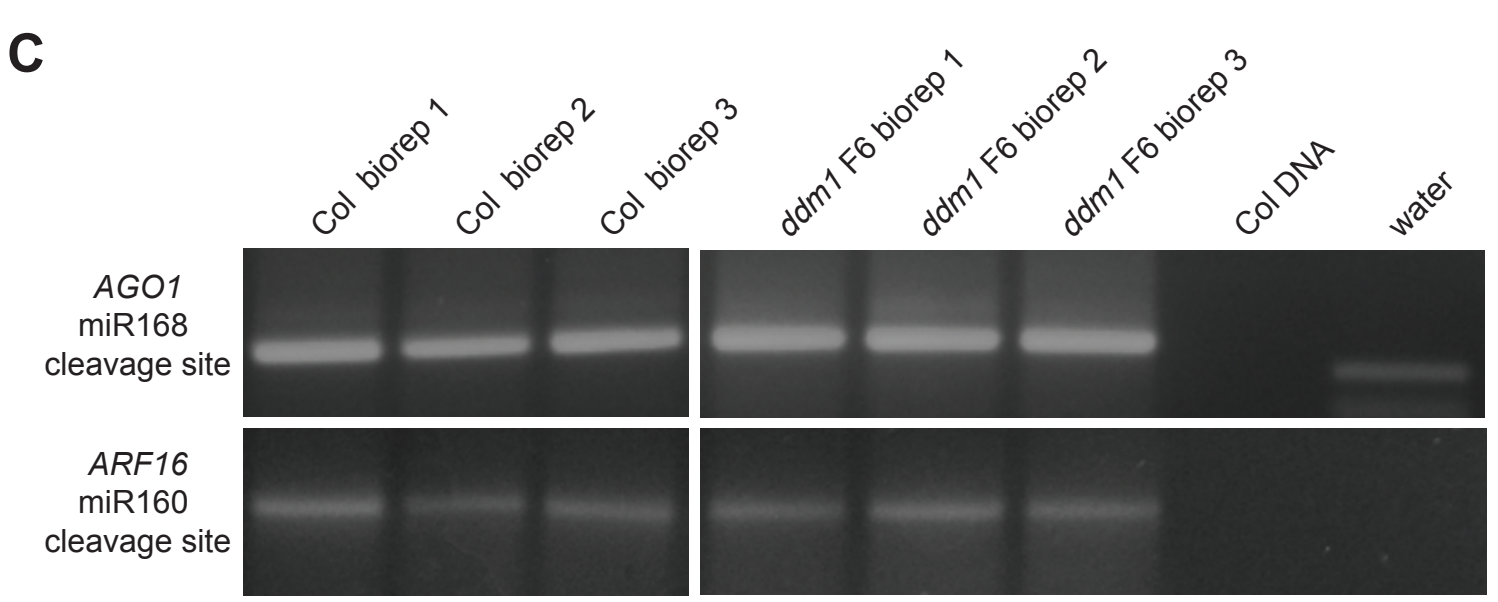
Supplemental Figure 1. Small RNAs do not incorporate in AGO1 protein complexes after cell lysis

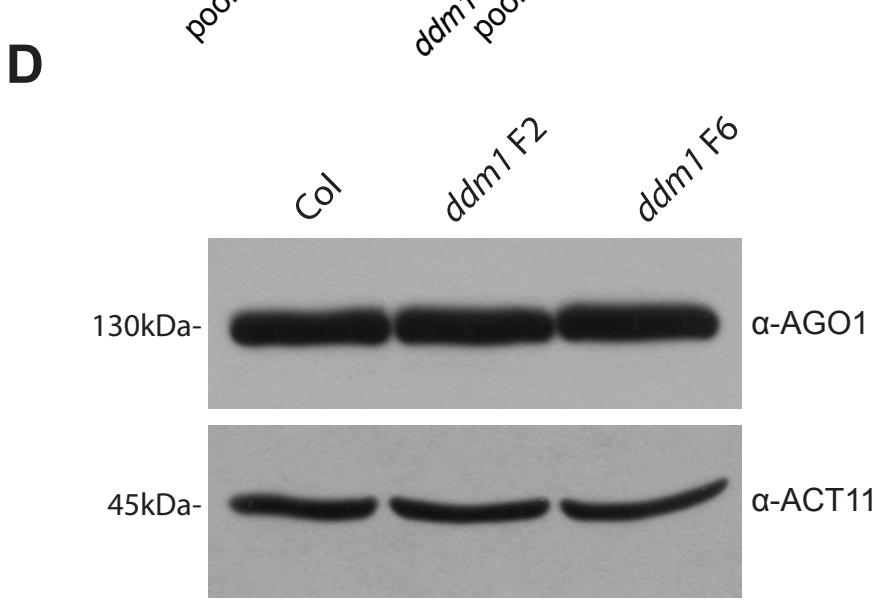
We performed AGO1-IPs from wild-type Columbia (wt Col) seedling and inflorescence (infl) tissues, and confirmed that the 20 nt microRNA156 is a seedling-enriched microRNA that accumulates at very low levels in infl tissue (Meng et al. 2012). MicroRNA166 accumulates to high levels in both wt Col seedling and infl, and is shown as an IP control. We isolated small RNAs from seedlings and spiked 4µg of purified seedling small RNA into infl crude protein extracts just after the cells were lysed. After each AGO1-IP, 1.2µg of small RNA was loaded per lane on the Northern blot. The purified seedling microRNA156 is not enriched in the spiked sample beyond the level it accumulates in the infl AGO1-IP control sample, indicated that AGO1 does not bind small RNAs after cell lysis.

Supplemental Figure 2









Supplemental Figure 2. AGO1 protein and mRNA levels are unchanged in *ddm1* F6.

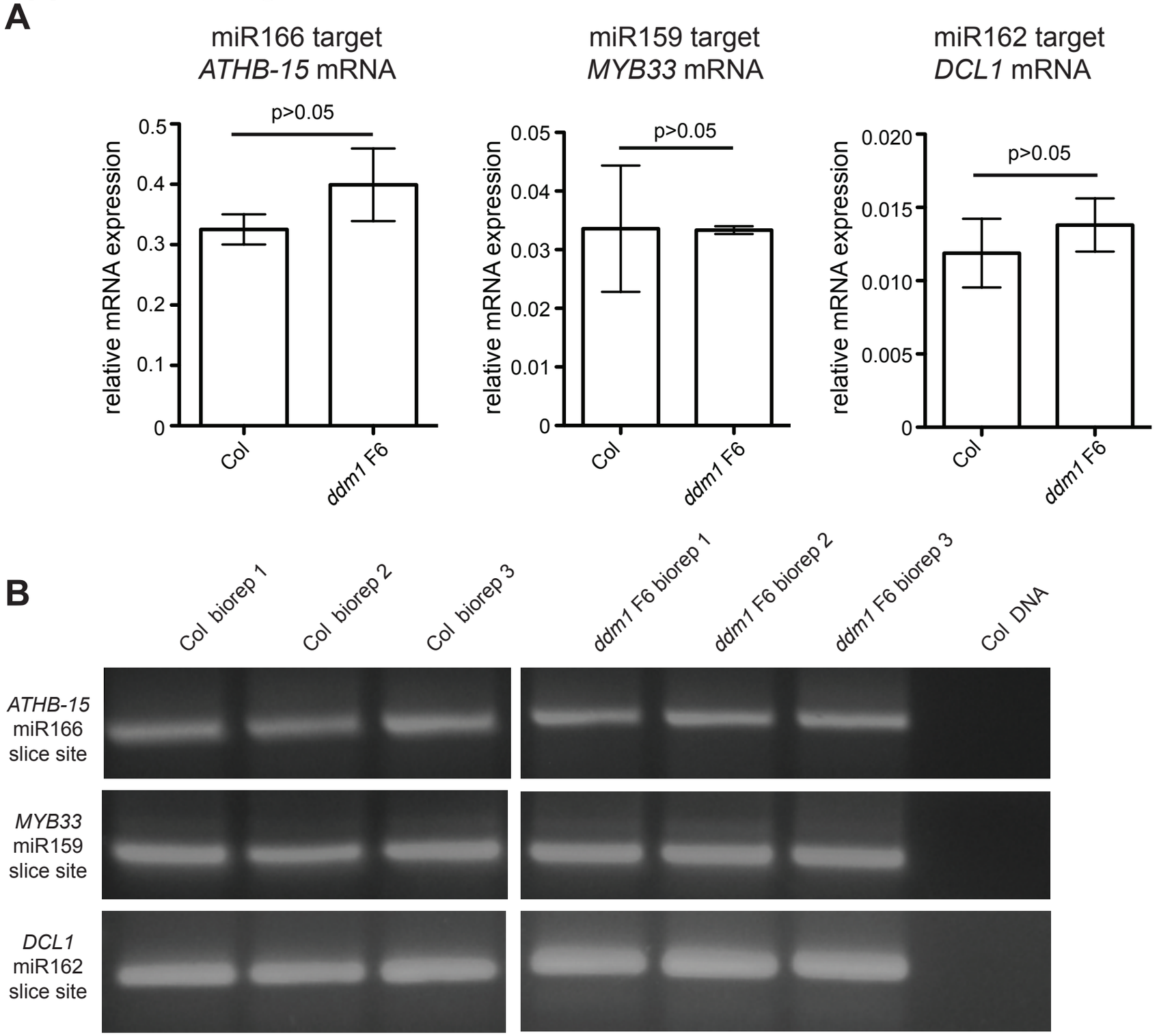
A. qRT-PCR analysis of expression of AGO1 mRNA. AGO1 mRNA levels are unchanged in *ddm1* F6 inflorescences compared to wt Col.

B. MicroRNA168 (which targets AGO1 mRNA) accumulation in *ddm1* F6 AGO1-IP does not change compared to wt Col AGO1-IP.

C. Modified 5' RACE RT-PCR was used to assess changes in the levels of cleaved mRNA at discrete microRNA168 slice sites. Accumulation of AGO1 mRNA sliced at the miR168 target site does not change in *ddm1* F6 samples. ARF16 mRNA sliced at the miR160 target site is used as a control, as miR160 accumulation does not change in *ddm1* F6 AGO1-IP.

D. Western blot analysis of AGO1 protein accumulation. AGO1 protein accumulation does not change in *ddm1* F6 inflorescences. ACT11 is used as a protein loading control.

Supplemental Figure 3

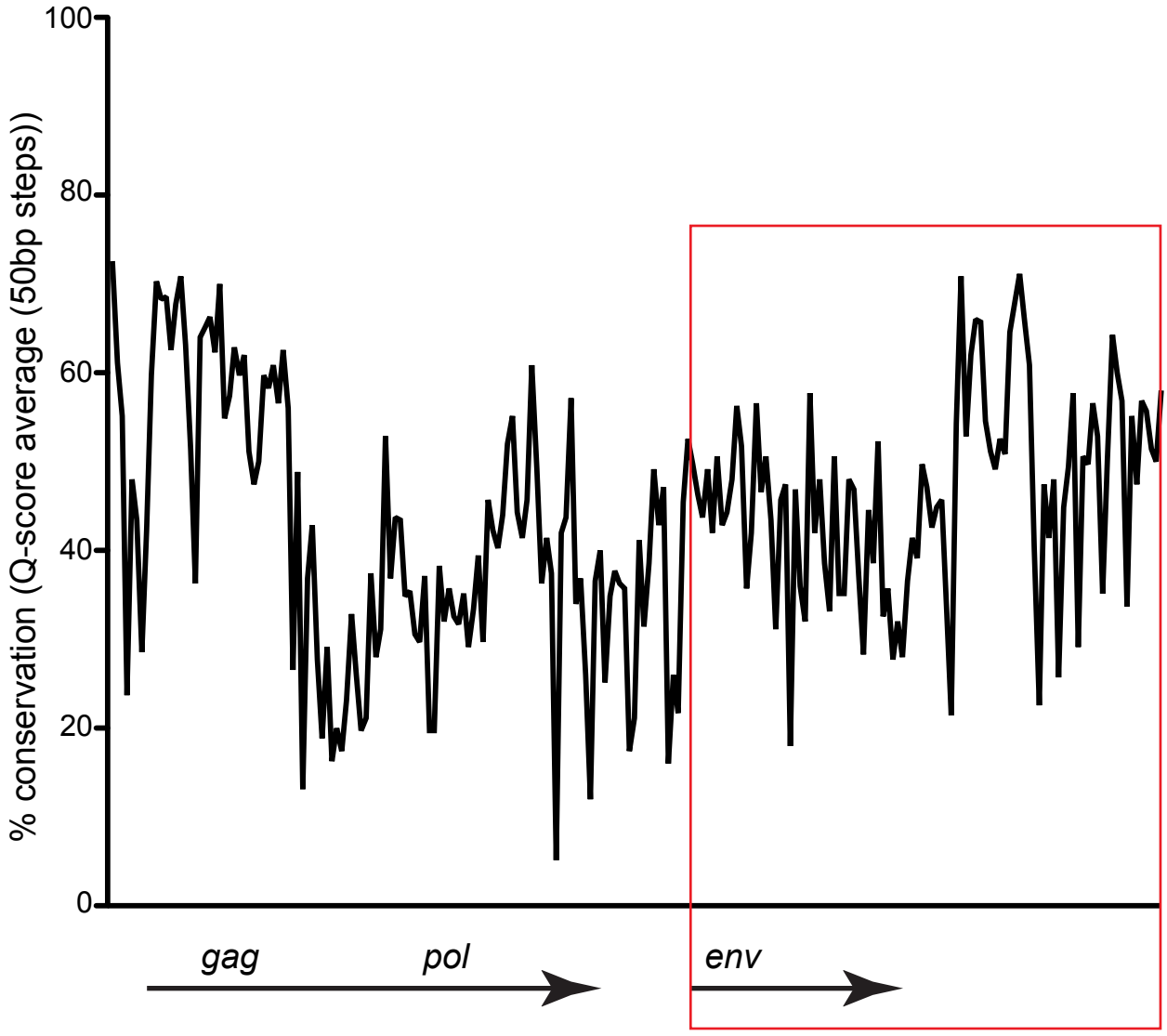


Supplemental Figure 3. Changes in microRNA accumulation in *ddm1* F6 mutants do not affect target mRNA accumulation.

A. qRT-PCR analysis of expression of microRNA targets, ATHB-16, MYB33, and DCL1, indicates that changes in microRNA accumulation do not affect changes in accumulation of their target mRNA. PCR primers were used in this assay that span the microRNA cleavage site, thus detecting only un-sliced mRNAs.

B. Modified 5' RACE was used to assess changes in the levels of cleaved mRNA at discrete slice sites. Accumulation of sliced ATHB-16, MYB33, and DCL1 mRNA (at their microRNA166, microRNA159, and microRNA162 target sites, respectively) does not change in *ddm1* F6 mutants.

Supplemental Figure 4



Supplemental Figure 4. DNA identity and conservation between *Athila* subfamily elements

Individual *Athila* consensus elements for the 9 *Athila* subfamiles were downloaded from the RepBase repeat masking of the Arabidopsis genome (http://www.girinst.org/repbase/update/browse.php). These *Athila* subfamily consensus elements were used in DNA identity alignments generated by ClustalW2. The x-axis represents the consensus *Athila6A* element, with two protein coding regions: *gag/pol* and *env*. The red box represents the region of 21-22 nt siRNA production from Figure 2D. Portions of the non-protein coding region 3' of *env* have just as much DNA sequence conservaton as the *gag* protein coding domain.

Supplemental Table 1

21-22 nt TE siRNAs that accumulate to over 100 RPM in all combined wt Col AGO1-IPs

siRNA Sequence	siRNA size (nt)	TE family	siRNA RPM in Col AGO1-IP	siRNA RPM in *ddm1* F6 AGO1-IP
UAUGGAAGAAAUUGUAGUAUU	21	VANDAL4	314	539
UUGAGAAGAGAUAGAAUAGAA	21	ATHILA4	242	282
UUUGGACUGAAGGGAGCUCCU	21	ATGP3	228	110
UUUGGGAGUAGCCAUAUAGCCU	22	RathE2_cons	166	13
UGAGCUGUGAUGAAAUUGGCU	21	HELITRONY1B	147	38

21-22 nt TE siRNAs that accumulate to over 100 RPM in the combined *ddm1* F6 AGO1-IPs

siRNA Sequence	siRNA size (nt)	TE family	siRNA RPM in Col AGO1-IP	siRNA RPM in *ddm1* F6 AGO1-IP	fold increase in *ddm1* F6
UGGCGCUCAACUCUGCAAGGU	21	ATHILA6A	4	10625	2491
UCCCCAGAAGUCGUUCAGCUC	21	ATHILA6A	11	6552	588
UUCGAGGAGAUAUGACGCGCC	21	ATHILA2	19	4887	254
UUGGCGCUCAACUCUGCAAGG	21	ATHILA6A	2	4868	2731
UUGAUCCAAGUAGCUGACUCU	21	ATHILA6A	1	4031	5276
UUGAGAGAUCCCCUGUUACUG	21	ATHILA2	5	3917	799
UUUGGCGCUCAACUCUGCAAG	21	ATHILA6A	2	3787	1608
UUACGAGACUCUAGCCCAGCU	21	ATHILA6A	3	3733	1086
UACCCGUACGUCGCUUACAAG	21	ATHILA6A	5	3223	693
CGAGAGAUUACAGGGACUGUC	21	ATHILA2	3	3198	930
UUAAUCCAAGUAGCUGACUCU	21	ATHILA2	1	2805	3388
AUUGACGUCGAGUAUGAGCCU	21	ATHILA6A	7	2734	373
UUUGGCGCUCAACUCUGCAAGG	22	ATHILA6A	5	2546	482
UUACCCGUACGUCGCUUACAAG	22	ATHILA6A	25	2330	93
UCUAAAUCCAUCAUCCUCGGA	21	ATHILA6A	1	2013	1506
UAGCUAACAAGAACUCUUUCU	21	ATHILA6A	1	1828	2871
UUCCCCUAGAAUUCUUUCCCU	21	ATHILA6A	1	1646	2154
UCCACCGACUGAUGACAAUGU	21	ATHILA6A	2	1524	772
UGACGGACAAGAUAAGUUGCU	21	ATHILA6A	1	1505	1576
UGAAGGACAAGCUCAGCUGCU	21	ATHILA2	3	1483	518
UCUCAUGUAGUUCUAGUUCGCA	22	ATHILA2	1	1437	1881
UUCAGGGUGAGAACAUUGACU	21	ATHILA6A	1	1291	1690
UUAGACACGGUGCCUGUAGAUU	22	ATHILA6A	16	1275	79
UUUGGCACUCAACUCUGCAAG	21	ATHILA6A	3	1274	408
UUCGAGAACUCCCUGACCCGA	21	ATHILA6A	1	1272	1537
UCGAAUGAUGAAUGCCUUGCA	21	ATHILA6A	4	1259	287
UCUGUAUGCAUAACUUGGGAC	21	ATHILA6A	5	1212	221
UGGCGCUCAACUCUGCGAGGU	21	ATHILA6A	1	1187	1434
UUUAGGAUUGUUGCAUAUGCA	21	ATHILA2	1	1164	2032
ACAAAACUGUUGAACAAGCCU	21	ATHILA6A	2	1107	561
AUCCAAGUAGCUGACUCUCCU	21	ATHILA2	1	1104	1020
CUUGGCAUCGAAUUUGAACUC	21	ATHILA6B	0	1059	2771
UUUAACAACUAAGGUUCCUGU	21	ATHILA2	0	1055	5524
UUCUGAAGGACAAGCUCAGCU	21	ATHILA2	1	1012	1987
AAACAGGACAAGUUACUCGCC	21	ATHILA2	5	986	209
CUCAGGCUCAUACUCGACGUC	21	ATHILA6A	2	968	475
UUGGCGCUCAACUCUGCAAGGU	22	ATHILA6A	6	955	163
UACUGGAGGACGUACAGCACU	21	ATHILA6A	1	949	994
UAUGGAGAUGAUCGCAAUGGC	21	ATHILA6A	3	937	300
UUGAAAGACUUGUGGAUCACC	21	ATHILA2	4	926	217
UAGGCCUGAGAUUGGACGCCU	21	ATHILA2	1	875	723
UGGCACUCAACUCUGCAAGGU	21	ATHILA6A	1	834	819
UACUUCCAGCGUUCUGUAGCC	21	ATHILA2	2	826	360
UGACACCGAUUCUGAUAGCUU	21	ATHILA2	1	823	862
UUUGAUCCGAGGAUGAUGGAU	21	ATHILA6A	0	816	4275
UCGAAUGACGAAUGCCUAGCC	21	ATHILA2	3	814	312
UGAGAGAUCCCCUGUUACUGA	21	ATHILA2	1	786	1122
AUUUGAACUCAUGGAUACCCU	21	ATHILA2	0	768	3015
UUGAGAAGAUACAUUGACGGU	21	ATHILA	0	731	3825
UAACUCUACCCUUUGCACUCG	21	ATHILA6A	0	727	2855
UCUGUAUGCAUAACUUGGGACU	22	ATHILA6A	7	686	103
UCCCAGGCCAUAGACGAACCU	21	ATHILA2	1	684	672
UUGGACGCCUCUACUAUGAGA	21	ATHILA2	0	679	1523
UUUGGUUCUGAGUCCCCGCCU	21	ATHILA6A	1	669	1168
CGAAUGACGAAUGCCUAGCCU	21	ATHILA2	1	662	612
UUGGUACAGGUGCUGAACAUC	21	ATHILA2	1	652	731
UUUGAGAGAUCCCCUGUUACUG	22	ATHILA2	2	632	310
UAUCAGAAUCGGUGUCACAAC	21	ATHILA2	1	614	439
UUGGCACUCAACUCUGCAAGG	21	ATHILA6A	0	611	1918
UGUGGUGACUUGGCUCAGGCC	21	ATHILA6A	0	609	2391
UGUUGAUCCAAGUAGCUGACU	21	ATHILA6A	0	608	608
UCCAAGUAGCUGACUCUCCUU	21	ATHILA2	0	596	4683
UGAAUGACAAACUGGACAAGCU	22	ATHILA6B	2	583	241
UGUUACGAGACUCUAGCCCAG	21	ATHILA6A	1	574	1126
UUCCCCAGAAGUCGUUCAGCUC	22	ATHILA6A	9	558	60
UUAGACACGGUGCCUGUAGAU	21	ATHILA2	1	552	619
UUGUUGAUCCAAGUAGCUGACU	22	ATHILA6A	0	539	8473
UAUAGGGCUUGAAAGAAAGUC	21	ATHILA2	0	535	2801
UAUUGACGUCGAGUAUGAGCCU	22	ATHILA6A	27	517	19
UUGGGAGAACUAUGACACGAG	21	ATHILA	0	515	4045
CUUCGAGGAGAUAUGACGCGCC	22	ATHILA2	47	513	11
UAGACACGGUGCCUGUAGAUU	21	ATHILA6A	1	505	529
UCUGAACUCAAGGCACCCAAA	21	ATHILA6A	0	493	1549
UGAAGUCAAUGUUCUCACCCU	21	ATHILA6A	1	486	545
UUUCUGACGGACAAGAUAAGU	21	ATHILA6A	0	480	1257
UGAAGGAUUUGUGGUUAACCA	21	ATHILA6A	1	474	744
UAACUCUACCCUUUGCACUCA	21	ATHILA6B	0	473	1239
UCUGUAUGCAUAGCUUGGGACU	22	ATHILA2	1	466	915
CACCGCGGUCGCGUAAGCUAC	21	ATHILA6B	2	466	198
UUCACAUGUCCGGGCUAGGCA	21	ATHILA2	0	461	1208
UAGUGACCGAGUAGUACCACC	21	ATHILA6A	0	461	1035
UUUCCGUUGGUGUGCGCCCAC	21	ATHILA6A	0	458	1799
UUCCAGAACUAAUGAAUGUUA	21	ATHILA2	0	448	1172
UUACGAGACUCUAGCCCAACU	21	ATHILA6A	1	447	780
CCACCGACUGAUGACAAUGUC	21	ATHILA6A	0	446	2334

UUGGACGUCUCUACUAUGAGA	21 ATHILA2	0	437	6871
UCCCGAGGCUCGAAUGAUGAA	21 ATHILA6A	2	433	272
UCUAGUUCACAUUUUUCGGAC	21 ATHILA2	0	427	3350
AUAGCUAACAAGAACUCUUUCU	22 ATHILA2	0	426	3342
UCGAACAAGAGCUGAACGUCU	21 ATHILA	0	423	949
UCUAGUUCGCAUUUUUUGGAC	21 ATHILA2	0	421	2205
UGAAGUCAAUGUUCCUGCCCU	21 ATHILA2	1	418	468
UGACGUCGAGUAUGAGCCUGA	21 ATHILA6A	1	416	654
UGAAGGACAAGAUCAGCUGCU	21 ATHILA2	2	415	167
UGCAUAACUUGGGACUUACCU	21 ATHILA6B	2	413	180
UCAGAAUCGGUGUCACAACGC	21 ATHILA6A	1	411	807
UACCGGAGGACGUACAUAGCU	21 ATHILA6A	0	401	6304
CUUCCCCUAGAAUUCUUUCCC	21 ATHILA2	0	401	1049
UGGAUUCCGGCUGCAUACUCC	21 ATHILA5	9	392	42
UUUAGAGAUCCCCUGUUACUG	21 ATHILA2	1	387	760
UUAACUCUACCCUUUGCACUC	21 ATHILA6A	0	380	1992
UGCACUCGCUAGGUCUGGCAG	21 ATHILA6A	0	378	990
UGACACCGAUUCUGAUUGCAU	21 ATHILA6A	0	377	1479
UUUGGCCUGAGGUUGGACGCC	21 ATHILA2	1	367	641
UCUUCGACUGAGGUAAGCGCCU	22 ATHILA2	16	355	22
UUCUGAAGGACAAGAUCAGCU	21 ATHILA2	1	351	502
AUUCGAGAACUCCCUGACCCG	21 ATHILA6A	0	350	1830
UUGCAGAGUGGAGAGAAACUC	21 ATHILA6A	1	347	495
UAUGCUUCUGUUGAUCCACCU	21 ATHILA6A	1	344	601
CUUAAAUCACACAGUCCACUG	21 ATHILA2	0	342	1789
UUGGCAUCGAAUUUGAACUCA	21 ATHILA6B	0	339	5325
UUAGACACGGUGCCUGUAGAC	21 ATHILA2	2	335	150
UAUCCUGAGAGCGGUGCUGGC	21 ATHILA2	0	334	875
UUGGCGACCGAUCUCUGAAAG	21 ATHILA2	2	334	188
UCGAGGGCAGGAACAUUGACU	21 ATHILA2	1	334	375
UAUGCAUAACUUGGGACUUACC	22 ATHILA6A	20	333	17
UUAGCACCGAGGAUGAUGGACU	22 ATHILA2	5	330	66
UUAGACACGGUACCUGUAGAUU	22 ATHILA6A	3	329	115
UUUGGCACUCAACUCUGCAAGG	22 ATHILA6A	2	325	213
CAAACUGGACAAGCUACUGCU	21 ATHILA6B	0	324	848
UUCAUCUGCAGUAAGUCCCUG	21 ATHILA6A	0	314	1645
UUCUGACGGACAAGAUAAGCU	21 ATHILA6A	0	313	1229
CUACUCGGUCACUAGGCUCAG	21 ATHILA6A	0	311	814
UUAUCAACGAACUCUUGGCCC	21 ATHILA5	12	310	25
UACGAGACUCUAGCCCAGCUU	21 ATHILA6A	1	307	438
UUCUGUAGCACGAGGUAUCCU	21 ATHILA2	1	302	365
UAAAACUGAACCAUGCCUAGA	21 ATHILA2	0	302	1583
UACCGGAGGACGUACAACACC	21 ATHILA6A	1	302	431
UCUAGUUCGCGUUCUUCAGAC	21 ATHILA6A	0	300	4713
UAUGGCCUGGGAGCAAUCGCA	21 ATHILA2	0	299	1174
UAAUAAGGAGAGUCAGCUACU	21 ATHILA2	0	298	298
UAUCUCUGUCGUUACGAACCU	21 ATHILA6A	0	295	2318
UUAGCACCGAGGAUGAUGGAC	21 ATHILA2	6	291	48
CUUAUCAACGAACUCUUGGCC	21 ATHILA5	11	290	27
UAAGCAUUUUGAUUCACCGGA	21 ATHILA2	0	285	4479
UGUGGUGACUUGGCUCAGGCCU	22 ATHILA6A	2	283	131
CAAAUUCGAGAACUCCCUGAC	21 ATHILA6A	0	283	283
UUCCAGAAUUGGCGUCACAAC	21 ATHILA6A	0	283	1481
UCCGCUAGAUAUAUCAAACUG	21 ATHILA2	0	281	4421
UGUCCCAACUUAACUCUACCCU	22 ATHILA6A	0	279	1459
UCUGUACCGCUGAAUUCUUCC	21 ATHILA2	2	275	120
CGUCACUGCGAAUUCCUGGAG	21 ATHILA2	1	272	475
UCCUAUCCAGUCUGAAGAACGC	22 ATHILA6A	0	272	1068
UUGGCCUGAGGUUGGACGCCU	21 ATHILA2	1	272	534
UACGUCACUGCGAAUUCCUGGA	22 ATHILA2	4	271	75
UAAGUGCUGUACGUCCUCCAG	21 ATHILA6A	0	271	1417
UGUAGAUUCCCUGGGGUACAG	21 ATHILA6A	1	271	425
CCUGAGCCUAGUGACCGAGUA	21 ATHILA6A	1	270	531
UUACCCGUACGUCGCUUAUAAG	22 ATHILA6A	1	267	191
UCGAGUGAGUGUAGCCUUCCU	21 ATHILA2	2	266	174
UUCUUCAGACUGGAUAGGACU	21 ATHILA6A	0	265	4162
AUUCGAGAACUCCCUGACCCGA	22 ATHILA6A	0	265	594
UGAAAUAAAACUGAACCAUGCC	22 ATHILA2	0	263	825
UUGAGAGCCUUGUAGUAGUCU	21 ATHILA	1	262	458
UUGAGAGCACUCCACCGACUG	21 ATHILA6A	0	261	2050
CUCGGGAGAAAGAAGAAGGCU	21 ATHILA6A	1	259	453
UGACGGACAAGAUAAGCUGCU	21 ATHILA6A	0	259	580
UCUGAUUGCUCUUUGACCUGG	21 ATHILA2	0	258	1012
UCUGUCAGAAACUUGAUGGCCU	22 ATHILA6A	2	256	154
AAUUCGAGAACUCCCUGACCC	21 ATHILA6A	0	255	2003
UAUAGGGCUUGAAAGAAAGUU	21 ATHILA6B	0	252	252
UCGAGUAUGAGCCUGAGUCAUG	22 ATHILA6A	1	250	393
UCAUGUAGUUCUAGUUCGCCU	21 ATHILA6A	0	245	962
UCGAGUGACUUUGGAGCCAUU	21 ATHILA6B	2	244	147
UGAGACACAACAGGGAGAUUC	21 ATHILA6A	0	244	956
CUACCGGGACUCGAAUGACGA	21 ATHILA2	0	242	1904
UUAACUCUACCCUUUGCACUCA	22 ATHILA6A	0	240	538
UAUUGACGUCGAGUAUGAGCC	21 ATHILA6A	1	237	466
UAUCCAUUGCUCGCGGCUCGA	21 ATHILA2	0	236	3710
UCCCAACCCAUGAUCUAAGCG	21 ATHILA6A	0	236	3700
UAACAAGAACUCUUUCUUUUCU	22 ATHILA2	0	235	3689
CUAGAAUUCUUUCCCUUUCCU	21 ATHILA6A	0	235	1843
CUUCGACUGAGGUAAGCGCCU	21 ATHILA2	1	234	263
CGAAUAAGUGCUGUACGUCCU	21 ATHILA6A	1	234	459
UAGAGUGUUCAUGUAGUUGCA	21 ATHILA6A	0	232	1215
CUUACUGUUGUUUCUGUGAGCU	22 ATHILA6A	1	232	192
UCCUUCGUCGCGGCCAGCACC	21 ATHILA6B	2	231	140
UCCCGGGACUCGAAUGACGAA	21 ATHILA2	1	231	181
UUAGCCUGAGGUUGGACGCCU	21 ATHILA2	0	231	1207
CAUGCAAUCAGAAUCGGUGUC	21 ATHILA6A	0	230	1807
UGAGAGCACUCCACCGACUGA	21 ATHILA6A	0	230	3605
UUUGAACUCAUGGAUACCCUA	21 ATHILA2	0	227	227

UUUGGGUUUGGGUUAACUGCU	21 ATHILA2	0	225	1765
UACACUCACUUGAUCUAGGAG	21 ATHILA2	0	223	1753
AUCAUCCUCGGAUCAAACCCU	21 ATHILA6A	0	222	3491
UGUGGAUACAAGAGCUGGGCU	21 ATHILA2	1	215	423
UCCAUUGCUCGCGGCUCGAGUC	22 ATHILA2	3	214	70
UUUAGCCUGAGGUUGGACGCC	21 ATHILA2	0	213	213
UAUGGUGACUUGGCUCAGGCC	21 ATHILA6A	0	212	1666
UACACAAAGGGCUCCUCGCACC	22 ATHILA6A	0	211	474
UCAUCCUCUGUAGCUUCCGUC	21 ATHILA6A	0	210	3296
UCCUGAGUACUCUCUUCCAAG	21 ATHILA2	0	209	1643
UUGAGAGAUCCCCUGUUACUGA	22 ATHILA6A	2	208	86
CUCACAAGUGAUAUAGGGCUU	21 ATHILA2	0	208	1631
UCUCAUGUAGUUCUAGUUCGCG	22 ATHILA6A	0	207	3251
UUCUUUCCGUUGGUGUGCGCC	21 ATHILA6A	0	205	205
AUUUGGCGCUCAACUCUGCAA	21 ATHILA6A	0	204	3199
AAAUAAAACUGAACCAUGCCU	21 ATHILA2	0	203	637
AAAGUCAAGAACCCCAACCCU	21 ATHILA6A	1	201	315
AUUUCAGUGAGCACGUACCUC	21 ATHILA6A	1	200	314
UAGAGUUAAGUUGGGACAGGA	21 ATHILA6B	0	199	1562
CAACUAACAACGAGGGCACUG	21 ATHILA6B	0	198	1552
UGAAUCUUGGUCAACUGGACC	21 ATHILA6A	1	197	282
CAAAUCCUUCAACUCUUCCCU	21 ATHILA6A	0	197	3098
UCUGUAUGCAUAGCUUGGGAC	21 ATHILA2	0	197	197
CUGGGGUACAGAACAUUCGCU	21 ATHILA6A	0	197	515
UGGGACUCCACAAGCUAUCAG	21 ATHILA2	0	197	772
UUAGGCCUGAGAUUGGACGCC	21 ATHILA2	0	196	1028
AUGGAUUUAGAUCACUUGCGUC	22 ATHILA6A	2	196	128
UUCCCGUUGGUGUGCGCCCAC	21 ATHILA6A	0	196	1538
UAGAAUUAUCAUGUCUUGGCA	21 ATHILA6B	0	194	3049
UGCUCGUAUCAUACUCCUCCU	21 ATHILA6A	0	194	1016
CUAGAUCGAGUGAGUGUAGCCU	22 ATHILA2	10	193	19
CAUGUCGUAUUCCAGAAACUC	21 ATHILA6A	0	192	1008
UGCUCGUGUCAAACUCCGCCU	21 ATHILA6A	4	192	47
UACCCGUACGUCGCCUACAAG	21 ATHILA6A	1	192	215
CUUCCCCUAGAAUUCUUUCCCU	22 ATHILA6A	1	192	334
CUUGCCCUUGUAGAAUCUGCU	21 ATHILA6B	0	191	999
CAUUGACUUCAAGCCUGCGCU	21 ATHILA6A	2	190	99
UCUUGGCAUCGAAUUUGAACUC	22 ATHILA6A	0	189	991
UACAGAAUAGGCUUAAGUAAC	21 ATHILA6B	0	189	2970
UCACCAUUGGCAGCUCUGUACC	22 ATHILA2	3	187	74
CCGAUUCUGAUUGCAUGUGGU	21 ATHILA6A	0	186	186
UAGACACGGUACCUGUAGAUU	21 ATHILA6A	0	185	970
UACCCGUACGUCGCUUAUAAG	21 ATHILA6A	0	185	1451
UGUCCUGAGGACGCUCUCCCU	21 ATHILA6A	0	184	961
UACUCGACCACACUGUUAGGA	21 ATHILA6A	0	183	1438
UCGAGUACACAGAAUGGGCUG	21 ATHILA6B	0	179	940
UUUUGCUUAGACUUAGAAACU	21 HELITRONY1E	2	179	112
UGGCAUCGAAUUUGAACUCAU	21 ATHILA6A	0	178	2800
UGUGAGUGUUUGUGAGGUCUU	21 ATHILA2	0	178	178
UUGGCCUGAGGUUGGACACCU	21 ATHILA6A	0	178	399
UUAGACACGGUGCCUGUAGACU	22 ATHILA2	11	177	16
UACUGGAGGACGUACAACACU	21 ATHILA6A	1	176	307
UUCCCCAGAAGUCGUUCAGCU	21 ATHILA6A	1	175	306
CUCGAAUGAUGAAUGCCUUGC	21 ATHILA2	1	175	275
UUUGAUUCACCGGAUAAACUC	21 ATHILA2	0	175	1374
UCGACCACACUGUCAUGAUCU	21 ATHILA2	0	174	174
UAGGGAGAAGGAUGUUAGCUC	21 ATHILA2	0	172	450
UCUUGUCUUGAAACUUGCACC	21 ATHILA	0	171	894
UUGACGACCAACUCCGCUCCU	21 ATHILA6A	0	170	669
UCGAAUGACGAAUGCCUAGCCU	22 ATHILA2	5	170	33
UUCUUCCCGUUGGUGUGCGCC	21 ATHILA6A	1	170	267
CAAGAACCCGCACGACACUCG	21 ATHILA	0	169	885
UCAGAAUCGGUGUCACAAUGC	21 ATHILA2	0	169	663
UCGAAUGACGAAUGCCUGGCC	21 ATHILA2	1	169	189
UAGAUCGAGUGAGUGUAGCCU	21 ATHILA2	1	168	220
UUUGUUAAACUCAUGGUCACCC	22 ATHILA2	0	165	165
UGCCAUGAUCGAGAGCUGCCU	21 ATHILA6A	0	164	1286
UCUAGUCCGAAAAAUGCGAAC	21 ATHILA2	0	163	163
UUGGCGACCGAUCUCUGAAAGU	22 ATHILA2	3	163	48
UCUAGUUCGCGUUUUUCAGAC	21 ATHILA6A	0	163	2562
UGGCAGUAGGAGUACACGACU	21 ATHILA6A	1	163	319
UAGUAACGGAUCACAGGGCUU	21 ATHILA6A	0	162	847
UUUGAGCACUCUACAGACAGG	21 ATHILA2	0	162	1269
CUAGAUCGAGUGAGUGUAGCC	21 ATHILA2	1	160	280
UUCGAGCACUCCCUGACCCGA	21 ATHILA6A	0	160	160
UUCUUGUGAACUUGACCGGGA	21 ATHILA5	2	158	75
UGAGAACAUUGACUUCAGACCU	22 ATHILA6A	2	158	85
UGAGAACGCUCUGCCAUUGGA	21 ATHILA2	0	158	2476
UACAAAUUCGAGCACUCCCUG	21 ATHILA6A	0	156	491
UUCCAGCGUUCUGUAGCCAAC	21 ATHILA2	0	156	613
CUACAAAUUCGAGCACUCCCU	21 ATHILA6A	0	156	1222
UUUGAGAGCACUCCACCGACU	21 ATHILA6A	0	156	2444
UUGGACCGCGCCGAGUUUAGC	21 ATHILA2	0	155	812
UAGAUCAAGUGAGUGUAGCCU	21 ATHILA2	0	155	607
UCUUGGCAUCGAAUUUGAACU	21 ATHILA6A	0	154	1211
UUUGAGCACUCCUUGACCCGA	21 ATHILA6A	0	154	807
UGACGCCAAUUCUGAAAGUUU	21 ATHILA2	0	154	1210
UUCUUCGACUGAGGUAAGCGCC	22 ATHILA2	2	154	89
ACUGAGCGCUGAUAGUAACGG	21 ATHILA6A	0	153	804
UUAUGCUUCUGUUGAUCCACC	21 ATHILA6A	0	153	601
UACCGGAGGACGUACAGCAUC	21 ATHILA2	1	153	120
UAUGGAGAUGAUCGCAAUGGCC	22 ATHILA2	2	152	72
UCAACGAACUCUUGGCCCUAGA	21 ATHILA5	18	152	8
UUGUGGAAUCCGUAGUCUGUA	22 ATHILA6B	3	152	58
CUGAGGUCACACGGAUAAUCG	22 ATHILA2	0	152	2381
UAAGACUGAGAUACGCGUGCCU	21 VANDAL9	49	152	3
UCCACUGUGUGAAUAAACUUG	21 ATHILA2	0	151	593

UGUCCCUACGGAAUAGCUGUA	21 ATHILA2	0	150	1182
UGUCUUACCCGUACGUCGCUU	21 ATHILA6A	1	150	197
UUAUGAGACUCUAGCCCAGCU	21 ATHILA6A	0	149	1174
UCGGGAGUAGAGUACAUUGGCU	22 ATHILA2	6	149	23
UGUAUGCAUAACUUGGGACUU	21 ATHILA6A	1	149	123
UAAUGACCGAGUAGUACCACC	21 ATHILA6A	0	149	468
UCGGCCUGAGGUUGGACGCCU	21 ATHILA6A	0	147	385
UUCGGUCUGGCCAUACUCGGC	21 ATHILA5	0	147	384
UUCACUGAGAACGUCAAGAAGC	22 ATHILA2	2	146	66
UCACCUCGCAUCUUAGAACUG	21 ATHILA	0	146	762
UCAAGAACUCCAACCCUUCACU	22 ATHILA6A	0	144	453
UCAACACUCUGAUACAUCUAG	21 ATHILA6A	0	143	143
AGUGAAUGAGGCGUGAUCUGC	21 ATHILA2	0	142	1116
UUCGCAGUGACGUAGGUGCUC	21 ATHILA6A	0	142	557
CAAAUGACGAAUGCCUAGCCC	22 ATHILA2	0	142	142
UAUCGAGCACCUACGUCACUGU	21 ATHILA2	4	142	36
UCUAGUUCGCAUUUUUCGGAC	21 ATHILA2	0	142	142
UUGUGAGUGUUUGUGAGGUCU	21 ATHILA2	0	141	141
UUGAGAGAUCCCUUGUUACUG	21 ATHILA6A	0	141	2218
UGAGCGCUGAUAGUAACGGAU	21 ATHILA6A	0	141	1104
UUGAGAGCACUCCACCGACUGA	22 ATHILA6A	0	140	1101
UGACUCAGGCUCAUACUCGAC	21 ATHILA6A	0	139	1095
UUUGUUAAACUCAUGGUCACC	21 ATHILA2	0	138	138
UUGGCAACCGAUCUCUGAAAG	21 ATHILA2	1	138	109
UCACUUUGCUGAACAUGUACC	21 ATHILA2	0	138	2164
UUAGAAUUAUCAUGUCUUGGC	21 ATHILA6A	0	138	138
UCGAUAUCCAUUGCUCGCGGCU	22 ATHILA2	5	137	29
UCCAGUCUGAAGAACGCGAAC	21 ATHILA6A	0	136	136
UUCCCUGGGGUACAGAACAUUC	22 ATHILA6A	3	135	46
UUUGUAUGCAUAACUUGGGAC	21 ATHILA5	0	135	2119
UCGGGAUCCUGCUGAAUGGUC	21 ATHILA6A	0	135	1057
UAAGGAGAGUCAGCUACUUGGA	22 ATHILA2	0	134	2102
CAACGCUCUUGAUACAUCUAG	21 ATHILA6A	0	133	133
UUUGGCCUGAGGUUGGACACC	21 ATHILA6A	0	133	697
UUUUAAUUCAAGUAGCUGACU	21 ATHILA6A	0	133	133
CGGUGCCUGUAGAUUCCCUGG	21 ATHILA6A	0	133	347
CUUCUUCAAGAAGAUCGUCCU	21 ATHILA2	0	132	295
UCCGGCGGAGAAUCCCUGUAAG	22 ATHILA2	5	131	25
UUGACUUCAGACCUGCGCGUG	21 ATHILA6A	0	131	131
UUGGCAUCGAAUUUGAACUCAU	22 ATHILA6B	0	131	131
UUACCCGUACGUCGCUUACAA	21 ATHILA6A	0	130	683
UCGGCUCAAACCUAACACGUU	21 ATHILA	0	129	2031
UUACCCGUACGUCGCUUACAG	21 ATHILA6A	1	129	185
UAAACUACGAGACUGCAGAAG	21 ATHILA2	1	129	156
UGCCUGUAGAUUCCCUAGAGU	21 ATHILA6A	0	129	1011
AUUGAUUCUGCACUCAAGGGC	21 ATHILA6A	0	128	287
UAUCCGUGUGACCUCAGGGCU	21 ATHILA2	0	128	2006
AUGCCUGUAGAUUCCCUAGAG	21 ATHILA6A	0	127	1000
AUACCCAAACCUGAACUUUCU	21 ATHILA6A	0	127	1999
UGGAGAUGAUAGAUUAUGCGC	21 ATHILA2	3	126	40
UCGGUCACUAGGCUCAGGCCU	21 ATHILA6A	1	126	165
UUAGACACGGUACCUGUAGAU	21 ATHILA6A	0	126	987
UGCCUAGAUUGCUCUACUCGA	21 ATHILA6A	0	125	1967
CAUCAAGAACCGGUCAUGCCU	21 ATHILA	0	125	491
UUUGAGAGCACUCCACCGACUG	22 ATHILA6A	0	125	980
UACUCGUGUCAAACUCCGCCU	21 ATHILA2	0	123	277
UCACUGUGAAUUCCUGGAGUU	22 ATHILA2	0	123	123
UUAACUCUACCCUUUGCACUCG	21 ATHILA6A	0	123	1937
UAUGAGUUGAUCGACGAAGAU	21 ATHILA6A	0	123	967
AAACACUCUAGACUCGAUCCU	21 ATHILA6A	0	123	386
UCUGGGUAGAUGGGAUCUUAUC	22 ATHILA2	0	123	643
UAUCGAGCACCUACGUCACUG	21 ATHILA2	0	123	386
UGUCACCGUAGAUUUCUUCCU	21 ATENSPM5	0	123	1926
CCACCGACUGAUGACAACGUC	21 ATHILA6A	0	122	122
UACGCUAGGGAGAUAUCUGCC	22 ATHILA	0	122	122
UAGAAUCUGCUGUAACAUGUU	21 ATHILA6B	0	122	122
UUCUAGUUCGCGUUCUUCAGAC	21 ATHILA6A	0	122	1913
CUUCUCUGUCAUACUUGGGCC	21 ATHILA6A	0	121	121
UCGACCACACUGUUAGGAUCU	21 ATHILA6A	0	121	121
UUCAACUCUUCCCUCUCGAACU	22 ATHILA6A	0	119	268
CUUUGCACUCAUGAAUCUUUC	21 ATHILA6A	0	119	467
UGGCGCUCAACUCUGCAAGGUC	21 ATHILA6A	1	119	233
UUUGCUGAACAUGUACCUCCA	22 ATHILA2	0	119	467
UACGCGACCGCGGUGCUGGCC	21 ATHILA2	0	119	372
UUUUGAGAGCCUUGUAGUAGU	21 ATHILA	0	118	465
CAACACACACUUCCUGAGCCC	21 ATHILA6A	0	118	620
UUUAUUCACACAGUGGACUGUG	22 ATHILA2	0	118	310
UCAACGCUCUGAUACAUCUAG	21 ATHILA6A	0	118	1855
UUCCCGGGACUCGAAUGACGA	21 ATHILA2	0	117	369
UGAGGUCGAGUAGAGCAAUCUA	22 ATHILA2	0	117	1842
UGCAAUCAGAAUCGGUGUCAC	21 ATHILA6A	0	116	116
UAUUGAUUUUUGGCCUGAGGU	21 ATHILA2	0	116	116
AGCACCGCUCUGAUGAUACUC	21 ATHILA6A	1	116	107
UCUCAUGUAGUUCUAGUUCACA	22 ATHILA2	0	115	115
UUUAAAACCGAGGACUUUUGC	21 ATHILA2	0	115	903
CUUAACUCUACCCUUUGCACU	21 ATHILA6A	0	115	1802
UGGGCGCUUAUACUUUGGGUU	21 ATHILA2	0	115	115
UGUGACACCGAUUCUGAUAGC	21 ATHILA2	0	115	901
UCCAUGGAGGAUUCGCCACUG	21 ATHILA6A	1	114	138
UUUGCCUGUUGAACUCGAGUA	21 ATHILA6B	1	114	179
UGAGUAGAAUUCGAUCAUAUC	21 ATHILA2	0	114	114
UGUGACACCGAUUCUGAUUGC	21 ATHILA6A	0	114	895
UAGUAACGGAUCACAGGGCUUC	22 ATHILA6A	0	113	891
CUGGAGGACGUACAGCACUUA	21 ATHILA6A	0	113	1778
UCCCGGAAUGCUGAAGAAGUA	21 ATHILA	0	113	296
UACUCCAGAAACUCACAACGA	21 ATHILA6A	0	113	113
AUGACGAAUGUUUGACAGCCU	21 ATHILA6B	0	113	1771

UUUGAUCCGAGGAUGAUGGAUU	22 ATHILA6A	0	112	1767
UGUGGUGUACCUCUCACGUCU	21 ATHILA6A	0	112	1763
UGCCUGUAGACUCCCUGGAGU	21 ATHILA2	3	112	34
UUCCGCAGGGAGAGCGUCCUC	21 ATHILA6A	0	112	876
UGAGCCGACAAGAGUAGUAUC	21 ATHILA	0	111	872
AACAAAACUGUUGAACAAGCCU	22 ATHILA6A	8	111	13
UACGGUGCCUGUAGAUUCGCU	21 ATHILA6A	0	111	1741
UGUGGAUACAAGAGUUGGGCU	21 ATHILA2	0	111	1739
UGUGGUCGAGUAGAGCAAUCU	21 ATHILA6A	0	111	869
UUCUGAUUGCAUGUGGUGUACC	22 ATHILA6A	1	110	158
UUGACCUUGGUUGUAUGGAAC	21 ATHILA6A	0	110	289
CUCACAAGUGAUAUAGGGCUUG	22 ATHILA6A	0	110	1724
CCUCCUUGUUCUGUAUCAGCU	21 ATHILA2	0	110	573
UGGAGAUGAUAGAUUAUGCGCU	22 ATHILA2	3	109	32
UUCCAAGCUCUUGAUAGAUAG	21 ATHILA6A	0	109	1713
UCUGAUUGCAUGUGGUGUACC	21 ATHILA6A	0	109	109
UGACGGAAGCUACAGAGGAUG	21 ATHILA6A	0	108	108
UGCCUGUAGAUUCCCUGGGGU	21 ATHILA6A	0	108	340
AUUGUGUAUAAUUUUGAGCCU	21 ATHILA2	0	108	1694
UAGAUAACAAGAACUCUUUCU	21 ATHILA2	0	107	337
UGACGGUUCAGAUUCAGGAGC	21 ATHILA5	0	107	107
UUUUUCGGACUAGAUAGGACU	21 ATHILA2	0	107	1677
UCCUGAGGACGCUCUCCCUGC	21 ATHILA6A	0	106	106
UGUGUAUGCAUAACUUGGGAC	21 ATHILA6A	0	106	1671
UUGAGAUAUCCCCUGUUACUG	21 ATHILA2	0	106	1669
UCUAUAGCCAAUGUACUCUACU	22 ATHILA2	1	106	76
UCUGUAGAGUGCUCAAACCUG	21 ATHILA2	0	106	416
UCUUCGACUGAGGUAAGCGCC	21 ATHILA2	0	106	333
UCACUCGACCACAACAGGCUG	21 ATHILA6B	2	106	69
UUGAAGGAUUUGUGGUUAACCA	22 ATHILA6A	1	106	87
UGUGGUGUACCUCUUACGUCU	21 ATHILA6A	0	106	1658
UAGAGUGCUCAAACCUGAACCU	22 ATHILA2	6	105	19
UUUUGAUUCACCGGAUAAACUC	22 ATHILA6A	1	104	182
UUAGACCUUGCAGAGUUGAGCGCC	22 ATHILA6A	10	104	10
UUGGUCACACAGUGGACUGUG	21 ATHILA6A	0	104	545
UCAUCUGCAGUAAGUCCCUGA	21 ATHILA6A	0	104	104
UCCCUGGGGUACAGAACAUUC	21 ATHILA6A	0	104	544
UCAGUAGAAUUCGAUCAUAUC	21 ATHILA2	0	104	1626
CGGAGGAAACUUAGCAGCGCC	21 ATHILA	0	103	271
CUUGUGAGUGUUUGUGAGGUC	21 ATHILA6A	0	103	103
UCAUCAAUGAACUCAUUUGGCU	22 ATHILA6A	0	103	270
UGAGAAGAGAUAGAAUAGAAUC	22 ATHILA4	85	103	1
UAGGCAGCUCUCGAUCAUGGC	21 ATHILA6A	0	103	1615
UUCUUCGGACUGGAUAGGACU	21 ATHILA6A	0	102	804
CUCAUGUAGUUCUAGUUCGCA	21 ATHILA2	0	102	102
UCAAGCGAUUGGAAGGAUUGUU	22 ATHILA2	0	102	532
UACAGGAAGUGGGCGCACACC	21 ATHILA6A	0	102	1595
UUGAACAAGCCUGAUGAAGUU	21 ATHILA6A	0	102	399
UCAUAUGGACUUUGGCUACACC	22 ATREP18	48	101	2
UGAGAUUGCUAGAGGAAAGAG	21 ATHILA6A	0	101	796
UUCGGACUGGAUAGGACUAGG	21 ATHILA6A	0	101	101
UUGCAGAGAUGGAUGUACAAC	21 ATENSPM2	4	101	27
UACGGGUAAGACAUCAGCGUCU	22 ATHILA6A	1	101	113
UAUCCUGAGAGCGGUGCUGGCC	22 ATHILA2	0	101	316
UCCCCAGAAGUCGUUCAGAUC	21 ATHILA6A	0	101	791
UUGAGGGCCAUUGCGAUCAUC	21 ATHILA2	0	101	1580
CUUUCCGUUGGUGUGCGCCCA	21 ATHILA6A	0	100	100
GCAAGUGAUGAUAAAAAGACA	21 ATENSPM10	17	100	6
UCGAGCACCUACGUCACUGCG	21 ATHILA2	0	100	1574
UAACCGGGGCAUGAGAGACUC	21 ATHILA2	0	100	1572
UACCGCUGUUCAUUCACUGAG	21 ATHILA2	1	100	75
Total		809	184767	
Average		2	423	981

Supplemental Table 2

Genes predicted to be targeted by 21-22nt TE siRNAs that accumulate to over 100 RPM in Col AGO1-IP

Gene ID	siRNA sequence	siRNA RPM in wt Col AGO1-IP	E value	Type of Inhibition	Description of target
AT1G01500	UUGAGAAGAGAUAGAAUAGAA	242	2.5	Cleavage	| Symbols: | Erythronate-4-phosphate dehydrogenase family protein | chr1:185133-186923 FORWARD LENGTH=1461
AT1G03550	UUUGGGAGUAGCCAUAUAGCCU	166	3.5	Translation	| Symbols: | Secretory carrier membrane protein (SCAMP) family protein | chr1:885623-887956 REVERSE LENGTH=1258
AT1G04110	UGAGCUGUGAUGAAAUUGGCU	147	4	Cleavage	| Symbols: SDD1 | Subtilase family protein | chr1:1061457-1063784 REVERSE LENGTH=2328
AT1G06770	UAUGGAAGAAAUUGUAGUAUU	314	3	Cleavage	| Symbols: DRIP1 | DREB2A-interacting protein 1 | chr1:2078911-2081939 REVERSE LENGTH=2204
AT1G06840	UAUGGAAGAAAUUGUAGUAUU	314	4.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:2097747-2103479 REVERSE LENGTH=3240
AT1G14820	UGAGCUGUGAUGAAAUUGGCU	147	4	Cleavage	| Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:5105018-5106861 REVERSE LENGTH=1346
AT1G30210	UUUGGACUGAAGGGAGCUCCU	228	3.5	Cleavage	| Symbols: TCP24 | TEOSINTE BRANCHED 1, cycloidea, and PCF family 24 | chr1:10627185-10630610 REVERSE LENGTH=1553
AT1G32380	UUGAGAAGAGAUAGAAUAGAA	242	3	Translation	| Symbols: PRS2 | phosphoribosyl pyrophosphate (PRPP) synthase 2 | chr1:11681752-11684478 FORWARD LENGTH=1733
AT1G36060	UAUGGAAGAAAUUGUAGUAUU	314	4	Cleavage	| Symbols: | Integrase-type DNA-binding superfamily protein | chr1:13454496-13456331 REVERSE LENGTH=1836
AT1G53230	UUUGGACUGAAGGGAGCUCCU	228	4.5	Cleavage	| Symbols: TCP3 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 3 | chr1:19849788-19851725 REVERSE LENGTH=1844
AT1G53770	UAUGGAAGAAAUUGUAGUAUU	314	4	Cleavage	| Symbols: | O-fucosyltransferase family protein | chr1:20071311-20073758 REVERSE LENGTH=2005
AT1G54710	UAUGGAAGAAAUUGUAGUAUU	314	2	Cleavage	| Symbols: ATATG18H, ATG18H | homolog of yeast autophagy 18 (ATG18) H | chr1:20416770-20421035 REVERSE LENGTH=3335
AT1G67855	UUUGGGAGUAGCCAUAUAGCCU	166	4	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:25442256-2544287
AT2G23760	UAUGGAAGAAAUUGUAGUAUU	314	3	Translation	| Symbols: BLH4, SAW2 | BEL1-like homeodomain 4 | chr2:10107709-10113213 REVERSE LENGTH=2386
AT2G26610	UGAGCUGUGAUGAAAUUGGCU	147	4	Cleavage	| Symbols: | Transducin family protein / WD-40 repeat family protein | chr2:11318771-11324174 FORWARD LENGTH=3750
AT2G26950	UUUGGACUGAAGGGAGCUCCU	228	2	Cleavage	| Symbols: AtMYB104, MYB104 | myb domain protein 104 | chr2:11500721-11502136 REVERSE LENGTH=1212
AT2G28620	UAUGGAAGAAAUUGUAGUAUU	314	3.5	Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12265167-12270020 REVERSE LENGTH=3129
AT2G29570	UUUGGACUGAAGGGAGCUCCU	228	3	Cleavage	| Symbols: PCNA2, ATPCNA2 | proliferating cell nuclear antigen 2 | chr2:12649906-12651703 REVERSE LENGTH=1133
AT2G31070	UUUGGACUGAAGGGAGCUCCU	228	3.5	Cleavage	| Symbols: TCP10 | TCP domain protein 10 | chr2:13220478-13222609 REVERSE LENGTH=2017
AT2G33350	UAUGGAAGAAAUUGUAGUAUU	314	3	Cleavage	| Symbols: | CCT motif family protein | chr2:14133929-14137154 FORWARD LENGTH=1738
AT2G34430	UGAGCUGUGAUGAAAUUGGCU	147	3	Cleavage	| Symbols: LHB1B1, LHCB1.4 | light-harvesting chlorophyll-protein complex II subunit B1 | chr2:14524756-14525763 FORWARD LENGTH=1008
AT2G35210	UUGAGAAGAGAUAGAAUAGAA	242	3.5	Cleavage	| Symbols: RPA, AGD10, MEE28 | root and pollen arfgap | chr2:14836062-14838149 FORWARD LENGTH=1535
AT3G02230	UUGAGAAGAGAUAGAAUAGAA	242	2.5	Cleavage	| Symbols: RGP1, ATRGP1 | reversibly glycosylated polypeptide 1 | chr3:415393-417547 FORWARD LENGTH=1387
AT3G04610	UGAGCUGUGAUGAAAUUGGCU	147	4	Cleavage	| Symbols: FLK | RNA-binding KH domain-containing protein | chr3:1250553-1254873 REVERSE LENGTH=2058
AT3G06510	UUGAGAAGAGAUAGAAUAGAA	242	2.5	Cleavage	| Symbols: SFR2, ATSFR2 | Glycosyl hydrolase superfamily protein | chr3:2016330-2019778 FORWARD LENGTH=2234
AT3G06530	UGAGCUGUGAUGAAAUUGGCU	147	3.5	Cleavage	| Symbols: | ARM repeat superfamily protein | chr3:2022596-2033791 FORWARD LENGTH=6748
AT3G09790	UUGAGAAGAGAUAGAAUAGAA	242	2.5	Cleavage	| Symbols: UBQ8 | ubiquitin 8 | chr3:3003862-3006192 REVERSE LENGTH=2331
AT3G14870	UAUGGAAGAAAUUGUAGUAUU	314	3.5	Cleavage	| Symbols: | Plant protein of unknown function (DUF641) | chr3:5002367-5005739 FORWARD LENGTH=1854
AT3G15030	UUUGGACUGAAGGGAGCUCCU	228	3.5	Cleavage	| Symbols: TCP4 | TCP family transcription factor 4 | chr3:5061681-5064115 FORWARD LENGTH=2033
AT3G17185	UUGAGAAGAGAUAGAAUAGAA	242	0	Cleavage	| Symbols: TASIR-ARF, TAS3, ATTAS3 | TAS3/TASIR-ARF (TRANS-ACTING SIRNA3); other RNA | chr3:5861491-5862437 FORWARD LENGTH=947
AT3G24130	UGAGCUGUGAUGAAAUUGGCU	147	3.5	Translation	| Symbols: | Pectin lyase-like superfamily protein | chr3:8711663-8713424 REVERSE LENGTH=1071
AT3G42630	UAUGGAAGAAAUUGUAGUAUU	314	3.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:14722250-14723857 FORWARD LENGTH=1534
AT3G47400	UGAGCUGUGAUGAAAUUGGCU	147	3	Translation	| Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:17465590-17468118 FORWARD LENGTH=2054
AT3G47580	UUUGGGAGUAGCCAUAUAGCCU	166	4	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17532648-17536059 FORWARD LENGTH=3324
AT3G48770	UGAGCUGUGAUGAAAUUGGCU	147	5	Cleavage	| Symbols: | DNA binding;ATP binding | chr3:18078474-18086817 REVERSE LENGTH=6125
AT3G56620	UUGAGAAGAGAUAGAAUAGAA	242	3	Translation	| Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:20972503-20974611 REVERSE LENGTH=1443
AT3G60460	UUUGGACUGAAGGGAGCUCCU	228	3	Cleavage	| Symbols: DUO1 | myb-like HTH transcriptional regulator family protein | chr3:22342429-22343491 REVERSE LENGTH=894
AT3G61740	UUUGGACUGAAGGGAGCUCCU	228	3	Translation	| Symbols: SDG14, ATX3 | SET domain protein 14 | chr3:22850837-22856972 REVERSE LENGTH=3669
AT3G63390	UUUGGGAGUAGCCAUAUAGCCU	166	5	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:23411166-2341196
AT3G66658	UUUGGACUGAAGGGAGCUCCU	228	3.5	Cleavage	| Symbols: ALDH22A1 | aldehyde dehydrogenase 22A1 | chr3:2095105-2099137 REVERSE LENGTH=2155
AT4G02050	UGAGCUGUGAUGAAAUUGGCU	147	3	Cleavage	| Symbols: STP7 | sugar transporter protein 7 | chr4:898307-900870 REVERSE LENGTH=1819
AT4G05420	UUGAGAAGAGAUAGAAUAGAA	242	2.5	Cleavage	| Symbols: DDB1A | damaged DNA binding protein 1A | chr4:2746121-2752943 FORWARD LENGTH=3714
AT4G15080	UUGAGAAGAGAUAGAAUAGAA	242	4.5	Cleavage	| Symbols: | DHHC-type zinc finger family protein | chr4:8608700-8612693 REVERSE LENGTH=2893
AT4G18390	UUUGGACUGAAGGGAGCUCCU	228	3.5	Cleavage	| Symbols: TCP2 | TEOSINTE BRANCHED 1, cycloidea and PCF transcription factor 2 | chr4:10162979-10165546 REVERSE LENGTH=1569
AT4G29658	UUUGGGAGUAGCCAUAUAGCCU	166	4	Cleavage	| Symbols: PRA1.C | prenylated RAB acceptor 1.C | chr4:14533447-14533830 REVERSE LENGTH=384
AT4G30000	UGAGCUGUGAUGAAAUUGGCU	147	3	Cleavage	| Symbols: | Dihydropterin pyrophosphokinase / Dihydropteroate synthase | chr4:14670156-14672463 REVERSE LENGTH=2013
AT4G32830	UUUGGGAGUAGCCAUAUAGCCU	166	5	Cleavage	| Symbols: AtAUR1, AUR1 | ataurora1 | chr4:15842453-15844536 FORWARD LENGTH=1171
AT4G36710	UGAGCUGUGAUGAAAUUGGCU	147	4	Cleavage	| Symbols: | GRAS family transcription factor | chr4:17305758-17307643 FORWARD LENGTH=1886
AT5G06100	UUUGGACUGAAGGGAGCUCCU	228	2.5	Cleavage	| Symbols: MYB33, ATMYB33 | myb domain protein 33 | chr5:1837914-1839997 FORWARD LENGTH=1579
AT5G07660	UGAGCUGUGAUGAAAUUGGCU	147	3.5	Cleavage	| Symbols: SMC6A | structural maintenance of chromosomes 6A | chr5:2422839-2429912 FORWARD LENGTH=3177
AT5G08110	UAUGGAAGAAAUUGUAGUAUU	314	3.5	Cleavage	| Symbols: | nucleic acid binding;ATP-dependent helicases;ATP binding;helicases;ATP-dependent helicases | chr5:2594722-2600114 REVERSE LENGTH=3558
AT5G18240	UUUGGGAGUAGCCAUAUAGCCU	166	4	Cleavage	| Symbols: MYR1 | myb-related protein 1 | chr5:6028285-6030801 REVERSE LENGTH=1665
AT5G26622	UGAGCUGUGAUGAAAUUGGCU	147	3.5	Cleavage	| Symbols: | Beta-galactosidase related protein | chr5:9355980-9357436 REVERSE LENGTH=1457
AT5G28740	UUUGGGAGUAGCCAUAUAGCCU	166	3	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:10780647-10783911 FORWARD LENGTH=2923
AT5G32460	UUUGGGAGUAGCCAUAUAGCCU	166	3.5	Cleavage	| Symbols: | Transcriptional factor B3 family protein | chr5:12081803-12084148 REVERSE LENGTH=1593
AT5G37160	UUUGGGAGUAGCCAUAUAGCCU	166	3.5	Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:14705426-14708376 FORWARD LENGTH=2616
AT5G37180	UGAGCUGUGAUGAAAUUGGCU	147	3.5	Cleavage	| Symbols: SUS5, ATSUS5 | sucrose synthase 5 | chr5:14718238-14722913 FORWARD LENGTH=2511
AT5G48060	UGAGCUGUGAUGAAAUUGGCU	147	4	Cleavage	| Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr5:19475296-19479002 FORWARD LENGTH=3235
AT5G54250	UGAGCUGUGAUGAAAUUGGCU	147	3	Cleavage	| Symbols: CNGC4 | cyclic nucleotide-gated cation channel 4 | chr5:22025475-22030099 REVERSE LENGTH=2296
AT5G54290	UUUGGGAGUAGCCAUAUAGCCU	166	3.5	Cleavage	| Symbols: CcdA | cytochrome c biogenesis protein family | chr5:22051034-22053974 FORWARD LENGTH=1182
AT5G56600	UUUGGGAGUAGCCAUAUAGCCU	166	4	Cleavage	| Symbols: PFN3, PRF3 | profilin 3 | chr5:22909685-22910821 REVERSE LENGTH=704
AT5G57490	UGAGCUGUGAUGAAAUUGGCU	147	4	Translation	| Symbols: VDAC4, ATVDAC4 | voltage dependent anion channel 4 | chr5:23283680-23285934 REVERSE LENGTH=1301
AT5G60610	UUUGGGAGUAGCCAUAUAGCCU	166	3	Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr5:24363591-24365528 FORWARD LENGTH=1441
AT5G61010	UUUGGGAGUAGCCAUAUAGCCU	166	3.5	Cleavage	| Symbols: ATEXO70E2, EXO70E2 | exocyst subunit exo70 family protein E2 | chr5:24553841-24556749 FORWARD LENGTH=2805
AT5G62130	UUGAGAAGAGAUAGAAUAGAA	242	4	Cleavage	| Symbols: | Per1-like family protein | chr5:24950264-24953232 REVERSE LENGTH=2039

Genes predicted to be targeted by 21-22 nt TE siRNAs that accumulate to over 100 RPM in *ddm1* F6 AGO1-IP

Gene ID	siRNA sequence	siRNA RPM in *ddm1* F6 AGO1-IP	E value	Inhibition	Description of target
AT1G01020	UGUGGAUACAAGAGCUGGGCU	215	3.5	Translation	| Symbols: ARV1 | Arv1-like protein | chr1:5928-8737 REVERSE LENGTH=1623
AT1G01030	UCACUUUGCUGAACAUGUACC	138	4	Translation	| Symbols: NGA3 | AP2/B3-like transcriptional factor family protein | chr1:11649-13714 REVERSE LENGTH=1905
AT1G01060	UGAAUGACAAACUGGACAAGCU	583	3	Translation	| Symbols: LHY, LHY1 | Homeodomain-like superfamily protein | chr1:33379-37757 REVERSE LENGTH=2517
AT1G01160	UGUCCCAACUUAACUCUACCCU	279	4	Translation	| Symbols: GIF2 | GRF1-interacting factor 2 | chr1:72339-74096 FORWARD LENGTH=1045
AT1G01225	UAUGCAUAACUUGGGACUUACC	333	5	Cleavage	| Symbols: | NC domain-containing protein-related | chr1:95987-97407 FORWARD LENGTH=1025
AT1G01320	UUCAUCUGCAGUAAGUCCCUG	314	2.5	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:121124-130570 REVERSE LENGTH=6015
AT1G01340	UUUUAAUUCAAGUAGCUGACU	133	4	Cleavage	| Symbols: CNGC10 | cyclic nucleotide gated channel 10 | chr1:132330-135831 REVERSE LENGTH=2397
AT1G01390	GCAAGUGAUGAUAAAAAGACA	100	3	Translation	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:148120-149806 REVERSE LENGTH=1687
AT1G01610	AUUUGGCGCUCAACUCUGCAA	204	4.5	Cleavage	| Symbols: ATGPAT4, GPAT4 | glycerol-3-phosphate acyltransferase 4 | chr1:221691-224340 REVERSE LENGTH=1856
AT1G01880	UUGGUCACACAGUGGACUGUG	104	4	Cleavage	| Symbols: | 5'-3' exonuclease family protein | chr1:306480-309109 REVERSE LENGTH=1993
AT1G01910	UGACGGUUCAGAUUCAGGAGC	107	3.5	Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:313229-315902 REVERSE LENGTH=1374
AT1G02010	UAGAGUUAAGUUGGGACAGGA	199	3	Cleavage	| Symbols: SEC1A | secretory 1A | chr1:347891-352480 FORWARD LENGTH=2460
AT1G02060	UUUUUCGGACUAGAUAGGACU	107	3.5	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:360918-363094 REVERSE LENGTH=2177
AT1G02090	UAGUGACCGAGUAGUACCACC	461	4	Cleavage	| Symbols: FUS5, CSN7, COP15, ATCSN7 | Proteasome component (PCI) domain protein | chr1:387281-389647 REVERSE LENGTH=1655
AT1G02700	UUUGUUAAACUCAUGGUCACCC	165	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G02140.1); Has 49 Bla
AT1G02720	UUGAUCCAAGUAGCUGACUCU	4031	4	Cleavage	| Symbols: GATL5 | galacturonosyltransferase 5 | chr1:591826-593289 FORWARD LENGTH=1464
AT1G02730	UUCGAGCACUCCCUGACCGA	160	5	Translation	| Symbols: ATCSLD5, CSLD5, SOS6 | cellulose synthase-like D5 | chr1:594573-598657 REVERSE LENGTH=3854

AT1G02850	UCGAGGGCAGGAACAUUGACU	334	3	Cleavage	| Symbols: BGLU11 | beta glucosidase 11 | chr1:630505-633259 FORWARD LENGTH=1651
AT1G02860	UCUAGUUCGCAUUUUUUGGAC	421	3	Cleavage	| Symbols: NLA | SPX (SYG1/Pho81/XPR1) domain-containing protein | chr1:635144-637262 FORWARD LENGTH=1511
AT1G02890	UUAGCACCGAGGAUGAUGGACU	330	3.5	Cleavage	| Symbols: | AAA-type ATPase family protein | chr1:645092-651907 REVERSE LENGTH=4047
AT1G02910	UUGGCGCUCAACUCUGCAAGG	4868	4.5	Cleavage	| Symbols: LPA1 | tetratricopeptide repeat (TPR)-containing protein | chr1:655577-658148 REVERSE LENGTH=1557
AT1G02950	CCUGAGCCUAGUGACCGAGUA	270	4	Translation	| Symbols: ATGSTF4, GST31, GSTF4 | glutathione S-transferase F4 | chr1:665168-666451 REVERSE LENGTH=903
AT1G03010	UUUGAGAGAUCCCCUGUUACUG	632	3.5	Cleavage	| Symbols: | Phototropic-responsive NPH3 family protein | chr1:693480-696382 FORWARD LENGTH=2099
AT1G03040	UUUGAGAGAUCCCCUGUUACUG	632	3.5	Cleavage	| Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:703906-706630 REVERSE LENGTH=1440
AT1G03060	UGAGGUCGAGUAGAGCAAUCUA	117	3.5	Cleavage	| Symbols: SPI | Beige/BEACH domain ;WD domain, G-beta repeat protein | chr1:712473-726891 REVERSE LENGTH=11304
AT1G03070	UAUCCUGAGAGCGGUGCUGGC	334	5	Cleavage	| Symbols: | Bax inhibitor-1 family protein | chr1:729935-731557 FORWARD LENGTH=1019
AT1G03100	CAAGAACCCGCACGACACUCG	169	4.5	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:743885-746479 REVERSE LENGTH=2595
AT1G03110	UACGCUAGGGAGAUAUCUGCC	122	4.5	Cleavage	| Symbols: TRM82, AtTRM82 | Transducin/WD40 repeat-like superfamily protein | chr1:749246-751963 FORWARD LENGTH=1564
AT1G03190	UACGAGACUCUAGCCCAGCUU	307	4.5	Cleavage	| Symbols: ATXPD, UVH6 | RAD3-like DNA-binding helicase protein | chr1:775527-780027 FORWARD LENGTH=2578
AT1G03250	UUUGAGAGAUCCCCUGUUACUG	632	4.5	Cleavage	| Symbols: | unknown protein; Has 89 Blast hits to 89 proteins in 31 species: Archae - 0; Bacteria - 0; Metazoa - 31; Fungi - 0; Plants - 48; Viruses - 0; Other Eukaryotes - 10 (source: NCBI BLink). | chr1:793353-795368 REVERSE LENGTH=1170
AT1G03350	UGAAGGAUUUGUGGUUAACCA	474	4.5	Cleavage	| Symbols: | BSD domain-containing protein | chr1:822638-824393 REVERSE LENGTH=1756
AT1G03365	UGUGGUGUACCUCUCACGUCU	112	4.5	Translation	| Symbols: | RING/U-box superfamily protein | chr1:826569-830383 FORWARD LENGTH=2836
AT1G03380	UAUGCAUAACUUGGGACUUACC	333	3	Cleavage	| Symbols: ATATG18G, ATG18G | homolog of yeast autophagy 18 (ATG18) G | chr1:835785-840940 FORWARD LENGTH=3732
AT1G03445	CUACUCGGUCACUAGGCUCAG	311	3.5	Cleavage	| Symbols: BSU1 | Serine/threonine protein phosphatase family protein | chr1:854410-859701 REVERSE LENGTH=2727
AT1G03457	UCUGUAUGCAUAACUUGGGAC	1212	3.5	Translation	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:860788-864075 REVERSE LENGTH=1694
AT1G03610	UUCUUCCCGUUGGUGUGCGCC	170	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF789) | chr1:900887-903003 FORWARD LENGTH=1675
AT1G03687	UUAUGCUUCUGUUGAUCCACC	153	3.5	Cleavage	| Symbols: | DTW domain-containing protein | chr1:918299-920507 FORWARD LENGTH=1356
AT1G03770	CUUAUCAACGAACUCUUGGCC	290	2.5	Translation	| Symbols: ATRING1B, RING1B | RING 1B | chr1:944595-947482 FORWARD LENGTH=1611
AT1G03850	UCCAAGUAGCUGACUCUCCUU	596	4	Translation	| Symbols: | Glutaredoxin family protein | chr1:977102-977761 REVERSE LENGTH=660
AT1G03900	UCUAGUCCGAAAAAUGCGAAC	163	4	Translation	| Symbols: ATNAP4, NAP4 | non-intrinsic ABC protein 4 | chr1:991139-993118 FORWARD LENGTH=1198
AT1G04070	UUGAGAGCACUCCACCGACUG	261	4.5	Translation	| Symbols: TOM22-I, ATTOM22-I | translocase of outer membrane 22-I | chr1:1050553-1051186 REVERSE LENGTH=634
AT1G04090	CUUGGCAUCGAAUUUGAACUC	1059	3.5	Translation	| Symbols: | Plant protein of unknown function (DUF946) | chr1:1057151-1059419 FORWARD LENGTH=1965
AT1G04120	UGAGGUCGAGUAGAGCAAUCUA	117	3.5	Cleavage	| Symbols: ATMRP5, MRP5, ATABCC5, ABCC5 | multidrug resistance-associated protein 5 | chr1:1064454-1070927 REVERSE LENGTH=5277
AT1G04150	UCCACCGACUGAUGACAAUGU	1524	3.5	Cleavage	| Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr1:1081208-1084246 REVERSE LENGTH=3039
AT1G04180	UCCGCUAGAUAUAUCAAACUG	281	3.5	Translation	| Symbols: YUC9 | YUCCA 9 | chr1:1104623-1105988 FORWARD LENGTH=1266
AT1G04350	UUGAAAGACUUGUGGAUCACC	926	4	Translation	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:1165165-1166768 FORWARD LENGTH=1444
AT1G04530	CUACUCGGUCACUAGGCUCAG	311	2	Cleavage	| Symbols: TPR4 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:1234176-1236034 REVERSE LENGTH=1352
AT1G04600	UCGGCUCAAACCUAACACGUU	129	4	Cleavage	| Symbols: XIA, ATXIA | myosin XI A | chr1:1262123-1272376 FORWARD LENGTH=5193
AT1G04710	UUAUGAGACUCUAGCCCAGCU	149	3.5	Cleavage	| Symbols: KAT1, PKT4 | peroxisomal 3-ketoacyl-CoA thiolase 4 | chr1:1321904-1324782 FORWARD LENGTH=1595
AT1G04890	UUCGAGCACUCCCUGACCGA	160	4	Translation	| Symbols: | Protein of unknown function, DUF593 | chr1:1380382-1382599 REVERSE LENGTH=2023
AT1G04920	UUAUCAACGAACUCUUGGCCC	310	2.5	Cleavage	| Symbols: ATSPS3F, SPS3F | sucrose phosphate synthase 3F | chr1:1391502-1395864 REVERSE LENGTH=3469
AT1G04950	UAUGGCCUGGGAGCAAUCGCA	299	5	Cleavage	| Symbols: TAFII59, TAF6, ATTAF6 | TATA BOX ASSOCIATED FACTOR II 59 | chr1:1403085-1407501 REVERSE LENGTH=2110
AT1G04985	UGAGAGAUCCCCUGUUACUGA	786	4.5	Translation	| Symbols: | unknown protein; Has 37 Blast hits to 37 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:1416343-1418482 REVERSE LENGTH=993
AT1G05020	UCUGAACUCAAGGCACCCAAA	493	4	Cleavage	| Symbols: | ENTH/ANTH/VHS superfamily protein | chr1:1435254-1437667 REVERSE LENGTH=2414
AT1G05040	UAAGCAUUUUGAUUCACCGGA	285	3.5	Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: Ubiquitin-associated (UBA) protein (TAIR:AT2G33010.1); Has 14 Blast hits to 12 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 14; Viruses - 0; Other Eukaryote
AT1G05055	UUCACAUGUCCGGGCUAGGCA	461	4.5	Cleavage	| Symbols: ATGTF2H2, GTF2H2 | general transcription factor II H2 | chr1:1448718-1450887 REVERSE LENGTH=1496
AT1G05061	UUGAACAAGCCUGAUGAAGUU	102	4	Cleavage	| Symbols: | Pseudogene of AT2G32630; pentatricopeptide (PPR) repeat-containing protein | chr1:1453216-1454260 REVERSE LENGTH=1045
AT1G05090	AUUCGAGAACUCCCUGACCCG	350	3.5	Cleavage	| Symbols: | dentin sialophosphoprotein-related | chr1:1463202-1465622 FORWARD LENGTH=2121
AT1G05120	UGAAGGACAAGCUCAGCUGCU	1483	4	Cleavage	| Symbols: | Helicase protein with RING/U-box domain | chr1:1471406-1476078 REVERSE LENGTH=2731
AT1G05200	UCUAGUUCGCGUUCUUCAGAC	300	3	Translation	| Symbols: ATGLR3.4, GLR3.4, GLUR3 | glutamate receptor 3.4 | chr1:1505317-1509152 FORWARD LENGTH=3257
AT1G05300	AUGACGAAUGUUUGACAGCCU	113	4.5	Cleavage	| Symbols: ZIP5 | zinc transporter 5 precursor | chr1:1545216-1547798 REVERSE LENGTH=1838
AT1G05360	UUGUGAGUGUUUGUGAGGUCU	141	3	Translation	| Symbols: | BEST Arabidopsis thaliana protein match is: SNARE associated Golgi protein family (TAIR:AT4G14950.1); Has 332 Blast hits to 326 proteins in 115 species: Archae - 0; Bacteria - 11; Metazoa - 174; Fungi - 0; Plants - 74; Viruses - 0; Othe
AT1G05400	CUUCGAGGAGAUAUGACGCGCC	513	3.5	Cleavage	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: sperm cell; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06810.1); Has 31 Blast hi
AT1G05570	UUACCCGUACGUCGCUUACAA	130	4.5	Cleavage	| Symbols: CALS1, GSL06, ATGSL6, ATGSL06, GSL6 | callose synthase 1 | chr1:1647706-1659437 REVERSE LENGTH=6231
AT1G05640	UUCCAGAACUAAUGAAUGUUA	448	4	Cleavage	| Symbols: | Ankyrin repeat family protein | chr1:1687436-1689501 REVERSE LENGTH=1884
AT1G05670	AUUUCAGUGAGCACGUACCUC	200	4.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:1697587-1701025 REVERSE LENGTH=3227
AT1G05690	UGUGGAUACAAGAGUUGGGCU	111	4	Cleavage	| Symbols: BT3 | BTB and TAZ domain protein 3 | chr1:1707011-1709347 FORWARD LENGTH=1660
AT1G05920	UCACCUCGCAUCUUAGAACUG	146	3	Translation	| Symbols: | Domain of unknown function (DUF313) | chr1:1796778-1798254 FORWARD LENGTH=1477
AT1G05960	UGACACCGAUUCUGAUAGCUU	823	3	Cleavage	| Symbols: | ARM repeat superfamily protein | chr1:1807973-1815474 REVERSE LENGTH=3631
AT1G06060	UUCUUUCCGUUGGUGUGCGCC	205	4	Cleavage	| Symbols: | LisH and RanBPM domains containing protein | chr1:1832943-1834861 FORWARD LENGTH=1115
AT1G06070	UUUGGUUCUGAGUCCCCGCCU	669	4	Cleavage	| Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr1:1834829-1837648 REVERSE LENGTH=1893
AT1G06225	UGCAUAACUUGGGACUUACCU	413	4	Cleavage	| Symbols: CLE3 | CLAVATA3/ESR-RELATED 3 | chr1:1905975-1906226 FORWARD LENGTH=252
AT1G06370	UGACGCCAAUUCUGAAAGUUU	154	3.5	Cleavage	| Symbols: | pseudogene, similar to putative glycolipid alpha-mannosyltransferase, blastp match of 41% identity and 9.6e-10 P-value to GP|13161358|dbj|BAB32949.1||AP002908 putative glycolipid alpha-mannosyltransferase {Oryza sativa (jap
AT1G06580	UUCACAUGUCCGGGCUAGGCA	461	3	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:2014003-2016054 REVERSE LENGTH=2052
AT1G06670	UCAUAUGGACUUUGGCUACACC	101	3	Cleavage	| Symbols: NIH | nuclear DEIH-boxhelicase | chr1:2040433-2047612 FORWARD LENGTH=5144
AT1G06730	UGUCACCGUAGAUUUCUUCCU	123	4	Cleavage	| Symbols: | pfkB-like carbohydrate kinase family protein | chr1:2067529-2070446 FORWARD LENGTH=1968
AT1G06800	UCACCUCGCAUCUUAGAACUG	146	4	Translation	| Symbols: PLA-I{gamma}1 | alpha/beta-Hydrolases superfamily protein | chr1:2090041-2091686 REVERSE LENGTH=1646
AT1G07050	UGACGGUUCAGAUUCAGGAGC	107	4.5	Cleavage	| Symbols: | CCT motif family protein | chr1:2164188-2165239 REVERSE LENGTH=833
AT1G07150	UGUAUGCAUAACUUGGGACUU	149	4	Cleavage	| Symbols: MAPKKK13 | mitogen-activated protein kinase kinase kinase 13 | chr1:2193941-2195798 REVERSE LENGTH=1586
AT1G07450	UGAGAGAUCCCCUGUUACUGA	786	4.5	Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:2287926-2289336 REVERSE LENGTH=975
AT1G07570	UGAGAACAUUGACUUCAGACCU	158	4	Cleavage	| Symbols: APK1A, APK1 | Protein kinase superfamily protein | chr1:2331226-2333633 REVERSE LENGTH=1576
AT1G07590	UUGGACGUCUCUACUAUGAGA	437	4	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:2336523-2339391 REVERSE LENGTH=2361
AT1G07670	CUACAAAUUCGAGCACUCCCU	156	3.5	Translation	| Symbols: ATECA4, ECA4 | endomembrane-type CA-ATPase 4 | chr1:2370052-2374545 REVERSE LENGTH=3538
AT1G07705	UGACACCGAUUCUGAUUGCAU	377	4	Cleavage	| Symbols: | NOT2 / NOT3 / NOT5 family | chr1:2381615-2386092 FORWARD LENGTH=2316
AT1G07725	UGACACCGAUUCUGAUAGCUU	823	4.5	Cleavage	| Symbols: ATEXO70H6, EXO70H6 | exocyst subunit exo70 family protein H6 | chr1:2394801-2397272 REVERSE LENGTH=2472
AT1G07810	CUACAAAUUCGAGCACUCCCU	156	3.5	Translation	| Symbols: ECA1, ATECA1, ACA3 | ER-type Ca2+-ATPase 1 | chr1:2416265-2420757 FORWARD LENGTH=3499
AT1G07950	UAAGGAGAGUCAGCUACUUGGA	134	3	Cleavage	| Symbols: MED22B | Surfeit locus protein 5 subunit 22 of Mediator complex | chr1:2465770-2467022 REVERSE LENGTH=796
AT1G07960	UGUGACACCGAUUCUGAUAGC	115	3	Cleavage	| Symbols: ATPDIL5-1, PDIL5-1 | PDI-like 5-1 | chr1:2467161-2469139 FORWARD LENGTH=849
AT1G08040	UACACUCACUUGAUCUAGGAG	223	2.5	Cleavage	| Symbols: | Protein of unknown function (DUF707) | chr1:2495342-2498641 REVERSE LENGTH=1501
AT1G08050	UGAAAUAAAACUGAACCAUGCC	263	4	Cleavage	| Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr1:2498836-2501427 REVERSE LENGTH=2294
AT1G08065	AUACCCAAACCUGAACUUUCU	127	4	Cleavage	| Symbols: ATACA5, ACA5 | alpha carbonic anhydrase 5 | chr1:2511647-2513454 REVERSE LENGTH=1088
AT1G08110	UUCUGUAGCACGAGGUAUCCU	302	4.5	Translation	| Symbols: | lactoylglutathione lyase family protein / glyoxalase I family protein | chr1:2535328-2537931 FORWARD LENGTH=944
AT1G08250	UCCUGAGUACUCUCUUCCAAG	209	3	Translation	| Symbols: ADT6 | arogenate dehydratase 6 | chr1:2588857-2590301 REVERSE LENGTH=1445
AT1G08260	UCGAGGGCAGGAACAUUGACU	334	3.5	Translation	| Symbols: EMB142, EMB2284, POL2A, TIL1, EMB529, ABO4, ESD7 | DNA polymerase epsilon catalytic subunit | chr1:2590944-2606892 FORWARD LENGTH=6486
AT1G08340	UGAGGUCGAGUAGAGCAAUCUA	117	4	Cleavage	| Symbols: | Rho GTPase activating protein with PAK-box/P21-Rho-binding domain | chr1:2631068-2632871 FORWARD LENGTH=1438
AT1G08350	UUUGGCCUGAGGUUGGACACC	133	4	Cleavage	| Symbols: | Endomembrane protein 70 protein family | chr1:2632810-2635852 REVERSE LENGTH=2013
AT1G08380	UCGGCUCAAACCUAACACGUU	129	4	Translation	| Symbols: PSAO | photosystem I subunit O | chr1:2640813-2641828 REVERSE LENGTH=703
AT1G08450	UUUGUAUGCAUAACUUGGGAC	135	2.5	Translation	| Symbols: CRT3, PSL1, EBS2, AtCRT3 | calreticulin 3 | chr1:2667839-2671825 REVERSE LENGTH=1307
AT1G08500	UGAAGGAUUUGUGGUUAACCA	474	3	Cleavage	| Symbols: ENODL18, AtENODL18 | early nodulin-like protein 18 | chr1:2689016-2690045 FORWARD LENGTH=945
AT1G08520	UCUAUAGCCAAUGUACUCUACU	106	4	Cleavage	| Symbols: ALB1, ALB-1V, V157, PDE166, CHLD | ALBINA 1 | chr1:2696412-2700959 FORWARD LENGTH=2549
AT1G08620	AAACACUCUAGACUCGAUCCU	123	4.5	Cleavage	| Symbols: PKDM7D | Transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein | chr1:2736774-2743758 FORWARD LENGTH=4181
AT1G08830	UACCGGAGGACGUACAUAGCU	401	4.5	Translation	| Symbols: CSD1 | copper/zinc superoxide dismutase 1 | chr1:2827118-2829315 FORWARD LENGTH=806
AT1G08890	AUGACGAAUGUUUGACAGCCU	113	5	Cleavage	| Symbols: | Major facilitator superfamily protein | chr1:2848348-2852270 FORWARD LENGTH=1675
AT1G08940	UUCCCCUAGAAUUCUUUCCCU	1646	4.5	Cleavage	| Symbols: | Phosphoglycerate mutase family protein | chr1:2877692-2879169 FORWARD LENGTH=913
AT1G08970	UUCUUCAGACUGGAUAGGACU	265	3.5	Translation	| Symbols: HAP5C, NF-YC9 | nuclear factor Y, subunit C9 | chr1:2882543-2884337 FORWARD LENGTH=1613
AT1G09000	UCGAGUAUGAGCCUGAGUCAUG	250	4	Cleavage	| Symbols: ANP1, MAPKKK1, NP1 | NPK1-related protein kinase 1 | chr1:2891037-2895182 FORWARD LENGTH=2270

AT1G09010	UUUGUUAAACUCAUGGUCACCC	165	4 Translation	| Symbols: | glycoside hydrolase family 2 protein | chr1:2895166-2899384 REVERSE LENGTH=3025
AT1G09020	AUUGACGUCGAGUAUGAGCCU	2734	4 Translation	| Symbols: SNF4, ATSNF4 | homolog of yeast sucrose nonfermenting 4 | chr1:2899914-2904815 REVERSE LENGTH=2302
AT1G09195	UGCACUCGCUAGGUCUGGCAG	378	4.5 Translation	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; CONTAINS InterPro DOMAIN/s: Metal-dependent phosphohydrolase, HD subdomain (InterPro:IPR006674), Ppx/
AT1G09400	UUUAGAGAUCCCCUGUUACUG	387	3 Cleavage	| Symbols: | FMN-linked oxidoreductases superfamily protein | chr1:3033512-3035036 REVERSE LENGTH=1182
AT1G09540	UUCUGAAGGACAAGAUCAGCU	351	3.5 Cleavage	| Symbols: MYB61, ATMYB61 | myb domain protein 61 | chr1:3086159-3087912 FORWARD LENGTH=1498
AT1G09550	UCUAGUCCGAAAAAUGCGAAC	163	5 Translation	| Symbols: | Pectinacetylesterase family protein | chr1:3089733-3092327 REVERSE LENGTH=1240
AT1G09680	UUUGAGCACUCUACAGACAGG	162	4.5 Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:3134107-3135930 REVERSE LENGTH=1824
AT1G09710	UGGCGCUCAACUCUGCGAGGU	1187	3.5 Translation	| Symbols: | Homeodomain-like superfamily protein | chr1:3140872-3144370 FORWARD LENGTH=2138
AT1G09800	AUGACGAAUGUUUGACAGCCU	113	3.5 Cleavage	| Symbols: | Pseudouridine synthase family protein | chr1:3176883-3180421 REVERSE LENGTH=1442
AT1G09812	UAUCUCUGUCGUUACGAACCU	295	3 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G58007.2); Has 93 Blast hits to 93 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 93; Viruses - 0; Other Eukaryo
AT1G09840	UUCACAUGUCCGGGCUAGGCA	461	4 Translation	| Symbols: ATSK41, SK41 | shaggy-like protein kinase 41 | chr1:3195824-3200254 REVERSE LENGTH=1791
AT1G09850	UUGAGAGAUCCCCUGUUACUG	3917	4 Cleavage	| Symbols: XBCP3 | xylem bark cysteine peptidase 3 | chr1:3201799-3204150 FORWARD LENGTH=1638
AT1G09870	UUGAUCCAAGUAGCUGACUCU	4031	3.5 Cleavage	| Symbols: | histidine acid phosphatase family protein | chr1:3205741-3208598 FORWARD LENGTH=1694
AT1G09940	UUCUGUAGCACGAGGUAUCCU	302	4 Cleavage	| Symbols: HEMA2 | Glutamyl-tRNA reductase family protein | chr1:3236995-3239554 REVERSE LENGTH=2114
AT1G09980	UUUGCCUGUUGAACUCGAGUA	114	3.5 Cleavage	| Symbols: | Putative serine esterase family protein | chr1:3256245-3261614 REVERSE LENGTH=3156
AT1G10070	UCUGUAUGCAUAGCUUGGGAC	197	5 Cleavage	| Symbols: ATBCAT-2, BCAT-2 | branched-chain amino acid transaminase 2 | chr1:3288087-3290471 FORWARD LENGTH=1558
AT1G10240	UGAAGUCAAUGUUCUCACCCU	486	2.5 Cleavage	| Symbols: FRS11 | FAR1-related sequence 11 | chr1:3356680-3359838 REVERSE LENGTH=2295
AT1G10290	UGCAUAACUUGGGACUUACCU	413	3.5 Cleavage	| Symbols: ADL6, DRP2A | dynamin-like protein 6 | chr1:3370558-3377463 FORWARD LENGTH=3304
AT1G10385	AUUCGAGAACUCCCUGACCGA	265	5 Cleavage	| Symbols: | Vps51/Vps67 family (components of vesicular transport) protein | chr1:3403224-3405856 FORWARD LENGTH=2265
AT1G10450	UGGAUUCCGGCUGCAUACUCC	392	5 Cleavage	| Symbols: SNL6 | SIN3-like 6 | chr1:3431780-3438370 FORWARD LENGTH=4024
AT1G10470	CGAGAGAUUACAGGGACUGUC	3198	4 Translation	| Symbols: ARR4, MEE7, ATRR1, IBC7 | response regulator 4 | chr1:3442327-3443957 REVERSE LENGTH=1275
AT1G10500	UUUGAGCACUCUACAGACAGG	162	3.5 Translation	| Symbols: ATCPISCA, CPISCA | chloroplast-localized ISCA-like protein | chr1:3460000-3461485 REVERSE LENGTH=848
AT1G10540	AUGGAUUUAGAUCACUUGCGUC	196	4.5 Cleavage	| Symbols: ATNAT8, NAT8 | nucleobase-ascorbate transporter 8 | chr1:3474864-3477927 REVERSE LENGTH=1951
AT1G10660	UAAAACUGAACCAUGCCUAGA	302	4.5 Translation	| Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62960.1); Has 35333 Blast h
AT1G10670	UCUGAACUCAAGGCACCCAAA	493	4.5 Cleavage	| Symbols: ACLA-1 | ATP-citrate lyase A-1 | chr1:3535387-3538281 FORWARD LENGTH=1660
AT1G10682	UUCACAUGUCCGGGCUAGGCA	461	4.5 Translation	| Symbols: | other RNA | chr1:3544991-3545471 REVERSE LENGTH=481
AT1G10720	UCCAGUCUGAAGAACGCGAAC	136	3.5 Cleavage	| Symbols: | BSD domain-containing protein | chr1:3562952-3564759 FORWARD LENGTH=1615
AT1G11220	UCAACGCUCUGAUACAUCUAG	118	3.5 Cleavage	| Symbols: | Protein of unknown function (DUF761) | chr1:3759862-3761165 REVERSE LENGTH=1093
AT1G11420	CUCAGGCUCAUACUCGACGUC	968	3.5 Translation	| Symbols: ATDUF2, DUF2 | DOMAIN OF UNKNOWN FUNCTION 724 2 | chr1:3844581-3846872 REVERSE LENGTH=1815
AT1G11490	UUGAGAGAUCCCCUGUUACUG	3917	4 Translation	| Symbols: | zinc finger (C2H2 type) family protein | chr1:3868884-3870065 REVERSE LENGTH=1098
AT1G11545	UAUUGAUUUUUGGCCUGAGGU	116	3.5 Translation	| Symbols: XTH8 | xyloglucan endotransglucosylase/hydrolase 8 | chr1:3878550-3880361 REVERSE LENGTH=1132
AT1G11560	AUCCAAGUAGCUGACUCUCCU	1104	3.5 Translation	| Symbols: | Oligosaccharyltransferase complex/magnesium transporter family protein | chr1:3881788-3882819 FORWARD LENGTH=1032
AT1G11592	CCGAUUCUGAUUGCAUGUGGU	186	2.5 Cleavage	| Symbols: | other RNA | chr1:3895268-3896934 REVERSE LENGTH=1073
AT1G11670	UUGCAGAGAUGGAUGUACAAC	101	3 Cleavage	| Symbols: | MATE efflux family protein | chr1:3928162-3931576 REVERSE LENGTH=1964
AT1G11710	UCCAAGUAGCUGACUCUCCUU	596	4 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:3948714-3951359 FORWARD LENGTH=2646
AT1G11840	UACAGGAAGUGGGCGCACACC	102	4.5 Cleavage	| Symbols: ATGLX1, GLX1 | glyoxalase I homolog | chr1:3995169-3997864 FORWARD LENGTH=1504
AT1G12110	UAAGACUGAGAUACGCGUGCCU	152	4.5 Cleavage	| Symbols: NRT1.1, CHL1-1, NRT1, B-1, ATNRT1, CHL1 | nitrate transporter 1.1 | chr1:4105233-4109545 FORWARD LENGTH=2136
AT1G12140	UAUGGCCUGGGAGCAAUCGCA	299	4.5 Cleavage	| Symbols: FMO GS-OX5 | flavin-monooxygenase glucosinolate S-oxygenase 5 | chr1:4121369-4123542 FORWARD LENGTH=1567
AT1G12300	UAGAAUUAUCAUGUCUUGGCA	194	3.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4183066-4186124 REVERSE LENGTH=3059
AT1G12350	CUGAGGUCACACGGAUAAUCG	152	2.5 Cleavage	| Symbols: ATCOAB, COAB | 4-phospho-panto-thenoylcysteine synthetase | chr1:4198413-4200802 FORWARD LENGTH=1279
AT1G12380	UUACGAGACUCUAGCCCAACU	447	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G62870.1); Has 173 Blast hits to 170 proteins in 34 species: Archae - 0; Bacteria - 4; Metazoa - 25; Fungi - 8; Plants - 123; Viruses - 7; Other Eul
AT1G12460	UCAAGAACUCCAACCCUUCACU	144	3 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:4247249-4250630 FORWARD LENGTH=3289
AT1G12470	UCACUGUGAAUUCCUGGAGUU	123	5 Cleavage	| Symbols: | zinc ion binding | chr1:4251032-4257392 FORWARD LENGTH=3236
AT1G12550	UAUCGAGCACCUACGUCACUGU	142	3.5 Translation	| Symbols: | D-isomer specific 2-hydroxyacid dehydrogenase family protein | chr1:4274594-4275981 FORWARD LENGTH=1177
AT1G12570	UCCCAACCCAUGAUCUAAGCG	236	3 Cleavage	| Symbols: | Glucose-methanol-choline (GMC) oxidoreductase family protein | chr1:4277993-4280862 REVERSE LENGTH=2027
AT1G12667	UUGAGAUAUCCCCUGUUACUG	106	4.5 Cleavage	| Symbols: | Encodes a Plant thionin family protein | chr1:4313858-4314204 FORWARD LENGTH=347
AT1G12770	CAAACUGGACAAGCUACUGCU	324	3.5 Cleavage	| Symbols: ISE1, EMB1586 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:4351064-4353685 FORWARD LENGTH=2069
AT1G12820	UGGAUUCCGGCUGCAUACUCC	392	5 Cleavage	| Symbols: AFB3 | auxin signaling F-box 3 | chr1:4368760-4371293 REVERSE LENGTH=2229
AT1G12850	UAGCUAACAAGAACUCUUUCU	1828	3 Translation	| Symbols: | Phosphoglycerate mutase family protein | chr1:4379707-4381612 REVERSE LENGTH=1568
AT1G12880	UUCCAGAACUAAUGAAUGUUA	448	3 Translation	| Symbols: atnudt12, NUDT12 | nudix hydrolase homolog 12 | chr1:4389751-4391151 FORWARD LENGTH=1002
AT1G12930	UGGCAGUAGGAGUACACGACU	163	5 Cleavage	| Symbols: | ARM repeat superfamily protein | chr1:4398375-4405605 REVERSE LENGTH=3341
AT1G12970	UCCUAUCCAGUCUGAAGAACGC	272	5 Cleavage	| Symbols: PIRL3 | plant intracellular ras group-related LRR 3 | chr1:4423640-4425789 FORWARD LENGTH=1639
AT1G12990	CAAAUUCGAGAACUCCCUGAC	283	4 Cleavage	| Symbols: | beta-1,4-N-acetylglucosaminyltransferase family protein | chr1:4433640-4436075 FORWARD LENGTH=2035
AT1G13000	UUUGAGCACUCCUUGACCCGA	154	4.5 Translation	| Symbols: | Protein of unknown function (DUF707) | chr1:4436105-4439476 REVERSE LENGTH=1675
AT1G13160	AUUGUGUAUAAUUUUGAGCCU	108	2.5 Translation	| Symbols: | ARM repeat superfamily protein | chr1:4484584-4488577 FORWARD LENGTH=2654
AT1G13210	AUGACGAAUGUUUGACAGCCU	113	5 Translation	| Symbols: ACA.I | autoinhibited Ca2+/ATPase II | chr1:4508963-4513938 REVERSE LENGTH=4065
AT1G13400	UCGAGUGACUUUGGAGCCAUU	244	4 Cleavage	| Symbols: NUB, JGL | C2H2 and C2HC zinc fingers superfamily protein | chr1:4597627-4598911 FORWARD LENGTH=781
AT1G13410	UACGCGACCGCGGUGCUGGCC	119	5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4601261-4603298 FORWARD LENGTH=1814
AT1G13448	UACACUCACUUGAUCUAGGAG	223	5 Cleavage	| Symbols: | other RNA | chr1:4612243-4612929 FORWARD LENGTH=592
AT1G13470	UUGAGAGCACUCCACCGACUG	261	4.5 Translation	| Symbols: | Protein of unknown function (DUF1262) | chr1:4620228-4621580 REVERSE LENGTH=1272
AT1G13490	UUAACUCUACCCUUUGCACUC	380	4.5 Cleavage	| Symbols: | Protein of unknown function (DUF1262) | chr1:4624715-4626064 REVERSE LENGTH=1092
AT1G13530	UUAACUCUACCCUUUGCACUC	380	4.5 Cleavage	| Symbols: | Protein of unknown function (DUF1262) | chr1:4633740-4635129 REVERSE LENGTH=1158
AT1G13560	UCGAGUGACUUUGGAGCCAUU	244	3 Cleavage	| Symbols: AAPT1, ATAAPT1 | aminoalcoholphosphotransferase 1 | chr1:4638514-4642088 REVERSE LENGTH=1649
AT1G13630	UGACGGAAGCUACAGAGGAUG	108	4.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4669784-4672826 REVERSE LENGTH=2421
AT1G13800	UUGAGAUAUCCCCUGUUACUG	106	3.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:4731056-4733707 REVERSE LENGTH=2652
AT1G13870	UAGAAUUAUCAUGUCUUGGCA	194	4 Cleavage	| Symbols: DRL1, AtKTI12 | calmodulin binding;purine nucleotide binding | chr1:4747265-4748642 REVERSE LENGTH=1148
AT1G13920	UCUAGUUCGCGUUUUUCAGAC	163	3 Translation	| Symbols: | Remorin family protein | chr1:4758188-4759754 FORWARD LENGTH=1038
AT1G14090	UUUUUCGGACUAGAUAGGACU	107	3.5 Cleavage	| Symbols: | pseudogene, pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat; blastp match of 33% identity and 1.5e-16 P-value to GP|20219038|gb|AAM15782.1|AC104428_3|AC104428 Putative indc
AT1G14220	UAACUCUACCCUUUGCACUCG	727	4.5 Cleavage	| Symbols: | Ribonuclease T2 family protein | chr1:4858642-4859601 REVERSE LENGTH=687
AT1G14300	AUGACGAAUGUUUGACAGCCU	113	4 Translation	| Symbols: | ARM repeat superfamily protein | chr1:4882376-4884791 REVERSE LENGTH=1403
AT1G14350	UUGACGACCAACUCCGCUCCU	170	4.5 Cleavage	| Symbols: FLP, MYB124 | Duplicated homeodomain-like superfamily protein | chr1:4907953-4911080 FORWARD LENGTH=2091
AT1G14390	UGUGGUGUACCUCUUACGUCU	106	4 Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:4924277-4926794 FORWARD LENGTH=2244
AT1G14440	UGAAAUAAAACUGAACCAUGCC	263	3.5 Cleavage	| Symbols: AtHB31, HB31, ZHD4 | homeobox protein 31 | chr1:4938824-4940903 REVERSE LENGTH=1577
AT1G14520	UUGAAGGAUUUGUGGUUAACCA	106	3 Cleavage	| Symbols: MIOX1 | myo-inositol oxygenase 1 | chr1:4968142-4970007 REVERSE LENGTH=1217
AT1G14685	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: BPC2, BBR/BPC2, ATBPC2 | basic pentacysteine 2 | chr1:5042323-5044294 FORWARD LENGTH=1453
AT1G14790	CAAGAACCCGCACGACACUCG	169	4.5 Cleavage	| Symbols: RDR1, ATRDRP1 | RNA-dependent RNA polymerase 1 | chr1:5093961-5098032 REVERSE LENGTH=3807
AT1G14920	UGGCGCUCAACUCUGCAAGGU	10625	3.5 Cleavage	| Symbols: GAI, RGA2 | GRAS family transcription factor family protein | chr1:5149226-5151354 FORWARD LENGTH=2129
AT1G14980	UAAUAAGGAGAGUCAGCUACU	298	4 Cleavage	| Symbols: CPN10 | chaperonin 10 | chr1:5165628-5166745 REVERSE LENGTH=690
AT1G15000	UCGACCACACUGUCAUGAUCU	174	3.5 Cleavage	| Symbols: scpl50 | serine carboxypeptidase-like 50 | chr1:5168596-5170066 FORWARD LENGTH=1471
AT1G15030	UUUGGCGCUCAACUCUGCAAG	3787	4.5 Translation	| Symbols: | Protein of unknown function (DUF789) | chr1:5177529-5180049 FORWARD LENGTH=1645
AT1G15165	UACACUCACUUGAUCUAGGAG	223	3 Cleavage	| Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:5217719-5220113 REVERSE LENGTH=1036
AT1G15250	UAAAACUGAACCAUGCCUAGA	302	3.5 Cleavage	| Symbols: | Zinc-binding ribosomal protein family protein | chr1:5248664-5249474 REVERSE LENGTH=542
AT1G15320	UUUGCUGAACAUGUACCUCCA	119	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; EXPRESSED IN: flower; EXPRESSED DURING: petal differentiation and expansion stage; Has 30201 Blast hits to 17322 protei
AT1G15470	UGCCUAGAUUGCUCUACUCGA	125	3.5 Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:5315507-5317863 FORWARD LENGTH=1416
AT1G15480	UCAUGUAGUUCUAGUUCGCCU	245	4 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:5318011-5320594 FORWARD LENGTH=2081
AT1G15700	UCUUCGACUGAGGUAAGCGCCU	355	3.5 Cleavage	| Symbols: ATPC2 | ATPase, F1 complex, gamma subunit protein | chr1:5402569-5403818 REVERSE LENGTH=1250
AT1G15720	UUUGAGAGAUCCCCUGUUACUG	632	3 Cleavage	| Symbols: TRFL5 | TRF-like 5 | chr1:5406025-5407486 FORWARD LENGTH=1462
AT1G15750	UUGCAGAGAUGGAUGUACAAC	101	3 Translation	| Symbols: WSIP1, TPL | Transducin family protein / WD-40 repeat family protein | chr1:5414817-5420630 REVERSE LENGTH=3829
AT1G15800	UUUAGCCUGAGGUUGGACGCC	213	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80610.1); Has 56 Blast hits to 52 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 56; Viruses - 0; Other Eukaryot

AT1G15860	CUCACAAGUGAUAUAGGGCUUG	110	4.5	Cleavage	| Symbols: | Domain of unknown function (DUF298) | chr1:5454785-5457022 FORWARD LENGTH=1077
AT1G15950	UUGAGAGCACUCCACCGACUG	261	4	Cleavage	| Symbols: CCR1, IRX4, ATCCR1 | cinnamoyl coa reductase 1 | chr1:5478754-5482180 FORWARD LENGTH=1401
AT1G16000	UUUGGUUCUGAGUCCCCGCCU	669	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G80890.1); Has 41 Blast hits to 40 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 41; Viruses - 0; Other Eukaryo
AT1G16010	UCAUCAAUGAACUCAUUUGGCU	103	3	Translation	| Symbols: MGT2 | magnesium transporter 2 | chr1:5495373-5497723 REVERSE LENGTH=1731
AT1G16030	UCAACACUCUGAUACAUCUAG	143	4	Cleavage	| Symbols: Hsp70b | heat shock protein 70B | chr1:5502206-5504535 REVERSE LENGTH=2330
AT1G16070	UUAGCCUGAGGUUGGACGCCU	231	4	Cleavage	| Symbols: AtTLP8, TLP8 | tubby like protein 8 | chr1:5511873-5513896 REVERSE LENGTH=1337
AT1G16090	UGUCCCAACUUAACUCUACCCU	279	4	Cleavage	| Symbols: WAKL7 | wall associated kinase-like 7 | chr1:5516259-5517822 FORWARD LENGTH=1310
AT1G16150	UUCUUCAGACUGGAUAGGACU	265	3.5	Cleavage	| Symbols: WAKL4 | wall associated kinase-like 4 | chr1:5532415-5534877 FORWARD LENGTH=2340
AT1G16220	UCUCAUGUAGUUCUAGUUCGCA	1437	4	Cleavage	| Symbols: | Protein phosphatase 2C family protein | chr1:5548653-5550553 FORWARD LENGTH=1476
AT1G16320	UGGAGAUGAUAGAUUAUGCGC	126	4.5	Cleavage	| Symbols: | Uncharacterized conserved protein (DUF2358) | chr1:5580855-5582143 FORWARD LENGTH=1129
AT1G16330	UCGAGUAUGAGCCUGAGUCAUG	250	3.5	Cleavage	| Symbols: CYCB3;1 | cyclin b3;1 | chr1:5582387-5587391 REVERSE LENGTH=1947
AT1G16430	UAAGGAGAGUCAGCUACUUGGA	134	3	Cleavage	| Symbols: | Surfeit locus protein 5 subunit 22 of Mediator complex | chr1:5614619-5615510 FORWARD LENGTH=579
AT1G16570	UUCCCGUUGGUGUGCGCCAC	196	4.5	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:5670577-5673600 REVERSE LENGTH=1636
AT1G16700	UGAGUAGAAUUCGAUCAUAUC	114	3.5	Cleavage	| Symbols: | Alpha-helical ferredoxin | chr1:5709725-5711902 FORWARD LENGTH=1061
AT1G16760	UUGAGAGAUCCCCUGUUACUG	3917	3.5	Cleavage	| Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:5734234-5737307 FORWARD LENGTH=2277
AT1G16920	UUGGUCACACAGUGGACUGUG	104	4.5	Cleavage	| Symbols: RAB11, ATRABA1B, RABA1b | RAB GTPase homolog A1B | chr1:5787330-5789249 REVERSE LENGTH=912
AT1G16950	UGAGUAGAAUUCGAUCAUAUC	114	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: stamen; EXPRESSED DURING: 4 anthesis; Has 17 Blast hits to 17 prote
AT1G16980	UCUAGUUCACAUUUUUCGGAC	427	3.5	Translation	| Symbols: ATTPS2, TPS2 | trehalose-phosphatase/synthase 2 | chr1:5807311-5811488 FORWARD LENGTH=2466
AT1G17140	UACACUCACUUGAUCUAGGAG	223	4	Cleavage	| Symbols: ICR1, RIP1 | interactor of constitutive active rops 1 | chr1:5856573-5858550 REVERSE LENGTH=1459
AT1G17210	UUUGAACUCAUGGAUACCCUA	227	4	Cleavage	| Symbols: ATILP1, ILP1 | IAP-like protein 1 | chr1:5880130-5884756 REVERSE LENGTH=3348
AT1G17345	CUCGGGAGAAAGAAGAAGGCU	259	2.5	Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr1:5940423-5941210 FORWARD LENGTH=788
AT1G17500	UUGAAGGAUUUGUGGUUAACCA	106	4	Translation	| Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:6018757-6023503 FORWARD LENGTH=3953
AT1G17580	AUUUGAACUCAUGGAUACCCU	768	4	Cleavage	| Symbols: MYA1, ATMYA1, XI-1 | myosin 1 | chr1:6039303-6049556 FORWARD LENGTH=4960
AT1G17665	AAUUCGAGAACUCCCUGACCC	255	4.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 11 growth stages; Has 149 B
AT1G17780	UGACACCGAUUCUGAUAGCUU	823	4	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G16575.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Vi
AT1G17790	UGACGGUUCAGAUUCAGGAGC	107	3.5	Translation	| Symbols: | DNA-binding bromodomain-containing protein | chr1:6125356-6127404 REVERSE LENGTH=1768
AT1G17830	UUUGUUAAACUCAUGGUCACCC	165	3.5	Translation	| Symbols: | Protein of unknown function (DUF789) | chr1:6135803-6138432 REVERSE LENGTH=1589
AT1G18060	UAAUAAGGAGAGUCAGCUACU	298	4	Cleavage	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 74 Blast hits to 74 proteins in 29 species: Archae - 0; Bacteria - 1
AT1G18190	UAACAAGAACUCUUUCUUUUCU	235	3.5	Cleavage	| Symbols: GC2 | golgin candidate 2 | chr1:6257851-6261457 REVERSE LENGTH=2251
AT1G18340	UACAGGAAGUGGGCGCACACC	102	3.5	Cleavage	| Symbols: | basal transcription factor complex subunit-related | chr1:6311483-6313931 REVERSE LENGTH=1232
AT1G18370	UUUUAAUUCAAGUAGCUGACU	133	3	Cleavage	| Symbols: HIK, ATNACK1, NACK1 | ATP binding microtubule motor family protein | chr1:6319650-6324222 REVERSE LENGTH=3118
AT1G18410	UAACUCUACCCUUUGCACUCG	727	4	Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:6336528-6342460 REVERSE LENGTH=3423
AT1G18480	UUCGAGAACUCCCUGACCCGA	1272	4	Translation	| Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr1:6361629-6363007 FORWARD LENGTH=1379
AT1G18520	UGUCCCAACUUAACUCUACCCU	279	3.5	Cleavage	| Symbols: TET11 | tetraspanin11 | chr1:6374932-6376316 FORWARD LENGTH=1073
AT1G18660	CGAGAGAUUACAGGGACUGUC	3198	3.5	Translation	| Symbols: | zinc finger (C3HC4-type RING finger) family protein | chr1:6421225-6425880 FORWARD LENGTH=1906
AT1G18800	UUUUGCUUAGACUUAGAAACU	179	2	Cleavage	| Symbols: NRP2 | NAP1-related protein 2 | chr1:6481113-6483596 REVERSE LENGTH=1257
AT1G19190	UUCCAGCGUUCUGUAGCCAAC	156	4	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:6623876-6624977 FORWARD LENGTH=1102
AT1G19340	UACAGAAUAGGCUUAAGUAAC	189	4	Translation	| Symbols: | Methyltransferase MT-A70 family protein | chr1:6684751-6687116 FORWARD LENGTH=1610
AT1G19350	CUUCGACUGAGGUAAGCGCCU	234	4	Cleavage	| Symbols: BES1, BZR2 | Brassinosteroid signalling positive regulator (BZR1) family protein | chr1:6688703-6690410 FORWARD LENGTH=1304
AT1G19450	UUCGGACUGGAUAGGACUAGG	101	4	Cleavage	| Symbols: | Major facilitator superfamily protein | chr1:6731434-6734882 REVERSE LENGTH=1953
AT1G19550	UAGAGUGUUCAUGUAGUUGCA	232	3.5	Cleavage	| Symbols: | Glutathione S-transferase family protein | chr1:6767451-6767983 REVERSE LENGTH=462
AT1G19570	UAGAGUGUUCAUGUAGUUGCA	232	3.5	Cleavage	| Symbols: DHAR1, ATDHAR1, DHAR5 | dehydroascorbate reductase | chr1:6773311-6774528 REVERSE LENGTH=905
AT1G19720	UUGAUCCAAGUAGCUGACUCU	4031	4	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:6819564-6822711 REVERSE LENGTH=3069
AT1G19770	UUCAGGGUGAGAACAUUGACU	1291	4.5	Cleavage	| Symbols: ATPUP14, PUP14 | purine permease 14 | chr1:6832347-6833837 FORWARD LENGTH=1396
AT1G19850	UUUGAUUCACCGGAUAAACUC	175	3	Translation	| Symbols: MP, ARF5, IAA24 | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr1:6886879-6891374 FORWARD LENGTH=3375
AT1G19910	CGAGAGAUUACAGGGACUGUC	3198	3	Cleavage	| Symbols: AVA-P2, AVA-2PE, ATVHA-C2 | ATPase, F0/V0 complex, subunit C protein | chr1:6913229-6914594 FORWARD LENGTH=858
AT1G19920	UUGAAAGACUUGUGGAUCACC	926	4	Cleavage	| Symbols: APS2, ASA1 | Pseudouridine synthase/archaeosine transglycosylase-like family protein | chr1:6914613-6916805 REVERSE LENGTH=1801
AT1G19940	CAACUAACAACGAGGGCACUG	198	4	Cleavage	| Symbols: AtGH9B5, GH9B5 | glycosyl hydrolase 9B5 | chr1:6918191-6920377 REVERSE LENGTH=1789
AT1G19970	UACAAAUUCGAGCACUCCCUG	156	4	Cleavage	| Symbols: | ER lumen protein retaining receptor family protein | chr1:6931012-6932689 REVERSE LENGTH=1093
AT1G20080	CAUCAAGAACCGGUCAUGCCU	125	5	Cleavage	| Symbols: SYTB, ATSYTB, NTMC2TYPE1.2, NTMC2T1.2, SYT2 | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:6962132-6965045 FORWARD LENGTH=1851
AT1G20400	UUUGGCACUCAACUCUGCAAG	1274	4	Cleavage	| Symbols: | Protein of unknown function (DUF1204) | chr1:7072192-7075838 REVERSE LENGTH=2835
AT1G20570	UGGCACUCAACUCUGCAAGGU	834	4	Cleavage	| Symbols: | Spc97 / Spc98 family of spindle pole body (SBP) component | chr1:7122018-7126559 REVERSE LENGTH=2931
AT1G20620	CGAGAGAUUACAGGGACUGUC	3198	3.5	Cleavage	| Symbols: CAT3, SEN2, ATCAT3 | catalase 3 | chr1:7143067-7146477 FORWARD LENGTH=1817
AT1G20750	UGACGGUUCAGAUUCAGGAGC	107	3.5	Cleavage	| Symbols: | RAD3-like DNA-binding helicase protein | chr1:7203302-7208998 REVERSE LENGTH=3435
AT1G20980	UGUGGAUACAAGAGCUGGGCU	215	4.5	Cleavage	| Symbols: SPL14, FBR6, SPL1R2, ATSPL14 | squamosa promoter binding protein-like 14 | chr1:7324588-7329385 FORWARD LENGTH=4014
AT1G21000	UUGGACGCCUCUACUAUGAGA	679	4.5	Translation	| Symbols: | PLATZ transcription factor family protein | chr1:7337819-7339437 FORWARD LENGTH=1194
AT1G21140	AUCAUCCUCGGAUCAAACCCU	222	3	Translation	| Symbols: | Vacuolar iron transporter (VIT) family protein | chr1:7404383-7405281 FORWARD LENGTH=899
AT1G21160	UUAACUCUACCCUUUGCACUCG	123	5	Cleavage	| Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:7407955-7412857 REVERSE LENGTH=3724
AT1G21210	UGCCUAGAUUGCUCUACUCGA	125	3.5	Cleavage	| Symbols: WAK4 | wall associated kinase 4 | chr1:7424106-7427041 FORWARD LENGTH=2588
AT1G21390	UCUGUAUGCAUAACUUGGGAC	1212	4	Cleavage	| Symbols: emb2170 | embryo defective 2170 | chr1:7489151-7490737 REVERSE LENGTH=1164
AT1G21590	UAACUCUACCCUUUGCACUCA	473	4.5	Translation	| Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr1:7566232-7569902 REVERSE LENGTH=2860
AT1G21630	UUCCGCAGGGAGAGCGUCCUC	112	2.5	Cleavage	| Symbols: | Calcium-binding EF hand family protein | chr1:7581152-7588151 FORWARD LENGTH=4317
AT1G21690	UGUUGAUCCAAGUAGCUGACU	608	3	Cleavage	| Symbols: EMB1968 | ATPase family associated with various cellular activities (AAA) | chr1:7615644-7618501 FORWARD LENGTH=1169
AT1G21710	UGCACUCGCUAGGUCUGGCAG	378	3	Translation	| Symbols: OGG1, ATOGG1 | 8-oxoguanine-DNA glycosylase 1 | chr1:7624396-7626116 FORWARD LENGTH=1388
AT1G21960	UUUGUUAAACUCAUGGUCACCC	165	3.5	Cleavage	| Symbols: | RING/U-box superfamily protein | chr1:7725972-7726586 FORWARD LENGTH=615
AT1G21990	UAUGGAGAUGAUCGCAAUGGC	937	4.5	Cleavage	| Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:7740530-7742106 REVERSE LENGTH=1398
AT1G22020	UUCACAUGUCCGGGCUAGGCA	461	4	Translation	| Symbols: SHM6 | serine hydroxymethyltransferase 6 | chr1:7754321-7757383 FORWARD LENGTH=2374
AT1G22170	UAGAAUUAUCAUGUCUUGGCA	194	3.5	Cleavage	| Symbols: | Phosphoglycerate mutase family protein | chr1:7826289-7828326 FORWARD LENGTH=1392
AT1G22180	UUCGAGGAGAUAUGACGCGCC	4887	3.5	Cleavage	| Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:7828328-7830275 REVERSE LENGTH=1101
AT1G22250	UUGGGAGAACUAUGACACGAG	515	2.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78170.1); Has 64 Blast hits to 64 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 64; Viruses - 0; Other Eukaryo
AT1G22300	UGGCGCUCAACUCUGCAAGGU	10625	5	Cleavage	| Symbols: GRF10, GF14 EPSILON | general regulatory factor 10 | chr1:7878867-7881219 REVERSE LENGTH=1185
AT1G22360	AUAGCUAACAAGAACUCUUUCU	426	4.5	Cleavage	| Symbols: AtUGT85A2, UGT85A2 | UDP-glucosyl transferase 85A2 | chr1:7894858-7897591 REVERSE LENGTH=1684
AT1G22410	AAAUAAAACUGAACCAUGCCU	203	3.5	Translation	| Symbols: | Class-II DAHP synthetase family protein | chr1:7912046-7915003 FORWARD LENGTH=1919
AT1G22570	UCCACCGACUGAUGACAAUGU	1524	4	Translation	| Symbols: | Major facilitator superfamily protein | chr1:7976620-7978573 REVERSE LENGTH=1698
AT1G22750	UUGCAGAGAUGGAUGUACAAC	101	3.5	Cleavage	| Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1475 (InterPro:IPR009943); Has 186 Blast hits to 155 proteins in 21 species: Archae - 0; Bacteria - 8; Metazoa - 3; Fungi - 0; Plants - 65; Viruses - 0; O
AT1G22770	UGGAUUCCGGCUGCAUACUCC	392	4	Cleavage	| Symbols: GI, FB | gigantea protein (GI) | chr1:8061844-8067716 FORWARD LENGTH=4136
AT1G22910	GCAAGUGAUGAUAAAAAGACA	100	3.5	Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:8105589-8108164 FORWARD LENGTH=1478
AT1G22930	UUUGUAUGCAUAACUUGGGAC	135	3.5	Translation	| Symbols: | T-complex protein 11 | chr1:8117732-8122127 FORWARD LENGTH=3577
AT1G22960	UGACGCCAAUUCUGAAAGUUU	154	4.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:8128086-8130242 REVERSE LENGTH=2157
AT1G22970	UUGUGGAAUCCGUAGUCUGUA	152	3.5	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71150.1); Has 134 Blast hits to 132 proteins in 48 species: Archae - 0; Bacteria - 0; Metazoa - 66; Fungi - 10; Plants - 48; Viruses - 0; Other Eul
AT1G22980	UAGAGUUAAGUUGGGACAGGA	199	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G22970.1); Has 52 Blast hits to 50 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 8; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryo
AT1G23170	UCUAUAGCCAAUGUACUCUACU	106	5	Translation	| Symbols: | Protein of unknown function DUF2359, transmembrane | chr1:8212724-8215516 FORWARD LENGTH=1710
AT1G23200	UUCUUGUGAACUUGACCGGGA	158	3.5	Translation	| Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr1:8227178-8229582 FORWARD LENGTH=1905
AT1G23210	UCUAGUUCGCGUUUUUCAGAC	163	4.5	Cleavage	| Symbols: AtGH9B6, GH9B6 | glycosyl hydrolase 9B6 | chr1:8240174-8242129 FORWARD LENGTH=1470
AT1G23260	UUGAUCCAAGUAGCUGACUCU	4031	3.5	Cleavage	| Symbols: MMZ1, UEV1A | MMS ZWEI homologue 1 | chr1:8256986-8258688 REVERSE LENGTH=815
AT1G23400	UAUGGUGACUUGGCUCAGGCC	212	4	Cleavage	| Symbols: CAF2, ATCAF2 | RNA-binding CRS1 / YhbY (CRM) domain-containing protein | chr1:8312076-8314744 REVERSE LENGTH=1822
AT1G23620	UUGUGAGUGUUUGUGAGGUCU	141	3	Translation	| Symbols: | pseudogene, hypothetical protein | chr1:8364662-8366449 REVERSE LENGTH=1788
AT1G23660	UCAACACUCUGAUACAUCUAG	143	4	Cleavage	| Symbols: | Domain of unknown function DUF220 | chr1:8371609-8372845 REVERSE LENGTH=868
AT1G23830	UGACGGACAAGAUAAGUUGCU	1505	4	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 9 growth stages; BEST Arabi

AT1G23870	UUUUUCGGACUAGAUAGGACU	107	5 Translation	| Symbols: ATTPS9, TPS9 | trehalose-phosphatase/synthase 9 | chr1:8432179-8435656 FORWARD LENGTH=2973
AT1G24240	UAUUGAUUUUUGGCCUGAGGU	116	3.5 Cleavage	| Symbols: | Ribosomal protein L19 family protein | chr1:8586353-8588116 FORWARD LENGTH=893
AT1G24265	UAGAUAACAAGAACUCUUUCU	107	3 Translation	| Symbols: | Protein of unknown function (DUF1664) | chr1:8600477-8603801 FORWARD LENGTH=1283
AT1G24320	CAAACUGGACAAGCUACUGCU	324	5 Cleavage	| Symbols: | Six-hairpin glycosidases superfamily protein | chr1:8626315-8630971 REVERSE LENGTH=2528
AT1G24430	UGCCAUGAUCGAGAGCUGCCU	164	3.5 Translation	| Symbols: | HXXXD-type acyl-transferase family protein | chr1:8658003-8659506 REVERSE LENGTH=1504
AT1G24510	CUUGGCAUCGAAUUUGAACUC	1059	3 Cleavage	| Symbols: | TCP-1/cpn60 chaperonin family protein | chr1:8685271-8688247 REVERSE LENGTH=2200
AT1G24590	UAUCCUGAGAGCGGUGCUGGC	334	4.5 Cleavage	| Symbols: DRNL, DRN-LIKE, SOB2, ESR2 | DORNROSCHEN-like | chr1:8714389-8715309 REVERSE LENGTH=921
AT1G24650	UGAAGGACAAGCUCAGCUGCU	1483	5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:8734570-8737315 FORWARD LENGTH=2661
AT1G25320	UGAGAUUGCUAGAGGAAAGAG	101	2 Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:8877857-8880310 FORWARD LENGTH=2370
AT1G25360	UAGAAUUAUCAUGUCUUGGCA	194	4 Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:8894428-8896800 FORWARD LENGTH=2373
AT1G25375	UGUGGAUACAAGAGUUGGGCU	111	3.5 Cleavage	| Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr1:8900153-8903257 REVERSE LENGTH=1738
AT1G25400	UCCUGAGUACUCUCUUCCAAG	209	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 20 plant structures; EXPRESSED DURING: 10 growth stages; BES
AT1G25682	UGAAGGACAAGAUCAGCUGCU	415	3.5 Cleavage	| Symbols: | Family of unknown function (DUF572) | chr1:9002285-9004646 REVERSE LENGTH=1244
AT1G26090	UGCACUCGCUAGGUCUGGCAG	378	5 Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:9020380-9022769 FORWARD LENGTH=1647
AT1G26130	UUCCCCUAGAAUUCUUUCCCU	1646	3 Cleavage	| Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:9033218-9038577 FORWARD LENGTH=4016
AT1G26650	UGACGGAAGCUACAGAGGAUG	108	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G69430.1); Has 205 Blast hits to 204 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 205; Viruses - 0; Other Euka
AT1G26690	CGGAGGAAACUUAGCAGCGCC	103	4 Cleavage	| Symbols: | emp24/gp25L/p24 family/GOLD family protein | chr1:9224145-9225775 REVERSE LENGTH=892
AT1G26770	UGUAUGCAUAACUUGGGACUU	149	5 Cleavage	| Symbols: ATEXPA10, AT-EXP10, ATEXP10, ATHEXP ALPHA 1.1, EXP10, EXPA10 | expansin A10 | chr1:9259605-9261313 FORWARD LENGTH=1366
AT1G26799	UUUAUUCACACAGUGGACUGUG	118	3.5 Cleavage	| Symbols: | Plant self-incompatibility protein S1 family | chr1:9283873-9284438 FORWARD LENGTH=566
AT1G26850	UCCCGGAAUGCUGAAGAAGUA	113	4 Translation	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:9300873-9304133 REVERSE LENGTH=2301
AT1G26890	UAUGCUUCUGUUGAUCCACCU	344	3.5 Cleavage	| Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:9317589-9319246 FORWARD LENGTH=1428
AT1G26900	UCGACCACACUGUCAUGAUCU	174	4 Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:9319756-9321474 REVERSE LENGTH=1719
AT1G26930	CUCACAAGUGAUAUAGGGCUU	208	4.5 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9336057-9337786 REVERSE LENGTH=1547
AT1G26940	CAAAUUCGAGAACUCCCUGAC	283	3.5 Translation	| Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr1:9343126-9345145 FORWARD LENGTH=931
AT1G27050	UUAGAAUUAUCAUGUCUUGGC	138	3.5 Cleavage	| Symbols: ATHB54, HB54 | homeobox protein 54 | chr1:9393690-9394592 FORWARD LENGTH=818
AT1G27080	AACAAAACUGUUGAACAAGCCU	111	4 Cleavage	| Symbols: NRT1.6 | nitrate transporter 1.6 | chr1:9400664-9403789 FORWARD LENGTH=1731
AT1G27190	UAUCCUGAGAGCGGUGCUGGC	334	4 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:9446657-9448825 REVERSE LENGTH=2169
AT1G27240	UUGAAAGACUUGUGGAUCACC	926	3 Cleavage	| Symbols: | Paired amphipathic helix (PAH2) superfamily protein | chr1:9466237-9467076 FORWARD LENGTH=561
AT1G27260	UUCUGAAGGACAAGCUCAGCU	1012	4 Cleavage	| Symbols: | Paired amphipathic helix (PAH2) superfamily protein | chr1:9469948-9470967 FORWARD LENGTH=669
AT1G27340	UCAUCCUCUGUAGCUUCCGUC	210	3 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr1:9495520-9498085 FORWARD LENGTH=1853
AT1G27595	UUCUUCAGACUGGAUAGGACU	265	2.5 Translation	| Symbols: | CONTAINS InterPro DOMAIN/s: Symplekin tight junction protein C-terminal (InterPro:IPR022075); BEST Arabidopsis thaliana protein match is: HEAT repeat-containing protein (TAIR:AT5G01400.1); Has 593 Blast hits to 297 proteins in
AT1G27690	UUUGGGUUUGGGUUAACUGCU	225	3 Cleavage	| Symbols: | Protein of unknown function (DUF620) | chr1:9636594-9638577 FORWARD LENGTH=1659
AT1G27750	UGAAUCUUGGUCAACUGGACC	197	4.5 Cleavage	| Symbols: | nucleic acid binding | chr1:9657385-9661958 FORWARD LENGTH=3476
AT1G27940	UAACUCUACCCUUUGCACUCG	727	2.5 Cleavage	| Symbols: PGP13 | P-glycoprotein 13 | chr1:9733597-9738129 REVERSE LENGTH=3738
AT1G28050	UUUGGCCUGAGGUUGGACGCC	367	3 Cleavage	| Symbols: | B-box type zinc finger protein with CCT domain | chr1:9775528-9777810 REVERSE LENGTH=1695
AT1G28090	CCGAUUCUGAUUGCAUGUGGU	186	4 Cleavage	| Symbols: | Polynucleotide adenylyltransferase family protein | chr1:9796153-9799063 FORWARD LENGTH=1692
AT1G28240	AAACAGGACAAGUUACUCGCC	986	3.5 Translation	| Symbols: | Protein of unknown function (DUF616) | chr1:9868316-9872211 REVERSE LENGTH=2364
AT1G28375	UUCAUCUGCAGUAAGUCCCUG	314	2.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: petal, leaf whorl, sepal, flower; EXPRESSED DURING: 4 anthesis, petal
AT1G28410	UCAUAUGGACUUUGGCUACACC	101	5 Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana pr
AT1G28680	UCUAGUUCGCGUUCUUCAGAC	300	4.5 Cleavage	| Symbols: | HXXXD-type acyl-transferase family protein | chr1:10078189-10080029 FORWARD LENGTH=1655
AT1G29050	UACGUCACUGCGAAUUCCUGGA	271	5 Translation	| Symbols: TBL38 | TRICHOME BIREFRINGENCE-LIKE 38 | chr1:10136230-10139208 REVERSE LENGTH=1415
AT1G29390	UGUGACACCGAUUCUGAUUGC	114	3.5 Cleavage	| Symbols: COR314-TM2, COR413IM2 | cold regulated 314 thylakoid membrane 2 | chr1:10286293-10287904 REVERSE LENGTH=823
AT1G29400	CUCACAAGUGAUAUAGGGCUU	208	4 Translation	| Symbols: AML5, ML5 | MEI2-like protein 5 | chr1:10290040-10294478 REVERSE LENGTH=2880
AT1G29560	UCCUGAGUACUCUCUUCCAAG	209	3 Cleavage	| Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:10332371-10335694 FORWARD LENGTH=2179
AT1G29570	UCCUGAGUACUCUCUUCCAAG	209	2 Cleavage	| Symbols: | Zinc finger C-x8-C-x5-C-x3-H type family protein | chr1:10335910-10337854 FORWARD LENGTH=966
AT1G29700	UCACCUCGCAUCUUAGAACUG	146	5 Translation	| Symbols: | Metallo-hydrolase/oxidoreductase superfamily protein | chr1:10384981-10387441 REVERSE LENGTH=1356
AT1G29750	CGGAGGAAACUUAGCAGCGCC	103	3.5 Cleavage	| Symbols: RKF1 | receptor-like kinase in flowers 1 | chr1:10413881-10420524 REVERSE LENGTH=3311
AT1G30290	UGUGUAUGCAUAACUUGGGAC	106	4 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:10670320-10672740 REVERSE LENGTH=2421
AT1G30410	UACCCGUACGUCGCUUACAAG	3223	4.5 Translation	| Symbols: ATMRP13, MRP13, ABCC12 | multidrug resistance-associated protein 13 | chr1:10738805-10747323 FORWARD LENGTH=4827
AT1G30420	UACCCGUACGUCGCUUACAAG	3223	4.5 Translation	| Symbols: ATMRP12, MRP12, ABCC11 | multidrug resistance-associated protein 12 | chr1:10748816-10756316 FORWARD LENGTH=4488
AT1G30450	AAACAGGACAAGUUACUCGCC	986	3.5 Cleavage	| Symbols: CCC1, ATCCC1, HAP5 | cation-chloride co-transporter 1 | chr1:10762739-10769227 FORWARD LENGTH=3260
AT1G30470	UUAAUCCAAGUAGCUGACUCU	2805	3.5 Cleavage	| Symbols: | SIT4 phosphatase-associated family protein | chr1:10779213-10786697 FORWARD LENGTH=2799
AT1G30490	UUCGGUCUGGCCAUACUCGGC	147	4 Translation	| Symbols: PHV, ATHB9 | Homeobox-leucine zipper family protein / lipid-binding START domain-containing protein | chr1:10796135-10800961 REVERSE LENGTH=2936
AT1G30600	UCCGCUAGAUAUAUCAAACUG	281	3.5 Translation	| Symbols: | Subtilase family protein | chr1:10841142-10845050 REVERSE LENGTH=2842
AT1G30620	UAAGCAUUUUGAUUCACCGGA	285	3.5 Cleavage	| Symbols: HSR8, MUR4, UXE1 | NAD(P)-binding Rossmann-fold superfamily protein | chr1:10854549-10858244 FORWARD LENGTH=1922
AT1G30660	CGUCACUGCGAAUUCCUGGAG	272	5 Translation	| Symbols: | nucleic acid binding;nucleic acid binding | chr1:10876853-10879017 FORWARD LENGTH=1014
AT1G30690	UCACCUCGCAUCUUAGAACUG	146	4.5 Cleavage	| Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr1:10887705-10890315 FORWARD LENGTH=1984
AT1G30710	UCUGGGUAGAUGGGAUCUUAUC	123	3.5 Cleavage	| Symbols: | FAD-binding Berberine family protein | chr1:10895280-10897109 FORWARD LENGTH=1830
AT1G30825	CGUCACUGCGAAUUCCUGGAG	272	4.5 Cleavage	| Symbols: ARPC2A, DIS2 | Arp2/3 complex, 34 kD subunit p34-Arc | chr1:10960941-10963182 FORWARD LENGTH=1305
AT1G30870	UUUCCGUUGGUGUGCGCCCAC	458	3.5 Cleavage	| Symbols: | Peroxidase superfamily protein | chr1:10991485-10993023 FORWARD LENGTH=1238
AT1G30925	UGAAGGAUUUGUGGUUAACCA	474	3.5 Translation	| Symbols: | phospholipase Cs | chr1:11009888-11011792 REVERSE LENGTH=1125
AT1G30950	UGAAUCUUGGUCAACUGGACC	197	4 Cleavage	| Symbols: UFO | F-box family protein | chr1:11036180-11037508 FORWARD LENGTH=1329
AT1G31040	UUGAGAGCACUCCACCGACUGA	140	5 Cleavage	| Symbols: | PLATZ transcription factor family protein | chr1:11069793-11072291 REVERSE LENGTH=841
AT1G31260	UGUCUUACCCGUACGUCGCUU	150	5 Cleavage	| Symbols: ZIP10 | zinc transporter 10 precursor | chr1:11175559-11177362 REVERSE LENGTH=1095
AT1G31490	UUCGAGAACUCCCUGACCCGA	1272	4 Translation	| Symbols: | HXXXD-type acyl-transferase family protein | chr1:11271228-11273294 REVERSE LENGTH=2067
AT1G31500	UGUGGAUACAAGAGCUGGGCU	215	3.5 Translation	| Symbols: | DNAse I-like superfamily protein | chr1:11273605-11276577 REVERSE LENGTH=1426
AT1G31540	UCUCAUGUAGUUCUAGUUCGCG	207	4 Translation	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr1:11290948-11293753 REVERSE LENGTH=2490
AT1G31670	AUGACGAAUGUUUGACAGCCU	113	5 Cleavage	| Symbols: | Copper amine oxidase family protein | chr1:11337558-11341889 FORWARD LENGTH=2226
AT1G31710	UAUGAGUUGAUCGACGAAGAU	123	4 Cleavage	| Symbols: | Copper amine oxidase family protein | chr1:11349840-11355486 FORWARD LENGTH=2208
AT1G31780	CAUUGACUUCAAGCCUGCGCU	190	4.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Conserved oligomeric complex COG6 (InterPro:IPR010490); Has 384 Blast hits to 379 proteins in 190 species: Archae - 0; Bacteria - 4; Metazoa - 151; Fungi - 156; Plants - 42; Viruses - 0; Other Eukaryot
AT1G31910	UGAAAUAAAACUGAACCAUGCC	263	4.5 Cleavage	| Symbols: | GHMP kinase family protein | chr1:11457127-11461825 FORWARD LENGTH=2442
AT1G31930	UCUAGUCCGAAAAAUGCGAAC	163	5 Cleavage	| Symbols: XLG3 | extra-large GTP-binding protein 3 | chr1:11465014-11469165 FORWARD LENGTH=3040
AT1G31960	UUGAAAGACUUGUGGAUCACC	926	3.5 Cleavage	| Symbols: | unknown protein; Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:11479133-11479654 REVERSE LENGTH=522
AT1G32430	UCAUCAAUGAACUCAUUUGGCU	103	2.5 Cleavage	| Symbols: | F-box and associated interaction domains-containing protein | chr1:11704932-11706325 REVERSE LENGTH=1143
AT1G32550	UAAUAAGGAGAGUCAGCUACU	298	4 Cleavage	| Symbols: FdC1 | 2Fe-2S ferredoxin-like superfamily protein | chr1:11771766-11774187 REVERSE LENGTH=819
AT1G32585	UUGAACAAGCCUGAUGAAGUU	102	3 Translation	| Symbols: | VQ motif-containing protein-related | chr1:11788515-11789177 REVERSE LENGTH=663
AT1G32600	AUCCAAGUAGCUGACUCUCCU	1104	5 Cleavage	| Symbols: | F-box associated ubiquitination effector family protein | chr1:11794802-11795683 FORWARD LENGTH=882
AT1G32740	UUCUUUCCGUUGGUGUGCGCC	205	4.5 Cleavage	| Symbols: | SBP (S-ribonuclease binding protein) family protein | chr1:11844877-11846347 FORWARD LENGTH=1210
AT1G32810	UGACGUCGAGUAUGAGCCUGA	416	5 Cleavage	| Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr1:11881810-11885843 FORWARD LENGTH=3207
AT1G33060	UAUUGAUUUUUGGCCUGAGGU	116	4.5 Cleavage	| Symbols: ANAC014, NAC014 | NAC 014 | chr1:11975340-11978521 REVERSE LENGTH=2153
AT1G33070	UGUCUUACCCGUACGUCGCUU	150	3.5 Cleavage	| Symbols: | MADS-box family protein | chr1:11982889-11985299 FORWARD LENGTH=498
AT1G33220	UGAAGGACAAGAUCAGCUGCU	415	3.5 Cleavage	| Symbols: | Glycosyl hydrolase superfamily protein | chr1:12044872-12045879 FORWARD LENGTH=1008
AT1G33270	UUCUGAUUGCAUGUGGUGUACC	110	4.5 Translation	| Symbols: | Acyl transferase/acyl hydrolase/lysophospholipase superfamily protein | chr1:12068063-12070374 REVERSE LENGTH=1588
AT1G33280	UUUGAGCACUCUACAGACAGG	162	2 Cleavage	| Symbols: ANAC015, BRN1, NAC015 | NAC domain containing protein 15 | chr1:12072741-12073839 FORWARD LENGTH=924
AT1G33350	CGAGAGAUUACAGGGACUGUC	3198	4.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:12089403-12091687 REVERSE LENGTH=2285
AT1G33475	CUUCCCCUAGAAUUCUUUCCC	401	4 Cleavage	| Symbols: | SNARE-like superfamily protein | chr1:12147276-12148249 REVERSE LENGTH=974
AT1G33920	UCCGCUAGAUAUAUCAAACUG	281	4.5 Cleavage	| Symbols: ATPP2-A4, PP2-A4 | phloem protein 2-A4 | chr1:12319905-12320870 FORWARD LENGTH=498
AT1G33990	CUAGAAUUCUUUCCCUUUCCU	235	3 Translation	| Symbols: ATMES14, MES14 | methyl esterase 14 | chr1:12355568-12358031 FORWARD LENGTH=1525
AT1G34020	UUUCUGACGGACAAGAUAAGU	480	4 Cleavage	| Symbols: | Nucleotide-sugar transporter family protein | chr1:12366854-12369178 FORWARD LENGTH=1463

AT1G34042	UUCUUCAGACUGGAUAGGACU	265	4	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr1:12379427-1237968
AT1G34050	CAACUAACAACGAGGGCACUG	198	3.5	Cleavage	| Symbols: | Ankyrin repeat family protein | chr1:12393495-12396006 FORWARD LENGTH=1722
AT1G34060	UGAAUCUUGGUCAACUGGACC	197	3.5	Translation	| Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr1:12396420-12398369 REVERSE LENGTH=1603
AT1G34140	AUACCCAAACCUGAACUUUCU	127	5	Cleavage	| Symbols: PAB1 | poly(A) binding protein 1 | chr1:12433356-12434735 REVERSE LENGTH=1224
AT1G34160	UCACUGUGAAUUCCUGGAGUU	123	4	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:12441393-12443256 FORWARD LENGTH=1777
AT1G34170	UUUAGCCUGAGGUUGGACGCC	213	4.5	Translation	| Symbols: ARF13 | AUXIN RESPONSE FACTOR 13 | chr1:12443578-12446764 REVERSE LENGTH=1641
AT1G34180	UGAGAGAUCCCCUGUUACUGA	786	4	Translation	| Symbols: anac016, NAC016 | NAC domain containing protein 16 | chr1:12448726-12451287 FORWARD LENGTH=1898
AT1G34190	AUCAUCCUCGGAUCAAACCCU	222	4	Cleavage	| Symbols: anac017, NAC017 | NAC domain containing protein 17 | chr1:12451451-12454142 FORWARD LENGTH=2180
AT1G34260	UCUAUAGCCAAUGUACUCUACU	106	4.5	Cleavage	| Symbols: FAB1D | FORMS APLOID AND BINUCLEATE CELLS 1A | chr1:12485967-12492169 FORWARD LENGTH=4741
AT1G34320	UAAGGAGAGUCAGCUACUUGGA	134	2.5	Cleavage	| Symbols: | Protein of unknown function (DUF668) | chr1:12520179-12524370 FORWARD LENGTH=2718
AT1G34380	UCAUCAAUGAACUCAUUUGGCU	103	3	Cleavage	| Symbols: | 5'-3' exonuclease family protein | chr1:12552670-12554358 REVERSE LENGTH=1272
AT1G34520	UGAAUCUUGGUCAACUGGACC	197	4	Translation	| Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:12623477-12624487 FORWARD LENGTH=1011
AT1G34770	UGGCGCUCAACUCUGCAAGGUC	119	4	Translation	| Symbols: | CONTAINS InterPro DOMAIN/s: MAGE protein (InterPro:IPR002190); Has 1274 Blast hits to 1260 proteins in 85 species: Archae - 0; Bacteria - 0; Metazoa - 1104; Fungi - 45; Plants - 49; Viruses - 0; Other Eukaryotes - 76 (source: NCBI E
AT1G35160	UGUGUAUGCAUAACUUGGGAC	106	4	Cleavage	| Symbols: GF14 PHI | GF14 protein phi chain | chr1:12867126-12868890 FORWARD LENGTH=1402
AT1G35190	UUUAGAGAUCCCCUGUUACUG	387	4.5	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:12890423-12892874 FORWARD LENGTH=1284
AT1G35220	UCACCAUUGGCAGCUCUGUACC	187	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has
AT1G35255	UAGCUAACAAGAACUCUUUCU	1828	4	Cleavage	| Symbols: | unknown protein; Has 3 Blast hits to 3 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 3; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:12935647-12936553 REVERSE LENGTH=907
AT1G35435	UGCACUCGCUAGGUCUGGCAG	378	3.5	Cleavage	| Symbols: | Putative membrane lipoprotein | chr1:13032806-13033247 REVERSE LENGTH=249
AT1G35460	UUAAUCCAAGUAGCUGACUCU	2805	4.5	Cleavage	| Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:13039916-13042102 FORWARD LENGTH=1151
AT1G35550	CAACGCUCUUGAUACAUCUAG	133	3	Cleavage	| Symbols: | elongation factor Tu C-terminal domain-containing protein | chr1:13112506-13113136 FORWARD LENGTH=631
AT1G35660	CAAACUGGACAAGCUACUGCU	324	3.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 11 growth stages; Has 309 Blast h
AT1G35750	UUCUGUAGCACGAGGUAUCCU	302	2.5	Cleavage	| Symbols: APUM10, PUM10 | pumilio 10 | chr1:13253398-13255570 REVERSE LENGTH=1587
AT1G35780	UCACCUCGCAUCUUAGAACUG	146	4.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G78150.2); Has 145 Blast hits to 144 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 145; Viruses - 0; Other Euka
AT1G36990	UGUUACGAGACUCUAGCCCAG	574	4.5	Cleavage	| Symbols: | unknown protein; LOCATED IN: chloroplast; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G08510.1); Has 5029 Blast hits to 1779 p
AT1G37020	UACUUCCAGCGUUCUGUAGCC	826	3.5	Cleavage	| Symbols: | Cysteine proteinases superfamily protein | chr1:14046735-14049742 FORWARD LENGTH=1836
AT1G42440	UACGCGACCGCGGUGCUGGCC	119	3.5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: ribosome biogenesis; LOCATED IN: nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: AARP2CN (InterPro:
AT1G42490	UUGGACGCCUCUACUAUGAGA	679	4	Cleavage	| Symbols: | pseudogene, glutamate dehydrogenase (fragment), blastp match of 78% identity and 1.6e-94 P-value to GP|15004984|dbj|BAB62170.1||AB066298 glutamate dehydrogenase {Brassica napus} | chr1:15945877-15946985 REVERSE LI
AT1G42560	UCUAGUUCGCGUUUUUCAGAC	163	4	Translation	| Symbols: MLO9, ATMLO9 | Seven transmembrane MLO family protein | chr1:15980135-15983328 REVERSE LENGTH=1457
AT1G43640	UAUCUCUGUCGUUACGAACCU	295	3.5	Translation	| Symbols: AtTLP5, TLP5 | tubby like protein 5 | chr1:16439435-16441844 REVERSE LENGTH=1594
AT1G43895	AAACAGGACAAGUUACUCGCC	986	3.5	Cleavage	| Symbols: | pseudogene, protein kinase -related | chr1:16648567-16649643 REVERSE LENGTH=1077
AT1G44110	UAUGAGUUGAUCGACGAAGAU	123	4.5	Cleavage	| Symbols: CYCA1;1 | Cyclin A1;1 | chr1:16774865-16777247 REVERSE LENGTH=1618
AT1G44575	UUGAGAGAUCCCUUGUUACUG	141	4	Translation	| Symbols: NPQ4, PSBS | Chlorophyll A-B binding family protein | chr1:16871696-16873378 FORWARD LENGTH=1520
AT1G44740	UGUGGUGUACCUCUCACGUCU	112	5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: embryo, leaf whorl, flower, seed; EXPRESSED DURING: F mature embryo stage
AT1G44810	UUCUUCAGACUGGAUAGGACU	265	3	Cleavage	| Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr1:16923543-16924821 FORWARD LENGTH=1279
AT1G44890	CCACCGACUGAUGACAACGUC	122	4.5	Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: homolog of yeast oxidase assembly 1 (OXA1) (TAIR:AT5G62050.1); Has 40 Blast hits to 40 proteins in 7 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 39; Viruses - 0; Other
AT1G45150	UAUCGAGCACCUACGUCACUG	123	3.5	Cleavage	| Symbols: | unknown protein; Has 219 Blast hits to 202 proteins in 78 species: Archae - 0; Bacteria - 166; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 17 (source: NCBI BLink). | chr1:17077448-17082503 REVERSE LENGTH=22
AT1G45170	UCAAGCGAUUGGAAGGAUUGUU	102	3	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BES
AT1G46264	UGAGCCGACAAGAGUAGUAUC	111	5	Cleavage	| Symbols: AT-HSFB4, HSFB4, SCZ | heat shock transcription factor B4 | chr1:17224842-17226280 FORWARD LENGTH=1206
AT1G47056	UUCCAGCGUUCUGUAGCCAAC	156	4.5	Translation	| Symbols: VFB1 | VIER F-box proteine 1 | chr1:17276103-17277659 REVERSE LENGTH=1557
AT1G47260	UCUGGGUAGAUGGGAUCUUAUC	123	4	Cleavage	| Symbols: APFI, GAMMA CA2 | gamma carbonic anhydrase 2 | chr1:17321173-17323484 REVERSE LENGTH=1185
AT1G47330	UUCUGUAGCACGAGGUAUCCU	302	3	Cleavage	| Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr1:17351050-17353875 FORWARD LENGTH=1819
AT1G47370	UGAGAACAUUGACUUCAGACCU	158	5	Cleavage	| Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:17365898-17368703 REVERSE LENGTH=1092
AT1G47380	CCACCGACUGAUGACAACGUC	122	4	Cleavage	| Symbols: | Protein phosphatase 2C family protein | chr1:17372537-17376075 REVERSE LENGTH=2046
AT1G47600	UGAAGGACAAGAUCAGCUGCU	415	3.5	Cleavage	| Symbols: BGLU34 | beta glucosidase 34 | chr1:17491732-17494754 FORWARD LENGTH=1737
AT1G47610	AUUUGAACUCAUGGAUACCCU	768	3.5	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr1:17504783-17505964 FORWARD LENGTH=1182
AT1G47625	UCGGCUCAAACCUAACACGUU	129	3.5	Cleavage	| Symbols: | pseudogene of seven transmembrane domain protein | chr1:17510810-17511489 REVERSE LENGTH=471
AT1G47630	UCAACGAACUCUUGGCCCUAGA	152	4	Translation	| Symbols: CYP96A7 | member of CYP96A | chr1:17516249-17517850 REVERSE LENGTH=1602
AT1G47640	UCGGCUCAAACCUAACACGUU	129	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPr
AT1G47750	UAUGAGUUGAUCGACGAAGAU	123	3.5	Translation	| Symbols: PEX11A | peroxin 11A | chr1:17569256-17570159 REVERSE LENGTH=904
AT1G47840	UUCUGAUUGCAUGUGGUGUACC	110	4.5	Cleavage	| Symbols: HXK3 | hexokinase 3 | chr1:17616107-17618894 REVERSE LENGTH=1653
AT1G47890	UGAGAUUGCUAGAGGAAAGAG	101	3.5	Cleavage	| Symbols: AtRLP7, RLP7 | receptor like protein 7 | chr1:17643976-17647035 FORWARD LENGTH=3060
AT1G47970	UCCUGAGUACUCUCUUCCAAG	209	4.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 11 growth stages; Has 93717 Blast hits to 40
AT1G47990	CUUUGCACUCAUGAAUCUUUC	119	3.5	Translation	| Symbols: ATGA2OX4, GA2OX4 | gibberellin 2-oxidase 4 | chr1:17698655-17700834 FORWARD LENGTH=966
AT1G48020	UUCUGAUUGCAUGUGGUGUACC	110	4.5	Translation	| Symbols: PMEI1, ATPMEI1 | pectin methylesterase inhibitor 1 | chr1:17716051-17716808 REVERSE LENGTH=758
AT1G48090	UUGUGGAAUCCGUAGUCUGUA	152	4.5	Cleavage	| Symbols: | calcium-dependent lipid-binding family protein | chr1:17732010-17758444 REVERSE LENGTH=12995
AT1G48120	UUAACUCUACCCUUUGCACUC	380	4	Cleavage	| Symbols: | hydrolases;protein serine/threonine phosphatases | chr1:17773688-17779955 REVERSE LENGTH=4346
AT1G48150	UGAAGGACAAGAUCAGCUGCU	415	4	Cleavage	| Symbols: | MADS-box transcription factor family protein | chr1:17785397-17786368 FORWARD LENGTH=972
AT1G48175	UUCCAGAACUAAUGAAUGUUA	448	4.5	Cleavage	| Symbols: emb2191 | Cytidine/deoxycytidylate deaminase family protein | chr1:17790507-17792331 FORWARD LENGTH=890
AT1G48360	UUUGAACUCAUGGAUACCCUA	227	3.5	Cleavage	| Symbols: | zinc ion binding;nucleic acid binding;hydrolases, acting on acid anhydrides, in phosphorus-containing anhydrides | chr1:17868650-17873032 FORWARD LENGTH=2707
AT1G48400	UGCAUAACUUGGGACUUACCU	413	5	Cleavage	| Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr1:17882136-17883855 REVERSE LENGTH=1542
AT1G48460	CCGAUUCUGAUUGCAUGUGGU	186	4	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabid
AT1G48540	UGACGCCAAUUCUGAAAGUUU	154	4.5	Cleavage	| Symbols: | Outer arm dynein light chain 1 protein | chr1:17945376-17950521 FORWARD LENGTH=3436
AT1G48650	UUCUUCGACUGAGGUAAGCGCC	154	3.5	Cleavage	| Symbols: | DEA(D/H)-box RNA helicase family protein | chr1:17989398-17995326 REVERSE LENGTH=3897
AT1G48670	UUGUGGAAUCCGUAGUCUGUA	152	4	Cleavage	| Symbols: | auxin-responsive GH3 family protein | chr1:17998946-18001200 REVERSE LENGTH=1578
AT1G48820	UACACAAAGGGCUCCUCGCACC	211	3.5	Cleavage	| Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr1:18055229-18059367 FORWARD LENGTH=1686
AT1G48830	UCUGUACCGCUGAAUUCUUCC	275	4	Cleavage	| Symbols: | Ribosomal protein S7e family protein | chr1:18059636-18061257 REVERSE LENGTH=837
AT1G48930	CAAAUUCGAGAACUCCCUGAC	283	3.5	Cleavage	| Symbols: AtGH9C1, GH9C1 | glycosyl hydrolase 9C1 | chr1:18101643-18104661 REVERSE LENGTH=2097
AT1G48980	UUUUAAUUCAAGUAGCUGACU	133	3	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr1:18118017-18120647 FORWARD LENGTH=1745
AT1G49110	UGCCAUGAUCGAGAGCUGCCU	164	5	Cleavage	| Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr1:18171595-18172450 FORWARD LENGTH=856
AT1G49130	UCACUGUGAAUUCCUGGAGUU	123	4.5	Cleavage	| Symbols: | B-box type zinc finger protein with CCT domain | chr1:18174740-18175964 REVERSE LENGTH=1010
AT1G49160	UAUGAGUUGAUCGACGAAGAU	123	3	Cleavage	| Symbols: WNK7 | Protein kinase superfamily protein | chr1:18179304-18182391 REVERSE LENGTH=2060
AT1G49190	UCACUUUGCUGAACAUGUACC	138	3.5	Cleavage	| Symbols: ARR19, RR19 | response regulator 19 | chr1:18191342-18193598 FORWARD LENGTH=1827
AT1G49300	UUAGCACCGAGGAUGAUGGACU	330	3.5	Cleavage	| Symbols: ATRAB7, ATRABG3E, RABG3E | RAB GTPase homolog G3E | chr1:18234724-18237231 FORWARD LENGTH=1002
AT1G49340	UGAAGGACAAGAUCAGCUGCU	415	3.5	Cleavage	| Symbols: ATPI4K ALPHA | Phosphatidylinositol 3- and 4-kinase family protein | chr1:18252355-18264462 FORWARD LENGTH=6455
AT1G49360	UACCGGAGGACGUACAUAGCU	401	4	Cleavage	| Symbols: | F-box family protein | chr1:18267231-18269448 REVERSE LENGTH=1578
AT1G49580	UUGAACAAGCCUGAUGAAGUU	102	4	Cleavage	| Symbols: | Calcium-dependent protein kinase (CDPK) family protein | chr1:18351458-18354619 FORWARD LENGTH=2209
AT1G49630	CGUCACUGCGAAUUCCUGGAG	272	4	Cleavage	| Symbols: ATPREP2, PREP2 | presequence protease 2 | chr1:18368261-18375381 REVERSE LENGTH=3432
AT1G49670	AUGACGAAUGUUUGACAGCCU	113	4.5	Cleavage	| Symbols: NQR | ARP protein (REF) | chr1:18381258-18386108 REVERSE LENGTH=2310
AT1G49730	UAGAGUGUUCAUGUAGUUGCA	232	3.5	Cleavage	| Symbols: | Protein kinase superfamily protein | chr1:18402530-18405563 REVERSE LENGTH=1975
AT1G49790	UUAGAAUUAUCAUGUCUUGGC	138	4	Translation	| Symbols: | F-box associated ubiquitination effector family protein | chr1:18435351-18437068 REVERSE LENGTH=921
AT1G49832	UCUUCGACUGAGGUAAGCGCCU	355	4	Cleavage	| Symbols: | | chr1:18447621-18448239 FORWARD LENGTH=619
AT1G49840	UUUGGGUUUGGGUUAACUGCU	225	3	Cleavage	| Symbols: | Protein of unknown function (DUF620) | chr1:18452070-18454358 FORWARD LENGTH=1859
AT1G49920	CUUCUUCAAGAAGAUCGUCCU	132	1.5	Cleavage	| Symbols: | MuDR family transposase | chr1:18481774-18484233 REVERSE LENGTH=2382
AT1G49980	UUGACGACCAACUCCGCUCCU	170	5	Cleavage	| Symbols: | DNA/RNA polymerases superfamily protein | chr1:18507971-18513172 FORWARD LENGTH=2734
AT1G50060	UCGGCCUGAGGUUGGACGCCU	147	4	Cleavage	| Symbols: | CAP (Cysteine-rich secretory proteins, Antigen 5, and Pathogenesis-related 1 protein) superfamily protein | chr1:18551186-18552578 FORWARD LENGTH=618
AT1G50260	UGUCUUACCCGUACGUCGCUU	150	4	Cleavage	| Symbols: NTMC2TYPE5.1, NTMC2T5.1 | N-terminal-transmembrane-C2 domain type 5.1 | chr1:18617593-18621690 REVERSE LENGTH=2334
AT1G50350	UUUGAUUCACCGGAUAAACUC	175	3.5	Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: RING/U-box superfamily protein (TAIR:AT3G19950.1); Has 37 Blast hits to 37 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes
AT1G50360	UACUGGAGGACGUACAGCACU	949	4.5	Translation	| Symbols: VIIIA, ATVIIIA | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:18649747-18657376 FORWARD LENGTH=4149
AT1G50400	UCGACCACACUGUUAGGAUCU	121	3.5	Cleavage	| Symbols: | Eukaryotic porin family protein | chr1:18668155-18670546 FORWARD LENGTH=1157

AT1G50570	UUGAUCCAAGUAGCUGACUCU	4031	5 Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr1:18726235-18728289 REVERSE LENGTH=1521
AT1G50630	UUCGGACUGGAUAGGACUAGG	101	3.5 Cleavage	| Symbols: | Protein of unknown function (DUF3537) | chr1:18751456-18753669 REVERSE LENGTH=1660
AT1G50770	CAAACUGGACAAGCUACUGCU	324	3.5 Translation	| Symbols: | Aminotransferase-like, plant mobile domain family protein | chr1:18818559-18820503 REVERSE LENGTH=1899
AT1G50780	UUUUGCUUAGACUUAGAAACU	179	3 Cleavage	| Symbols: | 2Fe-2S ferredoxin-like superfamily protein | chr1:18821267-18823077 FORWARD LENGTH=972
AT1G50790	UUGAGAGCCUUGUAGUAGUCU	262	2.5 Cleavage	| Symbols: | Plant mobile domain protein family | chr1:18824050-18826488 REVERSE LENGTH=2439
AT1G51070	UCUAGUUCGCAUUUUUCGGAC	142	3.5 Translation	| Symbols: bHLH115 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:18927887-18929762 FORWARD LENGTH=1061
AT1G51210	UCACCUCGCAUCUUAGAACUG	146	5 Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr1:18987809-18989110 FORWARD LENGTH=1302
AT1G51420	UUUGCUGAACAUGUACCUCCA	119	3.5 Cleavage	| Symbols: ATSPP1, SPP1 | sucrose-phosphatase 1 | chr1:19064768-19066704 REVERSE LENGTH=1356
AT1G51690	UUUGAUCCGAGGAUGAUGGAUU	112	3.5 Translation	| Symbols: ATB ALPHA, B ALPHA | protein phosphatase 2A 55 kDa regulatory subunit B alpha isoform | chr1:19165974-19170446 FORWARD LENGTH=2255
AT1G51700	UGAGAUUGCUAGAGGAAAGAG	101	3.5 Cleavage	| Symbols: ADOF1, DOF1 | DOF zinc finger protein 1 | chr1:19174070-19175189 FORWARD LENGTH=1120
AT1G51770	UGAGGUCGAGUAGAGCAAUCUA	117	4 Cleavage	| Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:19201789-19203224 FORWARD LENGTH=1270
AT1G51802	UUUGAACUCAUGGAUACCCUA	227	4.5 Translation	| Symbols: | Encodes a defensin-like (DEFL) family protein. | chr1:19218592-19218783 REVERSE LENGTH=192
AT1G51860	UCCCAACCCAUGAUCUAAGCG	236	4.5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19257634-19261479 REVERSE LENGTH=2673
AT1G51870	UCCCAACCCAUGAUCUAAGCG	236	4 Cleavage	| Symbols: | protein kinase family protein | chr1:19262879-19267001 REVERSE LENGTH=2514
AT1G51890	UCCCAACCCAUGAUCUAAGCG	236	5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:19274658-19278528 REVERSE LENGTH=2775
AT1G51965	UUUGGGUUUGGGUUAACUGCU	225	3 Cleavage	| Symbols: ABO5 | ABA Overly-Sensitive 5 | chr1:19312078-19314145 REVERSE LENGTH=1953
AT1G52110	UUCUGAAGGACAAGCUCAGCU	1012	3.5 Cleavage	| Symbols: | Mannose-binding lectin superfamily protein | chr1:19386789-19389740 REVERSE LENGTH=1848
AT1G52347	UGACGGACAAGAUAAGCUGCU	259	3.5 Cleavage	| Symbols: | other RNA | chr1:19496506-19497703 FORWARD LENGTH=628
AT1G52360	UACCGGAGGACGUACAUAGCU	401	4.5 Cleavage	| Symbols: | Coatomer, beta' subunit | chr1:19499343-19505757 FORWARD LENGTH=3099
AT1G52530	UUGAACAAGCCUGAUGAAGUU	102	4.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Hus1-like protein (InterPro:IPR007150); Has 129 Blast hits to 128 proteins in 49 species: Archae - 0; Bacteria - 0; Metazoa - 57; Fungi - 10; Plants - 47; Viruses - 0; Other Eukaryotes - 15 (source: NCBI BL
AT1G52580	UUGAGAGCACUCCACCGACUG	261	3.5 Translation	| Symbols: ATRBL5, RBL5 | RHOMBOID-like protein 5 | chr1:19587637-19589052 FORWARD LENGTH=1024
AT1G52590	CGAGAGAUUACAGGGACUGUC	3198	5 Cleavage	| Symbols: | Putative thiol-disulphide oxidoreductase DCC | chr1:19589009-19590273 REVERSE LENGTH=776
AT1G52690	CGUCACUGCGAAUUCCUGGAG	272	4.5 Cleavage	| Symbols: | Late embryogenesis abundant protein (LEA) family protein | chr1:19619745-19621534 FORWARD LENGTH=809
AT1G52870	UGUUGAUCCAAGUAGCUGACU	608	4 Translation	| Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr1:19685747-19687863 FORWARD LENGTH=1391
AT1G52920	UCUGUAUGCAUAGCUUGGGACU	466	4 Cleavage	| Symbols: GCR2, GPCR | G protein coupled receptor | chr1:19709275-19711052 REVERSE LENGTH=1322
AT1G52950	ACAAAACUGUUGAACAAGCCU	1107	4.5 Cleavage	| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr1:19725483-19728007 FORWARD LENGTH=1701
AT1G53160	UUUGGUUCUGAGUCCCCGCCU	669	4 Translation	| Symbols: SPL4 | squamosa promoter binding protein-like 4 | chr1:19806421-19807301 FORWARD LENGTH=803
AT1G53200	UACUCGACCACACUGUUAGGA	183	4 Translation	| Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr1:19840376-19843403
AT1G53210	UACCCGUACGUCGCUUACAAG	3223	4.5 Translation	| Symbols: | sodium/calcium exchanger family protein / calcium-binding EF hand family protein | chr1:19844632-19847836 FORWARD LENGTH=2219
AT1G53233	UACCGGAGGACGUACAGCAUC	153	4.5 Translation	| Symbols: | other RNA | chr1:19850031-19852127 FORWARD LENGTH=1938
AT1G53340	UUUGGCGCUCAACUCUGCAAGG	2546	4.5 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:19898928-19900931 REVERSE LENGTH=2004
AT1G53345	UCGACCACACUGUCAUGAUCU	174	4 Cleavage	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, F mature embryo stage, petal differentiation and expansion stag
AT1G53350	UAGUGACCGAGUAGUACCACC	461	3.5 Translation	| Symbols: | Disease resistance protein (CC-NBS-LRR class) family | chr1:19903899-19907515 FORWARD LENGTH=2784
AT1G53420	AUUGUGUAUAAUUUUGAGCCU	108	3.5 Cleavage	| Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:19926626-19931494 REVERSE LENGTH=2862
AT1G53440	AUUGUGUAUAAUUUUGAGCCU	108	4 Cleavage	| Symbols: | Leucine-rich repeat transmembrane protein kinase | chr1:19945959-19951562 FORWARD LENGTH=3108
AT1G53450	UGAGAUUGCUAGAGGAAAGAG	101	3 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G14830.2); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Vi
AT1G53645	UGACGGUUCAGAUUCAGGAGC	107	3 Translation	| Symbols: | hydroxyproline-rich glycoprotein family protein | chr1:20026147-20028635 REVERSE LENGTH=1907
AT1G53708	UAAGGAGAGUCAGCUACUUGGA	134	4 Cleavage	| Symbols: RTFL9 | ROTUNDIFOLIA like 9 | chr1:20052393-20053195 FORWARD LENGTH=630
AT1G53710	UCCAAGUAGCUGACUCUCCUU	596	3.5 Translation	| Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr1:20053259-20056318 REVERSE LENGTH=1797
AT1G53800	UGACGGACAAGAUAAGCUGCU	259	3.5 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53250.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Vi
AT1G53910	AUACCCAAACCUGAACUUUCU	127	4 Translation	| Symbols: RAP2.12 | related to AP2 12 | chr1:20135112-20136941 FORWARD LENGTH=1453
AT1G54090	UCAACACUCUGAUACAUCUAG	143	3 Cleavage	| Symbols: ATEXO70D2, EXO70D2 | exocyst subunit exo70 family protein D2 | chr1:20189567-20191900 FORWARD LENGTH=2334
AT1G54115	UAUGGAGAUGAUCGCAAUGGC	937	4.5 Cleavage	| Symbols: ATCCX4, CCX4 | cation calcium exchanger 4 | chr1:20202118-20204177 FORWARD LENGTH=2060
AT1G54340	UGCUCGUAUCAUACUCCUCCU	194	3.5 Cleavage	| Symbols: ICDH | isocitrate dehydrogenase | chr1:20283480-20286786 FORWARD LENGTH=1571
AT1G54710	UAGAAUUAUCAUGUCUUGGCA	194	4 Cleavage	| Symbols: ATATG18H, ATG18H | homolog of yeast autophagy 18 (ATG18) H | chr1:20416770-20421035 REVERSE LENGTH=3335
AT1G54730	UUUAAAACCGAGGACUUUUGC	115	3 Cleavage	| Symbols: | Major facilitator superfamily protein | chr1:20424410-20430123 FORWARD LENGTH=1980
AT1G54820	UAGUGACCGAGUAGUACCACC	461	5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr1:20447316-20450861 FORWARD LENGTH=1531
AT1G54840	UCCCAACCCAUGAUCUAAGCG	236	4 Cleavage	| Symbols: | HSP20-like chaperones superfamily protein | chr1:20452593-20454249 REVERSE LENGTH=1320
AT1G54980	UUGGCGCUCAACUCUGCAAGG	4868	3 Cleavage	| Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily protein | chr1:20507375-20508355 REVERSE LENGTH=543
AT1G55040	AUUGACGUCGAGUAUGAGCCU	2734	4.5 Cleavage	| Symbols: | zinc finger (Ran-binding) family protein | chr1:20534874-20539113 FORWARD LENGTH=2783
AT1G55250	UUUGGCACUCAACUCUGCAAG	1274	4.5 Cleavage	| Symbols: | histone mono-ubiquitination 2 | chr1:20610119-20612378 FORWARD LENGTH=1275
AT1G55280	UUUGAUCCGAGGAUGAUGGAUU	112	4.5 Cleavage	| Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr1:20622960-20624630 REVERSE LENGTH=1409
AT1G55350	UUCCAGCGUUCUGUAGCCAAC	156	3 Cleavage	| Symbols: DEK1, ATDEK1 | calpain-type cysteine protease family | chr1:20653820-20664622 REVERSE LENGTH=7133
AT1G55380	UUGGCGCUCAACUCUGCAAGG	4868	4 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:20676622-20678607 REVERSE LENGTH=1986
AT1G55390	UUUGGCGCUCAACUCUGCAAG	3787	4 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:20680876-20683043 REVERSE LENGTH=2168
AT1G55410	UGGCGCUCAACUCUGCAAGGU	10625	4 Cleavage	| Symbols: | pseudogene, CHP-rich zinc finger protein, putative, similar to putative CHP-rich zinc finger protein GB:CAB77744 GI:7268217 from (Arabidopsis thaliana) | chr1:20688614-20691034 REVERSE LENGTH=2421
AT1G55420	UUGGCGCUCAACUCUGCAAGG	4868	4 Translation	| Symbols: EDA11 | Cysteine/Histidine-rich C1 domain family protein | chr1:20691775-20693952 REVERSE LENGTH=2178
AT1G55430	UUCUGAAGGACAAGCUCAGCU	1012	3 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:20697649-20699622 REVERSE LENGTH=1974
AT1G55440	UUUGGCGCUCAACUCUGCAAGG	2546	4.5 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr1:20701499-20703460 REVERSE LENGTH=1962
AT1G55480	UAGAAUUAUCAUGUCUUGGCA	194	3.5 Cleavage	| Symbols: ZKT | protein containing PDZ domain, a K-box domain, and a TPR region | chr1:20713684-20715547 FORWARD LENGTH=1342
AT1G55740	UACCGGAGGACGUACAUAGCU	401	4 Cleavage	| Symbols: AtSIP1, SIP1 | seed imbibition 1 | chr1:20835366-20838778 REVERSE LENGTH=2477
AT1G55750	UCCGCUAGAUAUAUCAAACUG	281	4 Translation	| Symbols: | BSD domain (BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins) | chr1:20840195-20845182 REVERSE LENGTH=2077
AT1G55760	UUCCCCUAGAAUUCUUUCCCU	1646	2 Cleavage	| Symbols: | BTB/POZ domain-containing protein | chr1:20846908-20849054 REVERSE LENGTH=1746
AT1G55790	UUGACGACCAACUCCGCUCCU	170	4 Translation	| Symbols: | Domain of unknown function (DUF2431) | chr1:20852324-20856122 REVERSE LENGTH=1769
AT1G55810	UUUGCCUGUUGAACUCGAGUA	114	3.5 Cleavage	| Symbols: UKL3 | uridine kinase-like 3 | chr1:20860628-20864266 FORWARD LENGTH=1870
AT1G55860	UUCCAGAACUAAUGAAUGUUA	448	3 Cleavage	| Symbols: UPL1 | ubiquitin-protein ligase 1 | chr1:20879466-20893268 REVERSE LENGTH=11745
AT1G56190	CAAAUUCGAGAACUCCCUGAC	283	4 Cleavage	| Symbols: | Phosphoglycerate kinase family protein | chr1:21028216-21030614 FORWARD LENGTH=1689
AT1G56240	UGAGAAGAGAUAGAAUAGAAUC	103	3.5 Cleavage	| Symbols: AtPP2-B13, PP2-B13 | phloem protein 2-B13 | chr1:21056232-21057577 REVERSE LENGTH=1142
AT1G56340	UGUCCCAACUUAACUCUACCCU	279	4 Cleavage	| Symbols: CRT1, CRT1a, AtCRT1a | calreticulin 1a | chr1:21089880-21092659 REVERSE LENGTH=1446
AT1G56350	CCUGAGCCUAGUGACCGAGUA	270	4 Cleavage	| Symbols: | Peptide chain release factor 2 | chr1:21094778-21097988 FORWARD LENGTH=1673
AT1G56440	UAAUAAGGAGAGUCAGCUACU	298	4 Cleavage	| Symbols: TPR5 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:21138530-21141571 REVERSE LENGTH=1755
AT1G56490	UUCCAGAACUAAUGAAUGUUA	448	3.5 Cleavage	| Symbols: | pseudogene, pectinesterase, blastp match of 38% identity and 1.5e-56 P-value to GP|14495216|dbj|BAB60935.1||AP003578 putative pectin methylesterase {Oryza sativa (japonica cultivar-group)} | chr1:21155295-21157567 REVER
AT1G56550	UCGAGGGCAGGAACAUUGACU	334	3.5 Translation	| Symbols: RXGT1 | RhamnoGalacturonan speciﬁc Xylosyltransferase 1 | chr1:21185662-21188369 REVERSE LENGTH=1625
AT1G56612	UUCUUGUGAACUUGACCGGGA	158	3.5 Translation	| Symbols: | other RNA | chr1:21214158-21215389 REVERSE LENGTH=803
AT1G56690	CAUCAAGAACCGGUCAUGCCU	125	4 Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:21253817-21255931 FORWARD LENGTH=2115
AT1G57600	UUGUGAGUGUUUGUGAGGUCU	141	3 Cleavage	| Symbols: | MBOAT (membrane bound O-acyl transferase) family protein | chr1:21330512-21334727 REVERSE LENGTH=1950
AT1G57790	UGCACUCGCUAGGUCUGGCAG	378	4.5 Cleavage	| Symbols: | F-box family protein | chr1:21404408-21405956 REVERSE LENGTH=1318
AT1G57830	UCUAUAGCCAAUGUACUCUACU	106	4.5 Translation	| Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr1:21420309-21420803 FORWARD LENGTH=495
AT1G57980	UUGGGAGAACUAUGACACGAG	515	3.5 Translation	| Symbols: | Nucleotide-sugar transporter family protein | chr1:21439232-21440805 REVERSE LENGTH=1470
AT1G58025	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: | DNA-binding bromodomain-containing protein | chr1:21458123-21462196 REVERSE LENGTH=1960
AT1G58030	UCCUGAGUACUCUCUUCCAAG	209	3 Translation	| Symbols: CAT2 | cationic amino acid transporter 2 | chr1:21464001-21468420 REVERSE LENGTH=2371
AT1G58060	UAAGCAUUUUGAUUCACCGGA	285	4 Cleavage	| Symbols: | RNA helicase family protein | chr1:21489285-21501811 REVERSE LENGTH=4611
AT1G58190	UUGGACGUCUCUACUAUGAGA	437	4 Cleavage	| Symbols: AtRLP9, RLP9 | receptor like protein 9 | chr1:21540632-21544398 FORWARD LENGTH=2955
AT1G58200	UAUAGGGCUUGAAAGAAAGUC	535	2.5 Cleavage	| Symbols: MSL3 | MSCS-like 3 | chr1:21548187-21553085 REVERSE LENGTH=2517
AT1G58330	UCAACACUCUGAUACAUCUAG	143	3 Cleavage	| Symbols: ZW2 | transcription factor-related | chr1:21641130-21642041 FORWARD LENGTH=912
AT1G58350	UCCAAGUAGCUGACUCUCCUU	596	4 Translation	| Symbols: ZW18 | Putative serine esterase family protein | chr1:21662918-21667438 REVERSE LENGTH=2788
AT1G59453	UAGGCCUGAGAUUGGACGCCU	875	4 Cleavage	| Symbols: | B-block binding subunit of TFIIIC | chr1:21846902-21853384 REVERSE LENGTH=5190
AT1G59540	UAAGACUGAGAUACGCGUGCCU	152	4 Cleavage	| Symbols: ZCF125 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:21874012-21879539 FORWARD LENGTH=2735
AT1G59610	UGCAUAACUUGGGACUUACCU	413	3.5 Cleavage	| Symbols: ADL3, CF1, DRP2B, DL3 | dynamin-like 3 | chr1:21893221-21901086 FORWARD LENGTH=3261

AT1G59630	UUGUGAGUGUUUGUGAGGUCU	141	4	Translation	| Symbols: | F-box associated ubiquitination effector family protein | chr1:21907177-21907955 REVERSE LENGTH=720
AT1G59840	UUGGUCACACAGUGGACUGUG	104	3.5	Cleavage	| Symbols: CCB4 | cofactor assembly of complex C | chr1:22026546-22028419 FORWARD LENGTH=1162
AT1G59885	UACGAGACUCUAGCCCAGCUU	307	4.5	Translation	| Symbols: | unknown protein; Has 0 Blast hits to 0 proteins in 0 species (source: NCBI BLink). | chr1:22042308-22042815 FORWARD LENGTH=390
AT1G59900	UGAGAACGCUCUGCCAUUGGA	158	4	Cleavage	| Symbols: AT-E1 ALPHA, E1 ALPHA | pyruvate dehydrogenase complex E1 alpha subunit | chr1:22051295-22053885 FORWARD LENGTH=1468
AT1G60000	UAUCUCUGUCGUUACGAACCU	295	3	Translation	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:22093569-22094626 REVERSE LENGTH=972
AT1G60160	UGAGAACAUUGACUUCAGACCU	158	4	Cleavage	| Symbols: | Potassium transporter family protein | chr1:22188114-22191395 REVERSE LENGTH=2700
AT1G60300	UACUGGAGGACGUACAGCACU	949	5	Cleavage	| Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:22229780-22230748 REVERSE LENGTH=969
AT1G60380	UACUGGAGGACGUACAGCACU	949	4.5	Cleavage	| Symbols: | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:22246455-22247411 REVERSE LENGTH=957
AT1G60505	UGUGGAUACAAGAGCUGGGCU	215	4	Cleavage	| Symbols: | other RNA | chr1:22294677-22297220 REVERSE LENGTH=1928
AT1G60545	UGUGGAUACAAGAGCUGGGCU	215	4	Cleavage	| Symbols: | other RNA | chr1:22302492-22305156 FORWARD LENGTH=2305
AT1G60800	UUUUGCUUAGACUUAGAAACU	179	4	Cleavage	| Symbols: NIK3 | NSP-interacting kinase 3 | chr1:22383453-22387457 REVERSE LENGTH=2573
AT1G60850	UCAUAUGGACUUUGGCUACACC	101	3	Translation	| Symbols: ATRPAC42, AAC42 | DNA-directed RNA polymerase family protein | chr1:22397916-22400362 REVERSE LENGTH=1380
AT1G60860	UUUGGCACUCAACUCUGCAAG	1274	4	Translation	| Symbols: AGD2 | ARF-GAP domain 2 | chr1:22400927-22407777 REVERSE LENGTH=2786
AT1G60930	UCGAGUGACUUUGGAGCCAUU	244	3.5	Cleavage	| Symbols: RECQL4B, ATRECQ4B, RECQ4B | RECQ helicase L4B | chr1:22430847-22438877 REVERSE LENGTH=3877
AT1G60960	UGUGAGUGUUUGUGAGGUCUU	178	3.5	Translation	| Symbols: IRT3, ATIRT3 | iron regulated transporter 3 | chr1:22445310-22447214 REVERSE LENGTH=1532
AT1G60970	UCACUCGACCACAACAGGCUG	106	4	Translation	| Symbols: | SNARE-like superfamily protein | chr1:22447848-22449526 REVERSE LENGTH=833
AT1G61030	AUUUCAGUGAGCACGUACCUC	200	4	Cleavage	| Symbols: | WAPL (Wings apart-like protein regulation of heterochromatin) protein | chr1:22477896-22482380 FORWARD LENGTH=2896
AT1G61170	UUCGAGGAGAUAUGACGCGCC	4887	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 19 plant structures; EXPRESSED DURING: 12 growth stage
AT1G61215	UCCACCGACUGAUGACAAUGU	1524	5	Cleavage	| Symbols: BRD4 | bromodomain 4 | chr1:22572645-22575527 FORWARD LENGTH=2109
AT1G61240	CCUGAGCCUAGUGACCGAGUA	270	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF707) | chr1:22582024-22585203 FORWARD LENGTH=1674
AT1G61250	UCUAGUCCGAAAAAUGCGAAC	163	4.5	Cleavage	| Symbols: SC3 | secretory carrier 3 | chr1:22585899-22588905 FORWARD LENGTH=1247
AT1G61330	UGAGAGCACUCCACCGACUGA	230	4	Cleavage	| Symbols: | FBD, F-box and Leucine Rich Repeat domains containing protein | chr1:22622975-22624527 FORWARD LENGTH=1344
AT1G61360	UGUGGAUACAAGAGUUGGGCU	111	3.5	Cleavage	| Symbols: | S-locus lectin protein kinase family protein | chr1:22637728-22641825 REVERSE LENGTH=2825
AT1G61460	UCGAGUAUGAGCCUGAGUCAUG	250	3.5	Cleavage	| Symbols: | S-locus protein kinase, putative | chr1:22674198-22677713 REVERSE LENGTH=2585
AT1G61660	UCCAGUCUGAAGAACGCGAAC	136	5	Cleavage	| Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr1:22753736-22756300 REVERSE LENGTH=1521
AT1G61750	UGACGGACAAGAUAAGUUGCU	1505	4	Translation	| Symbols: | Receptor-like protein kinase-related family protein | chr1:22804613-22806318 REVERSE LENGTH=1026
AT1G61795	UUUUAAUUCAAGUAGCUGACU	133	4	Translation	| Symbols: | PAK-box/P21-Rho-binding family protein | chr1:22819632-22821029 FORWARD LENGTH=901
AT1G61820	UAUAGGGCUUGAAAGAAAGUC	535	3.5	Cleavage	| Symbols: BGLU46 | beta glucosidase 46 | chr1:22835078-22838615 FORWARD LENGTH=2096
AT1G61890	UCUGAACUCAAGGCACCCAAA	493	3.5	Cleavage	| Symbols: | MATE efflux family protein | chr1:22867770-22871280 REVERSE LENGTH=1956
AT1G61900	UUGUGGAAUCCGUAGUCUGUA	152	3.5	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G30700.1). | chr1:22882215-22885052 REVERSE LENGTH=1913
AT1G61940	CUACAAAUUCGAGCACUCCCU	156	4.5	Cleavage	| Symbols: AtTLP4, TLP4 | tubby like protein 4 | chr1:22897399-22898575 REVERSE LENGTH=735
AT1G61950	UGAGAACAUUGACUUCAGACCU	158	3.5	Cleavage	| Symbols: CPK19 | calcium-dependent protein kinase 19 | chr1:22899417-22901946 FORWARD LENGTH=1661
AT1G61990	UUACCCGUACGUCGCUUACAG	129	5	Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr1:22911205-22912935 FORWARD LENGTH=1731
AT1G62020	UGUGUAUGCAUAACUUGGGAC	106	3.5	Translation	| Symbols: | Coatomer, alpha subunit | chr1:22919534-22924024 FORWARD LENGTH=4098
AT1G62050	UUCUUCCCGUUGGUGUGCGCC	170	3.5	Cleavage	| Symbols: | Ankyrin repeat family protein | chr1:22936127-22939024 REVERSE LENGTH=2221
AT1G62085	UUACCCGUACGUCGCUUACAG	129	5	Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr1:22948757-22950142 REVERSE LENGTH=1386
AT1G62120	UACCCGUACGUCGCCUACAAG	192	5	Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr1:22960191-22961779 REVERSE LENGTH=1589
AT1G62150	UACCCGUACGUCGCUUACAAG	3223	4.5	Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr1:22970029-22971764 REVERSE LENGTH=1736
AT1G62305	AUUGAUUCUGCACUCAAGGGC	128	3	Translation	| Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:23026776-23029339 REVERSE LENGTH=1428
AT1G62330	UAUUGAUUUUUGGCCUGAGGU	116	4	Translation	| Symbols: | O-fucosyltransferase family protein | chr1:23046893-23050193 FORWARD LENGTH=2171
AT1G62490	UACCCGUACGUCGCCUACAAG	192	4.5	Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr1:23130405-23131533 REVERSE LENGTH=1005
AT1G62500	CUCACAAGUGAUAUAGGGCUU	208	3	Cleavage	| Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr1:23132045-23133502 FORWARD LENGTH=1458
AT1G62540	UUGGCGCUCAACUCUGCAAGG	4868	4.5	Cleavage	| Symbols: FMO GS-OX2 | flavin-monooxygenase glucosinolate S-oxygenase 2 | chr1:23151794-23155717 FORWARD LENGTH=1740
AT1G62560	UUGGACGCCUCUACUAUGAGA	679	3.5	Translation	| Symbols: FMO GS-OX3 | flavin-monooxygenase glucosinolate S-oxygenase 3 | chr1:23159823-23162649 FORWARD LENGTH=1576
AT1G62590	AUUGUGUAUAAUUUUGAGCCU	108	4	Cleavage	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:23176930-23179248 REVERSE LENGTH=2212
AT1G62740	UGAGUAGAAUUCGAUCAUAUC	114	3.5	Cleavage	| Symbols: Hop2 | stress-inducible protein, putative | chr1:23230956-23233543 FORWARD LENGTH=1949
AT1G62750	ACAAAACUGUUGAACAAGCCU	1107	4.5	Cleavage	| Symbols: ATSCO1, ATSCO1/CPEF-G, SCO1 | Translation elongation factor EFG/EF2 protein | chr1:23233434-23236447 REVERSE LENGTH=2666
AT1G62810	UUCGAGAACUCCCUGACCCGA	1272	5	Translation	| Symbols: | Copper amine oxidase family protein | chr1:23257726-23261966 REVERSE LENGTH=2860
AT1G62860	UACUGGAGGACGUACAGCACU	949	5	Cleavage	| Symbols: | pseudogene of pentatricopeptide (PPR) repeat-containing protein | chr1:23274676-23277017 REVERSE LENGTH=2342
AT1G62950	UCAAGAACUCCAACCCUUCACU	144	3	Cleavage	| Symbols: | leucine-rich repeat transmembrane protein kinase family protein | chr1:23315294-23318234 FORWARD LENGTH=2846
AT1G63100	CGUCACUGCGAAUUCCUGGAG	272	4	Cleavage	| Symbols: | GRAS family transcription factor | chr1:23399391-23401367 REVERSE LENGTH=1977
AT1G63170	AUACCCAAACCUGAACUUUCU	127	4	Cleavage	| Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr1:23425352-23427311 FORWARD LENGTH=1606
AT1G63230	UGUCACCGUAGAUUUCUUCCU	123	2	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:23450654-23452311 FORWARD LENGTH=1572
AT1G63430	UAAGGAGAGUCAGCUACUUGGA	134	3.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:23522608-23526770 FORWARD LENGTH=2602
AT1G63440	UGAAUGACAAACUGGACAAGCU	583	3.5	Cleavage	| Symbols: HMA5 | heavy metal atpase 5 | chr1:23527655-23531109 FORWARD LENGTH=2988
AT1G63450	UUGGACGUCUCUACUAUGAGA	437	3.5	Cleavage	| Symbols: RHS8 | root hair specific 8 | chr1:23531409-23534569 FORWARD LENGTH=3161
AT1G63480	CCGAUUCUGAUUGCAUGUGGU	186	4	Cleavage	| Symbols: | AT hook motif DNA-binding family protein | chr1:23539557-23542137 REVERSE LENGTH=1853
AT1G63490	UAUGCAUAACUUGGGACUUACC	333	4.5	Cleavage	| Symbols: | transcription factor jumonji (jmjC) domain-containing protein | chr1:23544656-23552030 REVERSE LENGTH=3717
AT1G63520	UAACAAGAACUCUUUCUUUUCU	235	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF3527) | chr1:23559887-23562143 FORWARD LENGTH=2073
AT1G63530	UAUAGGGCUUGAAAGAAAGUC	535	2.5	Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: hydroxyproline-rich glycoprotein family protein (TAIR:AT1G63540.1); Has 10212 Blast hits to 4024 proteins in 434 species: Archae - 1; Bacteria - 1259; Metazoa - 3608; Fungi - 2247; Plants -
AT1G63570	UUUAGGAUUGUUGCAUAUGCA	1164	4.5	Cleavage	| Symbols: | Receptor-like protein kinase-related family protein | chr1:23575450-23576304 FORWARD LENGTH=855
AT1G63640	UGGCGCUCAACUCUGCAAGGU	10625	3	Cleavage	| Symbols: | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | chr1:23589067-23595775 REVERSE LENGTH=3585
AT1G63710	UUUUGAUUCACCGGAUAAACUC	104	4	Translation	| Symbols: CYP86A7 | cytochrome P450, family 86, subfamily A, polypeptide 7 | chr1:23632178-23633942 REVERSE LENGTH=1765
AT1G63760	UGAGAACGCUCUGCCAUUGGA	158	4	Cleavage	| Symbols: ARI6, ATARI6 | pseudogene, ARI protein, similar to ARI protein (A Drosophila RING Finger Motif Involved in Axonal Path-finding in the Central Nervous System) GB:CAA66953 (Drosophila melanogaster); blastp match of 86% identity and
AT1G63820	UUCAACUCUUCCCUCUCGAACU	119	3	Cleavage	| Symbols: | CCT motif family protein | chr1:23682422-23684367 REVERSE LENGTH=1306
AT1G63850	UAGAAUUAUCAUGUCUUGGCA	194	4	Cleavage	| Symbols: | BTB/POZ domain-containing protein | chr1:23696962-23698708 FORWARD LENGTH=1647
AT1G64060	UAUGCUUCUGUUGAUCCACCU	344	3.5	Cleavage	| Symbols: ATRBOH F, ATRBOHF, RBOHAP108, RBOHF, RBOH F | respiratory burst oxidase protein F | chr1:23769774-23776931 FORWARD LENGTH=3941
AT1G64300	UUAGGCCUGAGAUUGGACGCC	196	4.5	Cleavage	| Symbols: | Protein kinase family protein | chr1:23863066-23866045 FORWARD LENGTH=2721
AT1G64350	UGAAUAAAACUGAACCAUGCC	263	3.5	Cleavage	| Symbols: SEH1H | Transducin/WD40 repeat-like superfamily protein | chr1:23881512-23883297 FORWARD LENGTH=1275
AT1G64430	CUCGGGAGAAAGAAGAAGGCU	259	3.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:23933380-23936867 FORWARD LENGTH=2372
AT1G64540	UGACGCCAAUUCUGAAAGUUU	154	3.5	Cleavage	| Symbols: | F-box/FBD-like domains containing protein | chr1:23966909-23968425 FORWARD LENGTH=1335
AT1G64570	CAUCAAGAACCGGUCAUGCCU	125	2.5	Cleavage	| Symbols: DUO3 | Homeodomain-like superfamily protein | chr1:23978868-23983925 FORWARD LENGTH=3720
AT1G64585	AUUGUGUAUAAUUUUGAGCCU	108	3.5	Cleavage	| Symbols: RTFL22, DVL12 | ROTUNDIFOLIA like 22 | chr1:23989933-23990097 REVERSE LENGTH=165
AT1G64740	UUGAGAGCACUCCACCGACUG	261	4	Cleavage	| Symbols: TUA1 | alpha-1 tubulin | chr1:24050006-24052487 FORWARD LENGTH=1652
AT1G64790	UAAAACUGAACCAUGCCUAGA	302	3.5	Translation	| Symbols: ILA | ILITYHIA | chr1:24065014-24083428 REVERSE LENGTH=8334
AT1G64800	AAUUCGAGAACUCCCUGACCC	255	4	Cleavage	| Symbols: | DNA binding;sequence-specific DNA binding transcription factors | chr1:24085086-24085433 FORWARD LENGTH=348
AT1G64840	UCGGCUCAAACCUAACACGUU	129	4	Translation	| Symbols: | Protein of unknown function (DUF295) | chr1:24093558-24095399 FORWARD LENGTH=1637
AT1G64980	UGUGGUGUACCUCUUACGUCU	106	5	Cleavage	| Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr1:24137517-24139276 REVERSE LENGTH=1235
AT1G65190	UUUCUGACGGACAAGAUAAGU	480	3	Cleavage	| Symbols: | Protein kinase superfamily protein | chr1:24215644-24217328 REVERSE LENGTH=1685
AT1G65280	UACCGGAGGACGUACAUAGCU	401	4.5	Cleavage	| Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:24245296-24248762 FORWARD LENGTH=2132
AT1G65320	UUGGUCACACAGUGGACUGUG	104	4.5	Cleavage	| Symbols: | Cystathionine beta-synthase (CBS) family protein | chr1:24259888-24262951 REVERSE LENGTH=1865
AT1G65365	UCUAUAGCCAAUGUACUCUACU	106	3	Cleavage	| Symbols: | pseudogene, putative protein kinase, blastp match of 45% identity and 1.7e-40 P-value to GP|21671940|gb|AAM74302.1|AC083944_20|AC083944 Putative protein kinase {Oryza sativa (japonica cultivar-group)} | chr1:24282516-24
AT1G65410	UUCUUCAGACUGGAUAGGACU	265	3.5	Cleavage	| Symbols: ATNAP11, TGD3, NAP11 | non-intrinsic ABC protein 11 | chr1:24295169-24297595 FORWARD LENGTH=1494
AT1G65420	UACGUCACUGCGAAUUCCUGGA	271	4	Translation	| Symbols: NPQ7 | Protein of unknown function (DUF565) | chr1:24297480-24298570 REVERSE LENGTH=979
AT1G65430	UUCUUCGGACUGGAUAGGACU	102	3.5	Translation	| Symbols: ARI8, ATARI8 | IBR domain-containing protein | chr1:24300898-24306236 REVERSE LENGTH=2048
AT1G65760	CAAAUUCGAGAACUCCCUGAC	283	4	Cleavage	| Symbols: | Protein of unknown function (DUF295) | chr1:24458591-24459715 FORWARD LENGTH=1089
AT1G65780	UGAGAGCACUCCACCGACUGA	230	4	Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:24462958-24466888 REVERSE LENGTH=3198
AT1G65860	UGAAGGACAAGCUCAGCUGCU	1483	3	Cleavage	| Symbols: FMO GS-OX1 | flavin-monooxygenase glucosinolate S-oxygenase 1 | chr1:24499066-24502745 REVERSE LENGTH=1591
AT1G65875	UACAGAAUAGGCUUAAGUAAC	189	5	Cleavage	| Symbols: | pseudogene, similar to EST AU070346(S12172) corresponds to a region of the predicted gene.~similar to AMP-binding protein. (X94625), blastp match of 57% identity and 4.5e-137 P-value to GP|6063549|dbj|BAA85409.1||AP0006

AT1G65880	UGUAUGCAUAACUUGGGACUU	149	4 Translation	| Symbols: BZO1 | benzoyloxyglucosinolate 1 | chr1:24508633-24510742 REVERSE LENGTH=1748
AT1G65890	UGUAUGCAUAACUUGGGACUU	149	4 Translation	| Symbols: AAE12 | acyl activating enzyme 12 | chr1:24512457-24514659 REVERSE LENGTH=1926
AT1G65910	UAUUGAUUUUUGGCCUGAGGU	116	3.5 Cleavage	| Symbols: anac028, NAC028 | NAC domain containing protein 28 | chr1:24520791-24524164 REVERSE LENGTH=2094
AT1G66173	UACGCGACCGCGGUGCUGGCC	119	4.5 Cleavage	| Symbols: | other RNA | chr1:24642586-24644068 FORWARD LENGTH=1483
AT1G66270	UUCUGACGGACAAGAUAAGCU	313	3.5 Cleavage	| Symbols: BGLU21 | Glycosyl hydrolase superfamily protein | chr1:24699990-24703041 REVERSE LENGTH=1735
AT1G66370	UGAAGGACAAGAUCAGCUGCU	415	2.5 Cleavage	| Symbols: MYB113, AtMYB113 | myb domain protein 113 | chr1:24753634-24754604 FORWARD LENGTH=741
AT1G66410	UCGGCUCAAACCUAACACGUU	129	4.5 Cleavage	| Symbols: CAM4 | calmodulin 4 | chr1:24774260-24775984 REVERSE LENGTH=850
AT1G66490	CAUCAAGAACCGGUCAUGCCU	125	3.5 Cleavage	| Symbols: | F-box and associated interaction domains-containing protein | chr1:24809421-24810549 REVERSE LENGTH=1083
AT1G66620	UAGCUAACAAGAACUCUUUCU	1828	4 Translation	| Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24852806-24854153 REVERSE LENGTH=1051
AT1G66660	UCUCAUGUAGUUCUAGUUCGCA	1437	3 Cleavage	| Symbols: | Protein with RING/U-box and TRAF-like domains | chr1:24861876-24863368 REVERSE LENGTH=1195
AT1G66830	UCAAGCGAUUGGAAGGAUUGUU	102	3.5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:24930665-24932918 REVERSE LENGTH=2177
AT1G66890	UCUGGGUAGAUGGGAUCUUAUC	123	3 Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match
AT1G66900	UUCCAGCGUUCUGUAGCCAAC	156	4.5 Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:24959334-24961616 FORWARD LENGTH=1398
AT1G66970	UGAGAGCACUCCACCGACUGA	230	4 Translation	| Symbols: SVL2 | SHV3-like 2 | chr1:24992553-24996117 REVERSE LENGTH=2663
AT1G67020	UCUGAACUCAAGGCACCCAAA	493	3.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; Has 72 Blast hits to 72 proteins in 9 species: Archae - 0; Ba
AT1G67090	UUGAAAGACUUGUGGAUCACC	926	3 Cleavage	| Symbols: RBCS1A | ribulose bisphosphate carboxylase small chain 1A | chr1:25048158-25049424 REVERSE LENGTH=1018
AT1G67120	UUCUUCAGACUGGAUAGGACU	265	2.5 Cleavage	| Symbols: | ATPases;nucleotide binding;ATP binding;nucleoside-triphosphatases;transcription factor binding | chr1:25069562-25095526 REVERSE LENGTH=16347
AT1G67130	UACUGGAGGACGUACAGCACU	949	4 Cleavage	| Symbols: | F-box family protein | chr1:25099262-25100625 REVERSE LENGTH=1176
AT1G67140	UAAGCAUUUUGAUUCACCGGA	285	3.5 Translation	| Symbols: SWEETIE | HEAT repeat-containing protein | chr1:25100908-25117372 REVERSE LENGTH=6774
AT1G67300	UGAAGGAUUUGUGGUUAACCA	474	4.5 Cleavage	| Symbols: | Major facilitator superfamily protein | chr1:25193704-25197089 REVERSE LENGTH=1811
AT1G67310	UGACGUCGAGUAUGAGCCUGA	416	4 Translation	| Symbols: | Calmodulin-binding transcription activator protein with CG-1 and Ankyrin domains | chr1:25198182-25203126 REVERSE LENGTH=3051
AT1G67320	UUGACUUCAGACCUGCGCGUG	131	5 Cleavage	| Symbols: | DNA primase, large subunit family | chr1:25205279-25209033 REVERSE LENGTH=1673
AT1G67340	UAAAACUGAACCAUGCCUAGA	302	2.5 Translation	| Symbols: | HCP-like superfamily protein with MYND-type zinc finger | chr1:25230265-25231840 FORWARD LENGTH=1416
AT1G67420	UGAGAACGCUCUGCCAUUGGA	158	4.5 Translation	| Symbols: | Zn-dependent exopeptidases superfamily protein | chr1:25255411-25260429 FORWARD LENGTH=2690
AT1G67510	UGACGGACAAGAUAAGUUGCU	1505	4 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:25297477-25300184 REVERSE LENGTH=2160
AT1G67550	CAUUGACUUCAAGCCUGCGCU	190	4.5 Translation	| Symbols: URE | urease | chr1:25312740-25317395 FORWARD LENGTH=3103
AT1G67610	UACACAAAGGGCUCCUCGCACC	211	4 Cleavage	| Symbols: | pseudogene, hypothetical protein | chr1:25339036-25340241 REVERSE LENGTH=1206
AT1G67645	UACACAAAGGGCUCCUCGCACC	211	4 Cleavage	| Symbols: | pseudogene, hypothetical protein | chr1:25354910-25356112 FORWARD LENGTH=1203
AT1G67720	CAAGAACCCGCACGACACUCG	169	3.5 Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr1:25386341-25391073 FORWARD LENGTH=3160
AT1G67750	UUAGCACCGAGGAUGAUGGACU	330	3 Translation	| Symbols: | Pectate lyase family protein | chr1:25401588-25403503 FORWARD LENGTH=1637
AT1G67780	UUUUGCUUAGACUUAGAAACU	179	3.5 Translation	| Symbols: | Zinc-finger domain of monoamine-oxidase A repressor R1 protein | chr1:25412816-25415530 FORWARD LENGTH=1539
AT1G67792	UUUGCUGAACAUGUACCUCCA	119	3.5 Cleavage	| Symbols: | other RNA | chr1:25417609-25420229 FORWARD LENGTH=2524
AT1G67930	UUCUGUAGCACGAGGUAUCCU	302	3.5 Cleavage	| Symbols: | Golgi transport complex protein-related | chr1:25474140-25477423 REVERSE LENGTH=2668
AT1G67960	UGUCACCGUAGAUUUCUUCCU	123	3.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Membrane protein,Tapt1/CMV receptor (InterPro:IPR008010); Has 447 Blast hits to 428 proteins in 176 species: Archae - 0; Bacteria - 0; Metazoa - 190; Fungi - 133; Plants - 49; Viruses - 0; Other Eukar
AT1G67980	UUACGAGACUCUAGCCCAGCU	3733	5 Cleavage	| Symbols: CCOAMT | caffeoyl-CoA 3-O-methyltransferase | chr1:25487714-25489158 FORWARD LENGTH=931
AT1G68170	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr1:25551922-25554258 FORWARD LENGTH=1074
AT1G68510	UGUGGUCGAGUAGAGCAAUCU	111	3.5 Cleavage	| Symbols: LBD42 | LOB domain-containing protein 42 | chr1:25706882-25708255 FORWARD LENGTH=1104
AT1G68530	UGUGGUCGAGUAGAGCAAUCU	111	4 Cleavage	| Symbols: CUT1, POP1, CER6, G2, KCS6 | 3-ketoacyl-CoA synthase 6 | chr1:25712588-25714807 REVERSE LENGTH=2220
AT1G68540	UCAGUAGAAUUCGAUCAUAUC	104	3.5 Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr1:25720024-25721410 FORWARD LENGTH=1055
AT1G68600	UUGGCGCUCAACUCUGCAAGG	4868	4.5 Translation	| Symbols: | Aluminium activated malate transporter family protein | chr1:25759842-25762934 FORWARD LENGTH=1875
AT1G68640	UUCAGGGUGAGAACAUUGACU	1291	4 Cleavage	| Symbols: PAN | bZIP transcription factor family protein | chr1:25769576-25772543 REVERSE LENGTH=1762
AT1G68690	UGAGACACAACAGGGAGAUUC	244	2.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr1:25788608-25792324 FORWARD LENGTH=3050
AT1G68720	AUUGAUUCUGCACUCAAGGGC	128	4 Translation	| Symbols: TADA, ATTADA | tRNA arginine adenosine deaminase | chr1:25804418-25808982 FORWARD LENGTH=4215
AT1G68750	UCACCUCGCAUCUUAGAACUG	146	3 Cleavage	| Symbols: ATPPC4, PPC4 | phosphoenolpyruvate carboxylase 4 | chr1:25822942-25828107 REVERSE LENGTH=3102
AT1G68780	UUUUGCUUAGACUUAGAAACU	179	4 Cleavage	| Symbols: | RNI-like superfamily protein | chr1:25831803-25833844 REVERSE LENGTH=1886
AT1G68820	GCAAGUGAUGAUAAAAAGACA	100	3.5 Translation	| Symbols: | Transmembrane Fragile-X-F-associated protein | chr1:25865660-25868985 FORWARD LENGTH=1784
AT1G68872	UCCCGGAAUGCUGAAGAAGUA	113	4.5 Translation	| Symbols: | Unknown gene | chr1:25890365-25891748 REVERSE LENGTH=1102
AT1G68930	AUUUCAGUGAGCACGUACCUC	200	4.5 Cleavage	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:25918314-25920545 FORWARD LENGTH=2232
AT1G68980	UUAUGCUUCUGUUGAUCCACC	153	3.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:25932998-25935030 FORWARD LENGTH=2033
AT1G69030	UUUGUUAAACUCAUGGUCACCC	165	3.5 Translation	| Symbols: | BSD domain-containing protein | chr1:25947265-25949262 REVERSE LENGTH=1118
AT1G69090	UGACGCCAAUUCUGAAAGUUU	154	4.5 Cleavage	| Symbols: | Protein of unknown function (DUF295) | chr1:25977501-25978706 REVERSE LENGTH=1206
AT1G69120	CUAGAAUUCUUUCCCUUUCCU	235	4 Translation	| Symbols: AP1, AGL7 | K-box region and MADS-box transcription factor family protein | chr1:25982330-25986313 REVERSE LENGTH=1228
AT1G69210	UGAAAUAAAACUGAACCAUGCC	263	3 Cleavage	| Symbols: | Uncharacterised protein family UPF0090 | chr1:26018438-26020058 REVERSE LENGTH=1153
AT1G69252	AAAUAAAACUGAACCAUGCCU	203	3.5 Cleavage	| Symbols: | other RNA | chr1:26036733-26037659 FORWARD LENGTH=927
AT1G69280	UUAUGCUUCUGUUGAUCCACC	153	3.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G03630.1); Has 885 Blast hits to 474 proteins in 40 species: Archae - 0; Bacteria - 4; Metazoa - 731; Fungi - 9; Plants - 68; Viruses - 0; Other Eul
AT1G69290	UUAUGCUUCUGUUGAUCCACC	153	3.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:26047372-26049348 REVERSE LENGTH=1977
AT1G69340	UAAGCAUUUUGAUUCACCGGA	285	5 Cleavage	| Symbols: | appr-1-p processing enzyme family protein | chr1:26065724-26069821 FORWARD LENGTH=2101
AT1G69380	UGAAGGACAAGAUCAGCUGCU	415	3.5 Cleavage	| Symbols: | Protein of unknown function (DUF155) | chr1:26081566-26083606 REVERSE LENGTH=1460
AT1G69430	UUGAGAGCACUCCACCGACUG	261	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G26650.1); Has 216 Blast hits to 215 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 216; Viruses - 0; Other Euka
AT1G69440	UUUGCCUGUUGAACUCGAGUA	114	3.5 Translation	| Symbols: AGO7, ZIP | Argonaute family protein | chr1:26101527-26105166 REVERSE LENGTH=3161
AT1G69450	UAGCUAACAAGAACUCUUUCU	1828	3 Cleavage	| Symbols: | Early-responsive to dehydration stress protein (ERD4) | chr1:26107120-26110148 REVERSE LENGTH=2278
AT1G69490	UAUGGAGAUGAUCGCAAUGGC	937	4 Cleavage	| Symbols: NAP, ANAC029, ATNAP | NAC-like, activated by AP3/PI | chr1:26122139-26123421 FORWARD LENGTH=1100
AT1G69572	UGAGCCGACAAGAGUAGUAUC	111	3.5 Cleavage	| Symbols: | other RNA | chr1:26161599-26162761 FORWARD LENGTH=1064
AT1G69587	UAGUGACCGAGUAGUACCACC	461	4.5 Cleavage	| Symbols: | Potential natural antisense gene, locus overlaps with AT1G69588 | chr1:26175654-26179351 REVERSE LENGTH=874
AT1G69630	CUCAGGCUCAUACUCGACGUC	968	4 Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr1:26191640-26193174 REVERSE LENGTH=1356
AT1G69670	AUACCCAAACCUGAACUUUCU	127	4 Cleavage	| Symbols: CUL3B, ATCUL3B | cullin 3B | chr1:26202031-26204442 REVERSE LENGTH=2337
AT1G69710	UCCUAUCCAGUCUGAAGAACGC	272	4 Cleavage	| Symbols: | Regulator of chromosome condensation (RCC1) family with FYVE zinc finger domain | chr1:26222072-26226652 FORWARD LENGTH=3501
AT1G69770	CUAGAAUUCUUUCCCUUUCCU	235	3 Translation	| Symbols: CMT3 | chromomethylase 3 | chr1:26248318-26253585 REVERSE LENGTH=2764
AT1G69800	UCCUAUCCAGUCUGAAGAACGC	272	4 Cleavage	| Symbols: | Cystathionine beta-synthase (CBS) protein | chr1:26274230-26276329 REVERSE LENGTH=1621
AT1G69890	UACAGAAUAGGCUUAAGUAAC	189	3 Cleavage	| Symbols: | Protein of unknown function (DUF569) | chr1:26323111-26324616 REVERSE LENGTH=1244
AT1G70080	UGUGGUGUACCUCUUACGUCU	106	4.5 Cleavage	| Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr1:26394669-26397565 REVERSE LENGTH=1836
AT1G70140	UUUGAUCCGAGGAUGAUGGAU	816	2.5 Cleavage	| Symbols: ATFH8, FH8 | formin 8 | chr1:26412688-26415230 REVERSE LENGTH=2465
AT1G70250	UUGAGAGAUCCCCUGUUACUG	3917	5 Cleavage	| Symbols: | receptor serine/threonine kinase, putative | chr1:26452965-26456088 FORWARD LENGTH=2410
AT1G70320	UUCCAGAACUAAUGAAUGUUA	448	3.5 Cleavage	| Symbols: UPL2 | ubiquitin-protein ligase 2 | chr1:26488522-26501281 REVERSE LENGTH=11200
AT1G70518	UCUGUAUGCAUAGCUUGGGACU	466	5 Cleavage	| Symbols: | Unknown gene | chr1:26583570-26584684 FORWARD LENGTH=649
AT1G70550	UUUGAUUCACCGGAUAAACUC	175	4.5 Cleavage	| Symbols: | Protein of Unknown Function (DUF239) | chr1:26597152-26600219 FORWARD LENGTH=1754
AT1G70610	CGUCACUGCGAAUUCCUGGAG	272	3.5 Cleavage	| Symbols: ATTAP1, TAP1 | transporter associated with antigen processing protein 1 | chr1:26621961-26626503 FORWARD LENGTH=2400
AT1G70650	UCGAGCACCUACGUCACUGCG	100	4 Translation	| Symbols: | Ran BP2/NZF zinc finger-like superfamily protein | chr1:26638075-26642268 FORWARD LENGTH=2190
AT1G70990	UUAUCAACGAACUCUUGGCCC	310	4 Cleavage	| Symbols: | proline-rich family protein | chr1:26767297-26768076 REVERSE LENGTH=780
AT1G71210	CAACUAACAACGAGGGCACUG	198	4.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr1:26838289-26841490 REVERSE LENGTH=3202
AT1G71240	UCAACGAACUCUUGGCCCUAGA	152	3.5 Cleavage	| Symbols: | Plant protein of unknown function (DUF639) | chr1:26855430-26859741 FORWARD LENGTH=2673
AT1G71340	UUGAAAGACUUGUGGAUCACC	926	4 Cleavage	| Symbols: | PLC-like phosphodiesterases superfamily protein | chr1:26885170-26888338 REVERSE LENGTH=2390
AT1G71460	UGAGUAGAAUUCGAUCAUAUC	114	4 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr1:26927984-26930316 REVERSE LENGTH=2333
AT1G71696	UCACUCGACCACAACAGGCUG	106	4 Cleavage	| Symbols: SQL1 | carboxypeptidase D, putative | chr1:26966887-26970572 FORWARD LENGTH=1793
AT1G71800	UUCUGAAGGACAAGCUCAGCU	1012	3 Cleavage	| Symbols: CSTF64 | cleavage stimulating factor 64 | chr1:26999452-27002342 FORWARD LENGTH=1929
AT1G71820	UACGAGACUCUAGCCCAGCUU	307	4.5 Cleavage	| Symbols: SEC6 | SEC6 | chr1:27009634-27017108 FORWARD LENGTH=2915
AT1G71900	UUAUCAACGAACUCUUGGCCC	310	3.5 Cleavage	| Symbols: | Protein of unknown function (DUF803) | chr1:27061486-27064496 FORWARD LENGTH=1743
AT1G72030	CUCACAAGUGAUAUAGGGCUU	208	4.5 Cleavage	| Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr1:27110865-27111932 FORWARD LENGTH=900
AT1G72090	UUGAGAGCACUCCACCGACUG	261	4.5 Cleavage	| Symbols: | Methylthiotransferase | chr1:27123567-27126895 FORWARD LENGTH=1984

AT1G72175	CUUCCCCUAGAAUUCUUUCCC	401	4 Cleavage	| Symbols: | RING/U-box protein with domain of unknown function (DUF 1232) | chr1:27157875-27159558 FORWARD LENGTH=860
AT1G72250	UAACUCUACCCUUUGCACUCG	727	3.5 Translation	| Symbols: | Di-glucose binding protein with Kinesin motor domain | chr1:27192902-27198314 FORWARD LENGTH=3784
AT1G72270	UAACUCUACCCUUUGCACUCG	727	4 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Ribosome 60S biogenesis N-terminal (InterPro:IPR021714); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G27010.1); Has 772 Blast hits to 657 proteins in 120 species: Archae
AT1G72310	UCCUAUCCAGUCUGAAGAACGC	272	5 Translation	| Symbols: ATL3 | RING/U-box superfamily protein | chr1:27225897-27227545 FORWARD LENGTH=1649
AT1G72390	AUGGAUUUAGAUCACUUGCGUC	196	3.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Spt20 family (InterPro:IPR021950); Has 8778 Blast hits to 7244 proteins in 477 species: Archae - 6; Bacteria - 326; Metazoa - 4198; Fungi - 1506; Plants - 923; Viruses - 22; Other Eukaryotes - 1797 (sour
AT1G72470	UUACGAGACUCUAGCCCAACU	447	4 Translation	| Symbols: ATEXO70D1, EXO70D1 | exocyst subunit exo70 family protein D1 | chr1:27283693-27285895 FORWARD LENGTH=2203
AT1G72670	AUUUCAGUGAGCACGUACCUC	200	4.5 Cleavage	| Symbols: iqd8 | IQ-domain 8 | chr1:27356683-27358853 REVERSE LENGTH=1656
AT1G72700	UUUGCCUGUUGAACUCGAGUA	114	3.5 Cleavage	| Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr1:27365896-27371733 FORWARD LENGTH=4404
AT1G72840	UCAUAUGGACUUUGGCUACACC	101	3.5 Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) | chr1:27409237-27413851 REVERSE LENGTH=4008
AT1G72852	UUAGCACCGAGGAUGAUGGACU	330	5 Cleavage	| Symbols: | Potential natural antisense gene, locus overlaps with AT1G72850 | chr1:27414415-27415173 REVERSE LENGTH=615
AT1G72880	UGAGCCGACAAGAGUAGUAUC	111	4.5 Cleavage	| Symbols: | Survival protein SurE-like phosphatase/nucleotidase | chr1:27423385-27426135 REVERSE LENGTH=1565
AT1G73040	AUUUGAACUCAUGGAUACCCU	768	5 Cleavage	| Symbols: | Mannose-binding lectin superfamily protein | chr1:27475060-27475962 REVERSE LENGTH=716
AT1G73150	UUGGACGCCUCUACUAUGAGA	679	4 Cleavage	| Symbols: GTE3 | global transcription factor group E3 | chr1:27504112-27506112 REVERSE LENGTH=1717
AT1G73230	UGUGGUGUACCUCUCACGUCU	112	2.5 Cleavage	| Symbols: | Nascent polypeptide-associated complex NAC | chr1:27540228-27541944 REVERSE LENGTH=901
AT1G73360	UUAUCAACGAACUCUUGGCCC	310	3.5 Cleavage	| Symbols: HDG11, EDT1, ATHDG11 | homeodomain GLABROUS 11 | chr1:27578696-27582521 REVERSE LENGTH=3067
AT1G73600	UAUGGAGAUGAUCGCAAUGGC	937	4.5 Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:27669152-27673572 FORWARD LENGTH=1759
AT1G73602	UAUGGAGAUGAUCGCAAUGGC	937	4.5 Cleavage	| Symbols: CPuORF32 | conserved peptide upstream open reading frame 32 | chr1:27670626-27673569 FORWARD LENGTH=1841
AT1G73603	UACCCGUACGUCGCCUACAAG	192	5 Cleavage	| Symbols: LCR64 | low-molecular-weight cysteine-rich 64 | chr1:27674288-27674953 FORWARD LENGTH=387
AT1G73810	UAUUGACGUCGAGUAUGAGCCU	517	4 Translation	| Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr1:27752400-27755297 REVERSE LENGTH=1452
AT1G73860	UAACUCUACCCUUUGCACUCG	727	3.5 Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:27770986-27776857 REVERSE LENGTH=3460
AT1G73920	UGGCGCUCAACUCUGCGAGGU	1187	4 Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:27790875-27794914 FORWARD LENGTH=2650
AT1G73960	UCUGGGUAGAUGGGAUCUUAUC	123	3 Cleavage	| Symbols: TAF2 | TBP-associated factor 2 | chr1:27805045-27814446 REVERSE LENGTH=4254
AT1G73980	UACUUCCAGCGUUCUGUAGCC	826	3 Cleavage	| Symbols: | Phosphoribulokinase / Uridine kinase family | chr1:27820149-27824036 REVERSE LENGTH=2211
AT1G74050	UUCUUCAGACUGGAUAGGACU	265	3.5 Translation	| Symbols: | Ribosomal protein L6 family protein | chr1:27847047-27848806 REVERSE LENGTH=1037
AT1G74060	UUCUUCAGACUGGAUAGGACU	265	3.5 Translation	| Symbols: | Ribosomal protein L6 family protein | chr1:27849833-27851374 REVERSE LENGTH=977
AT1G74090	UGAGAACAUUGACUUCAGACCU	158	3 Cleavage	| Symbols: SOT18, ATSOT18, ATST5B | desulfo-glucosinolate sulfotransferase 18 | chr1:27862909-27864193 FORWARD LENGTH=1285
AT1G74120	UAUGGAGAUGAUCGCAAUGGC	937	3.5 Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr1:27871274-27873260 REVERSE LENGTH=1987
AT1G74280	UACCGGAGGACGUACAUAGCU	401	3 Translation	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:27929662-27931364 FORWARD LENGTH=1453
AT1G74350	AAACAGGACAAGUUACUCGCC	986	5 Cleavage	| Symbols: | Intron maturase, type II family protein | chr1:27949022-27951283 REVERSE LENGTH=2262
AT1G74600	UCGACCACACUGUCAUGAUCU	174	4 Cleavage	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr1:28025153-28027840 REVERSE LENGTH=2688
AT1G74680	AUAGCUAACAAGAACUCUUUCU	426	4.5 Cleavage	| Symbols: | Exostosin family protein | chr1:28059188-28061119 FORWARD LENGTH=1861
AT1G74880	UUUGUUAAACUCAUGGUCACC	138	3 Cleavage	| Symbols: NDH-O | NAD(P)H:plastoquinone dehydrogenase complex subunit O | chr1:28129858-28131077 REVERSE LENGTH=788
AT1G74950	UGAGAUUGCUAGAGGAAAGAG	101	3 Translation	| Symbols: JAZ2, TIFY10B | TIFY domain/Divergent CCT motif family protein | chr1:28148575-28150444 REVERSE LENGTH=1280
AT1G75100	UCUAGUUCACAUUUUUCGGAC	427	4.5 Cleavage	| Symbols: JAC1 | J-domain protein required for chloroplast accumulation response 1 | chr1:28190816-28193800 REVERSE LENGTH=2279
AT1G75140	UUUUUCGGACUAGAUAGGACU	107	3 Cleavage	| Symbols: | unknown protein; LOCATED IN: endoplasmic reticulum; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G19370.1); Has 51 Blast hits t
AT1G75150	UAACUCUACCCUUUGCACUCG	727	3 Translation	| Symbols: | unknown protein; Has 38228 Blast hits to 24529 proteins in 1168 species: Archae - 169; Bacteria - 4103; Metazoa - 14594; Fungi - 5866; Plants - 1861; Viruses - 317; Other Eukaryotes - 11318 (source: NCBI BLink). | chr1:28204387-28
AT1G75250	AUAGCUAACAAGAACUCUUUCU	426	3 Cleavage	| Symbols: ATRL6, RSM3, RL6 | RAD-like 6 | chr1:28245073-28245453 REVERSE LENGTH=381
AT1G75380	UAUAGGGCUUGAAAGAAAGUU	252	4 Cleavage	| Symbols: ATBBD1, BBD1 | bifunctional nuclease in basal defense response 1 | chr1:28281389-28284036 REVERSE LENGTH=1462
AT1G75490	UUUGAACUCAUGGAUACCCUA	227	5 Cleavage	| Symbols: | Integrase-type DNA-binding superfamily protein | chr1:28335502-28336706 FORWARD LENGTH=1205
AT1G75560	UGUGACACCGAUUCUGAUUGC	114	4.5 Cleavage	| Symbols: | zinc knuckle (CCHC-type) family protein | chr1:28371141-28373241 REVERSE LENGTH=1134
AT1G75640	UAGCUAACAAGAACUCUUUCU	1828	4.5 Cleavage	| Symbols: | Leucine-rich receptor-like protein kinase family protein | chr1:28403466-28407051 REVERSE LENGTH=3586
AT1G76160	UCUAGUUCGCGUUUUUCAGAC	163	4 Cleavage	| Symbols: sks5 | SKU5 similar 5 | chr1:28577942-28581133 REVERSE LENGTH=2008
AT1G76210	UUUUAAUUCAAGUAGCUGACU	133	4 Cleavage	| Symbols: | Arabidopsis protein of unknown function (DUF241) | chr1:28594950-28595981 REVERSE LENGTH=1032
AT1G76270	UUACCCGUACGUCGCUUACAA	130	4.5 Cleavage	| Symbols: | O-fucosyltransferase family protein | chr1:28613207-28616739 REVERSE LENGTH=2268
AT1G76405	UCUGGGUAGAUGGGAUCUUAUC	123	4.5 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast envelope; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabid
AT1G76580	UCUUCGACUGAGGUAAGCGCCU	355	5 Cleavage	| Symbols: | Squamosa promoter-binding protein-like (SBP domain) transcription factor family protein | chr1:28734234-28738917 FORWARD LENGTH=3686
AT1G76740	UCUAGUUCGCGUUUUUCAGAC	163	3.5 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G76840.1); Has 3683 Blast hits to 2942 proteins in 407 species: Archae - 9; Bacteria - 440; Metazoa - 1472; Fungi - 269; Plants - 192; Viruses - 8
AT1G76750	UGAAGGACAAGAUCAGCUGCU	415	3.5 Cleavage	| Symbols: | Protein of unknown function (DUF1278) | chr1:28811040-28811721 FORWARD LENGTH=682
AT1G76810	UAACAAGAACUCUUUCUUUUCU	235	3 Cleavage	| Symbols: | eukaryotic translation initiation factor 2 (eIF-2) family protein | chr1:28831003-28836586 REVERSE LENGTH=4395
AT1G76870	UUUGGCGCUCAACUCUGCAAG	3787	5 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: sequence-specific DNA binding transcription factors (TAIR:AT1G21200.1); Has 406 Blast hits to 351 proteins in 76 species: Archae - 0; Bacteria - 2; Metazoa - 137; Fungi - 14; Plants - 127; Vir
AT1G76920	UCUGUAUGCAUAACUUGGGAC	1212	4 Cleavage	| Symbols: | F-box family protein | chr1:28892062-28893676 FORWARD LENGTH=1615
AT1G77020	UUAUGAGACUCUAGCCCAGCU	149	4.5 Cleavage	| Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr1:28944843-28947031 REVERSE LENGTH=1517
AT1G77080	UACUGGAGGACGUACAGCACU	949	5 Translation	| Symbols: MAF1, FLM, AGL27 | K-box region and MADS-box transcription factor family protein | chr1:28955637-28960096 FORWARD LENGTH=872
AT1G77130	CGUCACUGCGAAUUCCUGGAG	272	2.5 Cleavage	| Symbols: PGSIP2, GUX3 | plant glycogenin-like starch initiation protein 2 | chr1:28978894-28981345 REVERSE LENGTH=2146
AT1G77138	CGUCACUGCGAAUUCCUGGAG	272	5 Cleavage	| Symbols: | other RNA | chr1:28982766-28983469 FORWARD LENGTH=704
AT1G77180	ACUGAGCGCUGAUAGUAACGG	153	4 Translation	| Symbols: SKIP | chromatin protein family | chr1:28999608-29002135 REVERSE LENGTH=2405
AT1G77260	UGAGGUCGAGUAGAGCAAUCUA	117	4.5 Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr1:29023772-29026957 REVERSE LENGTH=2415
AT1G77290	AAAUAAAACUGAACCAUGCCU	203	3 Cleavage	| Symbols: | Glutathione S-transferase family protein | chr1:29038375-29039838 FORWARD LENGTH=1366
AT1G77470	UACGCUAGGGAGAUAUCUGCC	122	4 Translation	| Symbols: RFC3, RFC5 | replication factor C subunit 3 | chr1:29111948-29114435 REVERSE LENGTH=1468
AT1G77500	UGAAUGACAAACUGGACAAGCU	583	3.5 Cleavage	| Symbols: | Protein of unknown function (DUF630 and DUF632) | chr1:29121489-29125191 FORWARD LENGTH=3158
AT1G77510	UGAGAUUGCUAGAGGAAAGAG	101	3 Cleavage	| Symbols: ATPDIL1-2, PDI6, ATPDI6, PDIL1-2 | PDI-like 1-2 | chr1:29126650-29129612 FORWARD LENGTH=1798
AT1G77620	UUACCCGUACGUCGCUUACAAG	2330	4.5 Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:29167764-29172867 REVERSE LENGTH=3626
AT1G77660	CUUGGCAUCGAAUUUGAACUC	1059	3.5 Cleavage	| Symbols: | Histone H3 K4-specific methyltransferase SET7/9 family protein | chr1:29185899-29187825 REVERSE LENGTH=1765
AT1G77710	UUAGCACCGAGGAUGAUGGAC	291	3.5 Translation	| Symbols: | CONTAINS InterPro DOMAIN/s: Ubiquitin-like, Ufm1 (InterPro:IPR005375); Has 244 Blast hits to 244 proteins in 106 species: Archae - 0; Bacteria - 0; Metazoa - 149; Fungi - 0; Plants - 47; Viruses - 0; Other Eukaryotes - 48 (source: NCE
AT1G77960	CGAGAGAUUACAGGGACUGUC	3198	3 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G28630.4); Has 13187 Blast hits to 6837 proteins in 407 species: Archae - 0; Bacteria - 447; Metazoa - 4509; Fungi - 1333; Plants - 399; Viruses
AT1G78080	UUUGGUUCUGAGUCCCGCCU	669	3.5 Cleavage	| Symbols: RAP2.4 | related to AP2 4 | chr1:29364249-29366073 FORWARD LENGTH=1825
AT1G78130	UACACAAAGGGCUCCUCGCACC	211	4.5 Translation	| Symbols: UNE2 | Major facilitator superfamily protein | chr1:29400140-29401902 FORWARD LENGTH=1592
AT1G78190	UUUGCUGAACAUGUACCUCCA	119	4.5 Cleavage	| Symbols: | Trm112p-like protein | chr1:29418620-29418994 REVERSE LENGTH=375
AT1G78220	UGAAGGAUUUGUGGUUAACCA	474	4 Cleavage	| Symbols: GF14 PI, GRF13 | general regulatory factor 13 | chr1:29425721-29427181 REVERSE LENGTH=738
AT1G78260	UACCCGUACGUCGCCUACAAG	192	4 Translation	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr1:29446985-29450515 FORWARD LENGTH=1530
AT1G78300	UAUGGAGAUGAUCGCAAUGGC	937	4 Cleavage	| Symbols: GRF2, 14-3-3OMEGA, GF14 OMEGA | general regulatory factor 2 | chr1:29461671-29463385 FORWARD LENGTH=1325
AT1G78310	CUGGAGGACGUACAGCACUUA	113	3.5 Translation	| Symbols: | VQ motif-containing protein | chr1:29463656-29465053 REVERSE LENGTH=1398
AT1G78380	UUUGAGCACUCCUUGACCCGA	154	5 Translation	| Symbols: ATGSTU19, GST8, GSTU19 | glutathione S-transferase TAU 19 | chr1:29486413-29487906 REVERSE LENGTH=993
AT1G78470	AUUUGAACUCAUGGAUACCCU	768	5 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: F-box family protein (TAIR:AT1G67390.1); Has 40 Blast hits to 40 proteins in 4 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 40; Viruses - 0; Other Eukaryotes - 0 (source: N
AT1G78870	UACGUCACUGCGAAUUCCUGGA	271	4 Cleavage	| Symbols: UBC35, UBC13A | ubiquitin-conjugating enzyme 35 | chr1:29650455-29652593 FORWARD LENGTH=1089
AT1G78915	UGAAUCUUGGUCAACUGGACC	197	4.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr1:29667619-29671219 REVERSE LENGTH=1457
AT1G78920	UUUAAAACGAGGACUUUUGC	115	3.5 Cleavage	| Symbols: AVP2, AVPL1, AtVHP2;1, VHP2;1, VP2 | vacuolar H+-pyrophosphatase 2 | chr1:29671493-29676992 FORWARD LENGTH=3093
AT1G79010	UCUGGGUAGAUGGGAUCUUAUC	123	4 Cleavage	| Symbols: | Alpha-helical ferredoxin | chr1:29724879-29727028 REVERSE LENGTH=1023
AT1G79090	UAAGACUGAGAUACGCGUGCCU	152	5 Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro D
AT1G79150	UCUCAUGUAGUUCUAGUUCGCA	1437	3 Cleavage	| Symbols: | binding | chr1:29772588-29777989 REVERSE LENGTH=2736
AT1G79280	UCCAGUCUGAAGAACGCGAAC	136	4 Cleavage	| Symbols: NUA, AtTPR | nuclear pore anchor | chr1:29819176-29832978 REVERSE LENGTH=6451
AT1G79580	UUUGAGCACUCUACAGACAGG	162	3.5 Cleavage	| Symbols: SMB | NAC (No Apical Meristem) domain transcriptional regulator superfamily protein | chr1:29940932-29943602 REVERSE LENGTH=1338
AT1G79740	UGUGACACCGAUUCUGAUAGC	115	2.5 Translation	| Symbols: | hAT transposon superfamily | chr1:30004367-30007020 REVERSE LENGTH=2041
AT1G79810	UUCAGGGUGAGAACAUUGACU	1291	3.5 Cleavage	| Symbols: TED3, PEX2, ATPEX2 | Pex2/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein | chr1:30019744-30022486 FORWARD LENGTH=1532
AT1G79890	UGAAGGACAAGCUCAGCUGCU	1483	4 Cleavage	| Symbols: | RAD3-like DNA-binding helicase protein | chr1:30048655-30052203 FORWARD LENGTH=2649
AT1G79910	UACUCCAGAAACUCACAACGA	113	3.5 Cleavage	| Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr1:30054884-30057170 FORWARD LENGTH=1467
AT1G79970	AUGGAUUUAGAUCACUUGCGUC	196	4 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thali
AT1G80000	UUGAGAGAUCCCCUGUUACUG	3917	4 Cleavage	| Symbols: | CASC3/Barentsz eIF4AIII binding | chr1:30092924-30097165 FORWARD LENGTH=2345
AT1G80260	UAUGGAGAUGAUCGCAAUGGCC	152	5 Cleavage	| Symbols: emb1427 | Spc97 / Spc98 family of spindle pole body (SBP) component | chr1:30175785-30180681 FORWARD LENGTH=3297

AT1G80280	UAUCCUGAGAGCGGUGCUGGCC	101	4.5 Translation	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr1:30183541-30186586 REVERSE LENGTH=2687
AT1G80300	UGAGACACAACAGGGAGAUUC	244	3 Translation	| Symbols: NTT1, ATNTT1 | nucleotide transporter 1 | chr1:30191856-30194519 FORWARD LENGTH=2212
AT1G80380	UAUGCAUAACUUGGGACUUACC	333	3 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr1:30217219-30220004 FORWARD LENGTH=1422
AT1G80570	UUUGAUUCACCGGAUAAACUC	175	3 Translation	| Symbols: | RNI-like superfamily protein | chr1:30290454-30292418 FORWARD LENGTH=1837
AT1G80630	UUUGAUCCGAGGAUGAUGGAUU	112	4.5 Translation	| Symbols: | RNI-like superfamily protein | chr1:30308696-30310656 REVERSE LENGTH=1961
AT1G80640	AUCCAAGUAGCUGACUCUCCU	1104	3.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr1:30311666-30314375 FORWARD LENGTH=1730
AT1G80720	CAACGCUCUUGAUACAUCUAG	133	3.5 Translation	| Symbols: | Mitochondrial glycoprotein family protein | chr1:30336138-30337565 FORWARD LENGTH=942
AT1G80750	CUCACAAGUGAUAUAGGGCUU	208	4 Cleavage	| Symbols: | Ribosomal protein L30/L7 family protein | chr1:30348801-30350564 FORWARD LENGTH=975
AT1G80790	UUCCGCAGGGAGAGCGUCCUC	112	3 Cleavage	| Symbols: | XH/XS domain-containing protein | chr1:30359723-30363307 FORWARD LENGTH=2314
AT1G80800	UGAAUGACAAACUGGACAAGCU	583	5 Cleavage	| Symbols: | pseudogene, 40S ribosomal protein S12 (RPS12B), similar to ribosomal protein S12 GB:AAD39838 GI:5106775 from (Hordeum vulgare); blastp match of 65% identity and 4.7e-12 P-value to GP|23617253|dbj|BAC20920.1||AP005764
AT1G80810	UUUGGUUCUGAGUCCCCGCCU	669	3.5 Cleavage	| Symbols: | Tudor/PWWP/MBT superfamily protein | chr1:30365287-30368898 FORWARD LENGTH=2418
AT2G01260	UGGCGCUCAACUCUGCAAGGU	10625	4.5 Translation	| Symbols: | Protein of unknown function (DUF789) | chr2:135244-137803 REVERSE LENGTH=1573
AT2G01340	UUAACUCUACCCUUUGCACUCA	240	4.5 Translation	| Symbols: At17.1 | Encodes a protein whose expression is responsive to nematode infection. | chr2:163954-165290 FORWARD LENGTH=930
AT2G01422	UAGGCCUGAGAUUGGACGCCU	875	4 Cleavage	| Symbols: | | chr2:183940-184734 FORWARD LENGTH=795
AT2G01460	UGCCAUGAUCGAGAGCUGCCU	164	3.5 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:206136-211919 FORWARD LENGTH=3019
AT2G01580	UGGCAGUAGGAGUACACGACU	163	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07510.2); Has 129 Blast hits to 129 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 129; Viruses - 0; Other Euka
AT2G01670	UAGAUAACAAGAACUCUUUCU	107	3.5 Cleavage	| Symbols: atnudt17, NUDT17 | nudix hydrolase homolog 17 | chr2:296510-298101 REVERSE LENGTH=1211
AT2G01830	UCCGCUAGAUAUAUCAAACUG	281	5 Translation	| Symbols: WOL, CRE1, WOL1, AHK4, ATCRE1 | CHASE domain containing histidine kinase protein | chr2:363003-367680 REVERSE LENGTH=3637
AT2G01880	UCGAGGGCAGGAACAUUGACU	334	3 Cleavage	| Symbols: PAP7, ATPAP7 | purple acid phosphatase 7 | chr2:391423-394032 REVERSE LENGTH=1192
AT2G01905	UUCUUCGGACUGGAUAGGACU	102	4 Cleavage	| Symbols: CYCJ18 | cyclin J18 | chr2:410327-415330 FORWARD LENGTH=2604
AT2G01940	UUUGAUCCGAGGAUGAUGGAU	816	3 Translation	| Symbols: SGR5, ATIDD15 | C2H2-like zinc finger protein | chr2:432849-435077 FORWARD LENGTH=1501
AT2G01950	UAUCCUGAGAGCGGUGCUGGC	334	3 Cleavage	| Symbols: VH1, BRL2 | BRI1-like 2 | chr2:440636-444276 REVERSE LENGTH=3641
AT2G02020	UUGCAGAGAUGGAUGUACAAC	101	2.5 Cleavage	| Symbols: | Major facilitator superfamily protein | chr2:479101-481185 FORWARD LENGTH=1645
AT2G02070	UGAGAUUGCUAGAGGAAAGAG	101	3 Cleavage	| Symbols: AtIDD5, IDD5 | indeterminate(ID)-domain 5 | chr2:505487-509425 FORWARD LENGTH=2116
AT2G02080	UGUGGUGUACCUCUCACGUCU	112	3 Translation	| Symbols: AtIDD4, IDD4 | indeterminate(ID)-domain 4 | chr2:518159-521707 REVERSE LENGTH=1844
AT2G02170	GCAAGUGAUGAUAAAAAGACA	100	3 Cleavage	| Symbols: | Remorin family protein | chr2:556493-558715 REVERSE LENGTH=1668
AT2G02180	UUUGGCCUGAGGUUGGACACC	133	4.5 Cleavage	| Symbols: TOM3 | tobamovirus multiplication protein 3 | chr2:560864-563233 FORWARD LENGTH=1296
AT2G02250	UGGAGAUGAUAGAUUAUGCGCU	109	4 Cleavage	| Symbols: AtPP2-B2, PP2-B2 | phloem protein 2-B2 | chr2:594655-595852 REVERSE LENGTH=960
AT2G02370	CUUCGACUGAGGUAAGCGCCU	234	5 Cleavage	| Symbols: | SNARE associated Golgi protein family | chr2:621180-623285 FORWARD LENGTH=1379
AT2G02400	UCAUAUGGACUUUGGCUACACC	101	3 Translation	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:631236-632575 REVERSE LENGTH=1260
AT2G02430	UCUAGUUCGCGUUCUUCAGAC	300	4 Cleavage	| Symbols: | pseudogene, arginyl-tRNA synthetase | chr2:635456-636638 FORWARD LENGTH=1183
AT2G02510	UGACACCGAUUCUGAUAGCUU	823	2.5 Cleavage	| Symbols: | NADH dehydrogenase (ubiquinone)s | chr2:673305-674740 FORWARD LENGTH=506
AT2G02540	ACAAAACUGUUGAACAAGCCU	1107	4.5 Cleavage	| Symbols: ATHB21, ZFHD4, HB21, ZHD3 | homeobox protein 21 | chr2:683647-685309 FORWARD LENGTH=1205
AT2G02560	UAUCCUGAGAGCGGUGCUGGC	334	5 Cleavage	| Symbols: CAND1, ATCAND1, ETA2, TIP120, HVE | cullin-associated and neddylation dissociated | chr2:689788-697596 FORWARD LENGTH=4089
AT2G02610	UUUGGCGCUCAACUCUGCAAG	3787	4 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:710712-712819 FORWARD LENGTH=2108
AT2G02620	UACCGGAGGACGUACAGCAUC	153	4.5 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:717256-719380 FORWARD LENGTH=2125
AT2G02630	UGGCGCUCAACUCUGCAAGGU	10625	4.5 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:723565-725620 FORWARD LENGTH=2056
AT2G02640	UUGGCGCUCAACUCUGCAAGG	4868	4.5 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:732388-734271 FORWARD LENGTH=1884
AT2G02680	UUUGGCGCUCAACUCUGCAAGG	2546	4.5 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:745775-748573 FORWARD LENGTH=1950
AT2G02780	UGGGCGCUUAUACUUUGGGUU	115	3.5 Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr2:781847-784646 REVERSE LENGTH=2314
AT2G02835	UCGACCACACUGUCAUGAUCU	174	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G09840.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT2G02880	UUUGUUAAACUCAUGGUCACCC	165	3.5 Translation	| Symbols: | mucin-related | chr2:841246-843429 FORWARD LENGTH=1280
AT2G03150	UGAGUAGAAUUCGAUCAUAUC	114	3.5 Cleavage	| Symbols: emb1579 | ATP/GTP-binding protein family | chr2:951933-959188 FORWARD LENGTH=4398
AT2G03360	UAUCGAGCACCUACGUCACUGU	142	5 Cleavage	| Symbols: | Glycosyltransferase family 61 protein | chr2:1022287-1024391 REVERSE LENGTH=1486
AT2G03390	UCAUCCUCUGUAGCUUCCGUC	210	2.5 Cleavage	| Symbols: | uvrB/uvrC motif-containing protein | chr2:1030402-1032625 REVERSE LENGTH=1210
AT2G03470	UCUCAUGUAGUUCUAGUUCGCA	1437	4 Cleavage	| Symbols: | ELM2 domain-containing protein | chr2:1045456-1047684 REVERSE LENGTH=1707
AT2G03590	CAACUAACAACGAGGGCACUG	198	4 Translation	| Symbols: ATUPS1, UPS1 | ureide permease 1 | chr2:1094757-1096968 FORWARD LENGTH=1802
AT2G03680	UCUAGUUCACAUUUUUCGGAC	427	5 Cleavage	| Symbols: SPR1, SKU6 | spiral1 | chr2:1120922-1122055 FORWARD LENGTH=854
AT2G03730	UUUAUUCACACAGUGGACUGUG	118	4.5 Cleavage	| Symbols: ACR5 | ACT domain repeat 5 | chr2:1137635-1140186 REVERSE LENGTH=1800
AT2G03760	UUCGAGAACUCCCUGACCCGA	1272	3.5 Cleavage	| Symbols: ST, ATST1, RAR047, ST1, AtSOT1, AtSOT12, SOT12 | sulphotransferase 12 | chr2:1149337-1150663 REVERSE LENGTH=1327
AT2G03810	UCUGAACUCAAGGCACCCAAA	493	4 Cleavage	| Symbols: | 18S pre-ribosomal assembly protein gar2-related | chr2:1162523-1164573 FORWARD LENGTH=1787
AT2G03958	UUGAACAAGCCUGAUGAAGUU	102	5 Cleavage	| Symbols: | Encodes a defensin-like (DEFL) family protein. | chr2:1243663-1243992 FORWARD LENGTH=330
AT2G04046	UGAAGGACAAGCUCAGCUGCU	1483	3.5 Cleavage	| Symbols: | Defensin-like (DEFL) family protein | chr2:1315860-1316296 FORWARD LENGTH=333
AT2G04050	UUGUGGAAUCCGUAGUCUGUA	152	4 Translation	| Symbols: | MATE efflux family protein | chr2:1337386-1339270 REVERSE LENGTH=1431
AT2G04100	UGCACUCGCUAGGUCUGGCAG	378	4 Cleavage	| Symbols: | MATE efflux family protein | chr2:1376890-1379130 REVERSE LENGTH=1661
AT2G04350	UAUCCUGAGAGCGGUGCUGGCC	101	5 Cleavage	| Symbols: LACS8 | AMP-dependent synthetase and ligase family protein | chr2:1515828-1519307 FORWARD LENGTH=2406
AT2G04400	UAGGCCUGAGAUUGGACGCCU	875	4 Cleavage	| Symbols: | Aldolase-type TIM barrel family protein | chr2:1531148-1533737 FORWARD LENGTH=1428
AT2G04520	UGAGCCGACAAGAGUAGUAUC	111	4.5 Cleavage	| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr2:1574592-1575863 REVERSE LENGTH=817
AT2G04720	UUCCAGCGUUCUGUAGCCAAC	156	4.5 Cleavage	| Symbols: | pseudogene, GTP-binding protein -related, similar to GTP-binding protein GI:6624302 from (Carica papaya); blastp match of 60% identity and 5.0e-31 P-value to GP|6624302|dbj|BAA88497.1||AB035919 small GTP-binding protein {
AT2G04880	UGUGGAUACAAGAGUUGGGCU	111	4 Translation	| Symbols: ZAP1, ATWRKY1, WRKY1 | zinc-dependent activator protein-1 | chr2:1717888-1720526 FORWARD LENGTH=2028
AT2G05140	UUGGACGCCUCUACUAUGAGA	679	1.5 Cleavage	| Symbols: | phosphoribosylaminoimidazole carboxylase family protein / AIR carboxylase family protein | chr2:1853935-1854903 FORWARD LENGTH=489
AT2G05160	UUUGAGCACUCCUUGACCCGA	154	3.5 Cleavage	| Symbols: | CCCH-type zinc fingerfamily protein with RNA-binding domain | chr2:1858543-1861895 REVERSE LENGTH=2436
AT2G05171	UAGGCCUGAGAUUGGACGCCU	875	4.5 Cleavage	| Symbols: | Pseudogene of AT3G18310 | chr2:1874040-1874997 FORWARD LENGTH=958
AT2G05260	UGGAUUCCGGCUGCAUACUCC	392	4.5 Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:1918289-1920042 FORWARD LENGTH=1379
AT2G05370	UCACCAUUGGCAGCUCUGUACC	187	4.5 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: RNA-dependent RNA polymerase 6 (TAIR:AT3G49500.1); Has 65 Blast hits to 37 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 65; Viruses - 0; Other Eukaryot
AT2G05440	UGAGAAGAGAUAGAAUAGAAUC	103	3 Cleavage	| Symbols: ATGRP9, GRP9 | GLYCINE RICH PROTEIN 9 | chr2:1993082-1994166 FORWARD LENGTH=727
AT2G05803	UUCGAGCACUCCCUGACCCGA	160	4 Cleavage	| Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: N
AT2G05900	UUUGAUUCACCGGAUAAACUC	175	4 Cleavage	| Symbols: SDG11, SUVH10 | SET domain protein 11 | chr2:2256970-2257908 FORWARD LENGTH=939
AT2G06000	CAACUAACAACGAGGGCACUG	198	4.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:2327386-2329665 REVERSE LENGTH=2083
AT2G06090	AUUGAUUCUGCACUCAAGGGC	128	4.5 Cleavage	| Symbols: | Plant self-incompatibility protein S1 family | chr2:2371607-2372014 REVERSE LENGTH=408
AT2G06420	UUCUUCCCGUUGGUGUGCGCC	170	3 Translation	| Symbols: | Domain of unknown function (DUF1985) | chr2:2538743-2540365 FORWARD LENGTH=1470
AT2G06845	UUCGAGCACUCCCUGACCCGA	160	3.5 Cleavage	| Symbols: | Beta-galactosidase related protein | chr2:2754666-2756008 FORWARD LENGTH=948
AT2G06906	UUAGCACCGAGGAUGAUGGACU	330	4.5 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: nucleic acid binding;zinc ion binding (TAIR:AT2G06904.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT2G07560	AUACCCAAACCUGAACUUUCU	127	5 Cleavage	| Symbols: AHA6, HA6 | H(+)-ATPase 6 | chr2:3169972-3174012 REVERSE LENGTH=3332
AT2G07716	CUUCCCUAGAAUUCUUUCCC	401	3 Cleavage	| Symbols: | pseudogene, similar to orfx, blastp match of 85% identity and 5.5e-116 P-value to GP|287897|emb|CAA42649.1||X60046 orfx {Oenothera berteriana} | chr2:3413955-3414838 FORWARD LENGTH=884
AT2G07799	UAUGAGUUGAUCGACGAAGAU	123	3.5 Cleavage	| Symbols: | Pseudogene of ATMG00260 | chr2:3466756-3467061 FORWARD LENGTH=306
AT2G07826	UGAGAACAUUGACUUCAGACCU	158	5 Cleavage	| Symbols: | Pseudogene of ATMG01210 | chr2:3361110-3361415 FORWARD LENGTH=306
AT2G09840	UAUGGCCUGGGAGCAAUCGCA	299	4 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: nucleic acid binding;zinc ion binding (TAIR:AT2G06904.1); Has 10 Blast hits to 10 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 10; Viruses - 0; Other Eukaryot
AT2G10735	UUGACGACCAACUCCGCUCCU	170	4 Translation	| Symbols: | pseudogene, hypothetical protein | chr2:4224085-4226506 REVERSE LENGTH=2422
AT2G10931	UGAAGGAUUUGUGGUUAACCA	474	4.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1
AT2G10950	UGACGGUUCAGAUUCAGGAGC	107	4 Cleavage	| Symbols: | BSD domain-containing protein | chr2:4315411-4317862 REVERSE LENGTH=1196
AT2G11930	UUUGAACUCAUGGAUACCCUA	227	4 Translation	| Symbols: | pseudogene, hypothetical protein, and genefinder | chr2:4809841-4812236 FORWARD LENGTH=2396
AT2G12480	UUGAGAGCACUCCACCGACUGA	140	5 Translation	| Symbols: SCPL43 | serine carboxypeptidase-like 43 | chr2:5069590-5072533 REVERSE LENGTH=1670
AT2G13116	UUGAAGGAUUUGUGGUUAACCA	106	3 Cleavage	| Symbols: | pseudogene, hypothetical protein | chr2:5409925-5410530 REVERSE LENGTH=606
AT2G13145	UGUUACGAGACUCUAGCCCAG	574	4 Cleavage	| Symbols: | pseudogene, hypothetical protein | chr2:5428731-5430290 FORWARD LENGTH=1560
AT2G13273	UCAUAUGGACUUUGGCUACACC	101	4 Translation	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:5498542-5498667 F
AT2G13560	UUUGAGAGCACUCCACCGACUG	125	4.5 Translation	| Symbols: NAD-ME1 | NAD-dependent malic enzyme 1 | chr2:5649964-5655320 FORWARD LENGTH=2214
AT2G13950	UUUGAUUCACCGGAUAAACUC	175	3 Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:5857536-5859249 FORWARD LENGTH=1554
AT2G13975	UAUGGAGAUGAUCGCAAUGGC	937	3.5 Translation	| Symbols: | | chr2:5864884-5865600 REVERSE LENGTH=635

AT2G14095	UUGACGACCAACUCCGCUCCU	170	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 7 plant structures; EXPRESSED DURING: 4 anthesis, C globular stage, petal diffe
AT2G14100	UAUCCUGAGAGCGGUGCUGGC	334	4.5 Cleavage	| Symbols: CYP705A13 | cytochrome P450, family 705, subfamily A, polypeptide 13 | chr2:5934556-5936371 REVERSE LENGTH=1734
AT2G14260	UGUGGUCGAGUAGAGCAAUCU	111	4 Cleavage	| Symbols: PIP | proline iminopeptidase | chr2:6041253-6043705 REVERSE LENGTH=1408
AT2G14285	UUCAGGGUGAGAACAUUGACU	1291	4 Cleavage	| Symbols: | Small nuclear ribonucleoprotein family protein | chr2:6052332-6053994 REVERSE LENGTH=580
AT2G14580	UGUGAGUGUUUGUGAGGUCUU	178	4 Cleavage	| Symbols: ATPRB1, PRB1 | basic pathogenesis-related protein 1 | chr2:6225535-6226224 REVERSE LENGTH=690
AT2G14740	CUUUGCACUCAUGAAUCUUUC	119	2.5 Cleavage	| Symbols: ATVSR3, VSR3, VSR2;2, BP80-2;2 | vacuolar sorting receptor 3 | chr2:6308895-6312589 FORWARD LENGTH=2080
AT2G14800	CGAGAGAUUACAGGGACUGUC	3198	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44713.1); Has 41 Blast hits to 38 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 2; Plants - 16; Viruses - 0; Other Eukaryo
AT2G14820	CAAGAACCCGCACGACACUCG	169	4 Cleavage	| Symbols: NPY2 | Phototropic-responsive NPH3 family protein | chr2:6358864-6361300 FORWARD LENGTH=1905
AT2G14830	UAGAGUGUUCAUGUAGUUGCA	232	3.5 Cleavage	| Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr2:6362481-6364093 FORWARD LENGTH=684
AT2G15080	UUCACAUGUCCGGGCUAGGCA	461	4.5 Cleavage	| Symbols: AtRLP19, RLP19 | receptor like protein 19 | chr2:6533687-6536995 FORWARD LENGTH=3206
AT2G15220	CGGAGGAAACUUAGCAGCGCC	103	4.5 Cleavage	| Symbols: | Plant basic secretory protein (BSP) family protein | chr2:6608659-6609506 FORWARD LENGTH=848
AT2G15470	UUUUGCUUAGACUUAGAAACU	179	3.5 Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr2:6754330-6756051 FORWARD LENGTH=1215
AT2G15490	UUCUGACGGACAAGAUAAGCU	313	4.5 Cleavage	| Symbols: UGT73B4 | UDP-glycosyltransferase 73B4 | chr2:6761635-6763474 FORWARD LENGTH=1004
AT2G15780	UGACGUCGAGUAUGAGCCUGA	416	4 Cleavage	| Symbols: | Cupredoxin superfamily protein | chr2:6873545-6874741 REVERSE LENGTH=935
AT2G15830	UCUGUAUGCAUAGCUUGGGAC	197	4.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 16 plant structures; EXPRESSED DURING: 10 growth stages; BEST Arat
AT2G15840	UAGAUAACAAGAACUCUUUCU	107	3.5 Cleavage	| Symbols: | pseudogene, hypothetical protein | chr2:6897746-6900002 REVERSE LENGTH=2257
AT2G16110	CUCACAAGUGAUAUAGGGCUU	208	4 Cleavage	| Symbols: | pseudogene, similar to putative AP endonuclease/reverse transcriptase, blastp match of 34% identity and 5.9e-45 P-value to GP|21952510|gb|AAM82604.1|AF525305_2|AF525305 putative AP endonuclease/reverse transcriptase |
AT2G16510	UAUGAGUUGAUCGACGAAGAU	123	3 Cleavage	| Symbols: | ATPase, F0/V0 complex, subunit C protein | chr2:7159629-7160892 REVERSE LENGTH=954
AT2G16575	UGACACCGAUUCUGAUAGCUU	823	4 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G17780.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT2G16650	UUCCAGAACUAAUGAAUGUUA	448	4 Cleavage	| Symbols: PRORP2 | proteinaceous RNase P 2 | chr2:7215819-7218395 REVERSE LENGTH=1871
AT2G16810	UCUAGUCCGAAAAAUGCGAAC	163	4 Cleavage	| Symbols: | F-box and associated interaction domains-containing protein | chr2:7287412-7288945 REVERSE LENGTH=1534
AT2G16850	UGGCGCUCAACUCUGCGAGGU	1187	3.5 Cleavage	| Symbols: PIP3B, PIP2;8 | plasma membrane intrinsic protein 2;8 | chr2:7301581-7303437 FORWARD LENGTH=1160
AT2G16910	UUUGAUCCGAGGAUGAUGGAU	816	2 Cleavage	| Symbols: AMS | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:7331721-7334254 FORWARD LENGTH=1893
AT2G16950	UUCGGUCUGGCCAUACUCGGC	147	3 Translation	| Symbols: TRN1, ATTRN1 | transportin 1 | chr2:7353847-7361202 FORWARD LENGTH=3333
AT2G16990	UUUGAGAGAUCCCCUGUUACUG	632	4.5 Translation	| Symbols: | Major facilitator superfamily protein | chr2:7383035-7387854 FORWARD LENGTH=1506
AT2G17010	UAGCUAACAAGAACUCUUUCU	1828	3.5 Cleavage	| Symbols: | Mechanosensitive ion channel family protein | chr2:7392850-7395970 REVERSE LENGTH=2404
AT2G17270	UUUAACAACUAAGGUUCCUGU	1055	4 Translation	| Symbols: PHT3;3 | phosphate transporter 3;3 | chr2:7510100-7512387 FORWARD LENGTH=1555
AT2G17290	UUGGGAGAACUAUGACACGAG	515	3.5 Cleavage	| Symbols: CPK6, ATCDPK3, ATCPK6 | Calcium-dependent protein kinase family protein | chr2:7516415-7519633 FORWARD LENGTH=2332
AT2G17550	UUGGCCUGAGGUUGGACACCU	178	4.5 Cleavage	| Symbols: | unknown protein; Has 264 Blast hits to 258 proteins in 65 species: Archae - 5; Bacteria - 5; Metazoa - 66; Fungi - 16; Plants - 107; Viruses - 0; Other Eukaryotes - 65 (source: NCBI BLink). | chr2:7634283-7637832 REVERSE LENGTH=317
AT2G17640	UUGAGAGAUCCCUUGUUACUG	141	3 Cleavage	| Symbols: ATSERAT3;1, SAT-106 | Trimeric LpxA-like enzymes superfamily protein | chr2:7668078-7670495 REVERSE LENGTH=1401
AT2G17750	CAACGCUCUUGAUACAUCUAG	133	4 Cleavage	| Symbols: NIP1 | NEP-interacting protein 1 | chr2:7709192-7711151 REVERSE LENGTH=1237
AT2G17820	UAAGCAUUUUGAUUCACCGGA	285	3.5 Cleavage	| Symbols: ATHK1, AHK1, HK1 | histidine kinase 1 | chr2:7742924-7748220 REVERSE LENGTH=4040
AT2G17830	UGAGUAGAAUUCGAUCAUAUC	114	5 Cleavage	| Symbols: | F-box and associated interaction domains-containing protein | chr2:7754210-7755604 FORWARD LENGTH=1395
AT2G17845	UGGAUUCCGGCUGCAUACUCC	392	3 Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:7758846-7759881 FORWARD LENGTH=939
AT2G17930	UUCUGUAGCACGAGGUAUCCU	302	3.5 Translation	| Symbols: | Phosphatidylinositol 3- and 4-kinase family protein with FAT domain | chr2:7784288-7802230 REVERSE LENGTH=11744
AT2G17970	UUUUGAGAGCCUUGUAGUAGU	118	2 Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr2:7818940-7821373 REVERSE LENGTH=1797
AT2G17972	UCCACCGACUGAUGACAAUGU	1524	5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 14 gro
AT2G17990	UUCGGUCUGGCCAUACUCGGC	147	4 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: kinectin-related (TAIR:AT5G66250.3); Has 7578 Blast hits to 6129 proteins in 783 species: Archae - 220; Bacteria - 1045; Metazoa - 3605; Fungi - 575; Plants - 442; Viruses - 38; Other Eukary
AT2G18040	UGUGAGUGUUUGUGAGGUCUU	178	4.5 Cleavage	| Symbols: PIN1AT | peptidylprolyl cis/trans isomerase, NIMA-interacting 1 | chr2:7842164-7843870 FORWARD LENGTH=875
AT2G18140	CAUUGACUUCAAGCCUGCGCU	190	4.5 Cleavage	| Symbols: | Peroxidase superfamily protein | chr2:7887584-7888878 REVERSE LENGTH=1014
AT2G18150	CAUUGACUUCAAGCCUGCGCU	190	4.5 Cleavage	| Symbols: | Peroxidase superfamily protein | chr2:7892133-7893653 REVERSE LENGTH=1249
AT2G18170	UGAAGGACAAGCUCAGCUGCU	1483	3.5 Cleavage	| Symbols: ATMPK7, MPK7 | MAP kinase 7 | chr2:7907804-7909923 REVERSE LENGTH=1695
AT2G18180	UGACGGUUCAGAUUCAGGAGC	107	4 Cleavage	| Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr2:7911054-7913695 REVERSE LENGTH=1677
AT2G18193	UUUGGCCUGAGGUUGGACACC	133	3.5 Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:7917505-7919277 REVERSE LENGTH=1697
AT2G18220	UCAACACUCUGAUACAUCUAG	143	2.5 Cleavage	| Symbols: | Noc2p family | chr2:7928024-7931851 FORWARD LENGTH=2363
AT2G18290	UUCUAGUUCGCGUUCUUCAGAC	122	4.5 Translation	| Symbols: APC10 | anaphase promoting complex 10 | chr2:7948306-7950329 REVERSE LENGTH=1028
AT2G18390	UGUGGAUACAAGAGUUGGGCU	111	4.5 Cleavage	| Symbols: TTN5, HAL, ARL2, ATARLC1 | ADP-ribosylation factor family protein | chr2:7988165-7989525 FORWARD LENGTH=879
AT2G18560	UUACCCGUACGUCGCUUACAAG	2330	4.5 Translation	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr2:8059288-8061056 FORWARD LENGTH=1769
AT2G18640	UCAACACUCUGAUACAUCUAG	143	4.5 Cleavage	| Symbols: GGPS4 | geranylgeranyl pyrophosphate synthase 4 | chr2:8083740-8084888 REVERSE LENGTH=1149
AT2G18700	UCACUCGACCACAACAGGCUG	106	4 Translation	| Symbols: ATTPS11, TPS11, ATTPSB | trehalose phosphatase/synthase 11 | chr2:8109043-8112010 FORWARD LENGTH=2800
AT2G18730	UGUGACACCGAUUCUGAUUGC	114	4.5 Cleavage	| Symbols: ATDGK3, DGK3 | diacylglycerol kinase 3 | chr2:8118830-8121925 FORWARD LENGTH=1849
AT2G18810	CUUUGCACUCAUGAAUCUUUC	119	3 Cleavage	| Symbols: | Domain of unknown function (DUF313) | chr2:8147939-8149469 REVERSE LENGTH=705
AT2G18850	UCACUGUGAAUUCCUGGAGUU	123	3.5 Cleavage	| Symbols: | SET domain-containing protein | chr2:8160734-8163689 FORWARD LENGTH=1896
AT2G18880	AUUGAUUCUGCACUCAAGGGC	128	3.5 Cleavage	| Symbols: VEL2 | vernalization5/VIN3-like | chr2:8172189-8178995 FORWARD LENGTH=2108
AT2G18890	UAUGCUUCUGUUGAUCCACCU	344	3.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr2:8183890-8186796 FORWARD LENGTH=1383
AT2G19120	UUAUGAGACUCUAGCCCAGCU	149	4 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:8287036-8292498 REVERSE LENGTH=3659
AT2G19240	UUGCAGAGAUGGAUGUACAAC	101	3 Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr2:8349048-8352562 REVERSE LENGTH=2523
AT2G19280	UGCCUAGAUUGCUCUACUCGA	125	3.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:8362435-8366144 FORWARD LENGTH=3381
AT2G19390	CUUGUGAGUGUUUGUGAGGUC	103	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G29790.1); Has 203 Blast hits to 188 proteins in 60 species: Archae - 0; Bacteria - 11; Metazoa - 24; Fungi - 34; Plants - 93; Viruses - 0; Other Eu
AT2G19480	UCGACCACACUGUCAUGAUCU	174	4 Cleavage	| Symbols: NAP1;2 | nucleosome assembly protein 1;2 | chr2:8438393-8441384 FORWARD LENGTH=1671
AT2G19620	UUUGAGCACUCCUUGACCCGA	154	4 Translation	| Symbols: NDL3 | N-MYC downregulated-like 3 | chr2:8485991-8488720 REVERSE LENGTH=1253
AT2G19720	CUUUGCACUCAUGAAUCUUUC	119	3 Cleavage	| Symbols: rps15ab | ribosomal protein S15A B | chr2:8510020-8511339 REVERSE LENGTH=674
AT2G19860	UGAGAUUGCUAGAGGAAAGAG	101	3.5 Cleavage	| Symbols: ATHXK2, HXK2 | hexokinase 2 | chr2:8570750-8574000 FORWARD LENGTH=1815
AT2G19870	AUUCGAGAACUCCCUGACCCG	350	3.5 Cleavage	| Symbols: | tRNA/rRNA methyltransferase (SpoU) family protein | chr2:8575878-8577947 FORWARD LENGTH=2070
AT2G19880	AUGGAUUUAGAUCACUUGCGUC	196	4.5 Cleavage	| Symbols: | Nucleotide-diphospho-sugar transferases superfamily protein | chr2:8581460-8585478 FORWARD LENGTH=2041
AT2G19900	UUCUUCAGACUGGAUAGGACU	265	3.5 Cleavage	| Symbols: ATNADP-ME1, NADP-ME1 | NADP-malic enzyme 1 | chr2:8591899-8595478 REVERSE LENGTH=2028
AT2G19930	UAGCUAACAAGAACUCUUUCU	1828	4 Cleavage	| Symbols: | RNA-dependent RNA polymerase family protein | chr2:8607340-8612441 REVERSE LENGTH=3127
AT2G20010	UUCCCUGGGGUACAGAACAUUC	135	2 Cleavage	| Symbols: | Protein of unknown function (DUF810) | chr2:8637747-8641474 REVERSE LENGTH=3278
AT2G20110	CUUGGCAUCGAAUUUGAACUC	1059	3.5 Cleavage	| Symbols: | Tesmin/TSO1-like CXC domain-containing protein | chr2:8684496-8687218 FORWARD LENGTH=2085
AT2G20180	UUGGCCUGAGGUUGGACGCCU	272	5 Cleavage	| Symbols: PIL5, PIF1 | phytochrome interacting factor 3-like 5 | chr2:8704024-8706892 REVERSE LENGTH=1939
AT2G20190	UUACCCGUACGUCGCUUAUAAG	267	4 Translation	| Symbols: ATCLASP, CLASP | CLIP-associated protein | chr2:8711596-8719018 REVERSE LENGTH=4791
AT2G20230	UUUGUUAAACUCAUGGUCACCC	165	5 Cleavage	| Symbols: | Tetraspanin family protein | chr2:8725541-8727742 FORWARD LENGTH=1388
AT2G20330	UUCAUCUGCAGUAAGUCCCUG	314	2.5 Translation	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:8772687-8775614 REVERSE LENGTH=2244
AT2G20380	CUUCCCCUAGAAUUCUUUCCC	401	3.5 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr2:8794818-8795980 REVERSE LENGTH=1047
AT2G20410	CAACGCUCUUGAUACAUCUAG	133	4.5 Cleavage	| Symbols: | RNA-binding ASCH domain protein | chr2:8802344-8804373 FORWARD LENGTH=1324
AT2G20480	UGUUGAUCCAAGUAGCUGACU	608	4 Translation	| Symbols: | unknown protein; Has 19 Blast hits to 19 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 19; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:8830565-8831533 REVERSE LENGTH=379
AT2G20570	UACUGGAGGACGUACAGCACU	949	3.5 Cleavage	| Symbols: GPRI1, GLK1, ATGLK1 | GBF's pro-rich region-interacting factor 1 | chr2:8855358-8857756 FORWARD LENGTH=1625
AT2G20580	UGACACCGAUUCUGAUAGCUU	823	3.5 Cleavage	| Symbols: RPN1A, ATRPN1A | 26S proteasome regulatory subunit S2 1A | chr2:8858988-8864865 FORWARD LENGTH=3065
AT2G20613	UGAGAACGCUCUGCCAUUGGA	158	2.5 Translation	| Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr2:8886037-8886444 REVERSE LENGTH=408
AT2G20670	UACGCGACCGCGGUGCUGGCC	119	4.5 Cleavage	| Symbols: | Protein of unknown function (DUF506) | chr2:8911860-8913534 REVERSE LENGTH=1250
AT2G20690	AUUUCAGUGAGCACGUACCUC	200	3.5 Cleavage	| Symbols: | lumazine-binding family protein | chr2:8923305-8924974 FORWARD LENGTH=1206
AT2G20790	UGCCUAGAUUGCUCUACUCGA	125	3.5 Translation	| Symbols: | clathrin adaptor complexes medium subunit family protein | chr2:8950526-8952691 REVERSE LENGTH=1819
AT2G20830	UGUAUGCAUAACUUGGGACUU	149	4 Translation	| Symbols: | transferases;folic acid binding | chr2:8968209-8970727 REVERSE LENGTH=1195
AT2G20840	UCCAGUCUGAAGAACGCGAAC	136	4 Cleavage	| Symbols: | Secretory carrier membrane protein (SCAMP) family protein | chr2:8971712-8974485 REVERSE LENGTH=1147
AT2G20880	UUCACAUGUCCGGGCUAGGCA	461	3.5 Cleavage	| Symbols: | Integrase-type DNA-binding superfamily protein | chr2:8985973-8987263 FORWARD LENGTH=1291
AT2G21040	UAUCCUGAGAGCGGUGCUGGC	334	3.5 Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:9026157-9027310 FORWARD LENGTH=786
AT2G21187	UUUGAGCACUCUACAGACAGG	162	3.5 Cleavage	| Symbols: | Potential natural antisense gene, locus overlaps with AT2G21185 | chr2:9076292-9077468 FORWARD LENGTH=816
AT2G21390	UGUGUAUGCAUAACUUGGGAC	106	3.5 Translation	| Symbols: | Coatomer, alpha subunit | chr2:9152006-9156878 FORWARD LENGTH=4190
AT2G21540	CUUAACUCUACCCUUUGCACU	115	4 Cleavage	| Symbols: SFH3 | SEC14-like 3 | chr2:9220764-9224374 REVERSE LENGTH=1941

AT2G21740	UGACGGAAGCUACAGAGGAUG	108	4	Cleavage	| Symbols: | Protein of unknown function (DUF1278) | chr2:9281986-9282363 REVERSE LENGTH=378
AT2G21750	UGACGGAAGCUACAGAGGAUG	108	3	Cleavage	| Symbols: | Protein of unknown function (DUF1278) | chr2:9283367-9283744 REVERSE LENGTH=378
AT2G21895	UGACGGAAGCUACAGAGGAUG	108	4	Cleavage	| Symbols: | Encodes a ECA1 gametogenesis related family protein [pseudogene] | chr2:9333002-9333336 REVERSE LENGTH=335
AT2G21910	UUUAUUCACACAGUGGACUGUG	118	5	Cleavage	| Symbols: CYP96A5 | cytochrome P450, family 96, subfamily A, polypeptide 5 | chr2:9341498-9343030 FORWARD LENGTH=1533
AT2G22010	UCUUCGACUGAGGUAAGCGCCU	355	4	Cleavage	| Symbols: RKP | related to KPC1 | chr2:9363721-9369307 REVERSE LENGTH=4368
AT2G22060	UAGAGUUAAGUUGGGACAGGA	199	4	Translation	| Symbols: | BEST Arabidopsis thaliana protein match is: Galactose oxidase/kelch repeat superfamily protein (TAIR:AT2G22030.1); Has 148 Blast hits to 148 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 148; Viruses
AT2G22125	UUAGCACCGAGGAUGAUGGAC	291	4.5	Cleavage	| Symbols: CSI1 | binding | chr2:9406263-9414518 FORWARD LENGTH=6941
AT2G22170	UACACUCACUUGAUCUAGGAG	223	4	Translation	| Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr2:9426849-9427817 REVERSE LENGTH=788
AT2G22190	UAGAAUUAUCAUGUCUUGGCA	194	4	Cleavage	| Symbols: TPPE | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:9433765-9436544 REVERSE LENGTH=1259
AT2G22400	UCCACCGACUGAUGACAAUGU	1524	4	Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:9504659-9508875 REVERSE LENGTH=2678
AT2G22500	UAGAAUUAUCAUGUCUUGGCA	194	4	Cleavage	| Symbols: UCP5, ATPUMP5, DIC1 | uncoupling protein 5 | chr2:9563224-9564751 REVERSE LENGTH=1528
AT2G22530	UGAGAUUGCUAGAGGAAAGAG	101	3.5	Cleavage	| Symbols: | Alkaline-phosphatase-like family protein | chr2:9572796-9577441 REVERSE LENGTH=3052
AT2G22540	CUCGGGAGAAAGAAGAAGGCU	259	3.5	Translation	| Symbols: SVP, AGL22 | K-box region and MADS-box transcription factor family protein | chr2:9579874-9583893 FORWARD LENGTH=1556
AT2G22650	UAUCCUGAGAGCGGUGCUGGC	334	4	Cleavage	| Symbols: | FAD-dependent oxidoreductase family protein | chr2:9624586-9626969 REVERSE LENGTH=1418
AT2G22680	UGAGAACGCUCUGCCAUUGGA	158	4	Cleavage	| Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr2:9645313-9647613 FORWARD LENGTH=2301
AT2G22750	CGAGAGAUUACAGGGACUGUC	3198	3	Translation	| Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:9672144-9673625 FORWARD LENGTH=920
AT2G22770	UUGAACAAGCCUGAUGAAGUU	102	4.5	Cleavage	| Symbols: NAI1 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:9684725-9686595 FORWARD LENGTH=1370
AT2G22950	UCGAGGGCAGGAACAUUGACU	334	4.5	Translation	| Symbols: | Cation transporter/ E1-E2 ATPase family protein | chr2:9766127-9769766 FORWARD LENGTH=3048
AT2G23110	AUUUGGCGCUCAACUCUGCAA	204	3.5	Translation	| Symbols: | Late embryogenesis abundant protein, group 6 | chr2:9840456-9841046 FORWARD LENGTH=591
AT2G23200	UGAGACACAACAGGGAGAUUC	244	4	Cleavage	| Symbols: | Protein kinase superfamily protein | chr2:9879276-9881908 FORWARD LENGTH=2633
AT2G23250	UCUAGUUCACAUUUUUCGGAC	427	4	Cleavage	| Symbols: UGT84B2 | UDP-glucosyl transferase 84B2 | chr2:9897809-9899125 REVERSE LENGTH=1317
AT2G23390	UGUGGUGUACCUCUCACGUCU	112	3	Translation	| Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF482 (InterPro:IPR007434), Acyl-CoA N-acyltransferase (InterPro:IPR016181); Has 2165 Blast hits to 2163 proteins in 543 species: Archae - 0; Bacteria - 1044; Metazoa -
AT2G23450	UGAAUGACAAACUGGACAAGCU	583	4.5	Cleavage	| Symbols: | Protein kinase superfamily protein | chr2:9988754-9991332 REVERSE LENGTH=2387
AT2G23460	UAGAUAACAAGAACUCUUUCU	107	4.5	Cleavage	| Symbols: XLG1, ATXLG1 | extra-large G-protein 1 | chr2:9995478-9999122 FORWARD LENGTH=3065
AT2G23520	UGUCACCGUAGAUUUCUUCCU	123	3.5	Cleavage	| Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr2:10013991-10016943 REVERSE LENGTH=2953
AT2G23790	UUGUGGAAUCCGUAGUCUGUA	152	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF607) | chr2:10125368-10127521 REVERSE LENGTH=1401
AT2G23810	UGUGGUCGAGUAGAGCAAUCU	111	3	Cleavage	| Symbols: TET8 | tetraspanin8 | chr2:10135605-10137561 REVERSE LENGTH=1285
AT2G24020	UCUAGUUCGCAUUUUUUGGAC	421	3.5	Cleavage	| Symbols: | Uncharacterised BCR, YbaB family COG0718 | chr2:10217701-10219352 REVERSE LENGTH=800
AT2G24050	UGAAAUAAAACUGAACCAUGCC	263	4	Cleavage	| Symbols: eIFiso4G2 | MIF4G domain-containing protein / MA3 domain-containing protein | chr2:10225225-10228638 REVERSE LENGTH=2701
AT2G24100	AUACCCAAACCUGAACUUUCU	127	4.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G30780.1); Has 101 Blast hits to 101 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 95; Viruses - 0; Other Eukar
AT2G24350	UUUUAAUUCAAGUAGCUGACU	133	3.5	Translation	| Symbols: | RNA binding (RRM/RBD/RNP motifs) family protein | chr2:10361126-10364492 FORWARD LENGTH=1996
AT2G24430	UUUGAGCACUCUACAGACAGG	162	4	Cleavage	| Symbols: ANAC038, NAC038 | NAC domain containing protein 38 | chr2:10383517-10386625 REVERSE LENGTH=1025
AT2G24570	UCCGCUAGAUAUAUCAAACUG	281	3	Cleavage	| Symbols: WRKY17, ATWRKY17 | WRKY DNA-binding protein 17 | chr2:10437398-10439298 REVERSE LENGTH=1320
AT2G24696	CUUUGCACUCAUGAAUCUUUC	119	4	Cleavage	| Symbols: | transcriptional factor B3 family protein | chr2:10509068-10510902 REVERSE LENGTH=1128
AT2G24730	UUCGGUCUGGCCAUACUCGGC	147	3.5	Cleavage	| Symbols: | 60S ribosomal protein L4/L1 (RPL4C), pseudogene, blastp match of 68% identity and 7.9e-28 P-value to SP|Q9XF97|RL4_PRUAR 60S ribosomal protein L4 (L1). (Apricot) {Prunus armeniaca} | chr2:10526349-10527025 REVERSE LENG
AT2G24750	UGUGAGUGUUUGUGAGGUCUU	178	3	Translation	| Symbols: | pseudogene, similar to Avr9/Cf-9 rapidly elicited protein 141, similar to GB:AAB61068; blastp match of 43% identity and 5.0e-152 P-value to GP|30013669|gb|AAP03877.1||AY220478 Avr9/Cf-9 rapidly elicited protein 141 {Nicotiana
AT2G24800	UUGACGACCAACUCCGCUCCU	170	3.5	Translation	| Symbols: | Peroxidase superfamily protein | chr2:10571255-10572570 REVERSE LENGTH=990
AT2G24860	UGCACUCGCUAGGUCUGGCAG	378	4.5	Cleavage	| Symbols: | DnaJ/Hsp40 cysteine-rich domain superfamily protein | chr2:10586775-10588329 REVERSE LENGTH=867
AT2G24940	UACCGGAGGACGUACAACACC	302	5	Cleavage	| Symbols: AtMAPR2, MAPR2 | membrane-associated progesterone binding protein 2 | chr2:10609394-10612232 FORWARD LENGTH=2839
AT2G24945	UACCGGAGGACGUACAACACC	302	5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G36925.1); Has 6 Blast hits to 6 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 6; Viruses - 0; Other Eukaryotes -
AT2G24950	UGAGCCGACAAGAGUAGUAUC	111	4.5	Cleavage	| Symbols: | Protein of Unknown Function (DUF239) | chr2:10613105-10615563 FORWARD LENGTH=1236
AT2G25010	UGUAUGCAUAACUUGGGACUU	149	3.5	Translation	| Symbols: | Aminotransferase-like, plant mobile domain family protein | chr2:10631531-10633663 FORWARD LENGTH=1806
AT2G25110	UCGAGUGACUUUGGAGCCAUU	244	3	Translation	| Symbols: SDF2, ATSDL, AtSDF2 | stromal cell-derived factor 2-like protein precursor | chr2:10684135-10686085 FORWARD LENGTH=1197
AT2G25290	CAAACUGGACAAGCUACUGCU	324	3.5	Translation	| Symbols: Phox1 | Octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein | chr2:10765717-10768665 REVERSE LENGTH=2723
AT2G25320	UGUGGUGACUUGGCUCAGGCCU	283	3.5	Translation	| Symbols: | TRAF-like family protein | chr2:10781851-10788065 REVERSE LENGTH=5122
AT2G25340	UGGCGCUCAACUCUGCAAGGU	10625	4	Cleavage	| Symbols: ATVAMP712, VAMP712 | vesicle-associated membrane protein 712 | chr2:10792664-10793832 REVERSE LENGTH=660
AT2G25490	UAUAGGGCUUGAAAGAAAGUU	252	3.5	Cleavage	| Symbols: EBF1, FBL6 | EIN3-binding F box protein 1 | chr2:10847375-10850532 REVERSE LENGTH=2787
AT2G25540	UCAAGCGAUUGGAAGGAUUGUU	102	3	Cleavage	| Symbols: CESA10 | cellulose synthase 10 | chr2:10866822-10872077 REVERSE LENGTH=3446
AT2G25660	UAGCUAACAAGAACUCUUUCU	1828	3.5	Translation	| Symbols: emb2410 | embryo defective 2410 | chr2:10916203-10927390 REVERSE LENGTH=6754
AT2G25730	UGCAUAACUUGGGACUUACCU	413	3	Cleavage	| Symbols: | unknown protein; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages. | chr2:10956301-10972927 REVERSE LENGTH=8028
AT2G25737	UUUGCCUGUUGAACUCGAGUA	114	3.5	Cleavage	| Symbols: | Sulfite exporter TauE/SafE family protein | chr2:10976936-10979900 FORWARD LENGTH=1892
AT2G25800	UAGGCCUGAGAUUGGACGCCU	875	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF810) | chr2:11005924-11009739 REVERSE LENGTH=3189
AT2G25940	UUCGAGCACUCCCUGACCCGA	160	4	Cleavage	| Symbols: ALPHA-VPE, ALPHAVPE | alpha-vacuolar processing enzyme | chr2:11063301-11066028 REVERSE LENGTH=1640
AT2G26040	AUUCGAGAACUCCCUGACCCG	350	3.5	Cleavage	| Symbols: PYL2, RCAR14 | PYR1-like 2 | chr2:11094832-11095404 REVERSE LENGTH=573
AT2G26180	UUUGUUAAACUCAUGGUCACCC	165	3.5	Cleavage	| Symbols: IQD6 | IQ-domain 6 | chr2:11143290-11145103 REVERSE LENGTH=1515
AT2G26250	UCAUGUAGUUCUAGUUCGCCU	245	3	Cleavage	| Symbols: FDH, KCS10 | 3-ketoacyl-CoA synthase 10 | chr2:11170418-11173142 REVERSE LENGTH=2117
AT2G26290	UAACAAGAACUCUUUCUUUUCU	235	3.5	Cleavage	| Symbols: ARSK1 | root-specific kinase 1 | chr2:11192137-11194259 REVERSE LENGTH=1375
AT2G26350	UCCAAGUAGCUGACUCUCCUU	596	3	Cleavage	| Symbols: PEX10, ATPEX10 | peroxin 10 | chr2:11217439-11220507 REVERSE LENGTH=1566
AT2G26360	UGUGGAUACAAGAGUUGGGCU	111	4	Cleavage	| Symbols: | Mitochondrial substrate carrier family protein | chr2:11221516-11223213 REVERSE LENGTH=1304
AT2G26420	UCUAUAGCCAAUGUACUCUACU	106	3	Cleavage	| Symbols: PIP5K3 | 1-phosphatidylinositol-4-phosphate 5-kinase 3 | chr2:11239434-11242239 REVERSE LENGTH=2118
AT2G26455	UUGGUCACACAGUGGACUGUG	104	2	Cleavage	| Symbols: | pseudogene, similar to Ubiquitin conjugating enzyme 7 interacting protein 4 (UbcM4- interacting protein 4) (RING finger protein 144). (Mouse), contains a Prosite:PS00518: Zinc finger, C3HC4 type (RING finger), signature and Pfam:P
AT2G26460	UCUGAACUCAAGGCACCCAAA	493	3.5	Cleavage	| Symbols: SMU2 | RED family protein | chr2:11254932-11258973 REVERSE LENGTH=1935
AT2G26560	UUCGGACUGGAUAGGACUAGG	101	4	Translation	| Symbols: PLP2, PLA IIA, PLA2A | phospholipase A 2A | chr2:11293769-11295806 REVERSE LENGTH=1465
AT2G26590	UUGAGAUAUCCCCUGUUACUG	106	3.5	Cleavage	| Symbols: RPN13 | regulatory particle non-ATPase 13 | chr2:11311004-11315096 REVERSE LENGTH=1183
AT2G26710	CUCAGGCUCAUACUCGACGUC	968	3.5	Cleavage	| Symbols: BAS1, CYP734A1, CYP72B1 | Cytochrome P450 superfamily protein | chr2:11380492-11383612 FORWARD LENGTH=1970
AT2G26730	UCAAGCGAUUGGAAGGAUUGUU	102	4	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr2:11388407-11391641 FORWARD LENGTH=2546
AT2G26790	UAACCGGGGCAUGAGAGACUC	100	3	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:11425270-11427669 REVERSE LENGTH=2400
AT2G26980	UCUGAUUGCAUGUGGUGUACC	109	3	Translation	| Symbols: CIPK3 | CBL-interacting protein kinase 3 | chr2:11514703-11518323 REVERSE LENGTH=1993
AT2G27040	AACAAAACUGUUGAACAAGCCU	111	3.5	Cleavage	| Symbols: AGO4 | Argonaute family protein | chr2:11536534-11542357 REVERSE LENGTH=3189
AT2G27060	UUGAGAGCACUCCACCGACUG	261	4	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr2:11551041-11554775 FORWARD LENGTH=3508
AT2G27090	CCGAUUCUGAUUGCAUGUGGU	186	3	Cleavage	| Symbols: | Protein of unknown function (DUF630 and DUF632) | chr2:11567436-11571856 REVERSE LENGTH=2679
AT2G27170	UUCAACUCUUCCCUCUCGAACU	119	3	Cleavage	| Symbols: TTN7, SMC3 | Structural maintenance of chromosomes (SMC) family protein | chr2:11609122-11617434 REVERSE LENGTH=3968
AT2G27220	UACAGAAUAGGCUUAAGUAAC	189	3.5	Translation	| Symbols: BLH5 | BEL1-like homeodomain 5 | chr2:11637164-11639537 REVERSE LENGTH=1492
AT2G27260	AUCAUCCUCGGAUCAAACCCU	222	2	Cleavage	| Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:11669655-11670644 FORWARD LENGTH=990
AT2G27360	UCCCGGAAUGCUGAAGAAGUA	113	4.5	Cleavage	| Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr2:11706198-11708065 FORWARD LENGTH=1380
AT2G27380	UUUGAUCCGAGGAUGAUGGAUU	112	3.5	Cleavage	| Symbols: ATEPR1, EPR1 | extensin proline-rich 1 | chr2:11713411-11715696 FORWARD LENGTH=2286
AT2G27389	UGAAUCUUGGUCAACUGGACC	197	4.5	Cleavage	| Symbols: | unknown protein; LOCATED IN: endomembrane system. | chr2:11720294-11721081 FORWARD LENGTH=788
AT2G27395	UUCCCCUAGAAUUCUUUCCCU	1646	3.5	Cleavage	| Symbols: | pseudogene of cysteine protease-related | chr2:11721051-11721324 REVERSE LENGTH=274
AT2G27580	UACCCGUACGUCGCCUACAAG	192	5	Cleavage	| Symbols: | A20/AN1-like zinc finger family protein | chr2:11776411-11777529 REVERSE LENGTH=855
AT2G27610	UAUCCUGAGAGCGGUGCUGGC	334	4	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:11783927-11786533 REVERSE LENGTH=2607
AT2G27690	UUACGAGACUCUAGCCCAACU	447	4.5	Cleavage	| Symbols: CYP94C1 | cytochrome P450, family 94, subfamily C, polypeptide 1 | chr2:11809306-11811215 FORWARD LENGTH=1910
AT2G27775	UUUUUCGGACUAGAUAGGACU	107	4	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match
AT2G27810	UAAGACUGAGAUACGCGUGCCU	152	5	Cleavage	| Symbols: ATNAT12, NAT12 | nucleobase-ascorbate transporter 12 | chr2:11852080-11856291 FORWARD LENGTH=2691
AT2G27830	UGACGGUUCAGAUUCAGGAGC	107	3	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22758.1); Has 131 Blast hits to 131 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 131; Viruses - 0; Other Euka
AT2G27960	UUUAGGAUUGUUGCAUAUGCA	1164	4.5	Cleavage	| Symbols: CKS1, CKS1AT | cyclin-dependent kinase-subunit 1 | chr2:11910723-11911685 REVERSE LENGTH=586
AT2G27970	UACCGGAGGACGUACAACACC	302	4.5	Translation	| Symbols: CKS2 | CDK-subunit 2 | chr2:11912212-11913297 REVERSE LENGTH=573
AT2G28270	CCUGAGCCUAGUGACCGAGUA	270	4	Translation	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:12053542-12054398 FORWARD LENGTH=857
AT2G28290	UGGGGCGCUUAUACUUUGGGUU	115	3.5	Cleavage	| Symbols: SYD, CHR3 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12056213-12073083 FORWARD LENGTH=10837
AT2G28320	UCGACCACACUGUCAUGAUCU	174	2.5	Cleavage	| Symbols: | Pleckstrin homology (PH) and lipid-binding START domains-containing protein | chr2:12094746-12099644 FORWARD LENGTH=2849

AT2G28420	UAAAACUGAACCAUGCCUAGA	302	3 Cleavage	| Symbols: | Lactoylglutathione lyase / glyoxalase I family protein | chr2:12157923-12158791 FORWARD LENGTH=869
AT2G28450	AAAUAAAACUGAACCAUGCCU	203	4 Cleavage	| Symbols: | zinc finger (CCCH-type) family protein | chr2:12162090-12166039 REVERSE LENGTH=2783
AT2G28460	UUGGCAUCGAAUUUGAACUCAU	131	4 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr2:12166573-12168874 FORWARD LENGTH=2302
AT2G28620	UUUGGGUUUGGGUUAACUGCU	225	3.5 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:12265167-12270020 REVERSE LENGTH=3129
AT2G28660	UGAAGGACAAGAUCAGCUGCU	415	4 Cleavage	| Symbols: | Chloroplast-targeted copper chaperone protein | chr2:12295327-12297117 FORWARD LENGTH=1063
AT2G28810	UCAACACUCUGAUACAUCUAG	143	5 Translation	| Symbols: | Dof-type zinc finger DNA-binding family protein | chr2:12363630-12365377 FORWARD LENGTH=1371
AT2G28930	UGGGCGCUUAUACUUUGGGUU	115	4.5 Cleavage	| Symbols: APK1B, PK1B | protein kinase 1B | chr2:12424342-12426674 FORWARD LENGTH=1557
AT2G28960	CUACAAAUUCGAGCACUCCCU	156	4 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr2:12437914-12442347 REVERSE LENGTH=2787
AT2G29010	CUACAAAUUCGAGCACUCCCU	156	4 Cleavage	| Symbols: | pseudogene, receptor protein kinase, contains a protein kinase domain (PS50011); contains a S-locus glycoprotein family domain (PF00954); contains LRR Leucine Rich Repeat domains; blastp match of 42% identity and 3.1e-185 P-va
AT2G29100	UAUGGAGAUGAUCGCAAUGGCC	152	4.5 Translation	| Symbols: ATGLR2.9, GLR2.9 | glutamate receptor 2.9 | chr2:12501092-12504912 REVERSE LENGTH=2823
AT2G29110	UUGAGAUAUCCCCUGUUACUG	106	4 Translation	| Symbols: ATGLR2.8, GLR2.8 | glutamate receptor 2.8 | chr2:12506880-12510552 REVERSE LENGTH=2844
AT2G29320	UACCCGUACGUCGCUUACAAG	3223	4.5 Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:12592148-12593686 FORWARD LENGTH=1151
AT2G29340	UACCCGUACGUCGCUUACAAG	3223	5 Cleavage	| Symbols: | NAD-dependent epimerase/dehydratase family protein | chr2:12597115-12598423 FORWARD LENGTH=922
AT2G29470	UUCACAUGUCCGGGCUAGGCA	461	4.5 Cleavage	| Symbols: ATGSTU3, GST21, GSTU3 | glutathione S-transferase tau 3 | chr2:12628541-12629543 REVERSE LENGTH=856
AT2G29670	CCUGAGCCUAGUGACCGAGUA	270	4 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:12681958-12685087 REVERSE LENGTH=2149
AT2G29940	UGAGCCGACAAGAGUAGUAUC	111	4.5 Cleavage	| Symbols: PDR3, ATPDR3 | pleiotropic drug resistance 3 | chr2:12760139-12766623 FORWARD LENGTH=4449
AT2G29960	UCAACGAACUCUUGGCCCUAGA	152	5 Translation	| Symbols: CYP5, ATCYP5, CYP19-4 | cyclophilin 5 | chr2:12769033-12770579 REVERSE LENGTH=777
AT2G30040	CCGAUUCUGAUUGCAUGUGGU	186	4.5 Cleavage	| Symbols: MAPKKK14 | mitogen-activated protein kinase kinase kinase 14 | chr2:12821710-12823169 FORWARD LENGTH=1460
AT2G30300	UUUAAAACCGAGGACUUUUGC	115	4.5 Translation	| Symbols: | Major facilitator superfamily protein | chr2:12919401-12921222 FORWARD LENGTH=1503
AT2G30330	UCCUAUCCAGUCUGAAGAACGC	272	3.5 Translation	| Symbols: BLOS1 | GCN5L1 family protein | chr2:12928767-12929737 REVERSE LENGTH=786
AT2G30505	UCUAGUUCGCGUUCUUCAGAC	300	3 Cleavage	| Symbols: | Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family | chr2:13000973-13002563 REVERSE LENGTH=1591
AT2G30670	UUUGGGUUUGGGUUAACUGCU	225	3.5 Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr2:13069313-13070904 REVERSE LENGTH=789
AT2G30770	UGUCCCAACUUAACUCUACCCU	279	5 Translation	| Symbols: CYP71A13 | cytochrome P450, family 71, subfamily A, polypeptide 13 | chr2:13109794-13112011 REVERSE LENGTH=1632
AT2G30790	UACUGGAGGACGUACAGCACU	949	3 Cleavage	| Symbols: PSBP-2 | photosystem II subunit P-2 | chr2:13118937-13120090 REVERSE LENGTH=901
AT2G30820	UGUAUGCAUAACUUGGGACUU	149	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06660.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Vi
AT2G31060	UGUGAGUGUUUGUGAGGUCUU	178	3.5 Cleavage	| Symbols: | elongation factor family protein | chr2:13213172-13218567 REVERSE LENGTH=2346
AT2G31081	UGCAUAACUUGGGACUUACCU	413	4.5 Cleavage	| Symbols: CLE4 | CLAVATA3/ESR-RELATED 4 | chr2:13238047-13238600 FORWARD LENGTH=554
AT2G31345	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G06135.1); H
AT2G31420	UUCCAGAACUAAUGAAUGUUA	448	3.5 Translation	| Symbols: | Domain of unknown function (DUF313) | chr2:13393364-13394001 REVERSE LENGTH=638
AT2G31470	CUGGGGUACAGAACAUUCGCU	197	3 Translation	| Symbols: DOR | F-box and associated interaction domains-containing protein | chr2:13407492-13408655 REVERSE LENGTH=1164
AT2G31560	UCACUCGACCACAACAGGCUG	106	4.5 Translation	| Symbols: | Protein of unknown function (DUF1685) | chr2:13436557-13438011 FORWARD LENGTH=1169
AT2G31570	UUCUAGUUCGCGUUCUUCAGAC	122	3.5 Cleavage	| Symbols: ATGPX2, GPX2 | glutathione peroxidase 2 | chr2:13437974-13439881 REVERSE LENGTH=853
AT2G31580	UUCUGAAGGACAAGCUCAGCU	1012	3.5 Translation	| Symbols: | tRNAHis guanylyltransferase | chr2:13440909-13445851 REVERSE LENGTH=1946
AT2G31585	UGAAAUAAAACUGAACCAUGCC	263	4 Translation	| Symbols: | other RNA | chr2:13446002-13446729 FORWARD LENGTH=728
AT2G31625	CAACUAACAACGAGGGCACUG	198	3.5 Translation	| Symbols: | unknown pseudogene | chr2:13453331-13455235 REVERSE LENGTH=1001
AT2G31660	UGAAUGACAAACUGGACAAGCU	583	4 Cleavage	| Symbols: SAD2, URM9 | ARM repeat superfamily protein | chr2:13464298-13471821 FORWARD LENGTH=3812
AT2G31720	CUUUGCACUCAUGAAUCUUUC	119	3 Cleavage	| Symbols: | Domain of unknown function (DUF313) | chr2:13485034-13485975 REVERSE LENGTH=942
AT2G31750	UUGAAAGACUUGUGGAUCACC	926	3.5 Translation	| Symbols: UGT74D1 | UDP-glucosyl transferase 74D1 | chr2:13497233-13500023 FORWARD LENGTH=1603
AT2G31810	CUCACAAGUGAUAUAGGGCUU	208	4 Translation	| Symbols: | ACT domain-containing small subunit of acetolactate synthase protein | chr2:13524222-13528501 FORWARD LENGTH=1718
AT2G31840	UUCUUCAGACUGGAUAGGACU	265	3 Cleavage	| Symbols: | Thioredoxin superfamily protein | chr2:13537912-13539758 REVERSE LENGTH=1184
AT2G31860	UGGAGAUGAUAGAUUAUGCGCU	109	4.5 Translation	| Symbols: | pseudogene, poly (ADP-ribose) glycohydrolase, putative, contains Pfam domain, PF05028: poly (ADP-ribose) glycohydrolase (PARG); blastp match of 59% identity and 1.4e-19 P-value to EGAD|134505|143482 114E2.c protein {Drosop
AT2G31890	UUUGAUCCGAGGAUGAUGGAU	816	2.5 Cleavage	| Symbols: ATRAP, RAP | RAP | chr2:13556500-13559767 REVERSE LENGTH=2668
AT2G31970	CUAGAAUUCUUUCCCUUUCCU	235	4 Cleavage	| Symbols: RAD50, ATRAD50 | DNA repair-recombination protein (RAD50) | chr2:13600491-13609069 FORWARD LENGTH=4371
AT2G32450	UCUGUAUGCAUAACUUGGGAC	1212	4 Cleavage	| Symbols: | Calcium-binding tetratricopeptide family protein | chr2:13778449-13781258 FORWARD LENGTH=2810
AT2G32740	UCGAGCACCUACGUCACUGCG	100	3.5 Translation	| Symbols: ATGT13, GT13 | galactosyltransferase 13 | chr2:13886826-13888232 FORWARD LENGTH=1407
AT2G32770	ACUGAGCGCUGAUAGUAACGG	153	4.5 Translation	| Symbols: PAP13, ATPAP13 | purple acid phosphatase 13 | chr2:13895838-13898203 FORWARD LENGTH=2104
AT2G32840	AUGACGAAUGUUUGACAGCCU	113	4.5 Cleavage	| Symbols: | proline-rich family protein | chr2:13932904-13934949 REVERSE LENGTH=1324
AT2G32930	CCGAUUCUGAUUGCAUGUGGU	186	4.5 Translation	| Symbols: ZFN2 | zinc finger nuclease 2 | chr2:13965990-13968957 REVERSE LENGTH=1900
AT2G32950	UUUUAAUUCAAGUAGCUGACU	133	4 Cleavage	| Symbols: COP1, ATCOP1, DET340, FUS1, EMB168 | Transducin/WD40 repeat-like superfamily protein | chr2:13977933-13983535 FORWARD LENGTH=2348
AT2G33000	UCUUCGACUGAGGUAAGCGCCU	355	4 Cleavage	| Symbols: | ubiquitin-associated (UBA)/TS-N domain-containing protein-related | chr2:14006135-14008535 FORWARD LENGTH=1800
AT2G33060	UUAGAAUUAUCAUGUCUUGGC	138	3.5 Cleavage	| Symbols: AtRLP27, RLP27 | receptor like protein 27 | chr2:14025483-14028196 FORWARD LENGTH=2714
AT2G33170	UUAGGCCUGAGAUUGGACGCC	196	4 Cleavage	| Symbols: | Leucine-rich repeat receptor-like protein kinase family protein | chr2:14056250-14060641 REVERSE LENGTH=4012
AT2G33205	UACGUCACUGCGAAUUCCUGGA	271	4.5 Cleavage	| Symbols: | Serinc-domain containing serine and sphingolipid biosynthesis protein | chr2:14070987-14073211 REVERSE LENGTH=1269
AT2G33210	UCUAGUUCACAUUUUUCGGAC	427	4 Cleavage	| Symbols: HSP60-2 | heat shock protein 60-2 | chr2:14074907-14078731 REVERSE LENGTH=2107
AT2G33255	UCACCAUUGGCAGCUCUGUACC	187	4 Cleavage	| Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr2:14098778-14100593 FORWARD LENGTH=990
AT2G33320	UUUGAUCCGAGGAUGAUGGAU	816	3 Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr2:14119526-14122094 REVERSE LENGTH=2569
AT2G33350	UUGAAAGACUUGUGGAUCACC	926	2 Translation	| Symbols: | CCT motif family protein | chr2:14133929-14137154 FORWARD LENGTH=1735
AT2G33509	UUCCAGAACUAAUGAAUGUUA	448	4.5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:14193890-1419411
AT2G33560	AAACAGGACAAGUUACUCGCC	986	5 Cleavage	| Symbols: BUBR1 | BUB1-related (BUB1: budding uninhibited by benzymidazol 1) | chr2:14213601-14215999 REVERSE LENGTH=1478
AT2G33620	UCGAGUACACAGAAUGGGCUG	179	4 Cleavage	| Symbols: | AT hook motif DNA-binding family protein | chr2:14234026-14236862 FORWARD LENGTH=1389
AT2G33680	CUACAAAUUCGAGCACUCCCU	156	4 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:14249608-14251791 FORWARD LENGTH=2184
AT2G33740	UGAGAUUGCUAGAGGAAAGAG	101	3.5 Cleavage	| Symbols: CUTA | Nitrogen regulatory PII-like, alpha/beta | chr2:14269581-14271674 FORWARD LENGTH=828
AT2G33760	UUUUGCUUAGACUUAGAAACU	179	3 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:14275800-14277551 FORWARD LENGTH=1752
AT2G33790	AUGACGAAUGUUUGACAGCCU	113	4.5 Translation	| Symbols: ATAGP30, AGP30 | arabinogalactan protein 30 | chr2:14293561-14295271 REVERSE LENGTH=1055
AT2G33847	UCUGGGUAGAUGGGAUCUUAUC	123	4.5 Cleavage	| Symbols: | unknown protein; LOCATED IN: chloroplast; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G28395.3); Has 71 Blast hits to 71 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 71; '
AT2G34260	UUUGGCCUGAGGUUGGACGCC	367	4.5 Cleavage	| Symbols: | transducin family protein / WD-40 repeat family protein | chr2:14465876-14468531 FORWARD LENGTH=1281
AT2G34310	UUGAAAGACUUGUGGAUCACC	926	3.5 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BES
AT2G34410	UGACGGACAAGAUAAGUUGCU	1505	3.5 Cleavage	| Symbols: | O-acetyltransferase family protein | chr2:14518406-14522622 FORWARD LENGTH=2391
AT2G34450	CUCGGGAGAAAGAAGAAGGCU	259	3 Cleavage	| Symbols: | HMG-box (high mobility group) DNA-binding family protein | chr2:14527736-14529492 REVERSE LENGTH=685
AT2G34470	CAUUGACUUCAAGCCUGCGCU	190	4.5 Cleavage	| Symbols: UREG, PSKF109 | urease accessory protein G | chr2:14530735-14532505 REVERSE LENGTH=1087
AT2G34555	CUUUGCACUCAUGAAUCUUUC	119	3.5 Translation	| Symbols: ATGA2OX3, GA2OX3 | gibberellin 2-oxidase 3 | chr2:14556988-14558697 FORWARD LENGTH=1137
AT2G34630	AUGACGAAUGUUUGACAGCCU	113	4 Cleavage	| Symbols: GPPS, GPS1 | geranyl diphosphate synthase 1 | chr2:14578630-14581727 FORWARD LENGTH=1426
AT2G34680	UCCCAACCCAUGAUCUAAGCG	236	3.5 Translation	| Symbols: AIR9 | Outer arm dynein light chain 1 protein | chr2:14616622-14629129 REVERSE LENGTH=5739
AT2G34770	UCAUCUGCAGUAAGUCCCUGA	104	5 Cleavage	| Symbols: FAH1, ATFAH1 | fatty acid hydroxylase 1 | chr2:14665667-14668250 FORWARD LENGTH=1142
AT2G34780	UAACAAGAACUCUUUCUUUUCU	235	3.5 Translation	| Symbols: EMB1611, MEE22 | maternal effect embryo arrest 22 | chr2:14668653-14673904 FORWARD LENGTH=4191
AT2G34990	AUUUGAACUCAUGGAUACCCU	768	3.5 Cleavage	| Symbols: | RING/U-box superfamily protein | chr2:14750260-14751168 REVERSE LENGTH=909
AT2G35020	UAAGGAGAGUCAGCUACUUGGA	134	4 Cleavage	| Symbols: GlcNAc1pUT2 | N-acetylglucosamine-1-phosphate uridylyltransferase 2 | chr2:14756711-14760706 FORWARD LENGTH=1830
AT2G35075	AUUUGAACUCAUGGAUACCCU	768	3.5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:14786682-1478902
AT2G35200	UCUAUAGCCAAUGUACUCUACU	106	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G32690.1); Has 36 Blast hits to 36 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryot
AT2G35390	UGCCAUGAUCGAGAGCUGCCU	164	4 Cleavage	| Symbols: | Phosphoribosyltransferase family protein | chr2:14895279-14897822 REVERSE LENGTH=1702
AT2G35450	UUUGUUAAACUCAUGGUCACC	138	3 Translation	| Symbols: | catalytics;hydrolases | chr2:14903045-14905372 REVERSE LENGTH=1208
AT2G35620	UCCACCGACUGAUGACAAUGU	1524	5 Cleavage	| Symbols: FEI2 | Leucine-rich repeat protein kinase family protein | chr2:14961113-14965497 REVERSE LENGTH=2205
AT2G35630	UUCUGAUUGCAUGUGGUGUACC	110	3.5 Cleavage	| Symbols: MOR1, GEM1 | ARM repeat superfamily protein | chr2:14966678-14980606 FORWARD LENGTH=6332
AT2G35637	UACUGGAGGACGUACAGCACU	949	4 Translation	| Symbols: | other RNA | chr2:14982608-14983998 REVERSE LENGTH=1149
AT2G35720	UCUGGGUAGAUGGGAUCUUAUC	123	4 Cleavage	| Symbols: OWL1 | DNAJ heat shock N-terminal domain-containing protein | chr2:15016670-15020011 FORWARD LENGTH=1975
AT2G36100	UUCCAAGCUCUUGAUAGAUAG	109	3 Translation	| Symbols: | Uncharacterised protein family (UPF0497) | chr2:15159591-15160750 REVERSE LENGTH=855
AT2G36145	UUUGGCCUGAGGUUGGACGCC	367	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast stroma, chloroplast; EXPRESSED IN: 19 plant structures; EXPRESS
AT2G36190	GCAAGUGAUGAUAAAAAGACA	100	3 Cleavage	| Symbols: AtcwINV4, cwINV4 | cell wall invertase 4 | chr2:15174730-15177870 REVERSE LENGTH=2082
AT2G36240	UCGACCACACUGUCAUGAUCU	174	3 Cleavage	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr2:15195653-15197264 FORWARD LENGTH=1612

AT2G36307	UACCGGAGGACGUACAACACC	302	5 Translation	| Symbols: ZPR4 | ZPR4 (LITTLE ZIPPER 4); other RNA | chr2:15218040-15219415 REVERSE LENGTH=706
AT2G36340	UUUUGCUUAGACUUAGAAACU	179	3 Cleavage	| Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr2:15235723-15237728 FORWARD LENGTH=1619
AT2G36350	UUCCAGCGUUCUGUAGCCAAC	156	4 Cleavage	| Symbols: | Protein kinase superfamily protein | chr2:15238093-15241923 FORWARD LENGTH=3142
AT2G36370	UUUGAGCACUCCUUGACCCGA	154	3.5 Translation	| Symbols: | ubiquitin-protein ligases | chr2:15247793-15252967 FORWARD LENGTH=2965
AT2G36480	UGUGGAUACAAGAGCUGGGCU	215	4 Cleavage	| Symbols: | ENTH/VHS family protein | chr2:15302804-15306274 REVERSE LENGTH=2803
AT2G36680	UUUGGCCUGAGGUUGGACGCC	367	4 Cleavage	| Symbols: | Modifier of rudimentary (Mod(r)) protein | chr2:15368806-15370829 REVERSE LENGTH=1016
AT2G36850	UACCGGAGGACGUACAUAGCU	401	4.5 Cleavage	| Symbols: ATGSL08, GSL8, GSL08, ATGSL8, CHOR | glucan synthase-like 8 | chr2:15454697-15469889 REVERSE LENGTH=6176
AT2G37030	UUGUGGAAUCCGUAGUCUGUA	152	3.5 Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr2:15553732-15554106 FORWARD LENGTH=375
AT2G37050	UUCGAGAACUCCCUGACCCGA	1272	4.5 Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr2:15568986-15573726 FORWARD LENGTH=3355
AT2G37070	UACUGGAGGACGUACAGCACU	949	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G53320.1); Has 1323 Blast hits to 775 proteins in 176 species: Archae - 0; Bacteria - 113; Metazoa - 351; Fungi - 175; Plants - 115; Viruses - 13;
AT2G37230	UAUCUCUGUCGUUACGAACCU	295	3 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:15637046-15639522 REVERSE LENGTH=2477
AT2G37362	UUGGCGCUCAACUCUGCAAGG	4868	4 Translation	| Symbols: | Potential natural antisense gene, locus overlaps with AT2G37360 | chr2:15673687-15675978 FORWARD LENGTH=2292
AT2G37430	CCGAUUCUGAUUGCAUGUGGU	186	4.5 Cleavage	| Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr2:15706357-15707224 FORWARD LENGTH=868
AT2G37440	UUUAAAACCGAGGACUUUUGC	115	3 Cleavage	| Symbols: | DNAse I-like superfamily protein | chr2:15719788-15722108 FORWARD LENGTH=1777
AT2G37520	UUUGAUCCGAGGAUGAUGGAU	816	3.5 Cleavage	| Symbols: | Acyl-CoA N-acyltransferase with RING/FYVE/PHD-type zinc finger domain | chr2:15744769-15750107 REVERSE LENGTH=3246
AT2G37670	UUGAGAAGAUACAUUGACGGU	731	3 Translation	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:15797384-15800536 REVERSE LENGTH=2712
AT2G37690	UUGGACGCCUCUACUAUGAGA	679	1.5 Cleavage	| Symbols: | phosphoribosylaminoimidazole carboxylase, putative / AIR carboxylase, putative | chr2:15805715-15810552 FORWARD LENGTH=2406
AT2G37860	UUCCCCUAGAAUUCUUUCCCU	1646	3.5 Cleavage	| Symbols: LCD1 | Protein of unknown function (DUF3411) | chr2:15856632-15858920 FORWARD LENGTH=1531
AT2G37930	UGACACCGAUUCUGAUAGCUU	823	2.5 Cleavage	| Symbols: | Protein of unknown function (DUF3527) | chr2:15873117-15874972 FORWARD LENGTH=1773
AT2G37970	UUAGCCUGAGGUUGGACGCCU	231	4.5 Cleavage	| Symbols: SOUL-1 | SOUL heme-binding family protein | chr2:15890972-15891843 FORWARD LENGTH=872
AT2G38020	UAGAUAACAAGAACUCUUUCU	107	2.5 Cleavage	| Symbols: VCL1, MAN, EMB258 | vacuoleless1 (VCL1) | chr2:15909908-15914710 REVERSE LENGTH=2875
AT2G38025	UCUGUAUGCAUAGCUUGGGAC	197	4.5 Cleavage	| Symbols: | Cysteine proteinases superfamily protein | chr2:15914958-15916733 REVERSE LENGTH=1027
AT2G38070	AUCAUCCUCGGAUCAAACCCU	222	1.5 Cleavage	| Symbols: | Protein of unknown function (DUF740) | chr2:15928591-15930794 FORWARD LENGTH=2204
AT2G38080	UUCUGAAGGACAAGCUCAGCU	1012	3.5 Cleavage	| Symbols: IRX12, LAC4, ATLMCO4, LMCO4 | Laccase/Diphenol oxidase family protein | chr2:15934460-15937616 FORWARD LENGTH=2021
AT2G38120	CAACUAACAACGAGGGCACUG	198	5 Translation	| Symbols: AUX1, WAV5, PIR1, MAP1 | Transmembrane amino acid transporter family protein | chr2:15972993-15977180 FORWARD LENGTH=2135
AT2G38195	UGAAGGACAAGCUCAGCUGCU	1483	4 Cleavage	| Symbols: | RING/U-box superfamily protein | chr2:16003615-16006654 FORWARD LENGTH=1712
AT2G38260	CUUGGCAUCGAAUUUGAACUC	1059	3.5 Cleavage	| Symbols: | pseudogene, similar to carboxyl transferase alpha subunit, similar to GB:U34392, however, a substitution at base 93910 in our sequence causes a stop codon in the coding region. We sequenced four clones in that region which all co
AT2G38365	AUGGAUUUAGAUCACUUGCGUC	196	4.5 Cleavage	| Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:16070881-16072007 FORWARD LENGTH=1127
AT2G38420	UGACGCCAAUUCUGAAAGUUU	154	4 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr2:16091093-16092549 FORWARD LENGTH=1457
AT2G38440	UACCCGUACGUCGCCUACAAG	192	4.5 Cleavage	| Symbols: ITB1, SCAR2, DIS3, WAVE4, ATSCAR2 | SCAR homolog 2 | chr2:16095329-16101221 FORWARD LENGTH=4791
AT2G38450	AUGGAUUUAGAUCACUUGCGUC	196	3.5 Translation	| Symbols: | CONTAINS InterPro DOMAIN/s: Sel1-like (InterPro:IPR006597); BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G05360.1); Has 88 Blast hits to 88 proteins in 25 species: Archae - 0; Bacteria - 16; Metazoa - 0; Fı
AT2G38460	UAGAAUUAUCAUGUCUUGGCA	194	4 Cleavage	| Symbols: ATIREG1, IREG1, FPN1 | iron regulated 1 | chr2:16103311-16106177 FORWARD LENGTH=1877
AT2G38570	UACCGGAGGACGUACAUAGCU	401	5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: PRC-barrel-like (InterPro:IPR011033); Has 300 Blast hits to 300 proteins in 81 species: Archae - 0; Bacteria - 135; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryotes - 128 (source: NCBI BLir
AT2G38620	UGUGGUGUACCUCUUACGUCU	106	4 Cleavage	| Symbols: CDKB1;2 | cyclin-dependent kinase B1;2 | chr2:16152532-16154086 FORWARD LENGTH=1175
AT2G38630	CUUCGAGGAGAUAUGACGCGCC	513	4 Translation	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr2:16154067-16156579 REVERSE LENGTH=1897
AT2G38650	UCUAGUUCGCGUUUUUCAGAC	163	3.5 Translation	| Symbols: GAUT7, LGT7 | galacturonosyltransferase 7 | chr2:16161808-16165775 REVERSE LENGTH=2160
AT2G38840	UAGAGUUAAGUUGGGACAGGA	199	5 Cleavage	| Symbols: | Guanylate-binding family protein | chr2:16227051-16232456 FORWARD LENGTH=2428
AT2G38910	UUUAGAGAUCCCCUGUUACUG	387	3.5 Cleavage	| Symbols: CPK20 | calcium-dependent protein kinase 20 | chr2:16245214-16247483 REVERSE LENGTH=1752
AT2G38970	UCUAGUUCACAUUUUUCGGAC	427	1.5 Translation	| Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr2:16273901-16276872 FORWARD LENGTH=2534
AT2G38980	UACAGAAUAGGCUUAAGUAAC	189	3.5 Cleavage	| Symbols: | pseudogene, similar to fiber protein Fb12, blastp match of 53% identity and 1.2e-13 P-value to GP|25992543|gb|AAN77151.1||AF531371 fiber protein Fb12 {Gossypium barbadense} | chr2:16277009-16279354 REVERSE LENGTH=2
AT2G39100	UCAAGCGAUUGGAAGGAUUGUU	102	4 Cleavage	| Symbols: | RING/U-box superfamily protein | chr2:16317438-16319387 FORWARD LENGTH=1326
AT2G39120	UGGGGCGUUAUACUUUGGGUU	115	4.5 Cleavage	| Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr2:16321794-16322957 FORWARD LENGTH=1164
AT2G39220	UCACCAUUGGCAGCUCUGUACC	187	4.5 Cleavage	| Symbols: PLP6, PLA IIB | PATATIN-like protein 6 | chr2:16374896-16377020 REVERSE LENGTH=2016
AT2G39280	UUUUGCUUAGACUUAGAAACU	179	3.5 Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr2:16401587-16406650 REVERSE LENGTH=2512
AT2G39300	UGACGGAAGCUACAGAGGAUG	108	3.5 Translation	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 8 plant structures; EXPRESSED DURING: 4 anthesis, petal differentiation and expansion stage; BEST Arabidopsis thaliana protein mat
AT2G39470	UUCUUUCCGUUGGUGUGCGCC	205	4 Cleavage	| Symbols: PPL2 | PsbP-like protein 2 | chr2:16476216-16477843 FORWARD LENGTH=1000
AT2G39480	AUCCAAGUAGCUGACUCUCCU	1104	4 Cleavage	| Symbols: PGP6 | P-glycoprotein 6 | chr2:16477792-16485039 REVERSE LENGTH=4893
AT2G39550	UUUGAGCACUCCUUGACCCGA	154	4.5 Cleavage	| Symbols: ATGGT-IB, GGB, PGGT-I | Prenyltransferase family protein | chr2:16501623-16504304 FORWARD LENGTH=1331
AT2G39580	UUUAGAGAUCCCCUGUUACUG	387	3.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Putative zinc-finger domain (InterPro:IPR019607); Has 249 Blast hits to 219 proteins in 85 species: Archae - 0; Bacteria - 144; Metazoa - 29; Fungi - 8; Plants - 50; Viruses - 0; Other Eukaryotes - 18 (sour
AT2G39670	UUACGAGACUCUAGCCCAGCU	3733	3.5 Cleavage	| Symbols: | Radical SAM superfamily protein | chr2:16534230-16537318 FORWARD LENGTH=1692
AT2G39880	UUAGCACCGAGGAUGAUGGACU	330	3.5 Translation	| Symbols: MYB25, AtMYB25 | myb domain protein 25 | chr2:16647945-16649479 REVERSE LENGTH=1104
AT2G39950	UUCUUCAGACUGGAUAGGACU	265	3 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; Has
AT2G40070	UUACGAGACUCUAGCCCAACU	447	5 Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thalia
AT2G40190	UUUCUGACGGACAAGAUAAGU	480	4 Cleavage	| Symbols: LEW3 | UDP-Glycosyltransferase superfamily protein | chr2:16785194-16787530 FORWARD LENGTH=1703
AT2G40490	UUUUUCGGACUAGAUAGGACU	107	3.5 Translation	| Symbols: HEME2 | Uroporphyrinogen decarboxylase | chr2:16912845-16915177 FORWARD LENGTH=1490
AT2G40500	CUUCGAGGAGAUAUGACGCGCC	513	4.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr2:16916330-16917217 FORWARD LENGTH=888
AT2G40540	UGUCACCGUAGAUUUCUUCCU	123	3.5 Cleavage	| Symbols: KT2, ATKT2, SHY3, KUP2, ATKUP2, TRK2 | potassium transporter 2 | chr2:16931351-16934570 FORWARD LENGTH=2533
AT2G40570	UUAUGAGACUCUAGCCCAGCU	149	5 Cleavage	| Symbols: | initiator tRNA phosphoribosyl transferase family protein | chr2:16940835-16943492 FORWARD LENGTH=1999
AT2G40630	UGAAUGACAAACUGGACAAGCU	583	3 Cleavage	| Symbols: | Uncharacterised conserved protein (UCP030365) | chr2:16958146-16961144 FORWARD LENGTH=2106
AT2G40710	UUACGAGACUCUAGCCCAGCU	3733	4 Translation	| Symbols: | Haemolysin-III related integral membrane protein | chr2:16980943-16981368 REVERSE LENGTH=426
AT2G40802	UAGUGACCGAGUAGUACCACC	461	4.5 Translation	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:17028304-1702840
AT2G40995	UACGCUAGGGAGAUAUCUGCC	122	4 Cleavage	| Symbols: | Molecular chaperone Hsp40/DnaJ family protein | chr2:17109394-17109712 FORWARD LENGTH=246
AT2G41060	AAACAGGACAAGUUACUCGCC	986	4 Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr2:17126989-17129563 FORWARD LENGTH=1787
AT2G41080	UUCGGACUGGAUAGGACUAGG	101	4 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr2:17132853-17134593 FORWARD LENGTH=1741
AT2G41190	UAGAGUUAAGUUGGGACAGGA	199	3.5 Cleavage	| Symbols: | Transmembrane amino acid transporter family protein | chr2:17167279-17170407 REVERSE LENGTH=2155
AT2G41200	UUUCUGACGGACAAGAUAAGU	480	4 Cleavage	| Symbols: | unknown protein; Has 26 Blast hits to 26 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 26; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:17171625-17173131 FORWARD LENGTH=720
AT2G41300	UCGAGGGCAGGAACAUUGACU	334	3.5 Cleavage	| Symbols: SSL1 | strictosidine synthase-like 1 | chr2:17214237-17216292 REVERSE LENGTH=1260
AT2G41380	UUGUGAGUGUUUGUGAGGUCU	141	3 Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr2:17251941-17253057 FORWARD LENGTH=1021
AT2G41480	UUUGUUAAACUCAUGGUCACCC	165	3.5 Cleavage	| Symbols: | Peroxidase superfamily protein | chr2:17296812-17298731 REVERSE LENGTH=1202
AT2G41630	UUGACGACCAACUCCGCUCCU	170	3 Cleavage	| Symbols: TFIIB | transcription factor IIB | chr2:17355331-17357598 REVERSE LENGTH=1361
AT2G41700	UUCUGUAGCACGAGGUAUCCU	302	4 Cleavage	| Symbols: ABCA1, AtABCA1 | ATP-binding cassette A1 | chr2:17383042-17396110 REVERSE LENGTH=5846
AT2G41940	UUAUCAACGAACUCUUGGCCC	310	3.5 Translation	| Symbols: ZFP8 | zinc finger protein 8 | chr2:17507509-17508616 FORWARD LENGTH=1108
AT2G41960	UGUCCCAACUUAACUCUACCCU	279	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G58050.1); Has 11991 Blast hits to 7260 proteins in 458 species: Archae - 17; Bacteria - 481; Metazoa - 5028; Fungi - 1325; Plants - 615; Viruse
AT2G41980	UUGAGAUAUCCCCUGUUACUG	106	4 Translation	| Symbols: | Protein with RING/U-box and TRAF-like domains | chr2:17523494-17525914 REVERSE LENGTH=1335
AT2G42080	UGGCGCUCAACUCUGCGAGGU	1187	4.5 Translation	| Symbols: | Chaperone DnaJ-domain superfamily protein | chr2:17553240-17555504 REVERSE LENGTH=990
AT2G42200	UUUGAGAGCACUCCACCGACU	156	4.5 Cleavage	| Symbols: SPL9, AtSPL9 | squamosa promoter binding protein-like 9 | chr2:17587407-17589630 FORWARD LENGTH=1501
AT2G42300	UUUGGUUCUGAGUCCCCGCCU	669	3 Cleavage	| Symbols: | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr2:17621157-17624838 FORWARD LENGTH=1576
AT2G42320	UCGACCACACUGUUAGGAUCU	121	4 Translation	| Symbols: | nucleolar protein gar2-related | chr2:17627962-17630797 FORWARD LENGTH=2290
AT2G42388	UUUCUGACGGACAAGAUAAGU	480	4 Cleavage	| Symbols: | other RNA | chr2:17650225-17651083 FORWARD LENGTH=631
AT2G42400	UUCGAGGAGAUAUGACGCGCC	4887	3.5 Cleavage	| Symbols: VOZ2, ATVOZ2 | vascular plant one zinc finger protein 2 | chr2:17654232-17656839 REVERSE LENGTH=1834
AT2G42520	UCGAGCACCUACGUCACUGCG	100	4.5 Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr2:17704832-17708947 FORWARD LENGTH=2252
AT2G42570	UACGUCACUGCGAAUUCCUGGA	271	4 Translation	| Symbols: TBL39 | TRICHOME BIREFRINGENCE-LIKE 39 | chr2:17717367-17720080 REVERSE LENGTH=1394
AT2G42620	UGAGUAGAAUUCGAUCAUAUC	114	4.5 Cleavage	| Symbols: MAX2, ORE9, PPS | RNI-like superfamily protein | chr2:17756140-17758468 FORWARD LENGTH=2329
AT2G42670	UCAUGUAGUUCUAGUUCGCCU	245	4.5 Cleavage	| Symbols: | Protein of unknown function (DUF1637) | chr2:17771776-17774647 REVERSE LENGTH=1431
AT2G42720	UGACGGACAAGAUAAGCUGCU	259	4 Cleavage	| Symbols: | FBD, F-box, Skp2-like and Leucine Rich Repeat domains containing protein | chr2:17785409-17787421 FORWARD LENGTH=1786
AT2G42800	CUCGGGAGAAAGAAGAAGGCU	259	3 Cleavage	| Symbols: AtRLP29, RLP29 | receptor like protein 29 | chr2:17807942-17809590 REVERSE LENGTH=1649
AT2G42890	UAAGGAGAGUCAGCUACUUGGA	134	3.5 Cleavage	| Symbols: AML2, ML2 | MEI2-like 2 | chr2:17850531-17854532 FORWARD LENGTH=2921
AT2G42920	UUUUGCUUAGACUUAGAAACU	179	3.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr2:17858698-17863466 FORWARD LENGTH=4026
AT2G43040	UAAGGAGAGUCAGCUACUUGGA	134	3.5 Translation	| Symbols: NPG1 | tetratricopeptide repeat (TPR)-containing protein | chr2:17895883-17899374 REVERSE LENGTH=2582

AT2G43070	UGUGGUGUACCUCUCACGUCU	112	4.5	Cleavage	| Symbols: SPPL3, ATSPPL3 | SIGNAL PEPTIDE PEPTIDASE-LIKE 3 | chr2:17910888-17914870 REVERSE LENGTH=2062
AT2G43390	UUUGGGUUUGGGUUAACUGCU	225	3	Cleavage	| Symbols: | unknown protein; Has 7 Blast hits to 7 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr2:18020350-18020861 REVERSE LENGTH=512
AT2G43400	CUUUGCACUCAUGAAUCUUUC	119	4	Cleavage	| Symbols: ETFQO | electron-transfer flavoprotein:ubiquinone oxidoreductase | chr2:18021180-18025292 FORWARD LENGTH=2277
AT2G43420	UCUGUAUGCAUAGCUUGGGACU	466	5	Cleavage	| Symbols: | 3-beta hydroxysteroid dehydrogenase/isomerase family protein | chr2:18031268-18035098 REVERSE LENGTH=2073
AT2G43580	UGGAUUCCGGCUGCAUACUCC	392	4.5	Cleavage	| Symbols: | Chitinase family protein | chr2:18078649-18080028 REVERSE LENGTH=981
AT2G43820	CUCAUGUAGUUCUAGUUCGCA	102	4	Cleavage	| Symbols: GT, UGT74F2, ATSAGT1, SGT1, SAGT1 | UDP-glucosyltransferase 74F2 | chr2:18152227-18153908 FORWARD LENGTH=1595
AT2G43830	UACAGAAUAGGCUUAAGUAAC	189	3.5	Cleavage	| Symbols: | pseudogene, NPK1-related protein kinase 3, identical to NPK1-related protein kinase 3 (GI:2342427) (Arabidopsis thaliana);; blastp match of 91% identity and 2.1e-09 P-value to GP|456309|dbj|BAA05648.1||D26601 protein kinase {
AT2G43960	UUCCAAGCUCUUGAUAGAUAG	109	2.5	Cleavage	| Symbols: | SWAP (Suppressor-of-White-APricot)/surp domain-containing protein | chr2:18203312-18204912 REVERSE LENGTH=1481
AT2G44140	UCAUGUAGUUCUAGUUCGCCU	245	4	Cleavage	| Symbols: | Peptidase family C54 protein | chr2:18253497-18257239 REVERSE LENGTH=2911
AT2G44280	UAGUGACCGAGUAGUACCACC	461	5	Cleavage	| Symbols: | Major facilitator superfamily protein | chr2:18301350-18304201 REVERSE LENGTH=1791
AT2G44410	UUUGAUCCGAGGAUGAUGGAU	816	3.5	Translation	| Symbols: | RING/U-box superfamily protein | chr2:18328417-18330336 FORWARD LENGTH=1774
AT2G44470	AUUGACGUCGAGUAUGAGCCU	2734	4	Cleavage	| Symbols: BGLU29 | beta glucosidase 29 | chr2:18354186-18357481 FORWARD LENGTH=1605
AT2G44760	UUUAAAACCGAGGACUUUUGC	115	3	Translation	| Symbols: | Domain of unknown function (DUF3598) | chr2:18452851-18454809 REVERSE LENGTH=1613
AT2G44780	UGACGCCAAUUCUGAAAGUUU	154	4	Cleavage	| Symbols: | Encodes a Uclacyanin/Basic blue family protein [pseudogene] | chr2:18460687-18461194 REVERSE LENGTH=508
AT2G44790	UGACGCCAAUUCUGAAAGUUU	154	3.5	Cleavage	| Symbols: UCC2 | uclacyanin 2 | chr2:18461906-18463309 REVERSE LENGTH=962
AT2G44810	UCACUGUGAAUUCCUGGAGUU	123	4.5	Cleavage	| Symbols: DAD1 | alpha/beta-Hydrolases superfamily protein | chr2:18479053-18480197 FORWARD LENGTH=1145
AT2G44910	UCGGCUCAAACCUAACACGUU	129	4	Cleavage	| Symbols: ATHB4, ATHB-4, HB4 | homeobox-leucine zipper protein 4 | chr2:18517887-18519525 REVERSE LENGTH=957
AT2G44990	UUGAGAAGAUACAUUGACGGU	731	2.5	Cleavage	| Symbols: CCD7, MAX3, ATCCD7 | carotenoid cleavage dioxygenase 7 | chr2:18558938-18561621 FORWARD LENGTH=1890
AT2G45030	UUCGGACUGGAUAGGACUAGG	101	4	Translation	| Symbols: | Translation elongation factor EFG/EF2 protein | chr2:18572411-18576970 FORWARD LENGTH=2479
AT2G45070	UGAGAACAUUGACUUCAGACCU	158	4	Cleavage	| Symbols: SEC61 BETA | Preprotein translocase Sec, Sec61-beta subunit protein | chr2:18587082-18588259 REVERSE LENGTH=458
AT2G45126	UCUGUACCGCUGAAUUCUUCC	275	5	Translation	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr2:18605871-1860596
AT2G45340	AUGGAUUUAGAUCACUUGCGUC	196	3.5	Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr2:18691722-18694725 FORWARD LENGTH=2352
AT2G45360	UUGGACGUCUCUACUAUGAGA	437	4	Cleavage	| Symbols: | Protein of unknown function (DUF1442) | chr2:18698592-18699514 FORWARD LENGTH=829
AT2G45600	UGGAUUCCGGCUGCAUACUCC	392	3	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:18789588-18790952 FORWARD LENGTH=1365
AT2G45620	UCAACACUCUGAUACAUCUAG	143	5	Cleavage	| Symbols: | Nucleotidyltransferase family protein | chr2:18792864-18795904 FORWARD LENGTH=2528
AT2G45640	UCUAGUCCGAAAAAUGCGAAC	163	5	Cleavage	| Symbols: SAP18, ATSAP18 | SIN3 associated polypeptide P18 | chr2:18799610-18801383 REVERSE LENGTH=790
AT2G45840	AUACCCAAACCUGAACUUUCU	127	3.5	Translation	| Symbols: | Arabidopsis thaliana protein of unknown function (DUF821) | chr2:18869261-18871561 FORWARD LENGTH=1671
AT2G45970	CCACCGACUGAUGACAACGUC	122	5	Cleavage	| Symbols: CYP86A8, LCR | cytochrome P450, family 86, subfamily A, polypeptide 8 | chr2:18912260-18914739 REVERSE LENGTH=2480
AT2G46020	UGUGGAUACAAGAGUUGGGCU	111	3.5	Translation	| Symbols: CHR2, ATBRM, BRM, CHA2 | transcription regulatory protein SNF2, putative | chr2:18923304-18931934 FORWARD LENGTH=6747
AT2G46040	UGUUACGAGACUCUAGCCCAG	574	5	Cleavage	| Symbols: | ARID/BRIGHT DNA-binding domain;ELM2 domain protein | chr2:18935301-18938447 REVERSE LENGTH=2228
AT2G46110	AUCCAAGUAGCUGACUCUCCU	1104	4	Cleavage	| Symbols: PANB1, KPHMT1 | ketopantoate hydroxymethyltransferase 1 | chr2:18954570-18956530 REVERSE LENGTH=1400
AT2G46330	UGACGUCGAGUAUGAGCCUGA	416	4.5	Cleavage	| Symbols: AGP16, ATAGP16 | arabinogalactan protein 16 | chr2:19018508-19019255 REVERSE LENGTH=748
AT2G46470	UAUCUCUGUCGUUACGAACCU	295	4	Cleavage	| Symbols: OXA1L | inner membrane protein OXA1-like | chr2:19072313-19075123 FORWARD LENGTH=1618
AT2G46500	CCACCGACUGAUGACAACGUC	122	5	Cleavage	| Symbols: ATPI4K GAMMA 4, UBDK GAMMA 4, PI4K GAMMA 4 | phosphoinositide 4-kinase gamma 4 | chr2:19086561-19088964 REVERSE LENGTH=2311
AT2G46570	UAGAGUUAAGUUGGGACAGGA	199	4	Cleavage	| Symbols: LAC6 | laccase 6 | chr2:19126872-19129069 FORWARD LENGTH=1710
AT2G46590	GCAAGUGAUGAUAAAAAGACA	100	3.5	Translation	| Symbols: DAG2 | Dof-type zinc finger DNA-binding family protein | chr2:19133229-19135289 FORWARD LENGTH=2061
AT2G47020	UUUGCUGAACAUGUACCUCCA	119	3.5	Cleavage	| Symbols: | Peptide chain release factor 1 | chr2:19319812-19322391 REVERSE LENGTH=1631
AT2G47115	UUCUGUAGCACGAGGUAUCCU	302	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G10660.1); H
AT2G47170	UCGACCACACUGUCAUGAUCU	174	3.5	Translation	| Symbols: ARF1A1C | Ras-related small GTP-binding family protein | chr2:19366623-19368840 FORWARD LENGTH=1036
AT2G47500	UGAAUCUUGGUCAACUGGACC	197	3.5	Cleavage	| Symbols: | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | chr2:19492995-19498160 FORWARD LENGTH=3482
AT2G47600	UUCGAGGAGAUAUGACGCGCC	4887	4	Cleavage	| Symbols: ATMHX, MHX1, ATMHX1, MHX | magnesium/proton exchanger | chr2:19524160-19527413 REVERSE LENGTH=2147
AT2G47630	UUUAUUCACACAGUGGACUGUG	118	4	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr2:19534503-19537014 FORWARD LENGTH=1293
AT2G47770	UUGACUUCAGACCUGCGCGUG	131	4	Cleavage	| Symbols: ATTSPO, TSPO | TSPO(outer membrane tryptophan-rich sensory protein)-related | chr2:19568464-19569507 FORWARD LENGTH=1044
AT2G47800	UCUUGGCAUCGAAUUUGAACU	154	4	Cleavage	| Symbols: ATMRP4, EST3, MRP4, ABCC4 | multidrug resistance-associated protein 4 | chr2:19574864-19580599 FORWARD LENGTH=4847
AT2G48060	UGAGAGCACUCCACCGACUGA	230	4.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: shoot, sperm cell; CONTAINS InterPro DOMAIN/s: Protein of unknowı
AT2G48070	UCAAGCGAUUGGAAGGAUUGUU	102	3	Cleavage	| Symbols: RPH1 | resistance to phytophthora 1 | chr2:19662844-19664465 FORWARD LENGTH=949
AT3G01160	UGACACCGAUUCUGAUUGCAU	377	5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cytosol, nucleus; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: NUC
AT3G01175	UUGAACAAGCCUGAUGAAGUU	102	4	Translation	| Symbols: | Protein of unknown function (DUF1666) | chr3:59471-60845 FORWARD LENGTH=1219
AT3G01311	UCCAGUCUGAAGAACGCGAAC	136	4	Cleavage	| Symbols: | Protein of unknown function (DUF569) | chr3:103043-104287 REVERSE LENGTH=879
AT3G01350	UUUGCCUGUUGAACUCGAGUA	114	3	Cleavage	| Symbols: | Major facilitator superfamily protein | chr3:135024-137460 FORWARD LENGTH=1692
AT3G01380	UUGAAGGAUUUGUGGUUAACCA	106	4.5	Translation	| Symbols: | transferases;sulfuric ester hydrolases;catalytics;transferases | chr3:144288-149828 REVERSE LENGTH=2982
AT3G01390	UUGCAGAGAUGGAUGUACAAC	101	3	Cleavage	| Symbols: VMA10, AVMA10 | vacuolar membrane ATPase 10 | chr3:149999-151539 REVERSE LENGTH=680
AT3G01580	UUUUGCUUAGACUUAGAAACU	179	3.5	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:223529-225511 REVERSE LENGTH=1983
AT3G01810	UUUUGAUUCACCGGAUAAACUC	104	4.5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana proteir
AT3G02060	UGCCUAGAUUGCUCUACUCGA	125	4.5	Cleavage	| Symbols: | DEAD/DEAH box helicase, putative | chr3:354412-358833 FORWARD LENGTH=2888
AT3G02070	UGUCUUACCCGUACGUCGCUU	150	4.5	Cleavage	| Symbols: | Cysteine proteinases superfamily protein | chr3:360921-363429 FORWARD LENGTH=1142
AT3G02230	UGAGAAGAGAUAGAAUAGAAUC	103	2.5	Cleavage	| Symbols: RGP1, ATRGP1 | reversibly glycosylated polypeptide 1 | chr3:415393-417547 FORWARD LENGTH=1387
AT3G02320	AUGGAUUUAGAUCACUUGCGUC	196	4.5	Cleavage	| Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase | chr3:469934-473717 FORWARD LENGTH=2158
AT3G02360	UCGAGCACCUACGUCACUGCG	100	4	Translation	| Symbols: | 6-phosphogluconate dehydrogenase family protein | chr3:482028-484147 FORWARD LENGTH=1929
AT3G02370	CAUCAAGAACCGGUCAUGCCU	125	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G57360.1); Has 95 Blast hits to 95 proteins in 40 species: Archae - 0; Bacteria - 0; Metazoa - 53; Fungi - 2; Plants - 39; Viruses - 0; Other Eukary
AT3G02468	UUGAGAGAUCCCUUGUUACUG	141	4.5	Translation	| Symbols: CPuORF9 | conserved peptide upstream open reading frame 9 | chr3:509087-511557 FORWARD LENGTH=1876
AT3G02470	UUGAGAGAUCCCUUGUUACUG	141	4.5	Translation	| Symbols: SAMDC | S-adenosylmethionine decarboxylase | chr3:509096-511489 FORWARD LENGTH=1799
AT3G02490	UACGCUAGGGAGAUAUCUGCC	122	5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:513525-515925 FORWARD LENGTH=2401
AT3G02493	UACGUCACUGCGAAUCCUGGA	271	4	Translation	| Symbols: RTFL19, DVL2 | ROTUNDIFOLIA like 19 | chr3:515944-516358 REVERSE LENGTH=415
AT3G02560	UGACGGAAGCUACAGAGGAUG	108	4	Cleavage	| Symbols: | Ribosomal protein S7e family protein | chr3:541800-543385 FORWARD LENGTH=911
AT3G02620	UUUGAUUCACCGGAUAAACUC	175	4.5	Cleavage	| Symbols: | Plant stearoyl-acyl-carrier-protein desaturase family protein | chr3:560256-561880 FORWARD LENGTH=1332
AT3G02720	UGCAUAACUUGGGACUUACCU	413	4	Translation	| Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr3:586224-588365 FORWARD LENGTH=1556
AT3G02730	UGUGAGUGUUUGUGAGGUCUU	178	3.5	Translation	| Symbols: TRXF1, ATF1 | thioredoxin F-type 1 | chr3:588408-589685 REVERSE LENGTH=793
AT3G02750	UUCCAGAACUAAUGAAUGUUA	448	4	Cleavage	| Symbols: | Protein phosphatase 2C family protein | chr3:593207-595755 REVERSE LENGTH=2276
AT3G02810	UACCCGUACGUCGCUUAUAAG	185	4.5	Cleavage	| Symbols: | Protein kinase superfamily protein | chr3:608460-610985 REVERSE LENGTH=2146
AT3G02875	CGGAGGAAACUUAGCAGCGCC	103	4.5	Translation	| Symbols: ILR1 | Peptidase M20/M25/M40 family protein | chr3:631913-634074 FORWARD LENGTH=1624
AT3G02885	UUCCAGAACUAAUGAAUGUUA	448	4	Cleavage	| Symbols: GASA5 | GAST1 protein homolog 5 | chr3:638021-639055 REVERSE LENGTH=640
AT3G03040	CUCACAAGUGAUAUAGGGCUU	208	4	Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr3:684506-686544 FORWARD LENGTH=1748
AT3G03440	CUCGGGAGAAAGAAGAAGGCU	259	3.5	Cleavage	| Symbols: | ARM repeat superfamily protein | chr3:815644-818834 FORWARD LENGTH=1558
AT3G03570	UCUGAUUGCAUGUGGUGUACC	109	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF3550/UPF0682) | chr3:856876-860469 FORWARD LENGTH=2325
AT3G03580	UUACCCGUACGUCGCUUACAA	130	4	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:860512-863352 REVERSE LENGTH=2841
AT3G03630	UUUAACAACUAAGGUUCCUGU	1055	2.5	Cleavage	| Symbols: CS26 | cysteine synthase 26 | chr3:877928-880446 REVERSE LENGTH=1634
AT3G03702	AUUUCAGUGAGCACGUACCUC	200	4.5	Cleavage	| Symbols: | other RNA | chr3:916356-918834 REVERSE LENGTH=1451
AT3G03770	AUUGACGUCGAGUAUGAGCCU	2734	4.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr3:945135-949042 REVERSE LENGTH=2840
AT3G03810	UCACUGUGAAUUCCUGGAGUU	123	2.5	Cleavage	| Symbols: EDA30 | O-fucosyltransferase family protein | chr3:971672-976367 REVERSE LENGTH=2867
AT3G03970	UGUUACGAGACUCUAGCCCAG	574	5	Cleavage	| Symbols: | ARM repeat superfamily protein | chr3:1027997-1030592 REVERSE LENGTH=1946
AT3G04000	AUUGACGUCGAGUAUGAGCCU	2734	4	Translation	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:1035500-1036672 FORWARD LENGTH=1056
AT3G04020	AUACCCAAACCUGAACUUUCU	127	4	Cleavage	| Symbols: | unknown protein; Has 26 Blast hits to 25 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 23; Viruses - 0; Other Eukaryotes - 3 (source: NCBI BLink). | chr3:1040548-1042518 FORWARD LENGTH=1056
AT3G04310	UUAGAAUUAUCAUGUCUUGGC	138	3.5	Cleavage	| Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:1141581-1142528 REVERSE LENGTH=810
AT3G04340	CUAGAAUUCUUUCCCUUUCCU	235	2.5	Cleavage	| Symbols: emb2458 | FtsH extracellular protease family | chr3:1146800-1153341 REVERSE LENGTH=4106
AT3G04350	UUCCAGCGUUCUGUAGCCAAC	156	4.5	Cleavage	| Symbols: | Plant protein of unknown function (DUF946) | chr3:1153727-1156776 REVERSE LENGTH=2256
AT3G04360	CAUCAAGAACCGGUCAUGCCU	125	4.5	Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:1157004-1158310 REVERSE LENGTH=1307
AT3G04380	UUUGAACUCAUGGAUACCCUA	227	4	Translation	| Symbols: SUVR4, SDG31 | SET-domain containing protein lysine methyltransferase family protein | chr3:1161387-1164929 FORWARD LENGTH=2084
AT3G04530	UCUAGUUCGCAUUUUUUGGAC	421	3.5	Translation	| Symbols: PPCK2, PEPCK2, ATPPCK2 | phosphoenolpyruvate carboxylase kinase 2 | chr3:1221546-1222655 FORWARD LENGTH=1036

AT3G04670	UCUCAUGUAGUUCUAGUUCACA	115	5 Cleavage	| Symbols: WRKY39, ATWRKY39 | WRKY DNA-binding protein 39 | chr3:1266295-1268287 REVERSE LENGTH=1824
AT3G04790	UGAGAAGAGAUAGAAUAGAAUC	103	3.5 Cleavage	| Symbols: | Ribose 5-phosphate isomerase, type A protein | chr3:1313316-1315243 FORWARD LENGTH=1928
AT3G04940	UUGGACGCCUCUACUAUGAGA	679	3.5 Translation	| Symbols: ATCYSD1, CYSD1 | cysteine synthase D1 | chr3:1365165-1367759 FORWARD LENGTH=1369
AT3G05050	UACUCGACCACACUGUUAGGA	183	4 Translation	| Symbols: | Protein kinase superfamily protein | chr3:1408613-1411803 REVERSE LENGTH=2422
AT3G05060	AUUGAUUCUGCACUCAAGGGC	128	3 Cleavage	| Symbols: | NOP56-like pre RNA processing ribonucleoprotein | chr3:1412867-1415966 REVERSE LENGTH=2016
AT3G05100	UGACGGAAGCUACAGAGGAUG	108	4.5 Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:1424093-1426000 FORWARD LENGTH=1406
AT3G05155	UUCUGAAGGACAAGCUCAGCU	1012	3.5 Cleavage	| Symbols: | Major facilitator superfamily protein | chr3:1448570-1451213 FORWARD LENGTH=1287
AT3G05220	UAAGACUGAGAUACGCGUGCCU	152	3 Cleavage	| Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1488595-1491320 FORWARD LENGTH=2096
AT3G05420	UUUGGUUCUGAGUCCCCGCCU	669	4.5 Cleavage	| Symbols: ACBP4 | acyl-CoA binding protein 4 | chr3:1561778-1567250 FORWARD LENGTH=2315
AT3G05520	UGUCACCGUAGAUUUCUUCCU	123	3 Translation	| Symbols: | Subunits of heterodimeric actin filament capping protein Capz superfamily | chr3:1598547-1601310 FORWARD LENGTH=1167
AT3G05630	UUGGUCACACAGUGGACUGUG	104	3 Cleavage	| Symbols: PLDP2, PDLZ2, PLDZETA2 | phospholipase D P2 | chr3:1635200-1640348 FORWARD LENGTH=3505
AT3G05675	UCGAGCACCUACGUCACUGCG	100	4 Cleavage	| Symbols: | BTB/POZ domain-containing protein | chr3:1658271-1660306 REVERSE LENGTH=1927
AT3G05680	UCUGUACCGCUGAAUUCUUCC	275	4.5 Cleavage	| Symbols: EMB2016 | embryo defective 2016 | chr3:1660552-1672522 REVERSE LENGTH=6833
AT3G05685	UUUGCUGAACAUGUACCUCCA	119	3.5 Translation	| Symbols: | Cystatin/monellin superfamily protein | chr3:1673780-1674908 REVERSE LENGTH=543
AT3G05690	UGACGGUUCAGAUUCAGGAGC	107	4 Translation	| Symbols: UNE8, ATHAP2B, HAP2B, NF-YA2 | nuclear factor Y, subunit A2 | chr3:1676546-1678932 REVERSE LENGTH=1464
AT3G05700	UGAGACACAACAGGGAGAUUC	244	3 Cleavage	| Symbols: | Drought-responsive family protein | chr3:1682088-1684572 REVERSE LENGTH=1265
AT3G05790	UUCGAGAACUCCCUGACCCGA	1272	5 Cleavage	| Symbols: LON4 | lon protease 4 | chr3:1720154-1725182 REVERSE LENGTH=2829
AT3G05840	UUUGGCCUGAGGUUGGACACC	133	4 Cleavage	| Symbols: ATSK12 | Protein kinase superfamily protein | chr3:1740020-1743163 FORWARD LENGTH=1672
AT3G05880	AUUUGGCGCUCAACUCUGCAA	204	5 Cleavage	| Symbols: RCI2A | Low temperature and salt responsive protein family | chr3:1755497-1756540 REVERSE LENGTH=495
AT3G05990	UUGGCGCUCAACUCUGCAAGGU	955	4.5 Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr3:1796852-1799870 REVERSE LENGTH=1956
AT3G06020	UUUAGAGAUCCCCUGUUACUG	387	4.5 Cleavage	| Symbols: | Protein of unknown function (DUF3049) | chr3:1813267-1814169 FORWARD LENGTH=903
AT3G06130	UAAGCAUUUUGAUUCACCGGA	285	4 Cleavage	| Symbols: | Heavy metal transport/detoxification superfamily protein | chr3:1852884-1855063 REVERSE LENGTH=1643
AT3G06150	CUUUGCACUCAUGAAUCUUUC	119	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G19060.1); Has 61 Blast hits to 59 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 58; Viruses - 0; Other Eukaryo
AT3G06210	CAUUGACUUCAAGCCUGCGCU	190	5 Cleavage	| Symbols: | ARM repeat superfamily protein | chr3:1880093-1883491 FORWARD LENGTH=2697
AT3G06380	UCUAGUUCGCAUUUUUUGGAC	421	3.5 Cleavage	| Symbols: ATTLP9, TLP9 | tubby-like protein 9 | chr3:1936124-1938221 FORWARD LENGTH=1596
AT3G06510	UGAGAAGAGAUAGAAUAGAAUC	103	2 Cleavage	| Symbols: SFR2, ATSFR2 | Glycosyl hydrolase superfamily protein | chr3:2016330-2019778 FORWARD LENGTH=2234
AT3G06540	UUGAACAAGCCUGAUGAAGUU	102	3 Translation	| Symbols: REP, AthREP | Rab escort protein | chr3:2035003-2037788 REVERSE LENGTH=2016
AT3G06580	UUAGCACCGAGGAUGAUGGAC	291	3 Cleavage	| Symbols: GAL1, GALK | Mevalonate/galactokinase family protein | chr3:2048905-2052025 REVERSE LENGTH=1885
AT3G06910	UCUAGUUCACAUUUUUCGGAC	427	3.5 Translation	| Symbols: ULP1A, ELS1, AtULP1a | UB-like protease 1A | chr3:2178630-2181197 REVERSE LENGTH=1793
AT3G06980	AUGGAUUUAGAUCACUUGCGUC	196	3 Cleavage	| Symbols: | DEA(D/H)-box RNA helicase family protein | chr3:2201467-2204833 FORWARD LENGTH=2581
AT3G07220	UAACUCUACCCUUUGCACUCG	727	3 Cleavage	| Symbols: | SMAD/FHA domain-containing protein | chr3:2297886-2299572 FORWARD LENGTH=1210
AT3G07260	UAACUCUACCCUUUGCACUCG	727	3 Cleavage	| Symbols: | SMAD/FHA domain-containing protein | chr3:2309704-2310788 FORWARD LENGTH=914
AT3G07270	UUCGAGCACUCCCUGACCCGA	160	4.5 Cleavage	| Symbols: | GTP cyclohydrolase I | chr3:2313998-2317188 FORWARD LENGTH=1537
AT3G07400	UAUGCUUCUGUUGAUCCACCU	344	3.5 Cleavage	| Symbols: | lipase class 3 family protein | chr3:2367302-2372445 FORWARD LENGTH=3373
AT3G07440	UUGAGAGAUCCCCUGUUACUG	3917	3.5 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G48530.1); Has 37 Blast hits to 37 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 35; Viruses - 0; Other Eukaryo
AT3G07540	UUACGAGACUCUAGCCCAACU	447	4.5 Translation	| Symbols: | Actin-binding FH2 (formin homology 2) family protein | chr3:2404509-2407541 REVERSE LENGTH=2857
AT3G07565	UUAUGCUUCUGUUGAUCCACC	153	3.5 Translation	| Symbols: | Protein of unknown function (DUF3755) | chr3:2413642-2416259 FORWARD LENGTH=1435
AT3G07610	UGUCACCGUAGAUUUCUUCCU	123	3.5 Translation	| Symbols: IBM1 | Transcription factor jumonji (jmjC) domain-containing protein | chr3:2426069-2429358 FORWARD LENGTH=2368
AT3G07720	UAAAACUGAACCAUGCCUAGA	302	3.5 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:2465365-2467233 FORWARD LENGTH=1264
AT3G07730	UCUCAUGUAGUUCUAGUUCGCA	1437	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G01170.1); Has 1299 Blast hits to 1149 proteins in 206 species: Archae - 3; Bacteria - 100; Metazoa - 453; Fungi - 114; Plants - 108; Viruses - 2;
AT3G07800	UCUAGUUCGCGUUUUUCAGAC	163	3.5 Translation	| Symbols: | Thymidine kinase | chr3:2489387-2491087 REVERSE LENGTH=1426
AT3G08020	UCUAGUUCGCGUUUUUCAGAC	163	3 Cleavage	| Symbols: | PHD finger family protein | chr3:2557437-2561802 REVERSE LENGTH=2924
AT3G08040	UCACUGUGAAUUCCUGGAGUU	123	5 Cleavage	| Symbols: FRD3, MAN1, ATFRD3 | MATE efflux family protein | chr3:2566443-2572151 REVERSE LENGTH=1848
AT3G08500	UUUAGAGAUCCCCUGUUACUG	387	4.5 Translation	| Symbols: MYB83, AtMYB83 | myb domain protein 83 | chr3:2576794-2578246 REVERSE LENGTH=1370
AT3G08510	UGGCGCUCAACUCUGCAAGGU	10625	4 Translation	| Symbols: | phospholipase C 2 | chr3:2582382-2585851 REVERSE LENGTH=2136
AT3G08530	UUCUGAAGGACAAGAUCAGCU	351	3 Translation	| Symbols: | Clathrin, heavy chain | chr3:2586806-2595572 REVERSE LENGTH=5638
AT3G08720	UGAGAGCACUCCACCGACUGA	230	4.5 Translation	| Symbols: ATPK19, ATPK2 | serine/threonine protein kinase 2 | chr3:2648512-2650985 REVERSE LENGTH=1999
AT3G08850	UAUCCUGAGAGCGGUGCUGGC	334	4.5 Cleavage	| Symbols: RAPTOR1B, ATRAPTOR1B, RAPTOR1 | HEAT repeat ;WD domain, G-beta repeat protein protein | chr3:2686583-2695300 REVERSE LENGTH=4819
AT3G08870	UUUGAUCCGAGGAUGAUGGAUU	112	4 Cleavage	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:2700355-2702581 REVERSE LENGTH=2227
AT3G08960	UGACGUCGAGUAUGAGCCUGA	416	4.5 Translation	| Symbols: | ARM repeat superfamily protein | chr3:2729819-2736884 REVERSE LENGTH=3591
AT3G09035	UUUAACAACUAAGGUUCCUGU	1055	4 Cleavage	| Symbols: | Concanavalin A-like lectin family protein | chr3:2758820-2760347 FORWARD LENGTH=1528
AT3G09060	UUUAGGAUUGUUGCAUAUGCA	1164	4 Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:2766367-2768430 REVERSE LENGTH=2064
AT3G09320	UAUCGAGCACCUACGUCACUGU	142	5 Cleavage	| Symbols: | DHHC-type zinc finger family protein | chr3:2861743-2864245 REVERSE LENGTH=1392
AT3G09330	UUGGACGUCUCUACUAUGAGA	437	2.5 Cleavage	| Symbols: | Transmembrane amino acid transporter family protein | chr3:2864782-2867230 REVERSE LENGTH=1575
AT3G09340	UUGGACGUCUCUACUAUGAGA	437	2.5 Cleavage	| Symbols: | Transmembrane amino acid transporter family protein | chr3:2868050-2870526 REVERSE LENGTH=1587
AT3G09370	UUUGCCUGUUGAACUCGAGUA	114	3 Cleavage	| Symbols: MYB3R-3, AtMYB3R3 | myb domain protein 3r-3 | chr3:2879366-2882267 FORWARD LENGTH=1825
AT3G09400	UCUGUACCGCUGAAUUCUUCC	275	3 Cleavage	| Symbols: PLL3 | pol-like 3 | chr3:2891235-2893532 REVERSE LENGTH=1953
AT3G09510	ACAAAACUGUUGAACAAGCCU	1107	3.5 Cleavage	| Symbols: | Ribonuclease H-like superfamily protein | chr3:2921804-2923258 FORWARD LENGTH=1455
AT3G09550	UUCGGACUGGAUAGGACUAGG	101	4.5 Cleavage	| Symbols: | Ankyrin repeat family protein | chr3:2931865-2934354 FORWARD LENGTH=2121
AT3G09680	UGAAUCUUGGUCAACUGGACC	197	5 Cleavage	| Symbols: | Ribosomal protein S12/S23 family protein | chr3:2969045-2970371 REVERSE LENGTH=661
AT3G09850	AUCAUCCUCGGAUCAAACCCU	222	3 Cleavage	| Symbols: | D111/G-patch domain-containing protein | chr3:3023211-3025851 REVERSE LENGTH=2641
AT3G09880	UUUAGAGAUCCCCUGUUACUG	387	4.5 Cleavage	| Symbols: ATB' BETA | Protein phosphatase 2A regulatory B subunit family protein | chr3:3029511-3032256 FORWARD LENGTH=2216
AT3G09920	UGAGAACAUUGACUUCAGACCU	158	3.5 Cleavage	| Symbols: PIP5K9 | phosphatidyl inositol monophosphate 5 kinase | chr3:3040303-3043912 REVERSE LENGTH=2807
AT3G10040	UGCCAUGAUCGAGAGCUGCCU	164	5 Cleavage	| Symbols: | sequence-specific DNA binding transcription factors | chr3:3096415-3098071 REVERSE LENGTH=1657
AT3G10180	UUUUUCGGACUAGAUAGGACU	107	3 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:3146393-3154644 REVERSE LENGTH=3822
AT3G10200	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:3157608-3160188 FORWARD LENGTH=1958
AT3G10230	UGAGAUUGCUAGAGGAAAGAG	101	3.5 Cleavage	| Symbols: LYC | lycopene cyclase | chr3:3164075-3166038 REVERSE LENGTH=1964
AT3G10470	UUGACGACCAACUCCGCUCCU	170	4.5 Translation	| Symbols: | C2H2-type zinc finger family protein | chr3:3260351-3261854 FORWARD LENGTH=1504
AT3G10510	UUGAAAGACUUGUGGAUCACC	926	4 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:3274220-3275551 REVERSE LENGTH=1116
AT3G10550	CGGAGGAAACUAGCAGCGCC	103	3 Cleavage	| Symbols: MTM1, AtMTM1 | Myotubularin-like phosphatases II superfamily | chr3:3292899-3298522 REVERSE LENGTH=2904
AT3G10580	UGGCAGUAGGAGUACACGACU	163	4.5 Cleavage	| Symbols: | Homeodomain-like superfamily protein | chr3:3307051-3308237 REVERSE LENGTH=810
AT3G10650	UUAGCACCGAGGAUGAUGGACU	330	4 Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: nucleoporin-related (TAIR:AT5G20200.1); Has 61042 Blast hits to 31782 proteins in 2093 species: Archae - 202; Bacteria - 16480; Metazoa - 16017; Fungi - 12552; Plants - 1653; Viruses - 62
AT3G10690	CAACUAACAACGAGGGCACUG	198	5 Cleavage	| Symbols: GYRA | DNA GYRASE A | chr3:3339392-3346340 REVERSE LENGTH=3170
AT3G10700	UGCACUCGCUAGGUCUGGCAG	378	4.5 Cleavage	| Symbols: GalAK | galacturonic acid kinase | chr3:3346578-3351023 REVERSE LENGTH=1646
AT3G10800	UUUGGGUUUGGGUUAACUGCU	225	3 Cleavage	| Symbols: BZIP28 | Basic-leucine zipper (bZIP) transcription factor family protein | chr3:3379254-3381621 FORWARD LENGTH=2291
AT3G10840	UGUGUAUGCAUAACUUGGGAC	106	4 Translation	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:3391065-3393290 REVERSE LENGTH=1552
AT3G11010	UUGACGACCAACUCCGCUCCU	170	4.5 Translation	| Symbols: AtRLP34, RLP34 | receptor like protein 34 | chr3:3450496-3453683 REVERSE LENGTH=2952
AT3G11130	UUCUGAAGGACAAGAUCAGCU	351	2.5 Translation	| Symbols: | Clathrin, heavy chain | chr3:3482149-3491908 REVERSE LENGTH=5785
AT3G11270	UGGGCGCUUAUACUUUGGGUU	115	4 Cleavage	| Symbols: MEE34 | Mov34/MPN/PAD-1 family protein | chr3:3528801-3531565 FORWARD LENGTH=1360
AT3G11320	UCGAGUACACAGAAUGGGCUG	179	3.5 Cleavage	| Symbols: | Nucleotide-sugar transporter family protein | chr3:3546646-3548856 REVERSE LENGTH=1615
AT3G11325	UAUCUCUGUCGUUACGAACCU	295	4 Cleavage	| Symbols: | Phospholipid/glycerol acyltransferase family protein | chr3:3549771-3551661 REVERSE LENGTH=1395
AT3G11370	UAGGCCUGAGAUUGGACGCCU	875	4.5 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:3561099-3562880 FORWARD LENGTH=1782
AT3G11710	UUGACUUCAGACCUGCGCGUG	131	5 Cleavage	| Symbols: ATKRS-1 | lysyl-tRNA synthetase 1 | chr3:3702169-3705714 REVERSE LENGTH=2172
AT3G11830	UCGACCACACUGUUAGGAUCU	121	4.5 Translation	| Symbols: | TCP-1/cpn60 chaperonin family protein | chr3:3732661-3736374 FORWARD LENGTH=1965
AT3G11920	UUCGAGAACUCCCUGACCCGA	1272	3.5 Cleavage	| Symbols: | glutaredoxin-related | chr3:3772311-3774887 FORWARD LENGTH=1893
AT3G11950	UUUCUGACGGACAAGAUAAGU	480	4 Cleavage	| Symbols: | TRAF-like superfamily protein | chr3:3783111-3785660 REVERSE LENGTH=2010
AT3G12230	UUGGACGCCUCUACUAUGAGA	679	4.5 Cleavage	| Symbols: scpl14 | serine carboxypeptidase-like 14 | chr3:3899431-3901879 REVERSE LENGTH=1308
AT3G12280	UAUGGCCUGGGAGCAAUCGCA	299	4 Translation	| Symbols: RBR1 | retinoblastoma-related 1 | chr3:3913463-3919170 REVERSE LENGTH=3544
AT3G12350	UUCUGAUUGCAUGUGGUGUACC	110	4.5 Cleavage	| Symbols: | F-box family protein | chr3:3931555-3932849 FORWARD LENGTH=1159

AT3G12540	UGUGGUGUACCUCUCACGUCU	112	3	Cleavage	| Symbols: | Protein of unknown function, DUF547 | chr3:3975246-3977312 FORWARD LENGTH=1583
AT3G12550	CUUGUGAGUGUUUGUGAGGUC	103	4	Cleavage	| Symbols: | XH/XS domain-containing protein | chr3:3978005-3981762 FORWARD LENGTH=2491
AT3G12570	UAGCUAACAAGAACUCUUUCU	1828	4	Cleavage	| Symbols: FYD | FYD | chr3:3988743-3991052 FORWARD LENGTH=1748
AT3G12590	UGACGCCAAUUCUGAAAGUUU	154	3.5	Cleavage	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 50 Blast hits to 41 proteins in 15 species: Archae - 0; Bacteria - 0; Metazoa - 2; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 5 (source
AT3G12610	UUUCCGUUGGUGUGCGCCAC	458	5	Translation	| Symbols: DRT100 | Leucine-rich repeat (LRR) family protein | chr3:4006399-4007807 REVERSE LENGTH=1409
AT3G12650	UCUGAACUCAAGGCACCCAAA	493	5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; Has 31 Blast hits to
AT3G12710	UAACUCUACCCUUUGCACUCG	727	4	Translation	| Symbols: | DNA glycosylase superfamily protein | chr3:4040324-4041982 REVERSE LENGTH=1341
AT3G12730	UGGCAGUAGGAGUACACGACU	163	4.5	Cleavage	| Symbols: | Homeodomain-like superfamily protein | chr3:4047072-4048614 REVERSE LENGTH=1128
AT3G12750	UAUCGAGCACCUACGUCACUGU	142	4	Cleavage	| Symbols: ZIP1 | zinc transporter 1 precursor | chr3:4051651-4053201 REVERSE LENGTH=1412
AT3G12830	UUUAACAACUAAGGUUCCUGU	1055	4	Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr3:4078651-4079608 REVERSE LENGTH=958
AT3G12940	UUUGGCCUGAGGUUGGACGCC	367	4	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:4130007-4132467 REVERSE LENGTH=2215
AT3G12955	UGUGGUCGAGUAGAGCAAUCU	111	4.5	Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr3:4135500-4136143 REVERSE LENGTH=644
AT3G12960	AUCCAAGUAGCUGACUCUCCU	1104	4	Cleavage	| Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 14 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 44; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:4136488-4136828 FORWARD LENGTH=341
AT3G13030	UACACUCACUUGAUCUAGGAG	223	4.5	Cleavage	| Symbols: | hAT transposon superfamily protein | chr3:4169541-4171778 REVERSE LENGTH=2130
AT3G13120	UCACUGUGAAUUCCUGGAGUU	123	4.5	Cleavage	| Symbols: | Ribosomal protein S10p/S20e family protein | chr3:4219775-4221630 REVERSE LENGTH=1027
AT3G13380	UUUAAAACCGAGGACUUUUGC	115	3	Cleavage	| Symbols: BRL3 | BRI1-like 3 | chr3:4346557-4350923 FORWARD LENGTH=4274
AT3G13530	UAGGCCUGAGAUUGGACGCCU	875	4	Cleavage	| Symbols: MAPKKK7, MAP3KE1 | mitogen-activated protein kinase kinase kinase 7 | chr3:4411688-4419320 REVERSE LENGTH=4353
AT3G13560	UGUUGAUCCAAGUAGCUGACU	608	3.5	Cleavage	| Symbols: | O-Glycosyl hydrolases family 17 protein | chr3:4425227-4428179 REVERSE LENGTH=2119
AT3G13600	UUUAACAACUAAGGUUCCUGU	1055	3.5	Cleavage	| Symbols: | calmodulin-binding family protein | chr3:4445102-4447383 FORWARD LENGTH=1818
AT3G13610	UCGGCUCAAACCUAACACGUU	129	5	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:4449374-4450811 FORWARD LENGTH=1355
AT3G13640	UUUGGCCUGAGGUUGGACGCC	367	3.5	Cleavage	| Symbols: ATRLI1, RLI1 | RNAse l inhibitor protein 1 | chr3:4458461-4461733 REVERSE LENGTH=2197
AT3G13674	UUUGAUUCACCGGAUAAACUC	175	3	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 17 plant structures; EXPRESSED DURING: 11 growth stages; BEST Arabidopsis thali
AT3G13690	UUUAAAACCGAGGACUUUUGC	115	3.5	Translation	| Symbols: | Protein kinase protein with adenine nucleotide alpha hydrolases-like domain | chr3:4485735-4490231 FORWARD LENGTH=3321
AT3G13790	CAUUGACUUCAAGCCUGCGCU	190	5	Cleavage	| Symbols: ATBFRUCT1 | Glycosyl hydrolases family 32 protein | chr3:4532913-4535867 REVERSE LENGTH=1953
AT3G13882	UUAUCAACGAACUCUUGGCCC	310	3.5	Cleavage	| Symbols: | Ribosomal protein L34 | chr3:4574526-4576048 FORWARD LENGTH=714
AT3G13920	UUGGACGUCUCUACUAUGAGA	437	3.5	Translation	| Symbols: EIF4A1 | eukaryotic translation initiation factor 4A1 | chr3:4592615-4594999 REVERSE LENGTH=1467
AT3G13940	UACUGGAGGACGUACAGCACU	949	5	Cleavage	| Symbols: | DNA binding;DNA-directed RNA polymerases | chr3:4600492-4602486 REVERSE LENGTH=1558
AT3G14000	UACUUCCAGCGUUCUGUAGCC	826	3.5	Translation	| Symbols: ATBRXL2, BRX-LIKE2 | DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain containing protein | chr3:4630869-4633411 REVERSE LENGTH=1484
AT3G14050	ACAAAACUGUUGAACAAGCCU	1107	3.5	Cleavage	| Symbols: RSH2, AT-RSH2, ATRSH2 | RELA/SPOT homolog 2 | chr3:4650757-4653914 REVERSE LENGTH=2675
AT3G14170	UUUGAGCACUCCUUGACCCGA	154	4.5	Translation	| Symbols: | Plant protein of unknown function (DUF936) | chr3:4695965-4698120 REVERSE LENGTH=1799
AT3G14210	UGAAGGAUUUGUGGUUAACCA	474	4	Cleavage	| Symbols: ESM1 | epithiospecifier modifier 1 | chr3:4729823-4731803 FORWARD LENGTH=1483
AT3G14220	UCUGUACCGCUGAAUUCUUCC	275	3	Translation	| Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:4732893-4734609 FORWARD LENGTH=1364
AT3G14300	UCUUCGACUGAGGUAAGCGCCU	355	4	Cleavage	| Symbols: ATPMEPCRC, ATPME26, PME26 | pectinesterase family protein | chr3:4766905-4769898 REVERSE LENGTH=2907
AT3G14350	UCGGCUCAAACCUAACACGUU	129	5	Cleavage	| Symbols: SRF7 | STRUBBELIG-receptor family 7 | chr3:4782757-4787236 REVERSE LENGTH=2749
AT3G14520	UGUGGUGUACCUCUCACGUCU	112	4	Translation	| Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr3:4875748-4878336 REVERSE LENGTH=2031
AT3G14540	UGUGGUGUACCUCUCACGUCU	112	4	Translation	| Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr3:4881439-4883936 REVERSE LENGTH=1984
AT3G14650	UUCACAUGUCCGGGCUAGGCA	461	4.5	Cleavage	| Symbols: CYP72A11 | cytochrome P450, family 72, subfamily A, polypeptide 11 | chr3:4922131-4924694 FORWARD LENGTH=2143
AT3G14690	UUCACAUGUCCGGGCUAGGCA	461	4.5	Cleavage	| Symbols: CYP72A15 | cytochrome P450, family 72, subfamily A, polypeptide 15 | chr3:4937317-4939465 FORWARD LENGTH=1787
AT3G14720	CUUGGCAUCGAAUUUGAACUC	1059	4.5	Cleavage	| Symbols: ATMPK19, MPK19 | MAP kinase 19 | chr3:4945601-4949042 FORWARD LENGTH=2389
AT3G14730	UUAGGCCUGAGAUUGGACGCC	196	4.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:4949385-4951346 REVERSE LENGTH=1962
AT3G14790	UGAAGGACAAGCUCAGCUGCU	1483	3	Translation	| Symbols: RHM3, ATRHM3 | rhamnose biosynthesis 3 | chr3:4964155-4967075 FORWARD LENGTH=2348
AT3G14830	UACUUCCAGCGUUCUGUAGCC	826	4.5	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G53450.2); Has 73 Blast hits to 73 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 73; Viruses - 0; Other Eukaryo
AT3G14850	UCCUGAGUACUCUCUUCCAAG	209	2.5	Translation	| Symbols: TBL41 | TRICHOME BIREFRINGENCE-LIKE 41 | chr3:4996448-4997693 FORWARD LENGTH=988
AT3G14930	UCUAGUUCACAUUUUUCGGAC	427	3.5	Translation	| Symbols: HEME1 | Uroporphyrinogen decarboxylase | chr3:5020570-5022930 FORWARD LENGTH=1715
AT3G15030	UAGAGUGUUCAUGUAGUUGCA	232	4	Cleavage	| Symbols: TCP4 | TCP family transcription factor 4 | chr3:5061681-5064115 FORWARD LENGTH=2033
AT3G15060	UAGUGACCGAGUAGUACCACC	461	4.5	Translation	| Symbols: AtRABA1g, RABA1g | RAB GTPase homolog A1G | chr3:5069166-5070200 FORWARD LENGTH=902
AT3G15090	AAUUCGAGAACUCCCUGACCC	255	4.5	Cleavage	| Symbols: | GroES-like zinc-binding alcohol dehydrogenase family protein | chr3:5076689-5079117 FORWARD LENGTH=1506
AT3G15130	UACGCUAGGGAGAUAUCUGCC	122	5	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:5097153-5099222 REVERSE LENGTH=2070
AT3G15351	UCUGUAUGCAUAGCUUGGGACU	466	5	Cleavage	| Symbols: | unknown protein; Has 50 Blast hits to 50 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 7; Fungi - 0; Plants - 43; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:5176059-5177648 FORWARD LENGTH=688
AT3G15400	UUUUGAUUCACCGGAUAAACUC	104	4	Cleavage	| Symbols: ATA20 | anther 20 | chr3:5201644-5203197 FORWARD LENGTH=1414
AT3G15450	UCCUAUCCAGUCUGAAGAACGC	272	3.5	Cleavage	| Symbols: | Aluminium induced protein with YGL and LRDR motifs | chr3:5212984-5214119 FORWARD LENGTH=882
AT3G15470	CAACGCUCUUGAUACAUCUAG	133	3.5	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:5216262-5220218 REVERSE LENGTH=3370
AT3G15520	AUUGUGUAUAAUUUUGAGCCU	108	3.5	Translation	| Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr3:5249599-5252506 REVERSE LENGTH=1615
AT3G15530	UCCACCGACUGAUGACAAUGU	1524	3	Translation	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:5252875-5254562 REVERSE LENGTH=1508
AT3G15820	UAGGCCUGAGAUUGGACGCCU	875	4.5	Cleavage	| Symbols: ROD1 | phosphatidic acid phosphatase-related / PAP2-related | chr3:5351071-5353728 FORWARD LENGTH=1207
AT3G15980	UUGGGAGAACUAUGACACGAG	515	4	Cleavage	| Symbols: | Coatomer, beta' subunit | chr3:5411292-5418493 REVERSE LENGTH=3356
AT3G16000	CAACGCUCUUGAUACAUCUAG	133	4	Cleavage	| Symbols: MFP1 | MAR binding filament-like protein 1 | chr3:5430889-5433817 REVERSE LENGTH=2537
AT3G16230	UUCUGAAGGACAAGCUCAGCU	1012	4	Cleavage	| Symbols: | Predicted eukaryotic LigT | chr3:5500178-5503545 FORWARD LENGTH=1710
AT3G16250	CAACUAACAACGAGGGCACUG	198	4	Cleavage	| Symbols: NDF4 | NDH-dependent cyclic electron flow 1 | chr3:5506931-5508414 REVERSE LENGTH=869
AT3G16310	UCUAGUUCGCAUUUUUUGGAC	421	2	Cleavage	| Symbols: | mitotic phosphoprotein N' end (MPPN) family protein | chr3:5526414-5528602 REVERSE LENGTH=1341
AT3G16340	UUAGACCUUGCAGAGUUGAGCGCC	104	2.5	Translation	| Symbols: ATPDR1, PDR1 | pleiotropic drug resistance 1 | chr3:5539897-5546417 FORWARD LENGTH=4405
AT3G16560	UUCUGACGGACAAGAUAAGCU	313	4.5	Cleavage	| Symbols: | Protein phosphatase 2C family protein | chr3:5635596-5638482 REVERSE LENGTH=2166
AT3G16570	UUGAGAAGAUACAUUGACGGU	731	2.5	Cleavage	| Symbols: RALF23, ATRALF23 | rapid alkalinization factor 23 | chr3:5644698-5645414 FORWARD LENGTH=717
AT3G16610	UGUGGAUACAAGAGCUGGGCU	215	5	Translation	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr3:5656371-5658335 REVERSE LENGTH=1965
AT3G16785	UGACGCCAAUUCUGAAAGUUU	154	4.5	Cleavage	| Symbols: PLDP1, PLDZ1, PLDZETA1, PLD ZETA 1 | phospholipase D P1 | chr3:5711082-5719023 FORWARD LENGTH=3865
AT3G16800	CAACGCUCUUGAUACAUCUAG	133	3	Cleavage	| Symbols: | Protein phosphatase 2C family protein | chr3:5721105-5723185 FORWARD LENGTH=1406
AT3G16840	UUGAGAGCACUCCACCGACUG	261	4.5	Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:5737886-5743144 REVERSE LENGTH=2717
AT3G17000	UCUGUACCGCUGAAUUCUUCC	275	3.5	Cleavage	| Symbols: UBC32 | ubiquitin-conjugating enzyme 32 | chr3:5797179-5799683 FORWARD LENGTH=1263
AT3G17020	UUGAGAGAUCCCCUGUUACUG	3917	4	Cleavage	| Symbols: | Adenine nucleotide alpha hydrolases-like superfamily protein | chr3:5802536-5804157 REVERSE LENGTH=778
AT3G17120	UAGAGUUAAGUUGGGACAGGA	199	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G02380.1); Has 67 Blast hits to 67 proteins in 11 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 67; Viruses - 0; Other Eukaryo
AT3G17185	UGAGAAGAGAUAGAAUAGAAUC	103	0	Cleavage	| Symbols: TASIR-ARF, TAS3, ATTAS3 | TAS3/TASIR-ARF (TRANS-ACTING SIRNA3); other RNA | chr3:5861491-5862437 FORWARD LENGTH=947
AT3G17203	UUUUAAUUCAAGUAGCUGACU	133	4	Cleavage	| Symbols: GA2OX5 | a pseudogene initially named GA2ox5 and thought to be a member of the gibberellin 2-oxidase enzyme family. It was later shown to have a large DNA insert in the putative gene model. | chr3:5870787-5872854 FORWARD LE
AT3G17310	UAUGGAGAUGAUCGCAAUGGC	937	2.5	Cleavage	| Symbols: DRM3, AtDRM3 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:5909001-5913242 REVERSE LENGTH=2641
AT3G17440	UAUCGAGCACCUACGUCACUGU	142	4.5	Translation	| Symbols: NPSN13, ATNPSN13 | novel plant snare 13 | chr3:5969564-5972502 REVERSE LENGTH=1371
AT3G17590	UUUUUCGGACUAGAUAGGACU	107	3.5	Cleavage	| Symbols: BSH, CHE1 | transcription regulatory protein SNF5, putative (BSH) | chr3:6017212-6019666 REVERSE LENGTH=899
AT3G17630	UCGGGAUCCUGCUGAAUGGUC	135	3	Cleavage	| Symbols: ATCHX19, CHX19 | cation/H+ exchanger 19 | chr3:6029201-6031773 FORWARD LENGTH=2403
AT3G17700	UUGAGAAGAUACAUUGACGGU	731	3	Translation	| Symbols: CNBT1, CNGC20, ATCNGC20 | cyclic nucleotide-binding transporter 1 | chr3:6048916-6052552 FORWARD LENGTH=2556
AT3G17780	UGGAUUCCGGCUGCAUACUCC	392	5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: intracellular protein transport; LOCATED IN: endomembrane system, integral to membrane, endoplasmic reticulum; EXPRESSED IN: 23 plant structures; EXPRESSED DURIN
AT3G17810	UUUGAUCCGAGGAUGAUGGAU	816	2.5	Cleavage	| Symbols: PYD1 | pyrimidine 1 | chr3:6094098-6096566 FORWARD LENGTH=1739
AT3G17880	UUUUGCUUAGACUUAGAAACU	179	3	Cleavage	| Symbols: HIP, ATTDX, ATHIP2, TDX | tetraticopeptide domain-containing thioredoxin | chr3:6123409-6126281 FORWARD LENGTH=1415
AT3G18020	UUUAGGAUUGUUGCAUAUGCA	1164	3.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:6165449-6167515 FORWARD LENGTH=2067
AT3G18030	UCCGCUAGAUAUAUCAAACUG	281	4	Cleavage	| Symbols: ATHAL3A, HAL3A, HAL3, ATHAL3 | HAL3-like protein A | chr3:6167640-6168948 REVERSE LENGTH=1192
AT3G18160	CCUGAGCCUAGUGACCGAGUA	270	4	Cleavage	| Symbols: PEX3-1 | peroxin 3-1 | chr3:6220918-6223073 FORWARD LENGTH=1281
AT3G18210	UUUGAGCACUCUACAGACAGG	162	3	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:6237930-6240605 REVERSE LENGTH=1631
AT3G18230	UAUAGGGCUUGAAAGAAAGUC	535	3.5	Cleavage	| Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr3:6251483-6254221 FORWARD LENGTH=2263
AT3G18390	UUGAGAUAUCCCCUGUUACUG	106	4.5	Cleavage	| Symbols: EMB1865 | CRS1 / YhbY (CRM) domain-containing protein | chr3:6313485-6317971 FORWARD LENGTH=3021
AT3G18620	UGAAGGAUUUGUGGUUAACCA	474	3	Cleavage	| Symbols: | DHHC-type zinc finger family protein | chr3:6408318-6411064 FORWARD LENGTH=1917
AT3G18710	UCACCAUUGGCAGCUCUGUACC	187	3	Cleavage	| Symbols: PUB29, ATPUB29 | plant U-box 29 | chr3:6434083-6435561 REVERSE LENGTH=1479
AT3G18770	UAUGCAUAACUUGGGACUUACC	333	3	Cleavage	| Symbols: | Autophagy-related protein 13 | chr3:6459884-6463059 REVERSE LENGTH=2343

AT3G18790	UGUGGAUACAAGAGUUGGGCU	111	4	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: Isy1-like
AT3G18820	UUAGCACCGAGGAUGAUGGACU	330	3.5	Cleavage	| Symbols: ATRABG3F, ATRAB7B, RAB71, RABG3F, RAB7B | RAB GTPase homolog G3F | chr3:6484068-6486247 FORWARD LENGTH=1061
AT3G19050	CUAGAAUUCUUUCCCUUUCCU	235	2.5	Cleavage	| Symbols: POK2 | phragmoplast orienting kinesin 2 | chr3:6577724-6590188 FORWARD LENGTH=8598
AT3G19130	AUUGACGUCGAGUAUGAGCCU	2734	4	Cleavage	| Symbols: ATRBP47B, RBP47B | RNA-binding protein 47B | chr3:6611198-6614044 REVERSE LENGTH=1729
AT3G19180	UAGUGACCGAGUAGUACCACC	461	5	Cleavage	| Symbols: ARC6H, PARC6, ATCDP1, CDP1 | paralog of ARC6 | chr3:6632676-6637224 FORWARD LENGTH=2865
AT3G19190	UGACACCGAUUCUGAUAGCUU	823	4	Translation	| Symbols: ATATG2, ATG2 | autophagy 2 | chr3:6639711-6648857 FORWARD LENGTH=5990
AT3G19300	UAGAGUGUUCAUGUAGUUGCA	232	4	Cleavage	| Symbols: | Protein kinase superfamily protein | chr3:6690118-6693284 REVERSE LENGTH=2190
AT3G19340	UCUUCGACUGAGGUAAGCGCCU	355	5	Cleavage	| Symbols: | Protein of unknown function (DUF3754) | chr3:6701273-6704226 REVERSE LENGTH=1733
AT3G19460	UACAGAAUAGGCUUAAGUAAC	189	4.5	Cleavage	| Symbols: | Reticulon family protein | chr3:6747370-6749307 FORWARD LENGTH=1517
AT3G19510	AUUUGAACUCAUGGAUACCCU	768	4	Translation	| Symbols: HAT3.1 | Homeodomain-like protein with RING/FYVE/PHD-type zinc finger domain | chr3:6762764-6766588 REVERSE LENGTH=2769
AT3G19550	UAUGGAGAUGAUCGCAAUGGC	937	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 9 growth stages; Has 36 Blast hits to
AT3G19560	UCCGCUAGAUAUAUCAAACUG	281	3	Cleavage	| Symbols: | F-box family protein | chr3:6793311-6794802 FORWARD LENGTH=1267
AT3G19600	UUGAAGGAUUUGUGGUUAACCA	106	3	Cleavage	| Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr3:6810669-6811742 REVERSE LENGTH=950
AT3G19710	UCAUAUGGACUUUGGCUACACC	101	3.5	Cleavage	| Symbols: BCAT4 | branched-chain aminotransferase4 | chr3:6846969-6849497 REVERSE LENGTH=1366
AT3G19850	UAUUGAUUUUUGGCCUGAGGU	116	3	Cleavage	| Symbols: | Phototropic-responsive NPH3 family protein | chr3:6898181-6901255 REVERSE LENGTH=1965
AT3G19880	CUUCCCCUAGAAUUCUUUCCC	401	3.5	Translation	| Symbols: | F-box and associated interaction domains-containing protein | chr3:6911435-6912604 REVERSE LENGTH=1170
AT3G19910	UUGGGAGAACUAUGACACGAG	515	2.5	Translation	| Symbols: | RING/U-box superfamily protein | chr3:6926308-6929567 FORWARD LENGTH=1455
AT3G19960	UAGAAUUAUCAUGUCUUGGCA	194	3.5	Cleavage	| Symbols: ATM1 | myosin 1 | chr3:6948776-6956966 FORWARD LENGTH=4062
AT3G19990	UCUGAACUCAAGGCACCCAAA	493	3.5	Cleavage	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast stroma, chloroplast; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 118 Blast hits to 118 proteins in 41 species: A
AT3G20010	UUCUUGUGAACUUGACCGGGA	158	3.5	Translation	| Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related | chr3:6971352-6976595 FORWARD LENGTH=3399
AT3G20020	UCUAUAGCCAAUGUACUCUACU	106	4	Cleavage	| Symbols: ATPRMT6, PRMT6 | protein arginine methyltransferase 6 | chr3:6983705-6988099 REVERSE LENGTH=1746
AT3G20110	UUGGACGUCUCUACUAUGAGA	437	4	Translation	| Symbols: CYP705A20 | cytochrome P450, family 705, subfamily A, polypeptide 20 | chr3:7021332-7023279 FORWARD LENGTH=1862
AT3G20155	UAUCGAGCACCUACGUCACUGU	142	4.5	Translation	| Symbols: | unknown protein; Has 36 Blast hits to 36 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 36; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:7037135-7038375 FORWARD LENGTH=882
AT3G20170	UCUGAACUCAAGGCACCCAAA	493	3	Cleavage	| Symbols: | ARM repeat superfamily protein | chr3:7041727-7043341 FORWARD LENGTH=1615
AT3G20250	UAUGGCCUGGGAGCAAUCGCA	299	3.5	Cleavage	| Symbols: APUM5, PUM5 | pumilio 5 | chr3:7058902-7063240 REVERSE LENGTH=3213
AT3G20260	UCGAACAAGAGCUGAACGUCU	423	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF1666) | chr3:7064054-7066503 REVERSE LENGTH=2202
AT3G20300	UUCGGACUGGAUAGGACUAGG	101	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF3537) | chr3:7079617-7081921 REVERSE LENGTH=1686
AT3G20310	UUUGGUUCUGAGUCCCCGCCU	669	4	Cleavage	| Symbols: ATERF-7, ATERF7, ERF7 | ethylene response factor 7 | chr3:7084806-7086805 REVERSE LENGTH=2000
AT3G20350	UCUGGGUAGAUGGGAUCUUAUC	123	3	Cleavage	| Symbols: | unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: cotyledon; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G50660.1); Has 15095 Blast hits to 11
AT3G20440	UACAAAUUCGAGCACUCCCUG	156	3.5	Translation	| Symbols: EMB2729, BE1 | Alpha amylase family protein | chr3:7123197-7130436 REVERSE LENGTH=3088
AT3G20500	UUUAGAGAUCCCCUGUUACUG	387	5	Cleavage	| Symbols: ATPAP18, PAP18 | purple acid phosphatase 18 | chr3:7157906-7160417 FORWARD LENGTH=1507
AT3G20550	UGUGGUGUACCUCUCACGUCU	112	4.5	Cleavage	| Symbols: DDL | SMAD/FHA domain-containing protein | chr3:7174464-7177942 REVERSE LENGTH=1281
AT3G20580	UAUGGCCUGGGAGCAAUCGCA	299	4	Cleavage	| Symbols: COBL10 | COBRA-like protein 10 precursor | chr3:7187856-7190562 REVERSE LENGTH=2372
AT3G20680	UGAAGGACAAGCUCAGCUGCU	1483	4	Cleavage	| Symbols: | Domain of unknown function (DUF1995) | chr3:7230068-7231194 REVERSE LENGTH=1127
AT3G20865	UUCUGAAGGACAAGAUCAGCU	351	4	Cleavage	| Symbols: AGP40 | arabinogalactan protein 40 | chr3:7308504-7308962 REVERSE LENGTH=459
AT3G20890	UUCUGAAGGACAAGAUCAGCU	351	2.5	Translation	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:7319848-7321054 FORWARD LENGTH=970
AT3G20898	AUGGAUUUAGAUCACUUGCGUC	196	3	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G5135
AT3G21060	UAAGCAUUUUGAUUCACCGGA	285	2.5	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:7377434-7380213 FORWARD LENGTH=2303
AT3G21240	UACGAGACUCUAGCCCAGCUU	307	5	Cleavage	| Symbols: 4CL2, AT4CL2 | 4-coumarate:CoA ligase 2 | chr3:7454269-7457379 REVERSE LENGTH=1964
AT3G21540	UAGUGACCGAGUAGUACCACC	461	4.5	Cleavage	| Symbols: | transducin family protein / WD-40 repeat family protein | chr3:7585946-7590856 REVERSE LENGTH=3022
AT3G21690	UCUUGGCAUCGAAUUUGAACU	154	3.5	Cleavage	| Symbols: | MATE efflux family protein | chr3:7638663-7642205 FORWARD LENGTH=1952
AT3G22020	UCCUGAGUACUCUCUUCCAAG	209	3.5	Cleavage	| Symbols: | Receptor-like protein kinase-related family protein | chr3:7756577-7757491 FORWARD LENGTH=624
AT3G22050	UGAAGGAUUUGUGGUUAACCA	474	4	Cleavage	| Symbols: | Domain of unknown function (DUF26) | chr3:7764131-7765143 FORWARD LENGTH=777
AT3G22053	UCUGGGUAGAUGGGAUCUUAUC	123	4	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: Receptor protein kinase-related (TAIR:AT3G22030.1)
AT3G22090	UUCUGAAGGACAAGAUCAGCU	351	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G71470.2); Has 12 Blast hits to 12 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 12; Viruses - 0; Other Eukaryot
AT3G22170	UUUAGAGAUCCCCUGUUACUG	387	3.5	Cleavage	| Symbols: FHY3 | far-red elongated hypocotyls 3 | chr3:7822018-7825884 REVERSE LENGTH=2973
AT3G22220	CUUUGCACUCAUGAAUCUUUC	119	2.5	Cleavage	| Symbols: | hAT transposon superfamily | chr3:7839555-7842781 REVERSE LENGTH=2635
AT3G22380	UAGGCCUGAGAUUGGACGCCU	875	4	Cleavage	| Symbols: TIC | time for coffee | chr3:7912905-7919484 FORWARD LENGTH=5534
AT3G22415	AUUGACGUCGAGUAUGAGCCU	2734	4.5	Cleavage	| Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr3:7941014-7941564 FC
AT3G22425	UGAGAGCACUCCACCGACUGA	230	5	Cleavage	| Symbols: IGPD | imidazoleglycerol-phosphate dehydratase | chr3:7951055-7953223 FORWARD LENGTH=1238
AT3G22640	UACAAAUUCGAGCACUCCCUG	156	3	Cleavage	| Symbols: PAP85 | cupin family protein | chr3:8011724-8013902 REVERSE LENGTH=1658
AT3G22670	UACGUCACUGCGAAUUCCUGGA	271	4.5	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:8017771-8019459 REVERSE LENGTH=1689
AT3G22690	UACACUCACUUGAUCUAGGAG	223	4.5	Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1685 (InterPro:IPR012881), Pentatricopeptide repeat (InterPro:IPR002885); BEST Arabidopsis thaliana protein match is: Tetratricopeptide repeat (TPR)-like superfamil
AT3G22760	UUGACGACCAACUCCGCUCCU	170	5	Cleavage	| Symbols: SOL1 | Tesmin/TSO1-like CXC domain-containing protein | chr3:8044455-8047530 FORWARD LENGTH=2146
AT3G22860	UCUAGUCCGAAAAAUGCGAAC	163	3.5	Cleavage	| Symbols: TIF3C2, ATEIF3C-2, EIF3C-2, ATTIF3C2 | eukaryotic translation initiation factor 3 subunit C2 | chr3:8090654-8093248 REVERSE LENGTH=2418
AT3G22990	UUGGGAGAACUAUGACACGAG	515	3	Translation	| Symbols: LFR | ARM repeat superfamily protein | chr3:8163950-8166345 FORWARD LENGTH=1648
AT3G23050	CAUCAAGAACCGGUCAUGCCU	125	4.5	Cleavage	| Symbols: IAA7, AXR2 | indole-3-acetic acid 7 | chr3:8194679-8197153 FORWARD LENGTH=1258
AT3G23120	UAGAAUUAUCAUGUCUUGGCA	194	4.5	Cleavage	| Symbols: AtRLP38, RLP38 | receptor like protein 38 | chr3:8227222-8229576 REVERSE LENGTH=2355
AT3G23160	UGGCGCUCAACUCUGCAAGGU	10625	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF668) | chr3:8259855-8262028 REVERSE LENGTH=2174
AT3G23410	UCUAGUUCACAUUUUUCGGAC	427	3	Cleavage	| Symbols: ATFAO3, FAO3 | fatty alcohol oxidase 3 | chr3:8382805-8386148 FORWARD LENGTH=2420
AT3G23450	UGAGAACAUUGACUUCAGACCU	158	3	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 8 growth stages; Has 69454
AT3G23560	UCUUGGCAUCGAAUUUGAACU	154	3.5	Translation	| Symbols: ALF5 | MATE efflux family protein | chr3:8454116-8456681 REVERSE LENGTH=1772
AT3G23590	UGCAUAACUUGGGACUUACCU	413	4.5	Cleavage	| Symbols: RFR1, MED33A | REF4-related 1 | chr3:8467449-8473627 FORWARD LENGTH=4277
AT3G23660	UGUGGUGUACCUCUCACGUCU	112	3.5	Cleavage	| Symbols: | Sec23/Sec24 protein transport family protein | chr3:8513457-8517790 REVERSE LENGTH=2646
AT3G23860	UUCGAGAACUCCCUGACCCGA	1272	4.5	Cleavage	| Symbols: | GTP-binding protein-related | chr3:8616953-8617645 REVERSE LENGTH=693
AT3G23980	UGGAGAUGAUAGAUUAUGCGC	126	4	Cleavage	| Symbols: BLI, KOS1 | BLISTER | chr3:8662433-8667752 REVERSE LENGTH=2842
AT3G23990	UCUAGUUCACAUUUUUCGGAC	427	2	Cleavage	| Symbols: HSP60, HSP60-3B | heat shock protein 60 | chr3:8668918-8672578 FORWARD LENGTH=2129
AT3G24010	UUUGCUGAACAUGUACCUCCA	119	3.5	Cleavage	| Symbols: ING1, ATING1 | RING/FYVE/PHD zinc finger superfamily protein | chr3:8675956-8678220 REVERSE LENGTH=903
AT3G24120	UGACGUCGAGUAUGAGCCUGA	416	3.5	Translation	| Symbols: | Homeodomain-like superfamily protein | chr3:8705636-8708315 REVERSE LENGTH=1353
AT3G24220	UCUUGGCAUCGAAUUUGAACU	154	4	Cleavage	| Symbols: NCED6, ATNCED6 | nine-cis-epoxycarotenoid dioxygenase 6 | chr3:8761434-8763172 FORWARD LENGTH=1739
AT3G24255	UUCAUCUGCAGUAAGUCCCUG	314	4	Translation	| Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr3:8788854-8793368 FORWARD LENGTH=2777
AT3G24320	UCCGCUAGAUAUAUCAAACUG	281	4.5	Cleavage	| Symbols: MSH1, CHM1, ATMSH1, CHM | MUTL protein homolog 1 | chr3:8822979-8829694 REVERSE LENGTH=3730
AT3G24360	UCCCAACCCAUGAUCUAAGCG	236	5	Cleavage	| Symbols: | ATP-dependent caseinolytic (Clp) protease/crotonase family protein | chr3:8839728-8842831 REVERSE LENGTH=1393
AT3G24490	UCUAGUUCGCGUUCUUCAGAC	300	3.5	Translation	| Symbols: | Alcohol dehydrogenase transcription factor Myb/SANT-like family protein | chr3:8910770-8912196 FORWARD LENGTH=1427
AT3G24550	CUUGGCAUCGAAUUUGAACUC	1059	3.5	Cleavage	| Symbols: ATPERK1, PERK1 | proline extensin-like receptor kinase 1 | chr3:8960258-8963568 FORWARD LENGTH=2377
AT3G24630	UGACGGACAAGAUAAGUUGCU	1505	5	Cleavage	| Symbols: | unknown protein; Has 5348 Blast hits to 3182 proteins in 353 species: Archae - 0; Bacteria - 481; Metazoa - 1959; Fungi - 405; Plants - 180; Viruses - 10; Other Eukaryotes - 2313 (source: NCBI BLink). | chr3:8988055-8990873 FORWAI
AT3G24670	AUUGAUUCUGCACUCAAGGGC	128	3.5	Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr3:9005939-9008801 REVERSE LENGTH=1589
AT3G24820	UGUCCCAACUUAACUCUACCCU	279	3.5	Cleavage	| Symbols: | BSD domain-containing protein | chr3:9062365-9064378 REVERSE LENGTH=832
AT3G24890	UGACGGACAAGAUAAGUUGCU	1505	4	Cleavage	| Symbols: VAMP728 | vesicle-associated membrane protein 728 | chr3:9097514-9098945 FORWARD LENGTH=663
AT3G25060	UACUUCCAGCGUUCUGUAGCC	826	4	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9128516-9130321 FORWARD LENGTH=1806
AT3G25110	UUGAACAAGCCUGAUGAAGUU	102	3.5	Translation	| Symbols: AtFaTA, FaTA | fatA acyl-ACP thioesterase | chr3:9146271-9148486 REVERSE LENGTH=1620
AT3G25520	UGUGGAUACAAGAGCUGGGCU	215	3	Cleavage	| Symbols: ATL5, PGY3, OLI5, RPL5A | ribosomal protein L5 | chr3:9269293-9271390 REVERSE LENGTH=1249
AT3G25620	UUAGCACCGAGGAUGAUGGACU	330	4	Cleavage	| Symbols: | ABC-2 type transporter family protein | chr3:9316074-9319571 REVERSE LENGTH=2688
AT3G25640	UCUAGUUCACAUUUUUCGGAC	427	5	Translation	| Symbols: | Protein of unknown function, DUF617 | chr3:9333719-9334804 FORWARD LENGTH=1086
AT3G25670	UUAUCAACGAACUCUUGGCCC	310	4.5	Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr3:9344532-9346301 REVERSE LENGTH=1428
AT3G25860	UCGGGAUCCUGCUGAAUGGUC	135	3.5	Cleavage	| Symbols: LTA2, PLE2 | 2-oxoacid dehydrogenases acyltransferase family protein | chr3:9460560-9462787 FORWARD LENGTH=1717
AT3G26040	UUACGAGACUCUAGCCCAGCU	3733	5	Translation	| Symbols: | HXXXD-type acyl-transferase family protein | chr3:9519741-9521070 FORWARD LENGTH=1330
AT3G26060	UCGAGUACACAGAAUGGGCUG	179	3.5	Cleavage	| Symbols: ATPRX Q | Thioredoxin superfamily protein | chr3:9524733-9526374 FORWARD LENGTH=976
AT3G26085	UUUGGGUUUGGGUUAACUGCU	225	4	Cleavage	| Symbols: | CAAX amino terminal protease family protein | chr3:9530595-9532417 FORWARD LENGTH=983

AT3G26115	UUGGCGCUCAACUCUGCAAGGU	955	4 Translation	| Symbols: | Pyridoxal-5'-phosphate-dependent enzyme family protein | chr3:9542278-9544348 FORWARD LENGTH=1409
AT3G26125	CAACGCUCUUGAUACAUCUAG	133	3.5 Cleavage	| Symbols: CYP86C2 | cytochrome P450, family 86, subfamily C, polypeptide 2 | chr3:9551812-9553437 FORWARD LENGTH=1626
AT3G26160	UAUCGAGCACCUACGUCACUG	123	4 Cleavage	| Symbols: CYP71B17 | cytochrome P450, family 71, subfamily B, polypeptide 17 | chr3:9568280-9569886 REVERSE LENGTH=1524
AT3G26520	UUAGAAUUAUCAUGUCUUGGC	138	3.5 Translation	| Symbols: TIP2, SITIP, GAMMA-TIP2, TIP1;2 | tonoplast intrinsic protein 2 | chr3:9722443-9723815 REVERSE LENGTH=1201
AT3G26540	UCAGUAGAAUUCGAUCAUAUC	104	3 Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:9744542-9746644 REVERSE LENGTH=2103
AT3G26560	UCCGCUAGAUAUAUCAAACUG	281	3.5 Translation	| Symbols: | ATP-dependent RNA helicase, putative | chr3:9749904-9753772 REVERSE LENGTH=3778
AT3G26600	UUUAACAACUAAGGUUCCUGU	1055	3 Translation	| Symbols: ARO4 | armadillo repeat only 4 | chr3:9769744-9772035 FORWARD LENGTH=2292
AT3G26740	UCUAGUUCGCAUUUUUUGGAC	421	2.5 Cleavage	| Symbols: CCL | CCR-like | chr3:9827801-9828680 FORWARD LENGTH=712
AT3G26770	UAAGGAGAGUCAGCUACUUGGA	134	4.5 Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr3:9845396-9847148 FORWARD LENGTH=1088
AT3G26910	UCAUCCUCUGUAGCUUCCGUC	210	2.5 Translation	| Symbols: | hydroxyproline-rich glycoprotein family protein | chr3:9915128-9918743 REVERSE LENGTH=2253
AT3G26950	UGACGGAAGCUACAGAGGAUG	108	4 Cleavage	| Symbols: | unknown protein; Has 27 Blast hits to 27 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 27; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:9941138-9943480 REVERSE LENGTH=1780
AT3G26990	CUCACAAGUGAUAUAGGGCUUG	110	5 Cleavage	| Symbols: | ENTH/VHS family protein | chr3:9948223-9952041 REVERSE LENGTH=1960
AT3G27040	UGUGGUGUACCUCUCACGUCU	112	3 Cleavage	| Symbols: | Meprin and TRAF (MATH) homology domain-containing protein | chr3:9974912-9977927 REVERSE LENGTH=1077
AT3G27190	UGAAUCUUGGUCAACUGGACC	197	4 Cleavage	| Symbols: UKL2 | uridine kinase-like 2 | chr3:10039234-10043066 REVERSE LENGTH=1871
AT3G27200	UAGAUAACAAGAACUCUUUCU	107	3.5 Cleavage	| Symbols: | Cupredoxin superfamily protein | chr3:10043522-10044373 REVERSE LENGTH=774
AT3G27250	UGUCUUACCCGUACGUCGCUU	150	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G40800.1); Has 104 Blast hits to 104 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 104; Viruses - 0; Other Euka
AT3G27270	UUACGAGACUCUAGCCCAGCU	3733	4.5 Cleavage	| Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr3:10073280-10074160 FORWARD LENGTH=881
AT3G27340	UGAGACACAACAGGGAGAUUC	244	3.5 Translation	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: oxidation reduction; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro DOMAIN/s: Gamma-butyrobetaine dioxygenase/Trimet
AT3G27570	UCCCGGAAUGCUGAAGAAGUA	113	3.5 Cleavage	| Symbols: | Sucrase/ferredoxin-like family protein | chr3:10213996-10216736 REVERSE LENGTH=1475
AT3G27610	AUUUGAACUCAUGGAUACCCU	768	3.5 Translation	| Symbols: | Nucleotidylyl transferase superfamily protein | chr3:10225525-10228192 REVERSE LENGTH=1414
AT3G27670	AAAGUCAAGAACCCCAACCCU	201	4.5 Cleavage	| Symbols: RST1 | ARM repeat superfamily protein | chr3:10245134-10253293 FORWARD LENGTH=5865
AT3G27720	UCACUUUGCUGAACAUGUACC	138	4.5 Cleavage	| Symbols: ARI4, ATARI4 | IBR domain containing protein | chr3:10271876-10273621 FORWARD LENGTH=1482
AT3G27730	UGAAGGAUUUGUGGUUAACCA	474	3.5 Translation	| Symbols: RCK, MER3 | ATP binding;ATP-dependent helicases;DNA helicases | chr3:10273801-10280362 REVERSE LENGTH=3702
AT3G27831	UAUUGACGUCGAGUAUGAGCCU	517	4 Cleavage	| Symbols: | Gamma-thionin family protein | chr3:10319481-10320092 REVERSE LENGTH=234
AT3G27835	UAUUGACGUCGAGUAUGAGCCU	517	4 Cleavage	| Symbols: | Gamma-thionin family protein | chr3:10321741-10322306 REVERSE LENGTH=240
AT3G27910	UGUGGAUACAAGAGCUGGGCU	215	3.5 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr3:10357232-10358116 REVERSE LENGTH=885
AT3G27970	UAUCUCUGUCGUUACGAACCU	295	3 Cleavage	| Symbols: | Exonuclease family protein | chr3:10389609-10391544 FORWARD LENGTH=1074
AT3G27990	UGUGGAUACAAGAGCUGGGCU	215	4 Cleavage	| Symbols: | other RNA | chr3:10392675-10398175 REVERSE LENGTH=1527
AT3G28170	UUCUUGUGAACUUGACCGGGA	158	3.5 Translation	| Symbols: | unknown protein; Has 2 Blast hits to 1 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 2; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:10498361-10500360 FORWARD LENGTH=624
AT3G28223	UCUGUAUGCAUAACUUGGGAC	1212	4 Cleavage	| Symbols: | F-box family protein | chr3:10527477-10528961 REVERSE LENGTH=1408
AT3G28640	AAACACUCUAGACUCGAUCCU	123	3.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:10731518-10733032 REVERSE LENGTH=1515
AT3G28660	AAACACUCUAGACUCGAUCCU	123	3.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:10738715-10740930 REVERSE LENGTH=2142
AT3G28710	ACAAAACUGUUGAACAAGCCU	1107	4.5 Cleavage	| Symbols: | ATPase, V0/A0 complex, subunit C/D | chr3:10772903-10775727 REVERSE LENGTH=1430
AT3G28715	ACAAAACUGUUGAACAAGCCU	1107	4.5 Cleavage	| Symbols: | ATPase, V0/A0 complex, subunit C/D | chr3:10777837-10780614 FORWARD LENGTH=1484
AT3G28860	UCCCGGAAUGCUGAAGAAGUA	113	4 Cleavage	| Symbols: ATMDR1, ATMDR11, PGP19, MDR11, MDR1, ATPGP19, ABCB19, ATABCB19 | ATP binding cassette subfamily B19 | chr3:10870038-10877506 REVERSE LENGTH=4228
AT3G29255	UGAAAUAAAACUGAACCAUGCC	263	4 Translation	| Symbols: | catalytics;intramolecular transferases | chr3:11209586-11213909 FORWARD LENGTH=2121
AT3G29390	UCGACCACACUGUCAUGAUCU	174	5 Cleavage	| Symbols: RIK | RS2-interacting KH protein | chr3:11289613-11294774 FORWARD LENGTH=2049
AT3G29410	UCCACCGACUGAUGACAAUGU	1524	4 Cleavage	| Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr3:11302431-11305136 REVERSE LENGTH=2031
AT3G29630	UAAAACUGAACCAUGCCUAGA	302	4 Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:11447028-11448609 REVERSE LENGTH=1582
AT3G29638	UAUUGAUUUUUGGCUGAGGU	116	4 Cleavage	| Symbols: | General transcription factor 2-related zinc finger protein | chr3:11473584-11475559 FORWARD LENGTH=1239
AT3G29770	UAGUGACCGAGUAGUACCACC	461	4.5 Translation	| Symbols: ATMES11, MES11 | methyl esterase 11 | chr3:11648341-11650839 FORWARD LENGTH=1577
AT3G30120	UUAUGCUUCUGUUGAUCCACC	153	3.5 Cleavage	| Symbols: | pseudogene, similar to CTV.22, blastp match of 29% identity and 4.9e-74 P-value to GP|24461867|gb|AAN62354.1|AF506028_23|AF506028 CTV.22 {Poncirus trifoliata} | chr3:11752005-11756485 REVERSE LENGTH=4481
AT3G30222	UCGGCUCAAACCUAACACGUU	129	4.5 Cleavage	| Symbols: | unknown protein; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: N
AT3G30290	CUCAUGUAGUUCUAGUUCGCA	102	4 Cleavage	| Symbols: CYP702A8 | cytochrome P450, family 702, subfamily A, polypeptide 8 | chr3:11917230-11919546 REVERSE LENGTH=1227
AT3G30415	UUCUGAAGGACAAGCUCAGCU	1012	4 Translation	| Symbols: | pseudogene, putative urophorphyrin III methylase, blastp match of 80% identity and 2.7e-49 P-value to GP|20161485|dbj|BAB90408.1||AP003681 uroporphyrin-III C-methyltransferase-like protein {Oryza sativa (japonica cultivar-gr
AT3G31350	UUGAUCCAAGUAGCUGACUCU	4031	3.5 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: fruit; Has 2 Blast hits to 2 proteins in 1 species: Archae - 0; Bact
AT3G32896	UAUGAGUUGAUCGACGAAGAU	123	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; Has 10 Blast hits to 10 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Pla
AT3G32940	UGUGGAUACAAGAGUUGGGCU	111	4 Translation	| Symbols: | RNA-binding KH domain-containing protein | chr3:13490945-13493787 REVERSE LENGTH=2125
AT3G32990	UCUAGUCCGAAAAAUGCGAAC	163	4 Cleavage	| Symbols: | pseudogene, ATP synthase C subunit, blastp match of 86% identity and 9.3e-27 P-value to SP|P06286|ATPH_TOBAC ATP synthase C chain (EC 3.6.3.14) (Lipid-binding protein) (Subunit III). (Common tobacco) {Nicotiana tabacum} | ch
AT3G42047	UUUGAACUCAUGGAUACCCUA	227	4 Translation	| Symbols: | unknown pseudogene | chr3:14227679-14228304 REVERSE LENGTH=626
AT3G42310	UUGAUCCAAGUAGCUGACUCU	4031	5 Cleavage	| Symbols: | unknown protein; Has 66 Blast hits to 66 proteins in 13 species: Archae - 0; Bacteria - 0; Metazoa - 12; Fungi - 0; Plants - 18; Viruses - 31; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:14459818-14461497 FORWARD LENGTH=246
AT3G42550	UUGGACGCCUCUACUAUGAGA	679	4.5 Translation	| Symbols: | Eukaryotic aspartyl protease family protein | chr3:14665728-14669135 REVERSE LENGTH=1293
AT3G42670	CUGGAGGACGUACAGCACUUA	113	3.5 Cleavage	| Symbols: CHR38, CLSY | chromatin remodeling 38 | chr3:14755798-14760085 REVERSE LENGTH=3879
AT3G43120	UCUAGUCCGAAAAAUGCGAAC	163	4.5 Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr3:15094083-15095512 FORWARD LENGTH=849
AT3G43210	UCCCAACCCAUGAUCUAAGCG	236	4 Cleavage	| Symbols: TES, ATNACK2, NACK2 | ATP binding microtubule motor family protein | chr3:15190934-15196168 FORWARD LENGTH=3193
AT3G43290	UUGAGAUAUCCCCUGUUACUG	106	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: in 8 processes; LOCATED IN: cellular_component unknown; EXPRESSED IN: leaf; EXPRESSED DURING: LP.10 ten leaves visible; Has 1 Blast hits to 1 protein
AT3G43580	UGAGUAGAAUUCGAUCAUAUC	114	4 Cleavage	| Symbols: | Beta-galactosidase related protein | chr3:15502143-15503606 FORWARD LENGTH=1464
AT3G43660	AUCAUCCUCGGAUCAAACCCU	222	3 Translation	| Symbols: | Vacuolar iron transporter (VIT) family protein | chr3:15565224-15566047 FORWARD LENGTH=824
AT3G44090	UUCGGACUGGAUAGGACUAGG	101	3 Translation	| Symbols: | F-box family protein | chr3:15839123-15840759 FORWARD LENGTH=1350
AT3G44160	UCGGCUCAAACCUAACACGUU	129	4.5 Cleavage	| Symbols: | Outer membrane OMP85 family protein | chr3:15888902-15891988 REVERSE LENGTH=1586
AT3G44170	UCUUGGCAUCGAAUUUGAACUC	189	4.5 Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Plant self-incompatibility S1 (InterPro:IPR010264); BEST Arabidopsis tha
AT3G44290	UGAGUAGAAUUCGAUCAUAUC	114	3.5 Translation	| Symbols: anac060, NAC060 | NAC domain containing protein 60 | chr3:15972909-15975183 REVERSE LENGTH=1172
AT3G44460	UUCUUUCCGUUGGUGUGCGCC	205	3 Cleavage	| Symbols: DPBF2, AtbZIP67 | Basic-leucine zipper (bZIP) transcription factor family protein | chr3:16079976-16081906 REVERSE LENGTH=1232
AT3G44530	AUGGAUUUAGAUCACUUGCGUC	196	3.5 Translation	| Symbols: HIRA | homolog of histone chaperone HIRA | chr3:16115588-16121518 FORWARD LENGTH=3442
AT3G44713	UGACGGACAAGAUAAGCUGCU	259	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G14800.1); Has 69 Blast hits to 64 proteins in 24 species: Archae - 2; Bacteria - 10; Metazoa - 4; Fungi - 4; Plants - 36; Viruses - 1; Other Eukary
AT3G44716	UACCCGUACGUCGCUUACAAG	3223	4 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 13 Blast hits to 13 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fur
AT3G44800	UAUGCUUCUGUUGAUCCACCU	344	3.5 Translation	| Symbols: | Meprin and TRAF (MATH) homology domain-containing protein | chr3:16343333-16346027 FORWARD LENGTH=1695
AT3G44805	UAUGCUUCUGUUGAUCCACCU	344	4 Translation	| Symbols: | TRAF-like superfamily protein | chr3:16350395-16351437 FORWARD LENGTH=747
AT3G44890	ACAAAACUGUUGAACAAGCCU	1107	3 Cleavage	| Symbols: RPL9 | ribosomal protein L9 | chr3:16386434-16388466 FORWARD LENGTH=920
AT3G44900	UGCACUCGCUAGGUCUGGCAG	378	4.5 Cleavage	| Symbols: ATCHX4, CHX4 | cation/H+ exchanger 4 | chr3:16388724-16391360 FORWARD LENGTH=2454
AT3G44960	UUAGAAUUAUCAUGUCUUGGC	138	3.5 Translation	| Symbols: | unknown protein; Has 34 Blast hits to 34 proteins in 10 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 31; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr3:16427795-16429151 FORWARD LENGTH=624
AT3G44990	UACCCGUACGUCGCCUACAAG	192	4.5 Cleavage	| Symbols: XTR8, ATXTR8, XTH31 | xyloglucan endo-transglycosylase-related 8 | chr3:16446975-16448764 REVERSE LENGTH=1273
AT3G45040	AAACAGGACAAGUUACUCGCC	986	4.5 Translation	| Symbols: | phosphatidate cytidylyltransferase family protein | chr3:16472662-16475753 REVERSE LENGTH=1900
AT3G45280	UAUGGAGAUGAUCGCAAUGGCC	152	4.5 Cleavage	| Symbols: SYP72, ATSYP72 | syntaxin of plants 72 | chr3:16611413-16613340 REVERSE LENGTH=872
AT3G45310	UCAACACUCUGAUACAUCUAG	143	3.5 Cleavage	| Symbols: | Cysteine proteinases superfamily protein | chr3:16628384-16630521 REVERSE LENGTH=1442
AT3G45320	UCCCGGAAUGCUGAAGAAGUA	113	4 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G60330.1); Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 7; Viruses - 0; Other Eukaryotes -
AT3G45410	UCUGUACCGCUGAAUUCUUCC	275	3.5 Translation	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:16653899-16656013 REVERSE LENGTH=2115
AT3G45420	UCUGUACCGCUGAAUUCUUCC	275	3 Translation	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:16657263-16659266 REVERSE LENGTH=2004
AT3G45430	CCGAUUCUGAUUGCAUGUGGU	186	3.5 Translation	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:16660759-16662783 REVERSE LENGTH=2025
AT3G45620	UACGCGACCGCGGUGCUGGCC	119	4.5 Translation	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:16745882-16748156 FORWARD LENGTH=1747
AT3G45850	UUUGGCGCUCAACUCUGCAAG	3787	4.5 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:16855612-16861527 REVERSE LENGTH=3528
AT3G46160	UGGCAGUAGGAGUACACGACU	163	4 Cleavage	| Symbols: | Protein kinase superfamily protein | chr3:16950955-16952136 FORWARD LENGTH=1182
AT3G46290	UCUGUAUGCAUAACUUGGGAC	1212	3.5 Cleavage	| Symbols: HERK1 | hercules receptor kinase 1 | chr3:17012728-17015885 FORWARD LENGTH=3032
AT3G46330	UUUGGGUUUGGGUUAACUGCU	225	2 Translation	| Symbols: MEE39 | Leucine-rich repeat protein kinase family protein | chr3:17020747-17025011 REVERSE LENGTH=2904
AT3G46350	UUCUUCAGACUGGAUAGGACU	265	3.5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17036427-17041680 FORWARD LENGTH=2616
AT3G46360	UGACACCGAUUCUGAUUGCAU	377	3.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G44755.1); Has 4 Blast hits to 4 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 4; Viruses - 0; Other Eukaryotes -
AT3G46420	UUAGCACCGAGGAUGAUGGACU	330	3.5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17082108-17086534 FORWARD LENGTH=2517
AT3G46460	UUUCUGACGGACAAGAUAAGU	480	3 Cleavage	| Symbols: UBC13 | ubiquitin-conjugating enzyme 13 | chr3:17095878-17097452 REVERSE LENGTH=880
AT3G46510	UCGAGCACCUACGUCACUGCG	100	5 Cleavage	| Symbols: PUB13, ATPUB13 | plant U-box 13 | chr3:17123739-17126691 REVERSE LENGTH=2502

AT3G46650	UGAGAACAUUGACUUCAGACCU	158	4	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr3:17185453-17187812 REVERSE LENGTH=1416
AT3G46670	CGAGAGAUUACAGGGACUGUC	3198	4	Cleavage	| Symbols: UGT76E11 | UDP-glucosyl transferase 76E11 | chr3:17192589-17194397 REVERSE LENGTH=1732
AT3G46820	UAACAAGAACUCUUUCUUUUCU	235	3	Cleavage	| Symbols: TOPP5 | type one serine/threonine protein phosphatase 5 | chr3:17241781-17244277 REVERSE LENGTH=1583
AT3G46900	UAAAACUGAACCAUGCCUAGA	302	4	Cleavage	| Symbols: COPT2 | copper transporter 2 | chr3:17268875-17269510 FORWARD LENGTH=636
AT3G47030	CUGGGGUACAGAACAUUCGCU	197	3	Translation	| Symbols: | F-box and associated interaction domains-containing protein | chr3:17322119-17323545 FORWARD LENGTH=1427
AT3G47060	UUUGGCGCUCAACUCUGCAAG	3787	3	Translation	| Symbols: ftsh7 | FTSH protease 7 | chr3:17332985-17336966 FORWARD LENGTH=2776
AT3G47110	UGUGGAUACAAGAGUUGGGCU	111	4.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr3:17347103-17350296 REVERSE LENGTH=3078
AT3G47160	UUGCAGAGAUGGAUGUACAAC	101	4	Cleavage	| Symbols: | RING/U-box superfamily protein | chr3:17359988-17362118 REVERSE LENGTH=1227
AT3G47400	UACGCGACCGCGGUGCUGGCC	119	5	Cleavage	| Symbols: | Plant invertase/pectin methylesterase inhibitor superfamily | chr3:17465590-17468118 FORWARD LENGTH=2054
AT3G47470	CCACCGACUGAUGACAACGUC	122	3.5	Cleavage	| Symbols: LHCA4, CAB4 | light-harvesting chlorophyll-protein complex I subunit A4 | chr3:17493372-17495033 REVERSE LENGTH=1266
AT3G47890	UGUCCCAACUUAACUCUACCCU	279	3.5	Translation	| Symbols: | Ubiquitin carboxyl-terminal hydrolase-related protein | chr3:17666927-17673530 REVERSE LENGTH=4952
AT3G47930	UUUGGCGCUCAACUCUGCAAG	3787	4	Cleavage	| Symbols: ATGLDH, GLDH | L-galactono-1,4-lactone dehydrogenase | chr3:17684444-17687620 FORWARD LENGTH=2027
AT3G47960	UUUAACAACUAAGGUUCCUGU	1055	4	Cleavage	| Symbols: | Major facilitator superfamily protein | chr3:17697942-17700833 REVERSE LENGTH=2157
AT3G48170	UGACGCCAAUUCUGAAAGUUU	154	4	Cleavage	| Symbols: ALDH10A9 | aldehyde dehydrogenase 10A9 | chr3:17786140-17790008 REVERSE LENGTH=1752
AT3G48210	UGUGGAUACAAGAGCUGGGCU	215	2.5	Translation	| Symbols: | CONTAINS InterPro DOMAIN/s: Kinetochore-Ndc80 complex, subunit Spc25 (InterPro:IPR013255); Has 194 Blast hits to 194 proteins in 72 species: Archae - 0; Bacteria - 4; Metazoa - 72; Fungi - 39; Plants - 62; Viruses - 0; Other Eukary
AT3G48425	UUGGCGCUCAACUCUGCAAGGU	955	5	Cleavage	| Symbols: | DNAse I-like superfamily protein | chr3:17931818-17934744 FORWARD LENGTH=1438
AT3G48430	UCUUGGCAUCGAAUUUGAACUC	189	4	Translation	| Symbols: REF6 | relative of early flowering 6 | chr3:17935609-17940746 FORWARD LENGTH=4373
AT3G48460	UUCCAGAACUAAUGAAUGUUA	448	4	Cleavage	| Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr3:17949445-17951195 FORWARD LENGTH=1310
AT3G48540	UCUGAACUCAAGGCACCCAAA	493	4	Cleavage	| Symbols: | Cytidine/deoxycytidylate deaminase family protein | chr3:17989798-17992015 REVERSE LENGTH=699
AT3G48690	UGACACCGAUUCUGAUUGCAU	377	4.5	Cleavage	| Symbols: ATCXE12, CXE12 | alpha/beta-Hydrolases superfamily protein | chr3:18037047-18038234 REVERSE LENGTH=1188
AT3G48710	CUACAAAUUCGAGCACUCCCU	156	4.5	Cleavage	| Symbols: | DEK domain-containing chromatin associated protein | chr3:18040937-18044226 FORWARD LENGTH=1707
AT3G48770	CUGGAGGACGUACAGCACUUA	113	5	Cleavage	| Symbols: | DNA binding;ATP binding | chr3:18078474-18086817 REVERSE LENGTH=6125
AT3G48800	UCCUGAGUACUCUCUUCCAAG	209	4	Cleavage	| Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr3:18095825-18096661 REVERSE LENGTH=837
AT3G48870	UAUAGGGCUUGAAAGAAAGUC	535	4.5	Cleavage	| Symbols: ATCLPC, ATHSP93-III, HSP93-III | Clp ATPase | chr3:18122198-18126638 REVERSE LENGTH=3157
AT3G48880	UCGACCACACUGUUAGGAUCU	121	4.5	Cleavage	| Symbols: | RNI-like superfamily protein | chr3:18126870-18129172 FORWARD LENGTH=1191
AT3G48900	UGAGGUCGAGUAGAGCAAUCUA	117	4	Translation	| Symbols: | single-stranded DNA endonuclease family protein | chr3:18131829-18136341 FORWARD LENGTH=2031
AT3G48940	UGAAUCUUGGUCAACUGGACC	197	4.5	Cleavage	| Symbols: | Remorin family protein | chr3:18142863-18144163 REVERSE LENGTH=528
AT3G48960	UUUGAGAGCACUCCACCGACUG	125	4	Translation	| Symbols: | Ribosomal protein L13e family protein | chr3:18150444-18151412 REVERSE LENGTH=621
AT3G49070	UCGAGCACCUACGUCACUGCG	100	3	Translation	| Symbols: | Protein of unknown function (DUF677) | chr3:18192479-18193729 REVERSE LENGTH=1251
AT3G49240	UCAUCAAUGAACUCAUUUGGCU	103	4	Cleavage	| Symbols: emb1796 | Pentatricopeptide repeat (PPR) superfamily protein | chr3:18255979-18258100 FORWARD LENGTH=2122
AT3G49260	UCAAGCGAUUGGAAGGAUUGUU	102	3	Cleavage	| Symbols: iqd21 | IQ-domain 21 | chr3:18262399-18265979 FORWARD LENGTH=1740
AT3G49410	ACAAAACUGUUGAACAAGCCU	1107	4	Cleavage	| Symbols: | Transcription factor IIIC, subunit 5 | chr3:18324746-18329191 FORWARD LENGTH=1990
AT3G49500	UCACCAUUGGCAGCUCUGUACC	187	3.5	Cleavage	| Symbols: RDR6, SGS2, SDE1 | RNA-dependent RNA polymerase 6 | chr3:18349161-18353624 REVERSE LENGTH=3786
AT3G49710	UGAGUAGAAUUCGAUCAUAUC	114	3.5	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:18437845-18440010 FORWARD LENGTH=2166
AT3G49725	UGUCUUACCCGUACGUCGCUU	150	3.5	Translation	| Symbols: | GTP-binding protein, HflX | chr3:18442275-18445457 REVERSE LENGTH=2096
AT3G49830	UUGGCGACCGAUCUCUGAAAG	334	2	Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:18482383-18483940 FORWARD LENGTH=1422
AT3G49950	UUGGCCUGAGGUUGGACGCCU	272	3.5	Cleavage	| Symbols: | GRAS family transcription factor | chr3:18522510-18523906 FORWARD LENGTH=1397
AT3G50100	UGUGACACCGAUUCUGAUUGC	114	4	Cleavage	| Symbols: SDN1 | small RNA degrading nuclease 1 | chr3:18578353-18580594 FORWARD LENGTH=1288
AT3G50110	UUUGAUCCGAGGAUGAUGGAU	816	4	Cleavage	| Symbols: ATPEN3, PEN3 | PTEN 3 | chr3:18580609-18584535 REVERSE LENGTH=2251
AT3G50270	UCCCAACCCAUGAUCUAAGCG	236	4.5	Cleavage	| Symbols: | HXXXD-type acyl-transferase family protein | chr3:18635920-18637341 FORWARD LENGTH=1422
AT3G50295	UCGACCACACUGUUAGGAUCU	121	3.5	Translation	| Symbols: | pseudogene, hypothetical protein | chr3:18641798-18642664 FORWARD LENGTH=867
AT3G50310	UUGUGAGUGUUUGUGAGGUCU	141	3.5	Cleavage	| Symbols: MAPKKK20 | mitogen-activated protein kinase kinase kinase 20 | chr3:18648151-18649521 REVERSE LENGTH=1371
AT3G50350	UUGAGAGCACUCCACCGACUG	261	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF1685) | chr3:18672102-18674022 FORWARD LENGTH=935
AT3G50380	UAUCCUGAGAGCGGUGCUGGC	334	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF1162) | chr3:18686443-18700533 REVERSE LENGTH=9303
AT3G50390	UUACGAGACUCUAGCCCAGCU	3733	4	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr3:18702074-18703619 FORWARD LENGTH=1546
AT3G50670	CUAGAAUUCUUUCCCUUUCCU	235	5	Cleavage	| Symbols: U1-70K, U1SNRNP | U1 small nuclear ribonucleoprotein-70K | chr3:18826300-18829618 REVERSE LENGTH=1586
AT3G50720	UUGAACAAGCCUGAUGAAGUU	102	4.5	Cleavage	| Symbols: | Protein kinase superfamily protein | chr3:18847519-18849430 REVERSE LENGTH=1134
AT3G50950	UGCCAUGAUCGAGAGCUGCCU	164	4.5	Cleavage	| Symbols: ZAR1 | HOPZ-ACTIVATED RESISTANCE 1 | chr3:18935714-18938685 FORWARD LENGTH=2750
AT3G51010	UACCGGAGGACGUACAUAGCU	401	4	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion, plastid; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 24 Bla
AT3G51070	UACUCGACCACACUGUUAGGA	183	4.5	Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:18969068-18972291 FORWARD LENGTH=2688
AT3G51290	UUCGGUCUGGCCAUACUCGGC	147	3.5	Translation	| Symbols: | Protein of unknown function (DUF630) ;Protein of unknown function (DUF632) | chr3:19039980-19042569 FORWARD LENGTH=2037
AT3G51360	UCAAGCGAUUGGAAGGAUUGUU	102	2.5	Cleavage	| Symbols: | Eukaryotic aspartyl protease family protein | chr3:19064294-19066560 REVERSE LENGTH=1467
AT3G51370	AAACAGGACAAGUUACUCGCC	986	3.5	Translation	| Symbols: | Protein phosphatase 2C family protein | chr3:19069371-19072195 FORWARD LENGTH=1671
AT3G51460	UUCUUGUGAACUUGACCGGGA	158	3.5	Cleavage	| Symbols: RHD4 | Phosphoinositide phosphatase family protein | chr3:19092518-19097353 FORWARD LENGTH=2379
AT3G51490	CAAGAACCCGCACGACACUCG	169	5	Cleavage	| Symbols: TMT3 | tonoplast monosaccharide transporter3 | chr3:19104885-19107797 REVERSE LENGTH=2582
AT3G51895	UCUGUACCGCUGAAUUCUUCC	275	4	Cleavage	| Symbols: SULTR3;1, AST12 | sulfate transporter 3;1 | chr3:19251287-19255760 REVERSE LENGTH=2276
AT3G51970	UUUGCCUGUUGAACUCGAGUA	114	3.5	Cleavage	| Symbols: ATSAT1, ASAT1, ATASAT1 | acyl-CoA sterol acyl transferase 1 | chr3:19284339-19285582 FORWARD LENGTH=1244
AT3G52150	UCGACCACACUGUUAGGAUCU	121	3.5	Translation	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr3:19342024-19343448 FORWARD LENGTH=1064
AT3G52310	UUGAACAAGCCUGAUGAAGUU	102	3.5	Cleavage	| Symbols: | ABC-2 type transporter family protein | chr3:19398628-19402953 FORWARD LENGTH=2482
AT3G52340	AUACCCAAACCUGAACUUUCU	127	3.5	Cleavage	| Symbols: SPP2, ATSPP2 | sucrose-6F-phosphate phosphohydrolase 2 | chr3:19407052-19409335 FORWARD LENGTH=1568
AT3G52370	UAGAAUUAUCAUGUCUUGGCA	194	3.5	Cleavage	| Symbols: FLA15 | FASCICLIN-like arabinogalactan protein 15 precursor | chr3:19417490-19419782 FORWARD LENGTH=1603
AT3G52570	UGGCGCUCAACUCUGCAAGGU	10625	5	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:19501130-19502999 FORWARD LENGTH=1227
AT3G52600	UAACUCUACCCUUUGCACUCG	727	4	Translation	| Symbols: AtcwINV2, CWINV2 | cell wall invertase 2 | chr3:19506891-19509359 REVERSE LENGTH=2048
AT3G52840	AUACCCAAACCUGAACUUUCU	127	3	Translation	| Symbols: BGAL2 | beta-galactosidase 2 | chr3:19581113-19586299 FORWARD LENGTH=2517
AT3G52880	UGGCAGUAGGAGUACACGACU	163	5	Translation	| Symbols: ATMDAR1, MDAR1 | monodehydroascorbate reductase 1 | chr3:19601212-19604454 REVERSE LENGTH=1658
AT3G52930	UUGAGAGCCUUGUAGUAGUCU	262	3	Cleavage	| Symbols: | Aldolase superfamily protein | chr3:19626748-19629073 REVERSE LENGTH=1911
AT3G53020	UCACCUCGCAUCUUAGAACUG	146	3.5	Cleavage	| Symbols: STV1, RPL24B, RPL24 | Ribosomal protein L24e family protein | chr3:19660517-19662025 REVERSE LENGTH=837
AT3G53130	UUGGGAGAACUAUGACACGAG	515	4	Cleavage	| Symbols: LUT1, CYP97C1 | Cytochrome P450 superfamily protein | chr3:19692771-19697542 FORWARD LENGTH=3341
AT3G53170	CUAGAAUUCUUUCCCUUUCCU	235	3	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:19704485-19706417 REVERSE LENGTH=1615
AT3G53210	UGUGAGUGUUUGUGAGGUCUU	178	3	Translation	| Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr3:19720165-19721875 FORWARD LENGTH=1238
AT3G53250	UUGUGGAAUCCGUAGUCUGUA	152	4.5	Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr3:19742968-19743297 FORWARD LENGTH=330
AT3G53480	UUCUGAAGGACAAGCUCAGCU	1012	3.5	Cleavage	| Symbols: PIS1, PDR9, ATPDR9, ABCG37 | pleiotropic drug resistance 9 | chr3:19825307-19831797 FORWARD LENGTH=4565
AT3G53550	UUGGCGCUCAACUCUGCAAGG	4868	4	Cleavage	| Symbols: | FBD-like domain family protein | chr3:19856870-19858308 FORWARD LENGTH=771
AT3G53620	UACCGGAGGACGUACAUAGCU	401	4	Cleavage	| Symbols: AtPPa4, PPa4 | pyrophosphorylase 4 | chr3:19880504-19883672 FORWARD LENGTH=1296
AT3G53780	UGAGGUCGAGUAGAGCAAUCUA	117	3.5	Cleavage	| Symbols: ATRBL4, RBL4 | RHOMBOID-like protein 4 | chr3:19924568-19927026 REVERSE LENGTH=1654
AT3G53930	UGCCAUGAUCGAGAGCUGCCU	164	4	Translation	| Symbols: | Protein kinase superfamily protein | chr3:19966352-19970813 FORWARD LENGTH=2558
AT3G53940	UGGAUUCCGGCUGCAUACUCC	392	4.5	Cleavage	| Symbols: | Mitochondrial substrate carrier family protein | chr3:19971019-19973769 REVERSE LENGTH=1542
AT3G54050	UCACCAUUGGCAGCUCUGUACC	187	3.5	Translation	| Symbols: HCEF1 | high cyclic electron flow 1 | chr3:20016892-20018822 FORWARD LENGTH=1379
AT3G54100	UGAAGGAUUUGUGGUUAACCA	474	4	Cleavage	| Symbols: | O-fucosyltransferase family protein | chr3:20034071-20037953 REVERSE LENGTH=2376
AT3G54410	UGUAUGCAUAACUUGGGACUU	149	4	Cleavage	| Symbols: | Protein of unknown function (DUF1163) | chr3:20144551-20145489 FORWARD LENGTH=939
AT3G54430	UAACAAGAACUCUUUCUUUUCU	235	3.5	Cleavage	| Symbols: SRS6 | SHI-related sequence 6 | chr3:20147101-20148127 REVERSE LENGTH=951
AT3G54440	UCAUAUGGACUUUGGCUACACC	101	4.5	Cleavage	| Symbols: | glycoside hydrolase family 2 protein | chr3:20148336-20157138 REVERSE LENGTH=3601
AT3G54460	UAGAGUUAAGUUGGGACAGGA	199	3	Translation	| Symbols: | SNF2 domain-containing protein / helicase domain-containing protein / F-box family protein | chr3:20161942-20167293 REVERSE LENGTH=4352
AT3G54660	UCAAGCGAUUGGAAGGAUUGUU	102	3	Cleavage	| Symbols: GR, EMB2360, ATGR2 | glutathione reductase | chr3:20229744-20233182 REVERSE LENGTH=2196
AT3G54690	UGUGAGUGUUUGUGAGGUCUU	178	4.5	Cleavage	| Symbols: | Sugar isomerase (SIS) family protein | chr3:20246539-20248140 FORWARD LENGTH=1430
AT3G54720	UGACGGACAAGAUAAGCUGCU	259	4	Translation	| Symbols: AMP1, COP2, HPT, PT, MFO1 | Peptidase M28 family protein | chr3:20254725-20257848 REVERSE LENGTH=2278
AT3G54740	UUUAAAACCGAGGACUUUUGC	115	3.5	Cleavage	| Symbols: | Protein of unknown function, DUF593 | chr3:20262391-20264601 FORWARD LENGTH=1703
AT3G54780	UUUCUGACGGACAAGAUAAGU	480	5	Cleavage	| Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr3:20278954-20281544 FORWARD LENGTH=2045
AT3G54850	UGUGUAUGCAUAACUUGGGAC	106	3.5	Cleavage	| Symbols: ATPUB14, PUB14 | plant U-box 14 | chr3:20321422-20324020 FORWARD LENGTH=2173

AT3G54930	UUCCGCAGGGAGAGCGUCCUC	112	3 Cleavage	| Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr3:20350839-20352948 REVERSE LENGTH=1924
AT3G54940	UAACUCUACCCUUUGCACUCG	727	3 Cleavage	| Symbols: | Papain family cysteine protease | chr3:20354351-20356318 FORWARD LENGTH=1346
AT3G55070	UUGAGAGCCUUGUAGUAGUCU	262	3 Translation	| Symbols: | LisH/CRA/RING-U-box domains-containing protein | chr3:20408286-20411140 FORWARD LENGTH=1601
AT3G55170	UUCGAGCACUCCCUGACCCGA	160	3.5 Cleavage	| Symbols: | Ribosomal L29 family protein | chr3:20452969-20454342 REVERSE LENGTH=568
AT3G55254	UAACAAGAACUCUUUCUUUUCU	235	2.5 Cleavage	| Symbols: | Plant self-incompatibility protein S1 family | chr3:20482190-20482813 REVERSE LENGTH=624
AT3G55330	UUGAACAAGCCUGAUGAAGUU	102	4 Translation	| Symbols: PPL1 | PsbP-like protein 1 | chr3:20513825-20515351 REVERSE LENGTH=975
AT3G55370	UGAGAACGCUCUGCCAUUGGA	158	4.5 Translation	| Symbols: OBP3 | OBF-binding protein 3 | chr3:20527063-20529291 FORWARD LENGTH=1522
AT3G55410	AUUUGAACUCAUGGAUACCCU	768	3.5 Cleavage	| Symbols: | 2-oxoglutarate dehydrogenase, E1 component | chr3:20541435-20546034 FORWARD LENGTH=3494
AT3G55677	UCCGCUAGAUAUAUCAAACUG	281	4.5 Cleavage	| Symbols: | Plant self-incompatibility protein S1 family | chr3:20663983-20664576 FORWARD LENGTH=594
AT3G55820	UGACACCGAUUCUGAUUGCAU	377	4.5 Cleavage	| Symbols: | Fasciclin-like arabinogalactan family protein | chr3:20713709-20714805 FORWARD LENGTH=1097
AT3G56000	UACAAAUUCGAGCACUCCCUG	156	4 Cleavage	| Symbols: ATCSLA14, CSLA14 | cellulose synthase like A14 | chr3:20783318-20785796 REVERSE LENGTH=1864
AT3G56020	UGAGCCGACAAGAGUAGUAUC	111	4.5 Cleavage	| Symbols: | Ribosomal protein L41 family | chr3:20790570-20791085 REVERSE LENGTH=376
AT3G56120	AUGGAUUUAGAUCACUUGCGUC	196	3 Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:20823146-20826543 FORWARD LENGTH=1690
AT3G56230	UCUAGUUCGCAUUUUUUGGAC	421	3 Cleavage	| Symbols: | BTB/POZ domain-containing protein | chr3:20860778-20862265 REVERSE LENGTH=1100
AT3G56330	UGAGGUCGAGUAGAGCAAUCUA	117	4 Cleavage	| Symbols: | N2,N2-dimethylguanosine tRNA methyltransferase | chr3:20890250-20892002 FORWARD LENGTH=1371
AT3G56370	CGUCACUGCGAAUUCCUGGAG	272	4.5 Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr3:20899099-20902981 REVERSE LENGTH=3416
AT3G56480	UACAGGAAGUGGGCGCACACC	102	3.5 Cleavage	| Symbols: | myosin heavy chain-related | chr3:20936098-20939631 REVERSE LENGTH=2164
AT3G56650	UAAGGAGAGUCAGCUACUUGGA	134	3.5 Translation	| Symbols: | Mog1/PsbP/DUF1795-like photosystem II reaction center PsbP family protein | chr3:20984752-20986131 FORWARD LENGTH=1062
AT3G56850	UUGCAGAGAUGGAUGUACAAC	101	3 Cleavage	| Symbols: AREB3, DPBF3 | ABA-responsive element binding protein 3 | chr3:21046341-21048516 REVERSE LENGTH=1729
AT3G56920	UUGGCGACCGAUCUCUGAAAG	334	1 Cleavage	| Symbols: | DHHC-type zinc finger family protein | chr3:21070648-21072702 FORWARD LENGTH=1464
AT3G56950	CAAAUUCGAGAACUCCCUGAC	283	4 Cleavage	| Symbols: SIP2;1 | small and basic intrinsic protein 2;1 | chr3:21078297-21079856 REVERSE LENGTH=1109
AT3G57020	AUACCCAAACCUGAACUUUCU	127	3.5 Cleavage	| Symbols: | Calcium-dependent phosphotriesterase superfamily protein | chr3:21098315-21100359 REVERSE LENGTH=1327
AT3G57030	UUCUGUAGCACGAGGUAUCCU	302	4.5 Translation	| Symbols: | Calcium-dependent phosphotriesterase superfamily protein | chr3:21101457-21103293 REVERSE LENGTH=1410
AT3G57040	UUUUGCUUAGACUUAGAAACU	179	4.5 Cleavage	| Symbols: ARR9, ATRR4 | response regulator 9 | chr3:21109614-21111432 FORWARD LENGTH=1354
AT3G57170	UUUAUUCACACAGUGGACUGUG	118	5 Translation	| Symbols: | N-acetylglucosaminyl transferase component family protein / Gpi1 family protein | chr3:21159407-21163184 REVERSE LENGTH=2405
AT3G57200	UGAGAACGCUCUGCCAUUGGA	158	4 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41451.1); Has 94 Blast hits to 94 proteins in 31 species: Archae - 0; Bacteria - 12; Metazoa - 0; Fungi - 0; Plants - 77; Viruses - 0; Other Eukary
AT3G57240	UGACGUCGAGUAUGAGCCUGA	416	4.5 Cleavage	| Symbols: BG3 | beta-1,3-glucanase 3 | chr3:21181742-21183075 REVERSE LENGTH=1230
AT3G57330	UCCACCGACUGAUGACAAUGU	1524	4.5 Cleavage	| Symbols: ACA11 | autoinhibited Ca2+-ATPase 11 | chr3:21211456-21216375 REVERSE LENGTH=3277
AT3G57390	UAGAAUUAUCAUGUCUUGGCA	194	4 Cleavage	| Symbols: AGL18 | AGAMOUS-like 18 | chr3:21233701-21235911 FORWARD LENGTH=1156
AT3G57400	UACAGGAAGUGGGCGCACACC	102	4.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: N-terminal protein myristoylation; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G
AT3G57480	UAUGCUUCUGUUGAUCCACCU	344	2.5 Translation	| Symbols: | zinc finger (C2H2 type, AN1-like) family protein | chr3:21277936-21279354 REVERSE LENGTH=1132
AT3G57550	UUCGAGGAGAUAUGACGCGCC	4887	5 Cleavage	| Symbols: AGK2, GK-2 | guanylate kinase | chr3:21306723-21309464 FORWARD LENGTH=1774
AT3G57720	UGUGGAUACAAGAGCUGGGCU	215	4.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr3:21387722-21389726 FORWARD LENGTH=2005
AT3G57880	UCCCGGAAUGCUGAAGAAGUA	113	3.5 Translation	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) plant phosphoribosyltransferase family protein | chr3:21430983-21434600 REVERSE LENGTH=2960
AT3G57960	UCGAGUGACUUUGGAGCCAUU	244	2 Cleavage	| Symbols: | Emsy N Terminus (ENT) domain-containing protein | chr3:21463091-21464194 FORWARD LENGTH=672
AT3G58040	UUCGAGGAGAUAUGACGCGCC	4887	4.5 Translation	| Symbols: SINAT2 | seven in absentia of Arabidopsis 2 | chr3:21488516-21491488 FORWARD LENGTH=1601
AT3G58050	AUUUGAACUCAUGGAUACCCU	768	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G41960.1); Has 13384 Blast hits to 8116 proteins in 546 species: Archae - 41; Bacteria - 766; Metazoa - 5596; Fungi - 1431; Plants - 589; Viruse
AT3G58140	UCACCUCGCAUCUUAGAACUG	146	4 Translation	| Symbols: | phenylalanyl-tRNA synthetase class IIc family protein | chr3:21529731-21532572 REVERSE LENGTH=1733
AT3G58160	UCUGUAUGCAUAACUUGGGACU	686	4 Cleavage	| Symbols: XIJ, ATXIJ, ATMYOS3, MYA3, XI-16 | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr3:21534797-21541877 FORWARD LENGTH=3729
AT3G58190	UUGGGAGAACUAUGACACGAG	515	4 Cleavage	| Symbols: LBD29, ASL16 | lateral organ boundaries-domain 29 | chr3:21548484-21549558 REVERSE LENGTH=959
AT3G58250	CAAAUCCUUCAACUCUUCCCU	197	0 Cleavage	| Symbols: | TRAF-like family protein | chr3:21570745-21572143 REVERSE LENGTH=954
AT3G58260	UUAGACCUUGCAGAGUUGAGCGCC	104	3.5 Cleavage	| Symbols: | TRAF-like family protein | chr3:21573754-21575369 REVERSE LENGTH=1221
AT3G58270	UCGAGGGCAGGAACAUUGACU	334	2.5 Cleavage	| Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) with TRAF-like domain | chr3:21575887-21577830 REVERSE LENGTH=1223
AT3G58550	CUUGGCAUCGAAUUUGAACUC	1059	3 Cleavage	| Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr3:21649364-21650287 REVERSE LENGTH=730
AT3G58610	UGAGCCGACAAGAGUAGUAUC	111	3 Cleavage	| Symbols: | ketol-acid reductoisomerase | chr3:21671433-21675090 FORWARD LENGTH=2133
AT3G58680	UAAAACUGAACCAUGCCUAGA	302	4 Cleavage	| Symbols: MBF1B, ATMBF1B | multiprotein bridging factor 1B | chr3:21707276-21708911 FORWARD LENGTH=806
AT3G58800	UUACCCGUACGUCGCUUAUAAG	267	4.5 Translation	| Symbols: | unknown protein; Has 75 Blast hits to 75 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 53; Viruses - 17; Other Eukaryotes - 5 (source: NCBI BLink). | chr3:21748228-21749928 FORWARD LENGTH=1515
AT3G58980	UAUGCUUCUGUUGAUCCACCU	344	3.5 Translation	| Symbols: | F-box family protein | chr3:21794445-21797006 REVERSE LENGTH=1785
AT3G59040	UUUAGGAUUGUUGCAUAUGCA	1164	3 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:21821349-21824348 REVERSE LENGTH=2013
AT3G59050	UGUUACGAGACUCUAGCCCAG	574	3.5 Cleavage	| Symbols: ATPAO3, PAO3 | polyamine oxidase 3 | chr3:21824696-21827509 REVERSE LENGTH=2039
AT3G59052	UGUUACGAGACUCUAGCCCAG	574	3.5 Cleavage	| Symbols: CPuORF18 | conserved peptide upstream open reading frame 18 | chr3:21824696-21827509 REVERSE LENGTH=2039
AT3G59090	UCACUCGACCACAACAGGCUG	106	3.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1084 (InterPro:IPR009457); BEST Arabidopsis thaliana protein match is: tobamovirus multiplication 1 (TAIR:AT4G21790.1); Has 198 Blast hits to 197 proteins in 29 spec
AT3G59130	UUCUGAUUGCAUGUGGUGUACC	110	3.5 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr3:21860986-21862807 REVERSE LENGTH=1323
AT3G59140	UGUGAGUGUUUGUGAGGUCUU	178	3.5 Cleavage	| Symbols: ATMRP14, MRP14, ABCC10 | multidrug resistance-associated protein 14 | chr3:21863420-21868701 REVERSE LENGTH=4461
AT3G59570	UGCCUAGAUUGCUCUACUCGA	125	4 Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr3:22000832-22006056 REVERSE LENGTH=2631
AT3G59690	CAAGAACCCGCACGACACUCG	169	3 Translation	| Symbols: IQD13 | IQ-domain 13 | chr3:22048754-22051673 FORWARD LENGTH=2006
AT3G59740	UGUGGUCGAGUAGAGCAAUCU	111	3 Cleavage	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr3:22066987-22069058 REVERSE LENGTH=2072
AT3G59890	UCUAGUCCGAAAAAUGCGAAC	163	4 Cleavage	| Symbols: | Dihydrodipicolinate reductase, bacterial/plant | chr3:22124242-22126630 REVERSE LENGTH=1444
AT3G59910	UAACUCUACCCUUUGCACUCG	727	2.5 Translation	| Symbols: | Ankyrin repeat family protein | chr3:22130483-22133583 REVERSE LENGTH=2480
AT3G59920	UACCGGAGGACGUACAUAGCU	401	4.5 Cleavage	| Symbols: ATGDI2, GDI2 | RAB GDP dissociation inhibitor 2 | chr3:22134999-22138457 FORWARD LENGTH=1729
AT3G60030	UACUGGAGGACGUACAGCACU	949	5 Cleavage	| Symbols: SPL12 | squamosa promoter-binding protein-like 12 | chr3:22165654-22169572 REVERSE LENGTH=3148
AT3G60080	UGGCGCUCAACUCUGCAAGGU	10625	4.5 Translation	| Symbols: | RING/U-box superfamily protein | chr3:22187308-22188795 FORWARD LENGTH=1488
AT3G60100	UGACGGAAGCUACAGAGGAUG	108	4 Cleavage	| Symbols: CSY5 | citrate synthase 5 | chr3:22192730-22196447 FORWARD LENGTH=1754
AT3G60270	UGACGCCAAUUCUGAAAGUUU	154	4 Cleavage	| Symbols: | Cupredoxin superfamily protein | chr3:22278029-22278762 REVERSE LENGTH=564
AT3G60280	UGACGCCAAUUCUGAAAGUUU	154	4 Cleavage	| Symbols: UCC3 | uclacyanin 3 | chr3:22279664-22280675 REVERSE LENGTH=914
AT3G60286	UCUUGUCUUGAAACUUGCACC	171	2 Translation	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr3:22281741-2282824
AT3G60380	UGCAUAACUUGGGACUUACCU	413	5 Translation	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thali
AT3G60420	UGACGGUUCAGAUUCAGGAGC	107	4.5 Cleavage	| Symbols: | Phosphoglycerate mutase family protein | chr3:22334424-22335787 FORWARD LENGTH=912
AT3G60470	UUAAUCCAAGUAGCUGACUCU	2805	3 Translation	| Symbols: | Plant protein of unknown function (DUF247) | chr3:22344813-22347121 FORWARD LENGTH=1860
AT3G60550	UUCAGGGUGAGAACAUUGACU	1291	3.5 Translation	| Symbols: CYCP3;2 | cyclin p3;2 | chr3:22379805-22380641 FORWARD LENGTH=734
AT3G60740	UCGAGCACCUACGUCACUGCG	100	4.5 Cleavage	| Symbols: TTN1, EMB133, TFC D, CHO | ARM repeat superfamily protein | chr3:22447245-22453364 REVERSE LENGTH=3944
AT3G60770	UGAAGGACAAGAUCAGCUGCU	415	3.5 Translation	| Symbols: | Ribosomal protein S13/S15 | chr3:22460189-22461779 REVERSE LENGTH=915
AT3G60790	UAUGCUUCUGUUGAUCCACCU	344	3.5 Cleavage	| Symbols: | F-box family protein | chr3:22464623-22466948 FORWARD LENGTH=1467
AT3G60880	UAGAGUUAAGUUGGGACAGGA	199	3.5 Cleavage	| Symbols: DHDPS, DHDPS1 | dihydrodipicolinate synthase 1 | chr3:22494864-22496697 FORWARD LENGTH=1472
AT3G60955	UAUGGAGAUGAUCGCAAUGGC	937	4.5 Cleavage	| Symbols: CYP76C8P | a cytochrome P450 pseudogene. overlaps with a real gene on the other strand. | chr3:22529643-22532476 REVERSE LENGTH=2834
AT3G61020	UCUGGGUAGAUGGGAUCUUAUC	123	4 Cleavage	| Symbols: | pseudogene, similar to P0034A04.28, several hypothetical proteins - Arabidopsis thaliana; blastp match of 43% identity and 2.2e-46 P-value to GP|29837187|dbj|BAC75569.1||AP004333 P0034A04.28 {Oryza sativa (japonica cultivar
AT3G61060	UAUGAGUUGAUCGACGAAGAU	123	4.5 Cleavage	| Symbols: AtPP2-A13, PP2-A13 | phloem protein 2-A13 | chr3:22602910-22604578 FORWARD LENGTH=1374
AT3G61130	UUACGAGACUCUAGCCCAGCU	3733	4 Cleavage	| Symbols: GAUT1, LGT1 | galacturonosyltransferase 1 | chr3:22621969-22625716 FORWARD LENGTH=2569
AT3G61250	ACAAAACUGUUGAACAAGCCU	1107	4.5 Cleavage	| Symbols: AtMYB17, MYB17 | myb domain protein 17 | chr3:22671002-22672738 FORWARD LENGTH=1391
AT3G61360	AUUUGAACUCAUGGAUACCCU	768	5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr3:22704304-22706138 REVERSE LENGTH=1835
AT3G61420	UUUCCGUUGGUGUGCGCCCAC	458	3.5 Cleavage	| Symbols: | BSD domain (BTF2-like transcription factors, Synapse-associated proteins and DOS2-like proteins) | chr3:22727040-22731954 REVERSE LENGTH=2129
AT3G61580	UUUGAUUCACCGGAUAAACUC	175	3.5 Cleavage	| Symbols: | Fatty acid/sphingolipid desaturase | chr3:22786047-22787972 FORWARD LENGTH=1926
AT3G61670	UGCAUAACUUGGGACUUACCU	413	4 Cleavage	| Symbols: | Protein of unknown function (DUF3133) | chr3:22818589-22822020 FORWARD LENGTH=2873
AT3G61740	UACCCGUACGUCGCCUACAAG	192	4.5 Cleavage	| Symbols: SDG14, ATX3 | SET domain protein 14 | chr3:22850837-22856972 REVERSE LENGTH=3669
AT3G61980	UCGAGCACCUACGUCACUGCG	100	5 Translation	| Symbols: | serine protease inhibitor, Kazal-type family protein | chr3:22956139-22956883 REVERSE LENGTH=745
AT3G61990	UUGUGGAAUCCGUAGUCUGUA	152	4 Cleavage	| Symbols: OMTF3 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr3:22957054-22958995 REVERSE LENGTH=1222
AT3G62070	CAUCAAGAACCGGUCAUGCCU	125	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G46940.1); Has 137 Blast hits to 135 proteins in 12 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 137; Viruses - 0; Other Euka
AT3G62080	UAAUGACCGAGUAGUACCACC	149	4.5 Cleavage	| Symbols: | SNF7 family protein | chr3:22986174-22988777 FORWARD LENGTH=1666
AT3G62110	UGAGGUCGAGUAGAGCAAUCUA	117	3.5 Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr3:22997031-23000041 REVERSE LENGTH=2142

AT3G62130	UUCUGAAGGACAAGAUCAGCU	351	2.5	Cleavage	| Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr3:23004931-23007006 FORWARD LENGTH=1863
AT3G62360	UAACUCUACCCUUUGCACUCG	727	4.5	Cleavage	| Symbols: | Carbohydrate-binding-like fold | chr3:23072786-23080563 REVERSE LENGTH=4026
AT3G62590	UAACAAGAACUCUUUCUUUUCU	235	3	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr3:23147918-23150352 REVERSE LENGTH=2188
AT3G62600	CUCACAAGUGAUAUAGGGCUUG	110	4.5	Cleavage	| Symbols: ATERDJ3B, ERDJ3B | DNAJ heat shock family protein | chr3:23150790-23153510 REVERSE LENGTH=1453
AT3G62610	UGAGAAGAGAUAGAAUAGAAUC	103	2.5	Cleavage	| Symbols: ATMYB11, PFG2, MYB11 | myb domain protein 11 | chr3:23154758-23156585 FORWARD LENGTH=1246
AT3G62640	UACAAAUUCGAGCACUCCCUG	156	5	Translation	| Symbols: | Protein of unknown function (DUF3511) | chr3:23166289-23166900 REVERSE LENGTH=612
AT3G62700	UAUCCUGAGAGCGGUGCUGGC	334	4	Cleavage	| Symbols: ATMRP10, MRP10, ABCC14 | multidrug resistance-associated protein 10 | chr3:23190267-23195762 REVERSE LENGTH=4816
AT3G62780	UUCUGACGGACAAGAUAAGCU	313	4	Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr3:23221845-23222995 REVERSE LENGTH=1151
AT3G62840	UCUAGUUCACAUUUUUCGGAC	427	5	Cleavage	| Symbols: | Small nuclear ribonucleoprotein family protein | chr3:23235490-23236816 REVERSE LENGTH=684
AT3G62890	CUCACAAGUGAUAUAGGGCUUG	110	4.5	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr3:23246157-23248063 FORWARD LENGTH=1823
AT3G63070	UUUGUUAAACUCAUGGUCACCC	165	3	Translation	| Symbols: | Tudor/PWWP/MBT domain-containing protein | chr3:23302365-23309658 FORWARD LENGTH=4429
AT3G63130	AUUGACGUCGAGUAUGAGCCU	2734	5	Cleavage	| Symbols: RANGAP1, ATRANGAP1 | RAN GTPase activating protein 1 | chr3:23324621-23326913 FORWARD LENGTH=2040
AT3G63180	UGUGGUGUACCUCUUACGUCU	106	4	Cleavage	| Symbols: ATTKL, TKL | TIC-like | chr3:23336092-23340236 REVERSE LENGTH=3238
AT3G63290	UGAGACACAACAGGGAGAAUC	244	3.5	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr3:23381645-23383434 FORWARD LENGTH=1655
AT3G63380	UAGAAUUAUCAUGUCUUGGCA	194	3	Translation	| Symbols: | ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein | chr3:23406611-23410360 REVERSE LENGTH=3750
AT3G63400	AUAGCUAACAAGAACUCUUUCU	426	2.5	Translation	| Symbols: | Cyclophilin-like peptidyl-prolyl cis-trans isomerase family protein | chr3:23412024-23415659 FORWARD LENGTH=1535
AT3G63430	UUUGAUCCGAGGAUGAUGGAU	816	2.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G74160.1); Has 135 Blast hits to 119 proteins in 22 species: Archae - 0; Bacteria - 2; Metazoa - 3; Fungi - 3; Plants - 119; Viruses - 0; Other Euka
AT3G63440	UAUAGGGCUUGAAAGAAAGUC	535	2	Cleavage	| Symbols: ATCKX6, CKX6, ATCKX7 | cytokinin oxidase/dehydrogenase 6 | chr3:23424157-23426536 FORWARD LENGTH=2007
AT3G63520	UUUAGGAUUGUUGCAUAUGCA	1164	3	Cleavage	| Symbols: CCD1, ATCCD1, ATNCED1, NCED1 | carotenoid cleavage dioxygenase 1 | chr3:23452911-23456078 FORWARD LENGTH=1828
AT4G00110	UGUGGAUACAAGAGCUGGGCU	215	3.5	Translation	| Symbols: GAE3 | UDP-D-glucuronate 4-epimerase 3 | chr4:38504-40189 REVERSE LENGTH=1686
AT4G00225	UUUGUAUGCAUAACUUGGGAC	135	3	Cleavage	| Symbols: | pseudogene, similar to sucrose transporter SUC1, blastp match of 53% identity and 2.0e-09 P-value to GP|28371870|gb|AAO38059.1||AY190281 sucrose transporter SUC1 {Brassica napus} | chr4:92644-93147 REVERSE LENGTH=50
AT4G00236	CUACAAAUUCGAGCACUCCCU	156	3.5	Cleavage	| Symbols: | pseudogene, similar to leaf senescence-associated receptor-like protein kinase, blastp match of 56% identity and 4.7e-52 P-value to GP|9837280|gb|AAG00510.1||AF285172 leaf senescence-associated receptor-like protein kinase {
AT4G00238	UAGGCCUGAGAUUGGACGCCU	875	4.5	Cleavage	| Symbols: | DNA-binding storekeeper protein-related transcriptional regulator | chr4:103823-105217 REVERSE LENGTH=1395
AT4G00300	UUCACAUGUCCGGGCUAGGCA	461	4	Cleavage	| Symbols: | fringe-related protein | chr4:126509-130331 FORWARD LENGTH=2563
AT4G00355	UACUUCCAGCGUUCUGUAGCC	826	4.5	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G45980.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Vi
AT4G00416	UACUUCCAGCGUUCUGUAGCC	826	3	Cleavage	| Symbols: MBD3 | methyl-CPG-binding domain 3 | chr4:179022-179513 FORWARD LENGTH=492
AT4G00752	UUCAGGGUGAGAACAUUGACU	1291	3	Cleavage	| Symbols: | UBX domain-containing protein | chr4:317564-320895 REVERSE LENGTH=1719
AT4G00753	UUCAGGGUGAGAACAUUGACU	1291	3	Cleavage	| Symbols: | Pseudogene of AT5G37890; seven in absentia (SINA) protein, putative | chr4:322364-323033 FORWARD LENGTH=670
AT4G00760	UUCUAGUUCGCGUUCUUCAGAC	122	4	Translation	| Symbols: APRR8, PRR8 | pseudo-response regulator 8 | chr4:327025-333477 REVERSE LENGTH=3285
AT4G00970	CUCAGGCUCAUACUCGACGUC	968	3	Cleavage	| Symbols: CRK41 | cysteine-rich RLK (RECEPTOR-like protein kinase) 41 | chr4:418437-421694 FORWARD LENGTH=1998
AT4G00980	UUGUGGAAUCCGUAGUCUGUA	152	4	Cleavage	| Symbols: | zinc knuckle (CCHC-type) family protein | chr4:422478-424588 REVERSE LENGTH=1729
AT4G01170	UCUCAUGUAGUUCUAGUUCGCA	1437	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G07730.1); Has 211 Blast hits to 211 proteins in 60 species: Archae - 0; Bacteria - 22; Metazoa - 50; Fungi - 11; Plants - 77; Viruses - 0; Other Eu
AT4G01200	CCGAUUCUGAUUGCAUGUGGU	186	5	Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:506511-507626 REVERSE LENGTH=1116
AT4G01330	AAACACUCUAGACUCGAUCCU	123	3.5	Translation	| Symbols: | Protein kinase superfamily protein | chr4:550420-552941 FORWARD LENGTH=1837
AT4G01550	UACUGGAGGACGUACAGCACU	949	4.5	Cleavage	| Symbols: anac069, NAC069 | NAC domain containing protein 69 | chr4:673862-676411 REVERSE LENGTH=1723
AT4G01750	UCGAGGGCAGGAACAUUGACU	334	3	Translation	| Symbols: RGXT2 | rhamnogalacturonan xylosyltransferase 2 | chr4:756363-758590 FORWARD LENGTH=1501
AT4G02050	UAUUGACGUCGAGUAUGAGCC	237	4.5	Cleavage	| Symbols: STP7 | sugar transporter protein 7 | chr4:898307-900870 REVERSE LENGTH=1819
AT4G02180	UCCACCGACUGAUGACAAUGU	1524	4.5	Cleavage	| Symbols: | DC1 domain-containing protein | chr4:959964-963517 FORWARD LENGTH=2970
AT4G02195	UGACGGACAAGAUAAGUUGCU	1505	4.5	Cleavage	| Symbols: SYP42, TLG2B, ATSYP42, ATTLG2B | syntaxin of plants 42 | chr4:970007-972307 REVERSE LENGTH=1179
AT4G02200	UUUGGUUCUGAGUCCCCGCCU	669	3.5	Cleavage	| Symbols: | Drought-responsive family protein | chr4:972707-974692 FORWARD LENGTH=1053
AT4G02220	AACAAAACUGUUGAACAAGCCU	111	3.5	Translation	| Symbols: | zinc finger (MYND type) family protein / programmed cell death 2 C-terminal domain-containing protein | chr4:976278-979163 FORWARD LENGTH=1713
AT4G02410	UACACUCACUUGAUCUAGGAG	223	4.5	Cleavage	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr4:1059889-1062153 REVERSE LENGTH=2265
AT4G02430	UAUCUCUGUCGUUACGAACCU	295	3.5	Cleavage	| Symbols: SR34b, At-SR34b | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:1068974-1072183 FORWARD LENGTH=1513
AT4G02570	UUUGAGCACUCCUUGACCCGA	154	4	Cleavage	| Symbols: CUL1 | cullin 1 | chr4:1128515-1133774 FORWARD LENGTH=2793
AT4G02660	UGGCGCUCAACUCUGCAAGGU	10625	3.5	Translation	| Symbols: | Beige/BEACH domain ;WD domain, G-beta repeat protein | chr4:1159667-1174321 REVERSE LENGTH=11374
AT4G02930	UCUCAUGUAGUUCUAGUUCGCA	1437	3.5	Cleavage	| Symbols: | GTP binding Elongation factor Tu family protein | chr4:1295409-1298404 REVERSE LENGTH=1757
AT4G03030	UCCUAUCCAGUCUGAAGAACGC	272	4.5	Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:1335729-1337368 REVERSE LENGTH=1640
AT4G03270	UGAGACACAACAGGGAGAAUC	244	3.5	Translation	| Symbols: CYCD6;1 | Cyclin D6;1 | chr4:1432375-1433691 REVERSE LENGTH=909
AT4G03298	UAUCUCUGUCGUUACGAACCU	295	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 7 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0;
AT4G03330	CAACGCUCUUGAUACAUCUAG	133	4	Cleavage	| Symbols: SYP123, ATSYP123 | syntaxin of plants 123 | chr4:1466336-1467750 FORWARD LENGTH=1252
AT4G03400	UGAAAUAAAACUGAACCAUGCC	263	3	Cleavage	| Symbols: DFL2, GH3-10 | Auxin-responsive GH3 family protein | chr4:1497536-1499865 REVERSE LENGTH=2051
AT4G03510	UGACGGACAAGAUAAGUUGCU	1505	3.5	Cleavage	| Symbols: RMA1, ATRMA1 | RING membrane-anchor 1 | chr4:1557120-1559428 REVERSE LENGTH=1632
AT4G03550	UUUUGAGAGCCUUGUAGUAGU	118	2.5	Cleavage	| Symbols: ATGSL05, GSL05, ATGSL5, PMR4, GSL5 | glucan synthase-like 5 | chr4:1573348-1579696 FORWARD LENGTH=5835
AT4G03695	UACCCGUACGUCGCCUACAAG	192	4	Cleavage	| Symbols: | pseudogene, hypothetical protein | chr4:1637775-1638582 REVERSE LENGTH=808
AT4G03820	UGACACCGAUUCUGAUUGCAU	377	4	Cleavage	| Symbols: | Protein of unknown function (DUF3537) | chr4:1771863-1774421 REVERSE LENGTH=1606
AT4G04250	UUUGAACUCAUGGAUACCCUA	227	4	Translation	| Symbols: | pseudogene, hypothetical protein, contains Pfam profile: PF04642 protein of unknown function, DUF601 | chr4:2045957-2048347 REVERSE LENGTH=2391
AT4G04404	UCGAGCACCUACGUCACUCGCG	100	5	Translation	| Symbols: | C2H2 and C2HC zinc fingers superfamily protein | chr4:2166973-2167980 FORWARD LENGTH=693
AT4G04570	UGACGGACAAGAUAAGUUGCU	1505	4	Cleavage	| Symbols: CRK40 | cysteine-rich RLK (RECEPTOR-like protein kinase) 40 | chr4:2289959-2292391 FORWARD LENGTH=1938
AT4G04650	CUCACAAGUGAUAUAGGGCUU	208	3	Cleavage	| Symbols: | RNA-directed DNA polymerase (reverse transcriptase)-related family protein | chr4:2353989-2355213 REVERSE LENGTH=999
AT4G04660	UGAAUGACAAACUGGACAAGCU	583	3.5	Cleavage	| Symbols: | pseudogene, hypothetical protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277 | chr4:2365562-2366755 FORWARD LENGTH=1194
AT4G04700	UUCUUCAGACUGGAUAGGACU	265	3	Translation	| Symbols: CPK27 | calcium-dependent protein kinase 27 | chr4:2385276-2387986 REVERSE LENGTH=1458
AT4G04745	UUUAGGAUUGUUGCAUAUGCA	1164	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21902.1); Has 32 Blast hits to 32 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 32; Viruses - 0; Other Eukaryot
AT4G04800	UGUCACCGUAGAUUUCUUCCU	123	4.5	Cleavage	| Symbols: ATMSRB3, MSRB3 | methionine sulfoxide reductase B3 | chr4:2439546-2441205 FORWARD LENGTH=827
AT4G05018	UAUCUCUGUCGUUACGAACCU	295	3	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G21500.1); H
AT4G05040	UGUUACGAGACUCUAGCCCAG	574	4.5	Cleavage	| Symbols: | ankyrin repeat family protein | chr4:2578646-2581798 FORWARD LENGTH=1913
AT4G05090	UUGAGAGAUCCCCUGUUACUG	3917	3.5	Cleavage	| Symbols: | Inositol monophosphatase family protein | chr4:2609142-2611762 FORWARD LENGTH=1431
AT4G05160	UUGAACAAGCCUGAUGAAGUU	102	3	Translation	| Symbols: | AMP-dependent synthetase and ligase family protein | chr4:2664385-2666707 FORWARD LENGTH=1861
AT4G05320	CAACGCUCUUGAUACAUCUAG	133	3	Cleavage	| Symbols: UBQ10 | polyubiquitin 10 | chr4:2718170-2720308 FORWARD LENGTH=1835
AT4G05330	UCUAGUUCGCGUUCUUCAGAC	300	3.5	Translation	| Symbols: AGD13 | ARF-GAP domain 13 | chr4:2720561-2723125 REVERSE LENGTH=1322
AT4G05360	UCAACACUCUGAUACAUCUAG	143	3.5	Cleavage	| Symbols: | Zinc knuckle (CCHC-type) family protein | chr4:2728204-2732337 FORWARD LENGTH=2208
AT4G05420	AUUUCAGUGAGCACGUACCUC	200	3.5	Translation	| Symbols: DDB1A | damaged DNA binding protein 1A | chr4:2746122-2752896 FORWARD LENGTH=3603
AT4G05500	ACAAAACUGUUGAACAAGCCU	1107	3.5	Cleavage	| Symbols: | pseudogene, F-box protein family, AtFBL9/AtFBL23, contains similarity to N7 protein GI:3273101 from (Medicago truncatula); blastp match of 39% identity and 1.6e-34 P-value to GP|3273101|emb|CAA76808.1||Y17613 N7 protein
AT4G05540	UUGAGAGCACUCCACCGACUG	261	4.5	Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:2818776-2821065 REVERSE LENGTH=2070
AT4G06534	UAUGGCCUGGGAGCAAUCGCA	299	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 22 Blast hits to 22 proteins in 8 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fur
AT4G07320	UCUAGUUCGCAUUUUUUGGAC	421	3.5	Cleavage	| Symbols: | pseudogene, hypothetical protein | chr4:4115732-4119835 REVERSE LENGTH=4104
AT4G07868	UUGGACGCCUCUACUAUGAGA	679	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; M
AT4G07960	CUCGGGAGAAAGAAGAAGGCU	259	3	Cleavage	| Symbols: ATCSLC12, CSLC12 | Cellulose-synthase-like C12 | chr4:4802341-4805647 REVERSE LENGTH=2622
AT4G07990	CCUGAGCCUAGUGACCGAGUA	270	4.5	Translation	| Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:4825409-4829136 REVERSE LENGTH=1133
AT4G08210	UUUGAGAGAUCCCCUGUUACUG	632	3.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr4:5183813-5185873 REVERSE LENGTH=2061
AT4G08310	UGAAGGAUUUGUGGUUAACCA	474	2.5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro D
AT4G08500	UCGACCACACUGUUAGGAUCU	121	5	Cleavage	| Symbols: MEKK1, ATMEKK1, MAPKKK8, ARAKIN | MAPK/ERK kinase kinase 1 | chr4:5403753-5407301 REVERSE LENGTH=2490
AT4G08580	UUUAAAACCGAGGACUUUUGC	115	3.5	Translation	| Symbols: | microfibrillar-associated protein-related | chr4:5461483-5463907 FORWARD LENGTH=1595
AT4G08645	UGACGCCAAUUCUGAAAGUUU	154	3	Translation	| Symbols: | pseudogene, hypothetical protein | chr4:5514498-5515676 REVERSE LENGTH=1179
AT4G08810	AUACCCAAACCUGAACUUUCU	127	4.5	Cleavage	| Symbols: SUB1 | calcium ion binding | chr4:5616052-5617939 REVERSE LENGTH=1888
AT4G09040	CUUCCCCUAGAAUCUUUCCC	401	3.5	Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:5794530-5797375 REVERSE LENGTH=1384
AT4G09200	CUUCGAGGAGAUAUGACGCGCC	513	5	Cleavage	| Symbols: | SPla/RYanodine receptor (SPRY) domain-containing protein | chr4:5859257-5861803 FORWARD LENGTH=1449
AT4G09220	AAAGUCAAGAACCCCAACCCU	201	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G09270.1); Has 85 Blast hits to 85 proteins in 21 species: Archae - 0; Bacteria - 5; Metazoa - 52; Fungi - 7; Plants - 14; Viruses - 0; Other Eukary
AT4G09250	CUUCGAGGAGAUAUGACGCGCC	513	5	Cleavage	| Symbols: | SPla/RYanodine receptor (SPRY) domain-containing protein | chr4:5876578-5878978 FORWARD LENGTH=1159
AT4G09310	CUUCGAGGAGAUAUGACGCGCC	513	5	Cleavage	| Symbols: | SPla/RYanodine receptor (SPRY) domain-containing protein | chr4:5902826-5905372 FORWARD LENGTH=1449

AT4G09340	UACGCGACCGCGGUGCUGGCC	119	5	Cleavage	| Symbols: | SPla/RYanodine receptor (SPRY) domain-containing protein | chr4:5924602-5927635 REVERSE LENGTH=1795
AT4G09630	UAAAACUGAACCAUGCCUAGA	302	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF616) | chr4:6083713-6088134 FORWARD LENGTH=2615
AT4G09740	UGGCGCUCAACUCUGCAAGGU	10625	5	Cleavage	| Symbols: AtGH9B14, GH9B14 | glycosyl hydrolase 9B14 | chr4:6142706-6145003 REVERSE LENGTH=1437
AT4G09790	CAUCAAGAACCGGUCAUGCCU	125	3.5	Cleavage	| Symbols: | pseudogene of the F-box family protein | chr4:6163414-6164655 REVERSE LENGTH=1242
AT4G09810	UACAGAAUAGGCUUAAGUAAC	189	4	Cleavage	| Symbols: | Nucleotide-sugar transporter family protein | chr4:6175176-6177293 REVERSE LENGTH=1388
AT4G09940	UCACCAUUGGCAGCUCUGUACC	187	3.5	Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:6231786-6233397 FORWARD LENGTH=1185
AT4G10130	UAGAAUUAUCAUGUCUUGGCA	194	4.5	Cleavage	| Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr4:6320634-6321643 REVERSE LENGTH=1010
AT4G10170	UUCCCCUAGAAUUCUUUCCCU	1646	4.5	Cleavage	| Symbols: | SNARE-like superfamily protein | chr4:6344374-6345537 FORWARD LENGTH=1030
AT4G10320	CCGAUUCUGAUUGCAUGUGGU	186	5	Cleavage	| Symbols: | tRNA synthetase class I (I, L, M and V) family protein | chr4:6397330-6404596 REVERSE LENGTH=3856
AT4G10360	UACACAAAGGGCUCCUCGCACC	211	3.5	Cleavage	| Symbols: | TRAM, LAG1 and CLN8 (TLC) lipid-sensing domain containing protein | chr4:6420455-6422299 FORWARD LENGTH=1090
AT4G10457	UUCCCCUAGAAUUCUUUCCCU	1646	4.5	Cleavage	| Symbols: SCRL1 | SCR-like 1 | chr4:6466900-6467270 REVERSE LENGTH=279
AT4G10470	UCAACGAACUCUUGGCCCUAGA	152	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G33050.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT4G10570	CAAACUGGACAAGCUACUGCU	324	5	Cleavage	| Symbols: UBP9 | ubiquitin-specific protease 9 | chr4:6523255-6528173 REVERSE LENGTH=3289
AT4G10655	UACCCGUACGUCGCCUACAAG	192	5	Cleavage	| Symbols: | Encodes a defensin-like (DEFL) family protein. | chr4:6578839-6579024 FORWARD LENGTH=186
AT4G10740	UCUAUAGCCAAUGUACUCUACU	106	4	Cleavage	| Symbols: | F-box and associated interaction domains-containing protein | chr4:6617143-6618426 REVERSE LENGTH=1284
AT4G10760	CUCACAAGUGAUAUAGGGCUU	208	4	Translation	| Symbols: EMB1706, MTA | mRNAadenosine methylase | chr4:6619817-6623351 REVERSE LENGTH=2227
AT4G10920	UGAGACACAACAGGGAGAUUC	244	3.5	Cleavage	| Symbols: KELP | transcriptional coactivator p15 (PC4) family protein (KELP) | chr4:6696712-6699199 REVERSE LENGTH=1208
AT4G11000	UCGGCUCAAACCUAACACGUU	129	4	Cleavage	| Symbols: | Ankyrin repeat family protein | chr4:6731020-6732464 FORWARD LENGTH=1221
AT4G11110	UAAUAAGGAGAGUCAGCUACU	298	4	Cleavage	| Symbols: SPA2 | SPA1-related 2 | chr4:6771605-6777225 FORWARD LENGTH=3964
AT4G11150	CUUCGACUGAGGUAAGCGCCU	234	5	Cleavage	| Symbols: TUF, emb2448, TUFF, VHA-E1 | vacuolar ATP synthase subunit E1 | chr4:6799935-6801932 FORWARD LENGTH=1085
AT4G11175	UUUUGCUUAGACUUAGAAACU	179	4	Cleavage	| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr4:6818087-6819042 FORWARD LENGTH=737
AT4G11350	UAAUAAGGAGAGUCAGCUACU	298	4	Cleavage	| Symbols: | Protein of unknown function (DUF604) | chr4:6901682-6904225 FORWARD LENGTH=2464
AT4G11380	UGAAUCUUGGUCAACUGGACC	197	4	Cleavage	| Symbols: | Adaptin family protein | chr4:6920489-6925576 FORWARD LENGTH=3002
AT4G11393	UCUAGUUCGCGUUUUUCAGAC	163	3.5	Cleavage	| Symbols: | Defensin-like (DEFL) family protein | chr4:6932370-6932718 FORWARD LENGTH=237
AT4G11440	UGAAUCUUGGUCAACUGGACC	197	3.5	Cleavage	| Symbols: | Mitochondrial substrate carrier family protein | chr4:6955601-6958553 FORWARD LENGTH=2038
AT4G11500	UGAGAACGCUCUGCCAUUGGA	158	3.5	Cleavage	| Symbols: | pseudogene, similar to putative receptor-like serine-threonine protein kinase, blastp match of 59% identity and 6.5e-66 P-value to GP|18076583|emb|CAC84552.1||AJ306626 putative receptor-like serine-threonine protein kinase [
AT4G11730	UACCGGAGGACGUACAACACC	302	4.5	Cleavage	| Symbols: | Cation transporter/ E1-E2 ATPase family protein | chr4:7067035-7070968 FORWARD LENGTH=2442
AT4G11800	UUUGGUUCUGAGUCCCCGCCU	669	3.5	Cleavage	| Symbols: | Calcineurin-like metallo-phosphoesterase superfamily protein | chr4:7093542-7099697 REVERSE LENGTH=3540
AT4G11900	UUGAGAGCACUCCACCGACUG	261	4.5	Cleavage	| Symbols: | S-locus lectin protein kinase family protein | chr4:7150241-7153571 REVERSE LENGTH=2579
AT4G11940	UGCUCGUAUCAUACUCCUCCU	194	3	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G11930.1); Has 37 Blast hits to 37 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 37; Viruses - 0; Other Eukaryot
AT4G11960	UCGAGUAUGAGCCUGAGUCAUG	250	4.5	Cleavage	| Symbols: PGRL1B | PGR5-like B | chr4:7174903-7177805 REVERSE LENGTH=1433
AT4G11970	GCAAGUGAUGAUAAAAAGACA	100	4.5	Cleavage	| Symbols: | YTH family protein | chr4:7180437-7183677 FORWARD LENGTH=1871
AT4G12080	UGACGGAAGCUACAGAGGAUG	108	4	Translation	| Symbols: AHL1, ATAHL1 | AT-hook motif nuclear-localized protein 1 | chr4:7239219-7241494 FORWARD LENGTH=1566
AT4G12150	CUUUGCACUCAUGAAUCUUUC	119	3.5	Cleavage	| Symbols: | RING/U-box superfamily protein | chr4:7268837-7270267 REVERSE LENGTH=1074
AT4G12400	UCCGCUAGAUAUAUCAAACUG	281	3.5	Translation	| Symbols: Hop3 | stress-inducible protein, putative | chr4:7338659-7341361 REVERSE LENGTH=2006
AT4G12410	AUUGUGUAUAAUUUUGAGCCU	108	3.5	Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr4:7342956-7343590 REVERSE LENGTH=635
AT4G12450	UACUGGAGGACGUACAGCACU	949	5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G22560.1); Has 380 Blast hits to 380 proteins in 23 species: Archae - 0; Bacteria - 0; Metazoa - 1; Fungi - 4; Plants - 374; Viruses - 0; Other Euka
AT4G12640	UAAGCAUUUUGAUUCACCGGA	285	4	Cleavage	| Symbols: | RNA recognition motif (RRM)-containing protein | chr4:7462599-7467862 FORWARD LENGTH=2802
AT4G12700	UAUGGCCUGGGAGCAAUCGCA	299	4	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G04280.1); Has 136 Blast hits to 136 proteins in 17 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 125; Viruses - 0; Other Euka
AT4G12860	AUUUGAACUCAUGGAUACCCU	768	3.5	Cleavage	| Symbols: UNE14 | EF hand calcium-binding protein family | chr4:7538444-7538902 REVERSE LENGTH=459
AT4G12940	UCGAGUAUGAGCCUGAGUCAUG	250	4.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12930.1); H
AT4G12970	UAACUCUACCCUUUGCACUCG	727	5	Translation	| Symbols: STOMAGEN, EPFL9 | stomagen | chr4:7586143-7586849 REVERSE LENGTH=461
AT4G13262	UAUCGAGCACCUACGUCACUGU	142	3	Translation	| Symbols: | pseudogene, Phosphoribosylanthranilate transferase, similar to Phosphoribosylanthranilate transferase; blastp match of 28% identity and 1.1e-27 P-value to GP|1396054|dbj|BAA13032.1||D86180 phosphoribosylanthranilate trans
AT4G13460	UCACUUUGCUGAACAUGUACC	138	3	Cleavage	| Symbols: SDG22, SUVH9, SET22 | SU(VAR)3-9 homolog 9 | chr4:7824034-7826960 REVERSE LENGTH=2534
AT4G13570	UAGAAUUAUCAUGUCUUGGCA	194	4	Translation	| Symbols: HTA4 | histone H2A 4 | chr4:7884516-7885982 FORWARD LENGTH=759
AT4G13580	UUAUCAACGAACUCUUGGCCC	310	3.5	Cleavage	| Symbols: | Disease resistance-responsive (dirigent-like protein) family protein | chr4:7900374-7901328 FORWARD LENGTH=955
AT4G13650	UUUGAGCACUCUACAGACAGG	162	5	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:7938967-7942898 REVERSE LENGTH=3839
AT4G13820	UUCUUCGGACUGGAUAGGACU	102	4	Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr4:8007989-8010745 REVERSE LENGTH=2757
AT4G13920	UUCGGACUGGAUAGGACUAGG	101	4	Translation	| Symbols: AtRLP50, RLP50 | receptor like protein 50 | chr4:8043803-8046559 FORWARD LENGTH=2757
AT4G13930	UAGGCCUGAGAUUGGACGCCU	875	2.5	Cleavage	| Symbols: SHM4 | serine hydroxymethyltransferase 4 | chr4:8047692-8050106 REVERSE LENGTH=1822
AT4G13970	ACAAAACUGUUGAACAAGCCU	1107	4	Cleavage	| Symbols: | zinc ion binding | chr4:8070189-8075501 REVERSE LENGTH=2935
AT4G14060	UACGAGACUCUAGCCCAGCUU	307	5	Cleavage	| Symbols: | Polyketide cyclase/dehydrase and lipid transport superfamily protein | chr4:8107337-8108307 FORWARD LENGTH=673
AT4G14145	UAAAACUGAACCAUGCCUAGA	302	3.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 173
AT4G14150	CAAACUGGACAAGCUACUGCU	324	4	Cleavage	| Symbols: PAKRP1, KINESIN-12A | phragmoplast-associated kinesin-related protein 1 | chr4:8158572-8165008 REVERSE LENGTH=3952
AT4G14240	UCUUGGCAUCGAAUUUGAACUC	189	4.5	Cleavage	| Symbols: | CBS domain-containing protein with a domain of unknown function (DUF21) | chr4:8204347-8207408 REVERSE LENGTH=1985
AT4G14280	UUUAGGAUUGUUGCAUAUGCA	1164	2.5	Cleavage	| Symbols: | ARM repeat superfamily protein | chr4:8222518-8225185 FORWARD LENGTH=2508
AT4G14310	CAAAUUCGAGAACUCCCUGAC	283	3	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:8236759-8240324 REVERSE LENGTH=2977
AT4G14400	UCUAGUUCGCGUUCUUCAGAC	300	4	Cleavage	| Symbols: ACD6 | ankyrin repeat family protein | chr4:8294446-8298602 FORWARD LENGTH=2271
AT4G14430	AACAAAACUGUUGAACAAGCCU	111	4	Cleavage	| Symbols: IBR10, ATECI2, ECI2, ECHIB, PEC12 | indole-3-butyric acid response 10 | chr4:8304600-8305705 REVERSE LENGTH=1106
AT4G14740	UUGAGAGAUCCCCUGUUACUG	3917	4	Translation	| Symbols: | Plant protein of unknown function (DUF828) with plant pleckstrin homology-like region | chr4:8450292-8453085 REVERSE LENGTH=1692
AT4G14820	UGAGAUUGCUAGAGGAAAGAG	101	2.5	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:8507794-8510038 REVERSE LENGTH=2169
AT4G14900	UUUGAUUCACCGGAUAAACUC	175	3.5	Cleavage	| Symbols: | FRIGIDA-like protein | chr4:8521522-8523705 REVERSE LENGTH=1934
AT4G14970	UUCGAGGAGAUAUGACGCGCC	4887	4	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 14 plant structures; EXPRESSED DURING: 6 growth stages; Has 257 Blast hits to 16
AT4G15165	UUGACGACCAACUCCGCUCCU	170	4.5	Cleavage	| Symbols: | N-terminal nucleophile aminohydrolases (Ntn hydrolases) superfamily protein | chr4:8648832-8650382 FORWARD LENGTH=908
AT4G15210	UUUGGCACUCAACUCUGCAAG	1274	4	Cleavage	| Symbols: ATBETA-AMY, AT-BETA-AMY, RAM1 | beta-amylase 5 | chr4:8666338-8669470 REVERSE LENGTH=1890
AT4G15215	UCACCAUUGGCAGCUCUGUACC	187	4	Translation	| Symbols: PDR13, ATPDR13 | pleiotropic drug resistance 13 | chr4:8672070-8679176 FORWARD LENGTH=4475
AT4G15230	UCACCAUUGGCAGCUCUGUACC	187	3	Cleavage	| Symbols: ATPDR2, PDR2 | pleiotropic drug resistance 2 | chr4:8680182-8686880 FORWARD LENGTH=4316
AT4G15236	UCCCGGAAUGCUGAAGAAGUA	113	4	Cleavage	| Symbols: | ABC-2 and Plant PDR ABC-type transporter family protein | chr4:8696683-8702727 FORWARD LENGTH=4167
AT4G15430	AUUGACGUCGAGUAUGAGCCU	2734	4.5	Cleavage	| Symbols: | ERD (early-responsive to dehydration stress) family protein | chr4:8827876-8831504 FORWARD LENGTH=2585
AT4G15475	CAACUAACAACGAGGGCACUG	198	3.5	Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr4:8845875-8848869 FORWARD LENGTH=2053
AT4G15500	CUUAUCAACGAACUCUUGGCC	290	3.5	Cleavage	| Symbols: UGT84A4 | UDP-Glycosyltransferase superfamily protein | chr4:8856988-8858572 REVERSE LENGTH=1585
AT4G15550	UCUGUACCGCUGAAUUCUUCC	275	5	Cleavage	| Symbols: IAGLU | indole-3-acetate beta-D-glucosyltransferase | chr4:8877590-8879327 REVERSE LENGTH=1738
AT4G15730	UACGCUAGGGAGAUAUCUGCC	122	4	Cleavage	| Symbols: | CW-type Zinc Finger | chr4:8951533-8957632 REVERSE LENGTH=3952
AT4G15740	UCAUGUAGUUCUAGUUCGCCU	245	4	Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr4:8964745-8966318 REVERSE LENGTH=1574
AT4G15765	UGUGGUGUACCUCUUACGUCU	106	5	Cleavage	| Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr4:8975404-8977211 REVERSE LENGTH=1195
AT4G15810	UUUGUUAAACUCAUGGUCACCC	165	4	Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:8989162-8992591 REVERSE LENGTH=2757
AT4G15840	UGACACCGAUUCUGAUAGCUU	823	4	Cleavage	| Symbols: | BTB/POZ domain-containing protein | chr4:8996912-9001039 FORWARD LENGTH=2749
AT4G16030	UUAGCACCGAGGAUGAUGGACU	330	4.5	Cleavage	| Symbols: | Ribosomal protein L19e family protein | chr4:9083447-9084727 FORWARD LENGTH=1004
AT4G16050	UUGCAGAGAUGGAUGUACAAC	101	3.5	Translation	| Symbols: | Aminotransferase-like, plant mobile domain family protein | chr4:9092226-9094357 FORWARD LENGTH=2132
AT4G16070	UGGAUUCCGGCUGCAUACUCC	392	4	Cleavage	| Symbols: | Mono-/di-acylglycerol lipase, N-terminal;Lipase, class 3 | chr4:9096730-9100841 REVERSE LENGTH=2288
AT4G16150	UGAAGGAUUUGUGGUUAACCA	474	4	Cleavage	| Symbols: | calmodulin binding;transcription regulators | chr4:9148059-9153292 FORWARD LENGTH=3182
AT4G16155	UCACCAUUGGCAGCUCUGUACC	187	2	Translation	| Symbols: | dihydrolipoyl dehydrogenases | chr4:9153363-9157322 REVERSE LENGTH=2100
AT4G16280	AUGACGAAUGUUUGACAGCCU	113	4.5	Cleavage	| Symbols: FCA | RNA binding;abscisic acid binding | chr4:9207164-9214825 REVERSE LENGTH=4732
AT4G16350	UUCUGACGGACAAGAUAAGCU	313	3.5	Translation	| Symbols: CBL6, SCABP2 | calcineurin B-like protein 6 | chr4:9242320-9243912 REVERSE LENGTH=930
AT4G16470	UUCGGUCUGGCCAUACUCGGC	147	3.5	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:9287862-9289582 REVERSE LENGTH=1547
AT4G16563	UUCGAGAACUCCCUGACCCGA	1272	4.5	Cleavage	| Symbols: | Eukaryotic aspartyl protease family protein | chr4:9329657-9331523 REVERSE LENGTH=1867
AT4G16610	UUCCAGAACUAAUGAAUGUUA	448	3	Cleavage	| Symbols: | C2H2-like zinc finger protein | chr4:9354321-9355287 REVERSE LENGTH=967
AT4G16620	UGUCCCAACUUAACUCUACCCU	279	4.5	Cleavage	| Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr4:9358117-9360060 REVERSE LENGTH=1337
AT4G16807	UUUGUAUGCAUAACUUGGGAC	135	3	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G3352

AT4G16860	UUGAAAGACUUGUGGAUCACC	926	4	Cleavage	| Symbols: RPP4 | Disease resistance protein (TIR-NBS-LRR class) family | chr4:9488466-9495816 REVERSE LENGTH=3678
AT4G16900	UUGGCCUGAGGUUGGACGCCU	272	4	Translation	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:9511859-9516541 REVERSE LENGTH=3517
AT4G16940	UUAAUCCAAGUAGCUGACUCU	2805	4	Translation	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:9533149-9537604 REVERSE LENGTH=3538
AT4G16960	UUAAUCCAAGUAGCUGACUCU	2805	4	Translation	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr4:9546343-9551007 REVERSE LENGTH=3126
AT4G17140	UGUGGUGUACCUCUUACGUCU	106	3.5	Translation	| Symbols: | pleckstrin homology (PH) domain-containing protein | chr4:9613330-9636873 REVERSE LENGTH=13193
AT4G17250	UUUAUUCACACAGUGGACUGUG	118	4.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: heat acclimation; LOCATED IN: cellular_component unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsi
AT4G17260	AUGGAUUUAGAUCACUUGCGUC	196	4.5	Cleavage	| Symbols: | Lactate/malate dehydrogenase family protein | chr4:9673991-9675448 FORWARD LENGTH=1267
AT4G17270	UUCUGACGGACAAGAUAAGCU	313	3.5	Cleavage	| Symbols: | Mo25 family protein | chr4:9676127-9678777 FORWARD LENGTH=1520
AT4G17483	UUUAACAACUAAGGUUCCUGU	1055	4	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr4:9747344-9748892 REVERSE LENGTH=934
AT4G17610	UUCACAUGUCCGGGCUAGGCA	461	2	Cleavage	| Symbols: | tRNA/rRNA methyltransferase (SpoU) family protein | chr4:9805513-9814910 REVERSE LENGTH=5692
AT4G17616	CUUGGCAUCGAAUUUGAACUC	1059	5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:9819498-9821684 FORWARD LENGTH=2187
AT4G18100	ACAAAACUGUUGAACAAGCCU	1107	4.5	Cleavage	| Symbols: | Ribosomal protein L32e | chr4:10035485-10036541 REVERSE LENGTH=698
AT4G18120	UUGAUCCAAGUAGCUGACUCU	4031	4	Cleavage	| Symbols: AML3, ML3 | MEI2-like 3 | chr4:10038415-10042248 FORWARD LENGTH=2575
AT4G18340	CUUGUGAGUGUUUGUGAGGUC	103	3	Cleavage	| Symbols: | Glycosyl hydrolase superfamily protein | chr4:10130050-10132061 REVERSE LENGTH=1431
AT4G18370	UACCGGAGGACGUACAACACC	302	4	Cleavage	| Symbols: DEG5, DEGP5, HHOA | DEGP protease 5 | chr4:10149129-10151218 FORWARD LENGTH=1245
AT4G18470	UUAGGCCUGAGAUUGGACGCC	196	4	Cleavage	| Symbols: SNI1 | negative regulator of systemic acquired resistance (SNI1) | chr4:10192909-10195662 FORWARD LENGTH=1525
AT4G18490	UCUAGUUCGCAUUUUUUGGAC	421	3	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: shoot, shoot apex, embryo, flower, seed; EXPRESSED DURING: |
AT4G18530	UCGACCACACUGUCAUGAUCU	174	4	Cleavage	| Symbols: | Protein of unknown function (DUF707) | chr4:10217338-10220500 FORWARD LENGTH=1796
AT4G18600	UCUUCGACUGAGGUAAGCGCCU	355	3	Cleavage	| Symbols: WAVE5, ATSCAR-LIKE, SCARL | SCAR family protein | chr4:10239881-10247372 REVERSE LENGTH=6153
AT4G18640	UGAAGGACAAGCUCAGCUGCU	1483	3.5	Translation	| Symbols: MRH1 | Leucine-rich repeat protein kinase family protein | chr4:10259678-10263764 FORWARD LENGTH=2861
AT4G18730	UCUGUAUGCAUAACUUGGGAC	1212	4.5	Translation	| Symbols: RPL16B | ribosomal protein L16B | chr4:10302163-10303382 FORWARD LENGTH=800
AT4G18750	UUAACUCUACCCUUUGCACUC	380	4.5	Cleavage	| Symbols: DOT4 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:10304850-10307570 FORWARD LENGTH=2721
AT4G18910	UUCCAGAACUAAUGAAUGUUA	448	5	Translation	| Symbols: NIP1;2, NLM2, ATNLM2 | NOD26-like intrinsic protein 1;2 | chr4:10366059-10368381 FORWARD LENGTH=1239
AT4G18980	UAUCCUGAGAGCGGUGCUGGC	334	4	Cleavage	| Symbols: AtS40-3 | AtS40-3 | chr4:10398918-10399512 FORWARD LENGTH=595
AT4G19030	UUGAGAGCACUCCACCGACUG	261	3.5	Cleavage	| Symbols: NLM1, NIP1;1, AT-NLM1, ATNLM1 | NOD26-like major intrinsic protein 1 | chr4:10421525-10423487 REVERSE LENGTH=1172
AT4G19040	UGAGAUUGCUAGAGGAAAGAG	101	3.5	Cleavage	| Symbols: EDR2 | ENHANCED DISEASE RESISTANCE 2 | chr4:10431520-10437431 REVERSE LENGTH=2696
AT4G19090	UAGGCCUGAGAUUGGACGCCU	875	4	Translation	| Symbols: | Protein of unknown function (DUF594) | chr4:10449900-10452757 FORWARD LENGTH=2256
AT4G19150	UUCAGGGUGAGAACAUUGACU	1291	3	Cleavage	| Symbols: | Ankyrin repeat family protein | chr4:10471331-10472742 REVERSE LENGTH=1044
AT4G19160	GCAAGUGAUGAUAAAAAGACA	100	3.5	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:10477306-1048012
AT4G19170	UAUCGAGCACCUACGUCACUGU	142	4.5	Translation	| Symbols: NCED4, CCD4 | nine-cis-epoxycarotenoid dioxygenase 4 | chr4:10481786-10483857 FORWARD LENGTH=2072
AT4G19210	UAUUGAUUUUUGGCCUGAGGU	116	4	Cleavage	| Symbols: ATRLI2, RLI2 | RNAse l inhibitor protein 2 | chr4:10501200-10505217 FORWARD LENGTH=2279
AT4G19220	CAACGCUCUUGAUACAUCUAG	133	3.5	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:10505266-10508121 REVERSE LENGTH=2799
AT4G19490	UUGUGAGUGUUUGUGAGGUCU	141	3.5	Cleavage	| Symbols: ATVPS54, VPS54 | VPS54 | chr4:10615796-10623521 FORWARD LENGTH=3690
AT4G19520	UUGGCCUGAGGUUGGACACCU	178	4	Translation	| Symbols: | disease resistance protein (TIR-NBS-LRR class) family | chr4:10639269-10647079 REVERSE LENGTH=5463
AT4G19530	UUAGAAUUAUCAUGUCUUGGC	138	4	Cleavage	| Symbols: | disease resistance protein (TIR-NBS-LRR class) family | chr4:10651744-10657282 FORWARD LENGTH=3914
AT4G19570	UCACCAUUGGCAGCUCUGUACC	187	4.5	Translation	| Symbols: | Chaperone DnaJ-domain superfamily protein | chr4:10665294-10667318 FORWARD LENGTH=1892
AT4G19650	UAACAAGAACUCUUUCUUUUCU	235	2.5	Cleavage	| Symbols: | Mitochondrial transcription termination factor family protein | chr4:10691674-10695701 FORWARD LENGTH=2263
AT4G19720	CAUCAAGAACCGGUCAUGCCU	125	5	Cleavage	| Symbols: | Glycosyl hydrolase family protein with chitinase insertion domain | chr4:10730363-10731750 REVERSE LENGTH=1147
AT4G19740	UCAGUAGAAUUCGAUCAUAUC	104	4	Cleavage	| Symbols: | Glycosyl hydrolase superfamily protein | chr4:10739567-10740620 REVERSE LENGTH=954
AT4G19750	UCAGUAGAAUUCGAUCAUAUC	104	4.5	Cleavage	| Symbols: | Glycosyl hydrolase family protein with chitinase insertion domain | chr4:10745682-10747127 REVERSE LENGTH=1089
AT4G19880	UACAAAUUCGAGCACUCCCUG	156	3.5	Translation	| Symbols: | Glutathione S-transferase family protein | chr4:10784391-10786439 REVERSE LENGTH=1438
AT4G19900	UUGGGAGAACUAUGACACGAG	515	3.5	Cleavage	| Symbols: | alpha 1,4-glycosyltransferase family protein | chr4:10789096-10791433 REVERSE LENGTH=1983
AT4G19950	ACAAAACUGUUGAACAAGCCU	1107	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G44860.1); Has 338 Blast hits to 330 proteins in 72 species: Archae - 2; Bacteria - 94; Metazoa - 7; Fungi - 0; Plants - 232; Viruses - 0; Other Eul
AT4G20090	UCGACCACACUGUCAUGAUCU	174	4.5	Cleavage	| Symbols: EMB1025 | Pentatricopeptide repeat (PPR) superfamily protein | chr4:10868400-10870382 REVERSE LENGTH=1983
AT4G20140	UAUAGGGCUUGAAAGAAAGUC	535	2.5	Cleavage	| Symbols: GSO1 | Leucine-rich repeat transmembrane protein kinase | chr4:10884197-10888270 FORWARD LENGTH=3998
AT4G20210	UUUCUGACGGACAAGAUAAGU	480	3.5	Cleavage	| Symbols: | Terpenoid cyclases/Protein prenyltransferases superfamily protein | chr4:10913613-10918282 REVERSE LENGTH=1803
AT4G20410	UUUGAGCACUCUACAGACAGG	162	4	Cleavage	| Symbols: GSNAP, GAMMA-SNAP | gamma-soluble NSF attachment protein | chr4:11013895-11016576 REVERSE LENGTH=1202
AT4G20430	UUCAUCUGCAGUAAGUCCCUG	314	4	Cleavage	| Symbols: | Subtilase family protein | chr4:11017629-11021272 REVERSE LENGTH=2693
AT4G20460	UCUGAACUCAAGGCACCCAAA	493	3.5	Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:11029736-11032677 REVERSE LENGTH=1685
AT4G20720	AUUCGAGAACUCCCUGACCCG	350	3.5	Cleavage	| Symbols: | dentin sialophosphoprotein-related | chr4:11105318-11108053 FORWARD LENGTH=2493
AT4G20820	UCUCAUGUAGUUCUAGUUCGCG	207	4	Translation	| Symbols: | FAD-binding Berberine family protein | chr4:11150160-11151758 FORWARD LENGTH=1599
AT4G20850	UUGGUCACACAGUGGACUGUG	104	3.5	Translation	| Symbols: TPP2 | tripeptidyl peptidase ii | chr4:11160721-11169889 REVERSE LENGTH=4357
AT4G20890	UGAAUGACAAACUGGACAAGCU	583	4	Cleavage	| Symbols: TUB9 | tubulin beta-9 chain | chr4:11182092-11184072 FORWARD LENGTH=1693
AT4G20940	CCUGAGCCUAGUGACCGAGUA	270	3.5	Translation	| Symbols: | Leucine-rich receptor-like protein kinase family protein | chr4:11202728-11206280 FORWARD LENGTH=3176
AT4G21090	UACUGGAGGACGUACAACACU	176	4.5	Translation	| Symbols: ATMFDX2, MFDX2 | MITOCHONDRIAL FERREDOXIN 2 | chr4:11256459-11258587 REVERSE LENGTH=960
AT4G21100	AUUUCAGUGAGCACGUACCUC	200	3.5	Translation	| Symbols: DDB1B | damaged DNA binding protein 1B | chr4:11258761-11265463 REVERSE LENGTH=3576
AT4G21120	CCUGAGCCUAGUGACCGAGUA	270	4	Cleavage	| Symbols: AAT1, CAT1 | amino acid transporter 1 | chr4:11270045-11273973 FORWARD LENGTH=2256
AT4G21160	UUGAGAGAUCCCUUGUUACUG	141	4.5	Cleavage	| Symbols: ZAC, AGD12 | Calcium-dependent ARF-type GTPase activating protein family | chr4:11284147-11286767 FORWARD LENGTH=1377
AT4G21220	UUCUGACGGACAAGAUAAGCU	313	4.5	Translation	| Symbols: | Trimeric LpxA-like enzymes superfamily protein | chr4:11316828-11319067 REVERSE LENGTH=1065
AT4G21350	CUUCGACUGAGGUAAGCGCCU	234	4	Cleavage	| Symbols: B80, PUB8 | plant U-box 8 | chr4:11356143-11357267 REVERSE LENGTH=1125
AT4G21370	AUUGUGUAUAAUUUUGAGCCU	108	4.5	Cleavage	| Symbols: PSEUDOSRKA | S-locus protein kinase, putative | chr4:11383884-11387136 REVERSE LENGTH=2559
AT4G21390	UUUUGAUUCACCGGAUAAACUC	104	4	Translation	| Symbols: B120 | S-locus lectin protein kinase family protein | chr4:11394355-11397583 REVERSE LENGTH=2762
AT4G21490	UUCGAGGAGAUAUGACGCGCC	4887	4.5	Cleavage	| Symbols: NDB3 | NAD(P)H dehydrogenase B3 | chr4:11436495-11439326 REVERSE LENGTH=1743
AT4G21500	UCUAGUCCGAAAAAUGCGAAC	163	4.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G05018.1); H
AT4G21510	UUAUCAACGAACUCUUGGCCC	310	3.5	Cleavage	| Symbols: | F-box family protein | chr4:11445849-11447163 REVERSE LENGTH=1160
AT4G21530	UCUAUAGCCAAUGUACUCUACU	106	4	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:11450556-11456007 FORWARD LENGTH=2666
AT4G21534	UGAAUCUUGGUCAACUGGACC	197	4.5	Cleavage	| Symbols: | Diacylglycerol kinase family protein | chr4:11456230-11458820 FORWARD LENGTH=1446
AT4G21640	UUGGGAGAACUAUGACACGAG	515	3.5	Cleavage	| Symbols: | Subtilase family protein | chr4:11496834-11500618 REVERSE LENGTH=2202
AT4G21895	UCAUCCUCUGUAGCUUCCGUC	210	2.5	Cleavage	| Symbols: | DNA binding | chr4:11613314-11614941 REVERSE LENGTH=987
AT4G22010	UUGAUCCAAGUAGCUGACUCU	4031	3	Translation	| Symbols: sks4 | SKU5 similar 4 | chr4:11663324-11666715 FORWARD LENGTH=1983
AT4G22185	UUGAGAUAUCCCCUGUUACUG	106	4.5	Translation	| Symbols: | pseudogene, similar to P0537A05.16, similar to protein; blastp match of 28% identity and 3.1e-07 P-value to GP|13366010|dbj|BAB39287.1||AP002971 P0537A05.16 {Oryza sativa (japonica cultivar-group)} | chr4:11740053-117412
AT4G22350	UGAGGUCGAGUAGAGCAAUCUA	117	4.5	Cleavage	| Symbols: | Ubiquitin C-terminal hydrolases superfamily protein | chr4:11803834-11807178 REVERSE LENGTH=2011
AT4G22390	UUCAGGGUGAGAACAUUGACU	1291	3.5	Cleavage	| Symbols: | F-box associated ubiquitination effector family protein | chr4:11813425-11815133 REVERSE LENGTH=1408
AT4G22410	UGAGGUCGAGUAGAGCAAUCUA	117	5	Cleavage	| Symbols: | Ubiquitin C-terminal hydrolases superfamily protein | chr4:11818213-11820135 REVERSE LENGTH=1023
AT4G22540	UUUGGCCUGAGGUUGGACGCC	367	5	Cleavage	| Symbols: ORP2A | OSBP(oxysterol binding protein)-related protein 2A | chr4:11860444-11866364 REVERSE LENGTH=2782
AT4G22560	UACCGGAGGACGUACAUAGCU	401	5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G12450.1); Has 380 Blast hits to 380 proteins in 21 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 6; Plants - 374; Viruses - 0; Other Euk
AT4G22630	UUGAGAGCCUUGUAGUAGUCU	262	3.5	Translation	| Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr4:11909368-11909945 FORWARD LENGTH=489
AT4G22650	UUGAGAGCCUUGUAGUAGUCU	262	3.5	Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Plant lipid transfer protein/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612); BEST Arabidopsis thaliana protein match is: Bifunctional inhibitor/lipid-transfer protein/seed storage 2S a
AT4G22690	AAACAGGACAAGUUACUCGCC	986	4.5	Cleavage	| Symbols: CYP706A1 | cytochrome P450, family 706, subfamily A, polypeptide 1 | chr4:11929359-11931693 FORWARD LENGTH=2335
AT4G22710	AAACAGGACAAGUUACUCGCC	986	4.5	Cleavage	| Symbols: CYP706A2 | cytochrome P450, family 706, subfamily A, polypeptide 2 | chr4:11934969-11936755 FORWARD LENGTH=1787
AT4G22960	UUCAGGGUGAGAACAUUGACU	1291	4	Cleavage	| Symbols: | Protein of unknown function (DUF544) | chr4:12030020-12033137 FORWARD LENGTH=1708
AT4G22990	UGAGACACAACAGGGAGAUUC	244	3	Cleavage	| Symbols: | Major Facilitator Superfamily with SPX (SYG1/Pho81/XPR1) domain-containing protein | chr4:12048186-12051796 REVERSE LENGTH=2431
AT4G23010	UACAAAUUCGAGCACUCCCUG	156	4	Cleavage	| Symbols: ATUTR2, UTR2 | UDP-galactose transporter 2 | chr4:12060131-12062757 REVERSE LENGTH=1547
AT4G23130	UUAGCACCGAGGAUGAUGGACU	330	4	Cleavage	| Symbols: CRK5, RLK6 | cysteine-rich RLK (RECEPTOR-like protein kinase) 5 | chr4:12117598-12120134 REVERSE LENGTH=2082
AT4G23170	UUGAACAAGCCUGAUGAAGUU	102	3.5	Cleavage	| Symbols: EP1, CRK9 | receptor-like protein kinase-related family protein | chr4:12135093-12136157 FORWARD LENGTH=1065
AT4G23200	UGAGCCGACAAGAGUAGUAUC	111	4	Cleavage	| Symbols: CRK12 | cysteine-rich RLK (RECEPTOR-like protein kinase) 12 | chr4:12145380-12147934 REVERSE LENGTH=1947
AT4G23205	AUUGUGUAUAAUUUUGAGCCU	108	3.5	Cleavage	| Symbols: | other RNA | chr4:12144243-12144958 REVERSE LENGTH=490
AT4G23290	UAUGGAGAUGAUCGCAAUGGC	937	4.5	Cleavage	| Symbols: CRK21 | cysteine-rich RLK (RECEPTOR-like protein kinase) 21 | chr4:12177738-12180784 REVERSE LENGTH=2090
AT4G23320	UUCUUGUGAACUUGACCGGGA	158	4	Cleavage	| Symbols: CRK24 | cysteine-rich RLK (RECEPTOR-like protein kinase) 24 | chr4:12189182-12191977 REVERSE LENGTH=1314

AT4G23370	UUGUGAGUGUUUGUGAGGUCU	141	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF239, plant (InterPro
AT4G23380	CUUGUGAGUGUUUGUGAGGUC	103	4	Cleavage	| Symbols: | Protein of Unknown Function (DUF239) | chr4:12214667-12216333 REVERSE LENGTH=1203
AT4G23515	UAUGGAGAUGAUCGCAAUGGC	937	5	Translation	| Symbols: | Toll-Interleukin-Resistance (TIR) domain family protein | chr4:12271382-12272842 REVERSE LENGTH=996
AT4G23530	UGACGGAAGCUACAGAGGAUG	108	5	Cleavage	| Symbols: | Protein of unknown function (DUF793) | chr4:12279075-12280851 FORWARD LENGTH=1777
AT4G23540	CAAGAACCCGCACGACACUCG	169	4	Translation	| Symbols: | ARM repeat superfamily protein | chr4:12280413-12286420 REVERSE LENGTH=3530
AT4G23600	UUAUCAACGAACUCUUGGCCC	310	4	Cleavage	| Symbols: CORI3, JR2 | Tyrosine transaminase family protein | chr4:12311255-12313111 FORWARD LENGTH=1307
AT4G23750	UCCCGGAAUGCUGAAGAAGUA	113	3.5	Translation	| Symbols: CRF2, TMO3 | cytokinin response factor 2 | chr4:12376194-12378022 FORWARD LENGTH=1618
AT4G23990	UCGAGGGCAGGAACAUUGACU	334	2	Cleavage	| Symbols: ATCSLG3, CSLG3 | cellulose synthase like G3 | chr4:12456489-12460753 FORWARD LENGTH=2513
AT4G24010	UCGAGGGCAGGAACAUUGACU	334	2	Cleavage	| Symbols: ATCSLG1, CSLG1 | cellulose synthase like G1 | chr4:12466345-12469844 FORWARD LENGTH=2413
AT4G24100	UUUGUUAAACUCAUGGUCACCC	165	4	Cleavage	| Symbols: | Protein kinase superfamily protein | chr4:12515076-12519841 FORWARD LENGTH=2782
AT4G24240	UCACUGUGAAUUCCUGGAGUU	123	4	Cleavage	| Symbols: WRKY7, ATWRKY7 | WRKY DNA-binding protein 7 | chr4:12571766-12573725 FORWARD LENGTH=1505
AT4G24260	UUGAUCCAAGUAGCUGACUCU	4031	3.5	Translation	| Symbols: ATGH9A3, KOR3, GH9A3 | glycosyl hydrolase 9A3 | chr4:12577871-12580133 REVERSE LENGTH=1863
AT4G24280	UUUGUUAAACUCAUGGUCACCC	165	4	Translation	| Symbols: cpHsc70-1 | chloroplast heat shock protein 70-1 | chr4:12589988-12593630 FORWARD LENGTH=2456
AT4G24330	UUGGCAUCGAAUUUGAACUCA	339	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF1682) | chr4:12603521-12606328 REVERSE LENGTH=1863
AT4G24370	UGGAUUCCGGCUGCAUACUCC	392	4	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:12611396-1261213
AT4G24400	UUGGACGCCUCUACUAUGAGA	679	4.5	Translation	| Symbols: CIPK8, PKS11 | CBL-interacting protein kinase 8 | chr4:12617256-12620684 FORWARD LENGTH=1615
AT4G24430	UGAGUAGAAUUCGAUCAUAUC	114	3.5	Cleavage	| Symbols: | Rhamnogalacturonate lyase family protein | chr4:12630018-12633075 FORWARD LENGTH=2041
AT4G24450	UUUAGGAUUGUUGCAUAUGCA	1164	4	Cleavage	| Symbols: GWD3, PWD, ATGWD2 | phosphoglucan, water dikinase | chr4:12635426-12642797 FORWARD LENGTH=4150
AT4G24560	CGAGAGAUUACAGGGACUGUC	3198	4	Cleavage	| Symbols: UBP16 | ubiquitin-specific protease 16 | chr4:12679210-12684939 REVERSE LENGTH=3721
AT4G24580	UUUGGCCUGAGGUUGGACGCC	367	4	Cleavage	| Symbols: REN1 | Rho GTPase activation protein (RhoGAP) with PH domain | chr4:12687879-12694248 REVERSE LENGTH=2802
AT4G24680	CCGAUUCUGAUUGCAUGUGGU	186	4.5	Translation	| Symbols: MOS1 | modifier of snc1 | chr4:12732678-12740051 FORWARD LENGTH=4763
AT4G24800	UUCAGGGUGAGAACAUUGACU	1291	4.5	Cleavage	| Symbols: | MA3 domain-containing protein | chr4:12781916-12785197 FORWARD LENGTH=2658
AT4G24860	CUAGAAUUCUUUCCCUUUCCU	235	3	Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:12801549-12808190 REVERSE LENGTH=3400
AT4G24920	UUAGCACCGAGGAUGAUGGACU	330	4	Translation	| Symbols: | secE/sec61-gamma protein transport protein | chr4:12819511-12820736 REVERSE LENGTH=510
AT4G25420	CAACGCUCUUGAUACAUCUAG	133	3.5	Cleavage	| Symbols: GA5, GA20OX1, AT2301, ATGA20OX1 | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr4:12990884-12992458 REVERSE LENGTH=1281
AT4G25470	AUUGAUUCUGCACUCAAGGGC	128	4.5	Cleavage	| Symbols: CBF2, DREB1C, FTQ4, ATCBF2 | C-repeat/DRE binding factor 2 | chr4:13015277-13016220 REVERSE LENGTH=944
AT4G25620	UAUAGGGCUUGAAAGAAAGUC	535	4.5	Translation	| Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:13067186-13069679 REVERSE LENGTH=1994
AT4G25860	AUUGUGUAUAAUUUUGAGCCU	108	3.5	Cleavage	| Symbols: ORP4A | OSBP(oxysterol binding protein)-related protein 4A | chr4:13147326-13149606 FORWARD LENGTH=1271
AT4G25960	UGUGAGUGUUUGUGAGGUCUU	178	4	Cleavage	| Symbols: PGP2 | P-glycoprotein 2 | chr4:13177409-13183631 FORWARD LENGTH=4057
AT4G26250	UGUGAGUGUUUGUGAGGUCUU	178	3.5	Cleavage	| Symbols: AtGolS6, GolS6 | galactinol synthase 6 | chr4:13289641-13291084 FORWARD LENGTH=1042
AT4G26410	UGACACCGAUUCUGAUAGCUU	823	3.5	Cleavage	| Symbols: | Uncharacterised conserved protein UCP022280 | chr4:13346654-13349016 FORWARD LENGTH=1123
AT4G26580	UCACUUUGCUGAACAUGUACC	138	4	Cleavage	| Symbols: | RING/U-box superfamily protein | chr4:13411444-13413029 REVERSE LENGTH=1409
AT4G26650	AAACAGGACAAGUUACUCGCC	986	3.5	Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr4:13444938-13448212 FORWARD LENGTH=2306
AT4G26690	UGAGAGCACUCCACCGACUGA	230	4.5	Translation	| Symbols: SHV3, MRH5, GPDL2 | PLC-like phosphodiesterase family protein | chr4:13456434-13460060 REVERSE LENGTH=2809
AT4G26720	UCGACCACACUGUCAUGAUCU	174	3.5	Cleavage	| Symbols: PPX1, PPX-1 | protein phosphatase X 1 | chr4:13470032-13472342 REVERSE LENGTH=1471
AT4G26890	UGACGGACAAGAUAAGUUGCU	1505	4	Cleavage	| Symbols: MAPKKK16 | mitogen-activated protein kinase kinase kinase 16 | chr4:13511839-13513406 FORWARD LENGTH=1568
AT4G27050	UUGGGAGAACUAUGACACGAG	515	3.5	Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr4:13575800-13577993 REVERSE LENGTH=1923
AT4G27060	UGACACCGAUUCUGAUAGCUU	823	4	Cleavage	| Symbols: TOR1, SPR2, CN | ARM repeat superfamily protein | chr4:13581401-13585155 REVERSE LENGTH=2860
AT4G27100	AAAUAAAACUGAACCAUGCCU	203	4.5	Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr4:13595561-13598915 FORWARD LENGTH=1881
AT4G27180	UCUAGUUCGCGUUCUUCAGAC	300	3.5	Translation	| Symbols: ATK2, KATB | kinesin 2 | chr4:13614856-13619156 REVERSE LENGTH=2612
AT4G27250	UAUUGAUUUUUGGCCUGAGGU	116	3.5	Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:13642772-13644425 REVERSE LENGTH=1096
AT4G27370	UUAGAAUUAUCAUGUCUUGGC	138	3.5	Cleavage	| Symbols: VIIIB, ATVIIIB | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13694881-13700780 REVERSE LENGTH=3405
AT4G27440	UUUGAUUCACCGGAUAAACUC	175	3.5	Translation	| Symbols: PORB | protochlorophyllide oxidoreductase B | chr4:13725546-13727352 FORWARD LENGTH=1446
AT4G27640	UUUGGUUCUGAGUCCCCGCCU	669	3	Cleavage	| Symbols: | ARM repeat superfamily protein | chr4:13797658-13803063 REVERSE LENGTH=3589
AT4G27680	UGUGAGUGUUUGUGAGGUCUU	178	3	Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr4:13821106-13823342 FORWARD LENGTH=1613
AT4G27780	UGGCAUCGAAUUUGAACUCAU	178	3	Translation	| Symbols: ACBP2 | acyl-CoA binding protein 2 | chr4:13847549-13849887 FORWARD LENGTH=1548
AT4G27950	UCAUAUGGACUUUGGCUACACC	101	4	Translation	| Symbols: CRF4 | cytokinin response factor 4 | chr4:13909569-13910859 REVERSE LENGTH=1291
AT4G28030	UGACACCGAUUCUGAUAGCUU	823	4	Cleavage	| Symbols: | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:13937676-13939144 REVERSE LENGTH=877
AT4G28070	UUUGAUCCGAGGAUGAUGGAU	816	4	Cleavage	| Symbols: | AFG1-like ATPase family protein | chr4:13945892-13948627 FORWARD LENGTH=1677
AT4G28370	UUUGAGCACUCUACAGACAGG	162	3.5	Cleavage	| Symbols: | RING/U-box superfamily protein | chr4:14034654-14041322 FORWARD LENGTH=3919
AT4G28530	CAUUGACUUCAAGCCUGCGCU	190	2.5	Cleavage	| Symbols: anac074, NAC074 | NAC domain containing protein 74 | chr4:14090489-14094776 REVERSE LENGTH=1357
AT4G28550	UGAGACACAACAGGGAGAUUC	244	4	Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr4:14110884-14113748 FORWARD LENGTH=1685
AT4G28570	UGUGACACCGAUUCUGAUUGC	114	3	Cleavage	| Symbols: | Long-chain fatty alcohol dehydrogenase family protein | chr4:14119425-14122616 FORWARD LENGTH=2747
AT4G28680	UCGAGUGACUUUGGAGCCAUU	244	3	Translation	| Symbols: TYRDC, TYRDC1 | L-tyrosine decarboxylase | chr4:14155248-14158716 FORWARD LENGTH=1808
AT4G28720	CAAGAACCCGCACGACACUCG	169	3.5	Cleavage	| Symbols: YUC8 | Flavin-binding monooxygenase family protein | chr4:14192583-14194256 FORWARD LENGTH=1674
AT4G28860	UUCUUGUGAACUUGACCGGGA	158	3.5	Translation	| Symbols: ckl4 | casein kinase I-like 4 | chr4:14246283-14249014 FORWARD LENGTH=1404
AT4G28920	UUCUGUAGCACGAGGUAUCCU	302	4	Cleavage	| Symbols: | Protein of unknown function (DUF626) | chr4:14268415-14269885 REVERSE LENGTH=879
AT4G28940	UUUCUGACGGACAAGAUAAGU	480	3.5	Cleavage	| Symbols: | Phosphorylase superfamily protein | chr4:14274341-14277095 FORWARD LENGTH=1295
AT4G28990	UCACCAUUGGCAGCUCUGUACC	187	4	Translation	| Symbols: | RNA-binding protein-related | chr4:14291151-14293174 FORWARD LENGTH=1398
AT4G29033	UCUAGUUCGCAUUUUUCGGAC	142	4	Cleavage	| Symbols: | Defensin-like (DEFL) family protein | chr4:14308967-14309379 REVERSE LENGTH=246
AT4G29070	CUGGAGGACGUACAGCACUUA	113	4.5	Cleavage	| Symbols: | Phospholipase A2 family protein | chr4:14321813-14323307 FORWARD LENGTH=1121
AT4G29130	UGAGAUUGCUAGAGGAAAGAG	101	2.5	Cleavage	| Symbols: ATHXK1, GIN2, HXK1 | hexokinase 1 | chr4:14352037-14355103 REVERSE LENGTH=2030
AT4G29220	UCAUCCUCUGUAGCUUCCGUC	210	4	Cleavage	| Symbols: PFK1 | phosphofructokinase 1 | chr4:14403347-14406592 REVERSE LENGTH=2068
AT4G29260	UUGAGAGCCUUGUAGUAGUCU	262	3	Cleavage	| Symbols: | HAD superfamily, subfamily IIIB acid phosphatase | chr4:14422152-14423603 REVERSE LENGTH=1120
AT4G29380	UGUGGAUACAAGAGCUGGGCU	215	2.5	Cleavage	| Symbols: | protein kinase family protein / WD-40 repeat family protein | chr4:14458822-14464859 FORWARD LENGTH=4652
AT4G29440	UUUGAGAGCACUCCACCGACUG	125	4.5	Translation	| Symbols: | Regulator of Vps4 activity in the MVB pathway protein | chr4:14473757-14477877 REVERSE LENGTH=3614
AT4G29680	UUGAUCCAAGUAGCUGACUCU	4031	2.5	Translation	| Symbols: | Alkaline-phosphatase-like family protein | chr4:14537781-14539594 REVERSE LENGTH=1814
AT4G29830	UUGACUUCAGACCUGCGCGUG	131	3	Cleavage	| Symbols: VIP3 | Transducin/WD40 repeat-like superfamily protein | chr4:14597661-14599300 FORWARD LENGTH=1176
AT4G29890	UAGAGUGUUCAUGUAGUUGCA	232	4	Cleavage	| Symbols: | choline monooxygenase, putative (CMO-like) | chr4:14608833-14610998 FORWARD LENGTH=1397
AT4G29900	UCAUAUGGACUUUGGCUACACC	101	3.5	Cleavage	| Symbols: ACA10, CIF1, ATACA10 | autoinhibited Ca(2+)-ATPase 10 | chr4:14610883-14619573 REVERSE LENGTH=3762
AT4G29940	AUUUCAGUGAGCACGUACCUC	200	4	Cleavage	| Symbols: PRHA | pathogenesis related homeodomain protein A | chr4:14648164-14653303 REVERSE LENGTH=2629
AT4G29990	UCUUCGACUGAGGUAAGCGCCU	355	3.5	Cleavage	| Symbols: | Leucine-rich repeat transmembrane protein kinase protein | chr4:14665691-14670030 REVERSE LENGTH=3334
AT4G30090	UUAAUCCAAGUAGCUGACUCU	2805	3.5	Cleavage	| Symbols: emb1353 | embryo defective 1353 | chr4:14708712-14711612 REVERSE LENGTH=1498
AT4G30190	UUAGAAUUAUCAUGUCUUGGC	138	3.5	Translation	| Symbols: HA2 | H(+)-ATPase 2 | chr4:14770794-14776058 REVERSE LENGTH=3110
AT4G30230	UUUGAUUCACCGGAUAAACUC	175	3.5	Cleavage	| Symbols: | unknown protein; Has 42 Blast hits to 42 proteins in 5 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 42; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:14806345-14807425 FORWARD LENGTH=1081
AT4G30290	UCAUAUGGACUUUGGCUACACC	101	4.5	Cleavage	| Symbols: ATXTH19, XTH19 | xyloglucan endotransglucosylase/hydrolase 19 | chr4:14828712-14830016 REVERSE LENGTH=1127
AT4G30310	UUCUGUAGCACGAGGUAUCCU	302	4	Cleavage	| Symbols: | FGGY family of carbohydrate kinase | chr4:14832316-14835092 FORWARD LENGTH=1584
AT4G30340	UAAUAAGGAGAGUCAGCUACU	298	4	Translation	| Symbols: ATDGK7, DGK7 | diacylglycerol kinase 7 | chr4:14838291-14841067 REVERSE LENGTH=1779
AT4G30360	UCGAACAAGAGCUGAACGUCU	423	3	Translation	| Symbols: ATCNGC17, CNGC17 | cyclic nucleotide-gated channel 17 | chr4:14854811-14858003 REVERSE LENGTH=2636
AT4G30470	UAAUAAGGAGAGUCAGCUACU	298	3	Cleavage	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr4:14894105-14896815 FORWARD LENGTH=1379
AT4G30560	UUCUGACGGACAAGAUAAGCU	313	5	Cleavage	| Symbols: CNGC9 | cyclic nucleotide gated channel 9 | chr4:14926834-14930156 REVERSE LENGTH=2414
AT4G30720	UUGGCGCUCAACUCUGCAAGG	4868	4	Translation	| Symbols: | FAD/NAD(P)-binding oxidoreductase family protein | chr4:14971906-14975519 REVERSE LENGTH=2488
AT4G30800	UCUAGUUCGCAUUUUUUGGAC	421	3.5	Cleavage	| Symbols: | Nucleic acid-binding, OB-fold-like protein | chr4:15001134-15002671 FORWARD LENGTH=841
AT4G30850	UGUCACCGUAGAUUUCUUCCU	123	3	Cleavage	| Symbols: HHP2 | heptahelical transmembrane protein2 | chr4:15020415-15022445 REVERSE LENGTH=1369
AT4G30950	UCAACGCUCUGAUACAUCUAG	118	3.5	Translation	| Symbols: FAD6, FADC, SFD4 | fatty acid desaturase 6 | chr4:15056975-15059794 REVERSE LENGTH=1771
AT4G30990	CAAGAACCCGCACGACACUCG	169	3.5	Cleavage	| Symbols: | ARM repeat superfamily protein | chr4:15084098-15097920 FORWARD LENGTH=8101
AT4G31210	UUUGAUCCGAGGAUGAUGGAU	816	4	Cleavage	| Symbols: | DNA topoisomerase, type IA, core | chr4:15165156-15172738 FORWARD LENGTH=4183
AT4G31250	UUGAUCCAAGUAGCUGACUCU	4031	2.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr4:15178925-15181751 REVERSE LENGTH=2307
AT4G31340	UUUCUGACGGACAAGAUAAGU	480	4	Cleavage	| Symbols: | myosin heavy chain-related | chr4:15205480-15209601 FORWARD LENGTH=1885

AT4G31360	UCUGUACCGCUGAAUUCUUCC	275	4.5	Cleavage	| Symbols: | selenium binding | chr4:15221843-15223627 FORWARD LENGTH=980
AT4G31600	UAAAACUGAACCAUGCCUAGA	302	4	Cleavage	| Symbols: | UDP-N-acetylglucosamine (UAA) transporter family | chr4:15314885-15317135 REVERSE LENGTH=1633
AT4G31615	UGACGGAAGCUACAGAGGAUG	108	3.5	Cleavage	| Symbols: | Transcriptional factor B3 family protein | chr4:15320297-15322194 REVERSE LENGTH=1464
AT4G31640	UCAACGCUCUGAUACAUCUAG	118	3.5	Cleavage	| Symbols: | transcriptional factor B3 family protein | chr4:15328357-15329689 FORWARD LENGTH=1090
AT4G31720	UACCGGAGGACGUACAACACC	302	4	Cleavage	| Symbols: TAFII15, TAF10, STG1 | TBP-associated factor II 15 | chr4:15353952-15356346 REVERSE LENGTH=868
AT4G31860	UCCUAUCCAGUCUGAAGAACGC	272	4.5	Translation	| Symbols: | Protein phosphatase 2C family protein | chr4:15406439-15409000 REVERSE LENGTH=1540
AT4G31890	AACAAAACUGUUGAACAAGCCU	111	4	Cleavage	| Symbols: | ARM repeat superfamily protein | chr4:15426292-15429107 REVERSE LENGTH=2041
AT4G31950	UGUGGUGUACCUCUCACGUCU	112	4	Cleavage	| Symbols: CYP82C3 | cytochrome P450, family 82, subfamily C, polypeptide 3 | chr4:15455163-15457121 FORWARD LENGTH=1570
AT4G31970	CUCACAAGUGAUAUAGGGCUUG	110	4.5	Translation	| Symbols: CYP82C2 | cytochrome P450, family 82, subfamily C, polypeptide 2 | chr4:15462408-15464358 FORWARD LENGTH=1572
AT4G32010	UCUUCGACUGAGGUAAGCGCCU	355	4.5	Cleavage	| Symbols: HSL1, HSI2-L1, VAL2 | HSI2-like 1 | chr4:15479524-15485353 FORWARD LENGTH=3468
AT4G32030	UAGAGUUAAGUUGGGACAGGA	199	4.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G15800.1); Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Vi
AT4G32190	AUUUCAGUGAGCACGUACCUC	200	4	Translation	| Symbols: | Myosin heavy chain-related protein | chr4:15544878-15547855 FORWARD LENGTH=2692
AT4G32200	UCAUCAAUGAACUCAUUUGGCU	103	2	Cleavage	| Symbols: ASY2 | DNA-binding HORMA family protein | chr4:15548840-15555094 FORWARD LENGTH=4332
AT4G32320	UUACGAGACUCUAGCCCAACU	447	4.5	Cleavage	| Symbols: APX6 | ascorbate peroxidase 6 | chr4:15602721-15605400 FORWARD LENGTH=1212
AT4G32410	UCAAGCGAUUGGAAGGAUUGUU	102	2	Cleavage	| Symbols: CESA1, RSW1, AtCESA1 | cellulose synthase 1 | chr4:15640620-15646665 REVERSE LENGTH=3912
AT4G32440	UACUGGAGGACGUACAGCACU	949	4.5	Translation	| Symbols: | Plant Tudor-like RNA-binding protein | chr4:15656685-15660223 FORWARD LENGTH=2207
AT4G32551	CUCGGGAGAAAGAAGAAGGCU	259	3	Cleavage	| Symbols: LUG | LisH dimerisation motif;WD40/YVTN repeat-like-containing domain | chr4:15707481-15713662 FORWARD LENGTH=3595
AT4G32620	UUAUCAACGAACUCUUGGCCC	310	3.5	Cleavage	| Symbols: | Enhancer of polycomb-like transcription factor protein | chr4:15731508-15737272 FORWARD LENGTH=4925
AT4G32670	AUGACGAAUGUUUGACAGCCU	113	4	Cleavage	| Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr4:15759243-15762925 REVERSE LENGTH=2945
AT4G32730	UUUCCGUUGGUGUGCGCCCAC	458	3.5	Translation	| Symbols: PC-MYB1, MYB3R-1, ATMYB3R-1, ATMYB3R1, MYB3R1 | Homeodomain-like protein | chr4:15790345-15794252 FORWARD LENGTH=2639
AT4G32760	UGUGGAUACAAGAGCUGGGCU	215	3.5	Translation	| Symbols: | ENTH/VHS/GAT family protein | chr4:15799077-15804173 FORWARD LENGTH=2671
AT4G32770	UAACAAGAACUCUUUCUUUUCU	235	3	Cleavage	| Symbols: VTE1, ATSDX1 | tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1) | chr4:15804914-15807982 FORWARD LENGTH=1726
AT4G32820	UACUGGAGGACGUACAACACU	176	3	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15831576-15841643 REVERSE LENGTH=5884
AT4G32850	UUGGUCACACAGUGGACUGUG	104	4	Cleavage	| Symbols: nPAP | nuclear poly(a) polymerase | chr4:15849780-15854709 FORWARD LENGTH=2813
AT4G328500	UUGGUCACACAGUGGACUGUG	104	4	Cleavage	| Symbols: nPAP | nuclear poly(a) polymerase | chr4:15849780-15854460 FORWARD LENGTH=2786
AT4G32920	UACCCGUACGUCGCCUACAAG	192	4.5	Cleavage	| Symbols: | glycine-rich protein | chr4:15887270-15896006 REVERSE LENGTH=4763
AT4G32970	UUUUAAUUCAAGUAGCUGACU	133	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G32960.1); Has 552 Blast hits to 489 proteins in 85 species: Archae - 4; Bacteria - 14; Metazoa - 187; Fungi - 12; Plants - 225; Viruses - 0; Other
AT4G33010	UUGUGGAAUCCGUAGUCUGUA	152	3	Cleavage	| Symbols: AtGLDP1, GLDP1 | glycine decarboxylase P-protein 1 | chr4:15926670-15931332 REVERSE LENGTH=3474
AT4G33170	AUGGAUUUAGAUCACUUGCGUC	196	5	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:15995701-15998673 REVERSE LENGTH=2973
AT4G33310	UGCCAUGAUCGAGAGCUGCCU	164	5	Translation	| Symbols: | unknown protein; Has 5 Blast hits to 5 proteins in 1 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 5; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr4:16056156-16056416 FORWARD LENGTH=261
AT4G33470	UUGUGAGUGUUUGUGAGGUCU	141	4	Cleavage	| Symbols: hda14, ATHDA14 | histone deacetylase 14 | chr4:16102595-16105493 REVERSE LENGTH=1505
AT4G33680	AUUUCAGUGAGCACGUACCUC	200	4.5	Cleavage	| Symbols: AGD2 | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr4:16171694-16174686 REVERSE LENGTH=1595
AT4G34020	CGAGAGAUUACAGGGACUGUC	3198	4	Cleavage	| Symbols: | Class I glutamine amidotransferase-like superfamily protein | chr4:16298265-16300938 REVERSE LENGTH=1643
AT4G34090	UGGCAUCGAAUUUGAACUCAU	178	4.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thali
AT4G34220	CAUCAAGAACCGGUCAUGCCU	125	4	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr4:16381506-16384194 REVERSE LENGTH=2561
AT4G34370	AUAGCUAACAAGAACUCUUUCU	426	3.5	Cleavage	| Symbols: ATARI1, ARI1 | RING/U-box superfamily protein | chr4:16434333-16437309 FORWARD LENGTH=2280
AT4G34540	AUUGAUUCUGCACUCAAGGGC	128	3.5	Translation	| Symbols: | NmrA-like negative transcriptional regulator family protein | chr4:16498391-16502174 FORWARD LENGTH=2805
AT4G34610	UGCUCGUAUCAUACUCCUCCU	194	4	Cleavage	| Symbols: BLH6 | BEL1-like homeodomain 6 | chr4:16530346-16533034 REVERSE LENGTH=2123
AT4G34620	UACAGAAUAGGCUUAAGUAAC	189	4	Translation	| Symbols: SSR16 | small subunit ribosomal protein 16 | chr4:16534855-16536171 REVERSE LENGTH=650
AT4G34690	AUUUGAACUCAUGGAUACCCU	768	3	Cleavage	| Symbols: | unknown protein; Has 9 Blast hits to 9 proteins in 3 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 1 (source: NCBI BLink). | chr4:16555463-16556097 REVERSE LENGTH=624
AT4G34990	UUGAGAGAUCCCCUGUUACUG	3917	4.5	Translation	| Symbols: AtMYB32, MYB32 | myb domain protein 32 | chr4:16661329-16662367 REVERSE LENGTH=944
AT4G35025	UUUGAUUCACCGGAUAAACUC	175	4.5	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr4:16675528-1667574
AT4G35090	UGUGGUGUACCUCUCACGUCU	112	4	Cleavage	| Symbols: CAT2 | catalase 2 | chr4:16700596-16703325 REVERSE LENGTH=1930
AT4G35180	UGACACCGAUUCUGAUUGCAU	377	4.5	Cleavage	| Symbols: LHT7 | LYS/HIS transporter 7 | chr4:16738339-16740465 REVERSE LENGTH=1695
AT4G35335	UUCUGAAGGACAAGAUCAGCU	351	3.5	Cleavage	| Symbols: | Nucleotide-sugar transporter family protein | chr4:16807265-16810216 FORWARD LENGTH=1281
AT4G35440	UUCUGAAGGACAAGAUCAGCU	351	4.5	Translation	| Symbols: CLC-E, ATCLC-E, CLCE | chloride channel E | chr4:16835986-16839375 REVERSE LENGTH=2561
AT4G35480	UAUUGAUUUUUGGCCUGAGGU	116	4.5	Cleavage	| Symbols: RHA3B | RING-H2 finger A3B | chr4:16852074-16852947 REVERSE LENGTH=874
AT4G35520	AUCCAAGUAGCUGACUCUCCU	1104	4	Translation	| Symbols: MLH3, ATMLH3 | MUTL protein homolog 3 | chr4:16865488-16871764 FORWARD LENGTH=3747
AT4G35560	UGAAGGACAAGCUCAGCUGCU	1483	4.5	Cleavage	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr4:16881366-16887019 FORWARD LENGTH=3487
AT4G35600	UUCGAGAACUCCCUGACCCGA	1272	4	Cleavage	| Symbols: CONNEXIN 32 | Protein kinase superfamily protein | chr4:16896237-16898876 FORWARD LENGTH=1633
AT4G35650	UCCUGAGUACUCUCUUCCAAG	209	3.5	Cleavage	| Symbols: IDH-III | isocitrate dehydrogenase III | chr4:16908519-16910190 FORWARD LENGTH=1389
AT4G35670	UUCCAGAACUAAUGAAUGUUA	448	4	Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr4:16914996-16917201 FORWARD LENGTH=1185
AT4G35690	UUGAGAGAUCCCUUGUUACUG	141	3.5	Translation	| Symbols: | Arabidopsis protein of unknown function (DUF241) | chr4:16921803-16922963 FORWARD LENGTH=1161
AT4G35740	UGAGACACAACAGGGAGAUUC	244	3.5	Cleavage	| Symbols: RecQI3, ATRECQ3 | DEAD/DEAH box RNA helicase family protein | chr4:16936120-16940332 FORWARD LENGTH=2407
AT4G35800	UCACUUUGCUGAACAUGUACC	138	3.5	Translation	| Symbols: NRPB1, RPB1, RNA_POL_II_LSRNA_POL_II_LS, RNA_POL_II_LS | RNA polymerase II large subunit | chr4:16960657-16968128 REVERSE LENGTH=6126
AT4G35830	UUCUGAUUGCAUGUGGUGUACC	110	4	Cleavage	| Symbols: ACO1 | aconitase 1 | chr4:16972598-16978057 REVERSE LENGTH=3214
AT4G35840	UUUAACAACUAAGGUUCCUGU	1055	4	Cleavage	| Symbols: | RING/U-box superfamily protein | chr4:16980961-16982365 FORWARD LENGTH=932
AT4G36052	UUAUCAACGAACUCUUGGCCC	310	4.5	Cleavage	| Symbols: | other RNA | chr4:17052347-17053499 FORWARD LENGTH=1084
AT4G36140	UUGGCCUGAGGUUGGACGCCU	272	4	Translation	| Symbols: | disease resistance protein (TIR-NBS-LRR class), putative | chr4:17098956-17104479 REVERSE LENGTH=4824
AT4G36160	UUUGAGCACUCUACAGACAGG	162	4.5	Cleavage	| Symbols: ANAC076, VND2, NAC076 | NAC domain containing protein 76 | chr4:17110747-17114141 REVERSE LENGTH=1465
AT4G36180	UAACAAGAACUCUUUCUUUUCU	235	3.5	Cleavage	| Symbols: | Leucine-rich receptor-like protein kinase family protein | chr4:17120085-17123841 REVERSE LENGTH=3678
AT4G36210	UGGCAUCGAAUUUGAACUCAU	178	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF726) | chr4:17130246-17134656 FORWARD LENGTH=2617
AT4G36580	UCUCAUGUAGUUCUAGUUCGCA	1437	3.5	Cleavage	| Symbols: | AAA-type ATPase family protein | chr4:17257945-17260775 FORWARD LENGTH=2026
AT4G36650	UAGGCCUGAGAUUGGACGCCU	875	4.5	Cleavage	| Symbols: ATPBRP, PBRP | plant-specific TFIIB-related protein | chr4:17283134-17285599 REVERSE LENGTH=1733
AT4G36730	UUUGAGCACUCUACAGACAGG	162	4	Cleavage	| Symbols: GBF1 | G-box binding factor 1 | chr4:17309612-17312488 REVERSE LENGTH=1500
AT4G36760	UUGAAGGAUUUGUGGUUAACCA	106	4	Translation	| Symbols: ATAPP1, APP1 | aminopeptidase P1 | chr4:17326617-17330208 FORWARD LENGTH=2238
AT4G36770	UUCACAUGUCCGGGCUAGGCA	461	4.5	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr4:17330146-17331624 REVERSE LENGTH=1479
AT4G36810	UCCCAACCCAUGAUCUAAGCG	236	4	Cleavage	| Symbols: GGPS1 | geranylgeranyl pyrophosphate synthase 1 | chr4:17343374-17344865 FORWARD LENGTH=1492
AT4G36890	UACACAAAGGGCUCCUCGCACC	211	5	Cleavage	| Symbols: IRX14 | Nucleotide-diphospho-sugar transferases superfamily protein | chr4:17379175-17381780 REVERSE LENGTH=2187
AT4G36940	UUUGAUCCGAGGAUGAUGGAUU	112	3	Cleavage	| Symbols: NAPRT1 | nicotinate phosphoribosyltransferase 1 | chr4:17416855-17420252 FORWARD LENGTH=2132
AT4G37010	AACAAAACUGUUGAACAAGCCU	111	3	Translation	| Symbols: CEN2 | centrin 2 | chr4:17444348-17445615 FORWARD LENGTH=812
AT4G37080	CCGAUUCUGAUUGCAUGUGGU	186	4	Cleavage	| Symbols: | Protein of unknown function, DUF547 | chr4:17474166-17476952 FORWARD LENGTH=2069
AT4G37110	UCUAGUUCGCGUUUUUCAGAC	163	3	Translation	| Symbols: | Zinc-finger domain of monoamine-oxidase A repressor R1 | chr4:17484125-17486276 REVERSE LENGTH=1551
AT4G37130	CUUGGCAUCGAAUUUGAACUC	1059	4.5	Cleavage	| Symbols: | hydroxyproline-rich glycoprotein family protein | chr4:17489467-17492010 FORWARD LENGTH=1879
AT4G37225	UGGCAGUAGGAGUACACGACU	163	4	Translation	| Symbols: | other RNA | chr4:17516187-17516857 REVERSE LENGTH=587
AT4G37390	UAUGCUUCUGUUGAUCCACCU	344	3.5	Cleavage	| Symbols: YDK1, GH3.2, BRU6, GH3-2, AUR3 | Auxin-responsive GH3 family protein | chr4:17579657-17582022 FORWARD LENGTH=2131
AT4G37409	UCCUGAGUACUCUCUUCCAAG	209	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1
AT4G37430	UGUGAGUGUUUGUGAGGUCUU	178	3	Cleavage	| Symbols: CYP91A2, CYP81F1 | cytochrome P450, family 91, subfamily A, polypeptide 2 | chr4:17597110-17598958 FORWARD LENGTH=1764
AT4G37450	UAAGGAGAGUCAGCUACUUGGA	134	4	Cleavage	| Symbols: AGP18, ATAGP18 | arabinogalactan protein 18 | chr4:17605758-17606755 REVERSE LENGTH=819
AT4G37460	UUUUAAUUCAAGUAGCUGACU	133	3	Cleavage	| Symbols: SRFR1 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr4:17608378-17615776 REVERSE LENGTH=3646
AT4G37490	UCGACCACACUGUUAGGAUCU	121	3.5	Translation	| Symbols: CYC1, CYCB1;1, CYCB1 | CYCLIN B1;1 | chr4:17621886-17624285 REVERSE LENGTH=1607
AT4G37580	UAUAGGGCUUGAAAGAAAGUU	252	3.5	Translation	| Symbols: HLS1, COP3, UNS2 | Acyl-CoA N-acyltransferases (NAT) superfamily protein | chr4:17658612-17660878 FORWARD LENGTH=1846
AT4G37680	UUACGAGACUCUAGCCCAGCU	3733	4	Translation	| Symbols: HHP4 | heptahelical protein 4 | chr4:17700711-17702753 FORWARD LENGTH=1546
AT4G37750	UUCGGACUGGAUAGGACUAGG	101	4	Cleavage	| Symbols: ANT, DRG, CKC, CKC1 | Integrase-type DNA-binding superfamily protein | chr4:17739514-17742401 FORWARD LENGTH=2148
AT4G37770	UCUAGUCCGAAAAAUGCGAAC	163	3.5	Translation	| Symbols: ACS8 | 1-amino-cyclopropane-1-carboxylate synthase 8 | chr4:17752084-17754157 FORWARD LENGTH=1780
AT4G37910	UAGGCCUGAGAUUGGACGCCU	875	4.5	Cleavage	| Symbols: mtHsc70-1 | mitochondrial heat shock protein 70-1 | chr4:17825080-17828180 REVERSE LENGTH=2418
AT4G38150	CAUUGACUUCAAGCCUGCGCU	190	4	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr4:17900810-17902160 REVERSE LENGTH=1026
AT4G38190	CGAGAGAUUACAGGGACUGUC	3198	3.5	Cleavage	| Symbols: ATCSLD4, CSLD4 | cellulose synthase like D4 | chr4:17909919-17913641 REVERSE LENGTH=3513
AT4G38250	UGGGCGCUUAUACUUUGGGUU	115	4.5	Cleavage	| Symbols: | Transmembrane amino acid transporter family protein | chr4:17935402-17937068 FORWARD LENGTH=1667

AT4G38290	UUACGAGACUCUAGCCCAGCU	3733	4	Translation	| Symbols: | Haemolysin-III related integral membrane protein | chr4:17942871-17944047 FORWARD LENGTH=465
AT4G38350	UUCGAGCACUCCCUGACCCGA	160	4	Translation	| Symbols: | Patched family protein | chr4:17958177-17966962 REVERSE LENGTH=4085
AT4G38380	UUCGAGAACUCCCUGACCGA	1272	5	Cleavage	| Symbols: | MATE efflux family protein | chr4:17971855-17975100 REVERSE LENGTH=1913
AT4G38552	UAGAUAACAAGAACUCUUUCU	107	3.5	Translation	| Symbols: | Potential natural antisense gene, locus overlaps with AT4G38550 | chr4:18025620-18028492 REVERSE LENGTH=2771
AT4G38560	UUCGAGAACUCCCUGACCGA	1272	4.5	Cleavage	| Symbols: | Arabidopsis phospholipase-like protein (PEARLI 4) family | chr4:18029196-18031333 FORWARD LENGTH=1787
AT4G38640	UGAGAACGCUCUGCCAUUGGA	158	5	Cleavage	| Symbols: | Plasma-membrane choline transporter family protein | chr4:18059653-18062289 REVERSE LENGTH=2100
AT4G38650	UCCCGGAAUGCUGAAGAAGUA	113	3	Translation	| Symbols: | Glycosyl hydrolase family 10 protein | chr4:18063166-18065849 FORWARD LENGTH=1980
AT4G38830	UAGCUAACAAGAACUCUUUCU	1828	4.5	Cleavage	| Symbols: CRK26 | cysteine-rich RLK (RECEPTOR-like protein kinase) 26 | chr4:18122326-18124943 FORWARD LENGTH=2011
AT4G38920	UUCGAGGAGAUAUGACGCGCC	4887	4	Cleavage	| Symbols: AVA-P3, ATVHA-C3, VHA-C3 | vacuolar-type H(+)-ATPase C3 | chr4:18147211-18149267 FORWARD LENGTH=1028
AT4G38980	UGACGGUUCAGAUUCAGGAGC	107	3.5	Translation	| Symbols: | unknown protein; Has 44 Blast hits to 44 proteins in 19 species: Archae - 0; Bacteria - 2; Metazoa - 2; Fungi - 8; Plants - 24; Viruses - 0; Other Eukaryotes - 8 (source: NCBI BLink). | chr4:18166709-18168192 REVERSE LENGTH=1114
AT4G39040	UCCUGAGUACUCUCUUCCAAG	209	4	Cleavage	| Symbols: | RNA-binding CRS1 / YhbY (CRM) domain protein | chr4:18189072-18190556 REVERSE LENGTH=1089
AT4G39160	AUUUGAACUCAUGGAUACCCU	768	4.5	Translation	| Symbols: | Homeodomain-like superfamily protein | chr4:18236792-18239818 FORWARD LENGTH=1916
AT4G39340	UGACGGAAGCUACAGAGGAUG	108	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF1278) | chr4:18293129-18293512 REVERSE LENGTH=384
AT4G39350	CUCAGGCUCAUACUCGACGUC	968	4	Cleavage	| Symbols: CESA2, ATH-A, ATCESA2 | cellulose synthase A2 | chr4:18296797-18302192 FORWARD LENGTH=3838
AT4G39400	UAUAGGGCUUGAAAGAAAGUC	535	3	Cleavage	| Symbols: BRI1, CBB2, DWF2, BIN1, ATBRI1 | Leucine-rich receptor-like protein kinase family protein | chr4:18324661-18328826 FORWARD LENGTH=4166
AT4G39480	UGAGAAGAGAUAGAAUAGAAUC	103	3.5	Cleavage	| Symbols: CYP96A9 | cytochrome P450, family 96, subfamily A, polypeptide 9 | chr4:18362258-18364209 FORWARD LENGTH=1952
AT4G39490	UGAGAAGAGAUAGAAUAGAAUC	103	3	Cleavage	| Symbols: CYP96A10 | cytochrome P450, family 96, subfamily A, polypeptide 10 | chr4:18365049-18366888 FORWARD LENGTH=1840
AT4G39590	UUUGAGCACUCCUUGACCGA	154	2.5	Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18387331-18388732 REVERSE LENGTH=1402
AT4G39690	UGUUGAUCCAAGUAGCUGACU	608	4	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 26 plant structures; EXPRESSED DURING: 14 growth stages; CONTAINS InterPro DOMAIN/s: Mito
AT4G39700	UUAACUCUACCCUUUGCACUC	380	4	Cleavage	| Symbols: | Heavy metal transport/detoxification superfamily protein | chr4:18424265-18424906 FORWARD LENGTH=477
AT4G39756	AUUGUGUAUAAUUUUGAGCCU	108	3	Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr4:18441756-18443000 FORWARD LENGTH=1195
AT4G39850	UGCAUAACUUGGGACUUACCU	413	4	Cleavage	| Symbols: PXA1, PED3, CTS, ACN2, AtABCD1 | peroxisomal ABC transporter 1 | chr4:18488519-18497136 FORWARD LENGTH=4722
AT4G39960	UCACCAUUGGCAGCUCUGUACC	187	3.5	Translation	| Symbols: | Molecular chaperone Hsp40/DnaJ family protein | chr4:18533755-18536618 FORWARD LENGTH=1716
AT4G40040	UCAGUAGAAUUCGAUCAUAUC	104	3.5	Cleavage	| Symbols: | Histone superfamily protein | chr4:18557187-18558743 REVERSE LENGTH=861
AT5G01030	UUUAUUCACACAGUGGACUGUG	118	4.5	Translation	| Symbols: | Protein of unknown function (DUF3527) | chr5:9930-13235 FORWARD LENGTH=2728
AT5G01110	UUGGACGCCUCUACUAUGAGA	679	4.5	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:41768-44375 REVERSE LENGTH=2608
AT5G01130	UGGAUUCCGGCUGCAUACUCC	392	4.5	Translation	| Symbols: | Protein of unknown function (DUF674) | chr5:47570-49512 FORWARD LENGTH=1686
AT5G01215	UCCGCUAGAUAUAUCAAACUG	281	2.5	Cleavage	| Symbols: | other RNA | chr5:84736-86215 REVERSE LENGTH=1480
AT5G01220	UGACACCGAUUCUGAUUGCAU	377	4.5	Cleavage	| Symbols: SQD2 | sulfoquinovosyldiacylglycerol 2 | chr5:86585-89986 REVERSE LENGTH=1956
AT5G01240	UUACGAGACUCUAGCCCAGCU	3733	4	Cleavage	| Symbols: LAX1 | like AUXIN RESISTANT 1 | chr5:98533-101835 FORWARD LENGTH=1699
AT5G01550	CUUCGAGGAGAUAUGACGCGCC	513	5	Cleavage	| Symbols: LECRKA4.2 | lectin receptor kinase a4.1 | chr5:214517-216583 REVERSE LENGTH=2067
AT5G01560	UUCGAGGAGAUAUGACGCGCC	4887	4.5	Cleavage	| Symbols: LECRKA4.3 | lectin receptor kinase a4.3 | chr5:218138-220530 REVERSE LENGTH=2393
AT5G01590	UGACGGAAGCUACAGAGGAUG	108	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, chloroplast envelope; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages;
AT5G01715	UUUUGCUUAGACUUAGAAACU	179	4	Cleavage	| Symbols: | pseudogene, antisense mRNA to gene At5g01720, blastp match of 29% identity and 3.2e-13 P-value to GP|12848653|dbj|BAB28039.1||AK012109 unnamed protein product {Mus musculus} | chr5:267185-269354 FORWARD LENGTH
AT5G01740	UAUGCAUAACUUGGGACUUACC	333	3.5	Cleavage	| Symbols: | Nuclear transport factor 2 (NTF2) family protein | chr5:280722-281445 FORWARD LENGTH=724
AT5G01900	UUGAACAAGCCUGAUGAAGUU	102	4.5	Translation	| Symbols: WRKY62, ATWRKY62 | WRKY DNA-binding protein 62 | chr5:351008-352069 REVERSE LENGTH=976
AT5G01920	UGGCGCUCAACUCUGCAAGGU	10625	3.5	Cleavage	| Symbols: STN8 | Protein kinase superfamily protein | chr5:359107-362904 FORWARD LENGTH=3489
AT5G01930	UCAUGUAGUUCUAGUUCGCCU	245	4	Translation	| Symbols: MAN6, AtMAN6 | Glycosyl hydrolase superfamily protein | chr5:361081-362901 REVERSE LENGTH=1489
AT5G02050	UCUGAACUCAAGGCACCCAAA	493	3.5	Cleavage	| Symbols: | Mitochondrial glycoprotein family protein | chr5:402987-404323 REVERSE LENGTH=1135
AT5G02070	UAUGGCCUGGGAGCAAUCGCA	299	4.5	Cleavage	| Symbols: | Protein kinase family protein | chr5:405895-408220 REVERSE LENGTH=1974
AT5G02080	CUGAGGUCACACGGAUAAUCG	152	2.5	Cleavage	| Symbols: | DNA / pantothenate metabolism flavoprotein | chr5:409811-411557 FORWARD LENGTH=813
AT5G02170	UUGAGAGAUCCCCUGUUACUG	3917	3	Cleavage	| Symbols: | Transmembrane amino acid transporter family protein | chr5:427833-430695 FORWARD LENGTH=1635
AT5G02220	UUCAACUCUUCCCUCUCGAACU	119	4.5	Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:441707-442146 REV
AT5G02400	UCUGUACCGCUGAAUUCUUCC	275	3.5	Cleavage	| Symbols: PLL2 | pol-like 2 | chr5:513561-515896 FORWARD LENGTH=2025
AT5G02480	AUGGAUUUAGAUCACUUGCGUC	196	4.5	Cleavage	| Symbols: | HSP20-like chaperones superfamily protein | chr5:547563-549912 FORWARD LENGTH=2350
AT5G02520	UAUCUCUGUCGUUACGAACCU	295	4	Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: SANT associated (InterPro:IPR015216); BEST Arabidopsis thaliana protein match is: kinase interacting family protein (TAIR:AT1G58210.1); Has 842 Blast hits to 736 proteins in 154 species: Archae - 2; B
AT5G02780	UCGAGGGCAGGAACAUUGACU	334	3.5	Cleavage	| Symbols: GSTL1 | glutathione transferase lambda 1 | chr5:630876-632683 FORWARD LENGTH=987
AT5G02820	AUUGACGUCGAGUAUGAGCCU	2734	4.5	Translation	| Symbols: RHL2, BIN5 | Spo11/DNA topoisomerase VI, subunit A protein | chr5:642558-644394 FORWARD LENGTH=1655
AT5G02960	UGUGGAUACAAGAGUUGGGCU	111	3.5	Translation	| Symbols: | Ribosomal protein S12/S23 family protein | chr5:693079-694515 REVERSE LENGTH=749
AT5G03180	UAUGCUUCUGUUGAUCCACCU	344	4	Cleavage	| Symbols: | RING/U-box superfamily protein | chr5:754016-756494 REVERSE LENGTH=1669
AT5G03250	UUUGGGUUUGGGUUAACUGCU	225	3	Cleavage	| Symbols: | Phototropic-responsive NPH3 family protein | chr5:774401-777048 FORWARD LENGTH=2162
AT5G03310	CUCACAAGUGAUAUAGGGCUU	208	3.5	Cleavage	| Symbols: | SAUR-like auxin-responsive protein family | chr5:799224-799706 REVERSE LENGTH=483
AT5G03330	UCCUAUCCAGUCUGAAGAACGC	272	2	Translation	| Symbols: | Cysteine proteinases superfamily protein | chr5:807666-809763 FORWARD LENGTH=1288
AT5G03360	UGAAUGACAAACUGGACAAGCU	583	4	Translation	| Symbols: | DC1 domain-containing protein | chr5:817864-820139 FORWARD LENGTH=2276
AT5G03406	UUGAACAAGCCUGAUGAAGUU	102	5	Cleavage	| Symbols: | Class II aaRS and biotin synthetases superfamily protein | chr5:839885-841875 FORWARD LENGTH=1304
AT5G03520	UGGAGAUGAUAGAUUAUGCGC	126	3.5	Cleavage	| Symbols: ATRAB8C, ATRABE1D, ATRAB-E1D, RAB-E1D, RAB8C | RAB GTPase homolog 8C | chr5:883463-885422 FORWARD LENGTH=1135
AT5G03540	UUGACUUCAGACCUGCGCGUG	131	3.5	Translation	| Symbols: ATEXO70A1, EXO70A1 | exocyst subunit exo70 family protein A1 | chr5:889566-894167 FORWARD LENGTH=2208
AT5G03610	UUUAGGAUUGUUGCAUAUGCA	1164	3.5	Cleavage	| Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:915465-918485 FORWARD LENGTH=1424
AT5G03630	UCUGAACUCAAGGCACCCAAA	493	3.5	Cleavage	| Symbols: ATMDAR2 | Pyridine nucleotide-disulphide oxidoreductase family protein | chr5:922166-924683 REVERSE LENGTH=1587
AT5G03668	UUCGAGAACUCCCUGACCCGA	1272	4.5	Translation	| Symbols: | other RNA | chr5:947101-948967 REVERSE LENGTH=1667
AT5G03740	UUCCCCUAGAAUUCUUUCCCU	1646	3.5	Cleavage	| Symbols: HD2C, HDT3 | histone deacetylase 2C | chr5:981876-984200 FORWARD LENGTH=1242
AT5G03770	UCCGCUAGAUAUAUCAAACUG	281	3	Cleavage	| Symbols: KDTA | KDO transferase A | chr5:995160-997848 FORWARD LENGTH=1601
AT5G03900	CUAGAAUUCUUUCCCUUUCCU	235	4	Translation	| Symbols: | Iron-sulphur cluster biosynthesis family protein | chr5:1048295-1052387 FORWARD LENGTH=2013
AT5G03940	UGACACCGAUUCUGAUAGCUU	823	3.5	Cleavage	| Symbols: FFC, 54CP, CPSRP54, SRP54CP | chloroplast signal recognition particle 54 kDa subunit | chr5:1060134-1063319 REVERSE LENGTH=1888
AT5G04010	UAUGCUUCUGUUGAUCCACCU	344	4.5	Translation	| Symbols: | F-box family protein | chr5:1080105-1081074 REVERSE LENGTH=970
AT5G04020	UGAGACACAACAGGGAGAAUC	244	4.5	Cleavage	| Symbols: | calmodulin binding | chr5:1081611-1086546 REVERSE LENGTH=4780
AT5G04040	UUGAGAGCACUCCACCGACUGA	140	4.5	Translation	| Symbols: SDP1 | Patatin-like phospholipase family protein | chr5:1089342-1093179 FORWARD LENGTH=3275
AT5G04290	UUUGUUAAACUCAUGGUCACCC	165	4	Cleavage	| Symbols: KTF1, SPT5L | kow domain-containing transcription factor 1 | chr5:1196069-1202653 FORWARD LENGTH=4482
AT5G04320	UGGCGCUCAACUCUGCGAGGU	1187	4.5	Cleavage	| Symbols: | Shugoshin C terminus | chr5:1209197-1212578 FORWARD LENGTH=1945
AT5G04480	UCGAGUAUGAGCCUGAGUCAUG	250	3	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1271518-1277946 REVERSE LENGTH=3629
AT5G04530	UUAUGAGACUCUAGCCCAGCU	149	4	Cleavage	| Symbols: KCS19 | 3-ketoacyl-CoA synthase 19 | chr5:1291822-1293688 REVERSE LENGTH=1867
AT5G04540	UGACGUCGAGUAUGAGCCUGA	416	5	Cleavage	| Symbols: | Myotubularin-like phosphatases II superfamily | chr5:1296442-1302444 REVERSE LENGTH=3031
AT5G04620	UGAGAACGCUCUGCCAUUGGA	158	4	Cleavage	| Symbols: ATBIOF, BIOF | biotin F | chr5:1327213-1330091 FORWARD LENGTH=1667
AT5G04660	UACGUCACUGGCGAAUUCCUGGA	271	4	Translation	| Symbols: CYP77A4 | cytochrome P450, family 77, subfamily A, polypeptide 4 | chr5:1335995-1337670 FORWARD LENGTH=1676
AT5G04680	UUUGAGAGCACUCCACCGACU	156	3.5	Translation	| Symbols: | Ankyrin repeat family protein | chr5:1346238-1348857 REVERSE LENGTH=2165
AT5G04710	CGUCACUGCGAAUUCCUGGAG	272	5	Cleavage	| Symbols: | Zn-dependent exopeptidases superfamily protein | chr5:1356990-1360247 REVERSE LENGTH=1983
AT5G04740	UUGGACGUCUCUACUAUGAGA	437	4.5	Cleavage	| Symbols: | ACT domain-containing protein | chr5:1368542-1371480 REVERSE LENGTH=863
AT5G04860	UUAUGAGACUCUAGCCCAGCU	149	5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G11760.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; O
AT5G04870	AUUUGAACUCAUGGAUACCCU	768	5	Cleavage	| Symbols: CPK1, ATCPK1 | calcium dependent protein kinase 1 | chr5:1416783-1420338 REVERSE LENGTH=2526
AT5G04920	UGACGCCAAUUCUGAAAGUUU	154	4	Cleavage	| Symbols: | EAP30/Vps36 family protein | chr5:1438959-1441983 REVERSE LENGTH=1868
AT5G05000	UUCUUCAGACUGGAUAGGACU	265	2.5	Cleavage	| Symbols: TOC34, ATTOC34, OEP34 | translocon at the outer envelope membrane of chloroplasts 34 | chr5:1474113-1476019 REVERSE LENGTH=1142
AT5G05010	UAGAGUUAAGUUGGGACAGGA	199	2.5	Cleavage	| Symbols: | clathrin adaptor complexes medium subunit family protein | chr5:1476673-1480197 FORWARD LENGTH=2007
AT5G05200	AAAGUCAAGAACCCCAACCCU	201	2.5	Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:1544007-1547164 REVERSE LENGTH=1904
AT5G05280	UUGCAGAGAUGGAUGUACAAC	101	3.5	Cleavage	| Symbols: | RING/U-box superfamily protein | chr5:1565447-1566391 REVERSE LENGTH=945
AT5G05282	UUGCAGAGAUGGAUGUACAAC	101	3.5	Cleavage	| Symbols: CPuORF64 | conserved peptide upstream open reading frame 64 | chr5:1565447-1566391 REVERSE LENGTH=945
AT5G05470	UGACGCCAAUUCUGAAAGUUU	154	4	Cleavage	| Symbols: EIF2 ALPHA, ATEIF2-A2, EIF2-A2 | eukaryotic translation initiation factor 2 alpha subunit | chr5:1620458-1622340 FORWARD LENGTH=1282
AT5G05657	UAGUGACCGAGUAGUACCACC	461	4.5	Cleavage	| Symbols: | BEST Arabidopsis thaliana protein match is: Late embryogenesis abundant (LEA) hydroxyproline-rich glycoprotein family (TAIR:AT5G06330.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metaza
AT5G05690	UUUGGGUUUGGGUUAACUGCU	225	3.5	Cleavage	| Symbols: CPD, CYP90A, CYP90, CBB3, DWF3, CYP90A1 | Cytochrome P450 superfamily protein | chr5:1702688-1706787 REVERSE LENGTH=1635
AT5G05730	UCUGUAUGCAUAACUUGGGAC	1212	4	Cleavage	| Symbols: ASA1, TRP5, AMT1, WEI2, JDL1 | anthranilate synthase alpha subunit 1 | chr5:1719557-1722903 REVERSE LENGTH=2063

AT5G05760	UGACACCGAUUCUGAUUGCAU	377	4	Cleavage	| Symbols: SYP31, ATSED5, ATSYP31, SED5 | syntaxin of plants 31 | chr5:1728893-1731021 REVERSE LENGTH=1347
AT5G05880	UACCCGUACGUCGCUUACAAG	3223	4.5	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1769648-1771515 FORWARD LENGTH=1356
AT5G05890	UACCCGUACGUCGCUUACAAG	3223	4	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1772543-1774113 FORWARD LENGTH=1493
AT5G05900	UACCCGUACGUCGCUUACAAG	3223	4.5	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:1774513-1776381 FORWARD LENGTH=1353
AT5G05960	UCACUCGACCACAACAGGCUG	106	4	Translation	| Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:1790231-1790833 FORWARD LENGTH=515
AT5G06050	UUACGAGACUCUAGCCCAGCU	3733	3.5	Translation	| Symbols: | Putative methyltransferase family protein | chr5:1820132-1823771 FORWARD LENGTH=2312
AT5G06260	UAGAGUUAAGUUGGGACAGGA	199	4	Cleavage	| Symbols: | TLD-domain containing nucleolar protein | chr5:1902599-1905101 REVERSE LENGTH=1697
AT5G06510	UGACGGUUCAGAUUCAGGAGC	107	4	Translation	| Symbols: NF-YA10 | nuclear factor Y, subunit A10 | chr5:1984991-1987044 FORWARD LENGTH=1362
AT5G06540	UCUGUAUGCAUAACUUGGGAC	1212	3.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:1999181-2001049 REVERSE LENGTH=1869
AT5G06660	AUCAUCCUCGGAUCAAACCCU	222	4	Cleavage	| Symbols: | Protein of unknown function DUF106, transmembrane | chr5:2046810-2047794 FORWARD LENGTH=985
AT5G06780	UCGAGGGCAGGAACAUUGACU	334	3.5	Cleavage	| Symbols: | Emsy N Terminus (ENT)/ plant Tudor-like domains-containing protein | chr5:2093883-2097043 REVERSE LENGTH=1489
AT5G06850	AUGGAUUUAGAUCACUUGCGUC	196	4	Cleavage	| Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr5:2126975-2130443 REVERSE LENGTH=3081
AT5G06930	UGGCGCUCAACUCUGCAAGGU	10625	4	Cleavage	| Symbols: | LOCATED IN: chloroplast; EXPRESSED IN: 15 plant structures; EXPRESSED DURING: 7 growth stages; BEST Arabidopsis thaliana protein match is: nucleolar protein gar2-related (TAIR:AT2G42320.2); Has 3369 Blast hits to 1526 proteins
AT5G06960	UGCACUCGCUAGGUCUGGCAG	378	3.5	Translation	| Symbols: OBF5, TGA5 | OCS-element binding factor 5 | chr5:2154822-2157646 FORWARD LENGTH=1528
AT5G06970	UACACUCACUUGAUCUAGGAG	223	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF810) | chr5:2158228-2166398 REVERSE LENGTH=3781
AT5G07010	UACAAAUUCGAGCACUCCCUG	156	5	Cleavage	| Symbols: ATST2A, ST2A | sulfotransferase 2A | chr5:2174678-2176106 REVERSE LENGTH=1429
AT5G07150	CUCGGGAGAAAGAAGAAGGCU	259	3.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr5:2215820-2217983 FORWARD LENGTH=1662
AT5G07180	CAAACUGGACAAGCUACUGCU	324	5	Cleavage	| Symbols: ERL2 | ERECTA-like 2 | chr5:2227571-2233417 REVERSE LENGTH=3305
AT5G07250	UGUGACACCGAUUCUGAUAGC	115	4	Cleavage	| Symbols: ATRBL3, RBL3 | RHOMBOID-like protein 3 | chr5:2274260-2275990 REVERSE LENGTH=1132
AT5G07290	CUUCUUCAAGAAGAUCGUCCU	132	2.5	Cleavage	| Symbols: AML4, ML4 | MEI2-like 4 | chr5:2293353-2298976 FORWARD LENGTH=3695
AT5G07350	UUGGACGUCUCUACUAUGAGA	437	4	Cleavage	| Symbols: Tudor1, AtTudor1, TSN1 | TUDOR-SN protein 1 | chr5:2320021-2325419 REVERSE LENGTH=3182
AT5G07440	UUGGACGCCUCUACUAUGAGA	679	4.5	Cleavage	| Symbols: GDH2 | glutamate dehydrogenase 2 | chr5:2355940-2358194 FORWARD LENGTH=1520
AT5G07480	UCAUAUGGACUUUGGCUACACC	101	5	Cleavage	| Symbols: KUOX1 | KAR-UP oxidoreductase 1 | chr5:2367167-2369554 FORWARD LENGTH=1023
AT5G07560	UGUGGAUACAAGAGCUGGGCU	215	4	Cleavage	| Symbols: GRP20, ATGRP20 | glycine-rich protein 20 | chr5:2390207-2391075 REVERSE LENGTH=754
AT5G07630	UUAAUCCAAGUAGCUGACUCU	2805	3.5	Cleavage	| Symbols: | lipid transporters | chr5:2410703-2414711 FORWARD LENGTH=2024
AT5G07660	AUUUCAGUGAGCACGUACCUC	200	5	Cleavage	| Symbols: SMC6A | structural maintenance of chromosomes 6A | chr5:2422839-2429912 FORWARD LENGTH=3177
AT5G07670	UAUCCUGAGAGCGGUGCUGGC	334	5	Cleavage	| Symbols: | RNI-like superfamily protein | chr5:2430146-2432196 FORWARD LENGTH=1837
AT5G07710	UUGGCGACCGAUCUCUGAAAG	334	2	Cleavage	| Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:2453135-2455546 FORWARD LENGTH=1771
AT5G07770	UAGAUAACAAGAACUCUUUCU	107	3.5	Cleavage	| Symbols: | Actin-binding FH2 protein | chr5:2474684-2479402 FORWARD LENGTH=2600
AT5G07790	UUCUGUAGCACGAGGUAUCCU	302	3	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G6130
AT5G07990	UGACGGAAGCUACAGAGGAUG	108	4	Translation	| Symbols: TT7, CYP75B1, D501 | Cytochrome P450 superfamily protein | chr5:2560394-2563109 FORWARD LENGTH=1835
AT5G08020	UGUGGUGUACCUCUCACGUCU	112	4.5	Cleavage	| Symbols: ATRPA70B, RPA70B | RPA70-kDa subunit B | chr5:2572107-2574879 FORWARD LENGTH=1815
AT5G08030	CCGAUUCUGAUUGCAUGUGGU	186	3	Cleavage	| Symbols: | PLC-like phosphodiesterases superfamily protein | chr5:2575033-2576783 REVERSE LENGTH=1251
AT5G08080	UUCUGAUUGCAUGUGGUGUACC	110	3	Cleavage	| Symbols: SYP132, ATSYP132 | syntaxin of plants 132 | chr5:2588342-2591316 FORWARD LENGTH=1315
AT5G08185	UUUUUCGGACUAGAUAGGACU	107	4.5	Cleavage	| Symbols: MIR162A | microRNA162A | chr5:2634101-2635436 REVERSE LENGTH=580
AT5G08200	UUGAGAUAUCCCCUGUUACUG	106	4	Cleavage	| Symbols: | peptidoglycan-binding LysM domain-containing protein | chr5:2638036-2640824 FORWARD LENGTH=1895
AT5G08315	UUGAGAUAUCCCCUGUUACUG	106	4	Translation	| Symbols: | Defensin-like (DEFL) family protein | chr5:2676177-2676580 REVERSE LENGTH=249
AT5G08430	UGACGGAAGCUACAGAGGAUG	108	3.5	Translation	| Symbols: | SWIB/MDM2 domain;Plus-3;GYF | chr5:2716700-2720212 FORWARD LENGTH=2053
AT5G08450	UACAGAAUAGGCUUAAGUAAC	189	4.5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 25 plant structures; EXPRESSED DURING: 15 growth stages; CONTAINS InterPro D
AT5G08480	AACAAAACUGUUGAACAAGCCU	111	3	Translation	| Symbols: | VQ motif-containing protein | chr5:2743620-2745111 FORWARD LENGTH=918
AT5G08535	UUUAGCCUGAGGUUGGACGCC	213	4.5	Cleavage	| Symbols: | D111/G-patch domain-containing protein | chr5:2762029-2763432 FORWARD LENGTH=786
AT5G08540	UAAGCAUUUUGAUUCACCGGA	285	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast thylakoid membrane, chloroplast, chloroplast envelope; EXPRESSED IN: 24 plant structures; EXPRE
AT5G08650	CCUGAGCCUAGUGACCGAGUA	270	4.5	Cleavage	| Symbols: | Small GTP-binding protein | chr5:2806323-2813264 REVERSE LENGTH=2300
AT5G09350	CAUCAAGAACCGGUCAUGCCU	125	4	Cleavage	| Symbols: PI-4KBETA2, PI4KBETA2 | phosphatidylinositol 4-OH kinase beta2 | chr5:2899123-2906146 REVERSE LENGTH=4129
AT5G09410	UCACUUUGCUGAACAUGUACC	138	4	Cleavage	| Symbols: EICBP.B, CAMTA1 | ethylene induced calmodulin binding protein | chr5:2921268-2927416 FORWARD LENGTH=3284
AT5G09440	UAGUGACCGAGUAGUACCACC	461	4.5	Cleavage	| Symbols: EXL4 | EXORDIUM like 4 | chr5:2938347-2939461 FORWARD LENGTH=1115
AT5G09550	CUUCCCCUAGAAUUCUUUCCC	401	3.5	Cleavage	| Symbols: | GDP dissociation inhibitor family protein / Rab GTPase activator family protein | chr5:2963777-2966727 FORWARD LENGTH=1673
AT5G09640	UCAUCUGCAGUAAGUCCCUGA	104	3.5	Cleavage	| Symbols: SNG2, SCPL19 | serine carboxypeptidase-like 19 | chr5:2988314-2991156 FORWARD LENGTH=1647
AT5G09690	UUCUGAAGGACAAGAUCAGCU	351	4	Cleavage	| Symbols: ATMGT7, MGT7, MRS2-7 | magnesium transporter 7 | chr5:3000809-3003262 REVERSE LENGTH=1413
AT5G09820	UGGCAUCGAAUUUGAACUCAU	178	3.5	Cleavage	| Symbols: | Plastid-lipid associated protein PAP / fibrillin family protein | chr5:3055779-3057447 REVERSE LENGTH=1200
AT5G09840	UGAGAACAUUGACUUCAGACCU	158	4	Cleavage	| Symbols: | Putative endonuclease or glycosyl hydrolase | chr5:3058997-3061970 FORWARD LENGTH=2805
AT5G09850	UCUGUACCGCUGAAUUCUUCC	275	3.5	Translation	| Symbols: | Transcription elongation factor (TFIIS) family protein | chr5:3063251-3065889 REVERSE LENGTH=1967
AT5G09930	UCGAGUGACUUUGGAGCCAUU	244	3.5	Cleavage	| Symbols: ATGCN2, GCN2 | ABC transporter family protein | chr5:3097643-3100241 REVERSE LENGTH=2037
AT5G09980	UCGACCACACUGUCAUGAUCU	174	4.5	Cleavage	| Symbols: PROPEP4 | elicitor peptide 4 precursor | chr5:3122731-3123964 FORWARD LENGTH=541
AT5G10120	UCCCAACCCAUGAUCUAAGCG	236	4	Cleavage	| Symbols: | Ethylene insensitive 3 family protein | chr5:3169732-3171147 FORWARD LENGTH=1416
AT5G10160	UAGCUAACAAGAACUCUUUCU	1828	4	Cleavage	| Symbols: | Thioesterase superfamily protein | chr5:3185746-3187312 FORWARD LENGTH=886
AT5G10240	UGGCAGUAGGAGUACACGACU	163	3	Cleavage	| Symbols: ASN3 | asparagine synthetase 3 | chr5:3212688-3216466 REVERSE LENGTH=2028
AT5G10300	UUUAGGAUUGUUGCAUAUGCA	1164	3.5	Cleavage	| Symbols: ATMES5, MES5, HNL | methyl esterase 5 | chr5:3239617-3240870 FORWARD LENGTH=990
AT5G10320	UCUUCGACUGAGGUAAGCGCCU	355	4	Translation	| Symbols: | unknown protein; Has 54 Blast hits to 53 proteins in 19 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fungi - 0; Plants - 50; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:3243956-3246721 REVERSE LENGTH=1551
AT5G10370	UUGAGAGAUCCCCUGUUACUG	3917	4.5	Cleavage	| Symbols: | helicase domain-containing protein / IBR domain-containing protein / zinc finger protein-related | chr5:3261245-3267344 FORWARD LENGTH=5484
AT5G10420	UUUAGGAUUGUUGCAUAUGCA	1164	4	Cleavage	| Symbols: | MATE efflux family protein | chr5:3273553-3276490 REVERSE LENGTH=1495
AT5G10490	UAUAGGGCUUGAAAGAAAGUC	535	3	Cleavage	| Symbols: MSL2 | MSCS-like 2 | chr5:3300225-3304761 REVERSE LENGTH=2268
AT5G10540	UGACGGAAGCUACAGAGGAUG	108	2.5	Cleavage	| Symbols: | Zincin-like metalloproteases family protein | chr5:3328065-3334971 FORWARD LENGTH=2852
AT5G10660	UUCUUGUGAACUUGACCGGGA	158	2.5	Cleavage	| Symbols: | calmodulin-binding protein-related | chr5:3370518-3372348 FORWARD LENGTH=1394
AT5G10690	UGCCAUGAUCGAGAGCUGCCU	164	4.5	Translation	| Symbols: | pentatricopeptide (PPR) repeat-containing protein / CBS domain-containing protein | chr5:3374393-3377451 REVERSE LENGTH=1912
AT5G10750	UACGCUAGGGAGAUAUCUGCC	122	4	Cleavage	| Symbols: | Protein of unknown function (DUF1336) | chr5:3398951-3400156 FORWARD LENGTH=1206
AT5G10770	CUUCGACUGAGGUAAGCGCCU	234	4.5	Cleavage	| Symbols: | Eukaryotic aspartyl protease family protein | chr5:3403110-3405448 REVERSE LENGTH=1763
AT5G10810	UGGCGCUCAACUCUGCAAGGU	10625	4	Translation	| Symbols: ATER, ER | enhancer of rudimentary protein, putative | chr5:3418666-3420635 REVERSE LENGTH=640
AT5G10860	UCACCUCGCAUCUUAGAACUG	146	4.5	Cleavage	| Symbols: | Cystathionine beta-synthase (CBS) family protein | chr5:3428891-3430470 REVERSE LENGTH=1025
AT5G10910	UUCCCCUAGAAUUCUUUCCCU	1646	4.5	Cleavage	| Symbols: | mraW methylase family protein | chr5:3439553-3441582 FORWARD LENGTH=1405
AT5G10946	UGAGAACAUUGACUUCAGACCU	158	3.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; M
AT5G10950	UGAAAUAAAACUGAACCAUGCC	263	4.5	Translation	| Symbols: | Tudor/PWWP/MBT superfamily protein | chr5:3459273-3461734 REVERSE LENGTH=1574
AT5G11090	UGAAUGACAAACUGGACAAGCU	583	4.5	Cleavage	| Symbols: | serine-rich protein-related | chr5:3524680-3525846 FORWARD LENGTH=1167
AT5G11110	UAUCCUGAGAGCGGUGCUGGC	334	4.5	Cleavage	| Symbols: SPS1, ATSPS2F, KNS2, SPS2F | sucrose phosphate synthase 2F | chr5:3536226-3541133 FORWARD LENGTH=3576
AT5G11290	UCCGCUAGAUAUAUCAAACUG	281	4	Cleavage	| Symbols: | Plant protein of unknown function (DUF247) | chr5:3599001-3600472 FORWARD LENGTH=1472
AT5G11350	UCUAGUUCGCGUUUUUCAGAC	163	4	Cleavage	| Symbols: | DNAse I-like superfamily protein | chr5:3621561-3625645 FORWARD LENGTH=2520
AT5G11380	UAACCGGGGCAUGAGAGACUC	100	3	Cleavage	| Symbols: DXPS3 | 1-deoxy-D-xylulose 5-phosphate synthase 3 | chr5:3629998-3633441 FORWARD LENGTH=2468
AT5G11470	UAUGGCCUGGGAGCAAUCGCA	299	3.5	Cleavage	| Symbols: | bromo-adjacent homology (BAH) domain-containing protein | chr5:3662717-3667923 REVERSE LENGTH=2413
AT5G11540	UGUGACACCGAUUCUGAUUGC	114	3.5	Cleavage	| Symbols: | D-arabinono-1,4-lactone oxidase family protein | chr5:3703002-3704981 REVERSE LENGTH=1758
AT5G11690	UUGAGAGCACUCCACCGACUG	261	3.5	Translation	| Symbols: ATTIM17-3, TIM17-3 | translocase inner membrane subunit 17-3 | chr5:3761244-3762346 FORWARD LENGTH=856
AT5G11750	UGGGCGCUUAUACUUUGGGUU	115	4.5	Translation	| Symbols: | Ribosomal protein L19 family protein | chr5:3787230-3789212 FORWARD LENGTH=1089
AT5G11770	UUCGGACUGGAUAGGACUAGG	101	3.5	Translation	| Symbols: | NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial | chr5:3790806-3793000 REVERSE LENGTH=1070
AT5G12020	UACAGAAUAGGCUUAAGUAAC	189	3.5	Cleavage	| Symbols: HSP17.6II | 17.6 kDa class II heat shock protein | chr5:3882237-3882938 REVERSE LENGTH=702
AT5G12150	UCUAGUUCACAUUUUUCGGAC	427	4	Cleavage	| Symbols: | Rho GTPase activation protein (RhoGAP) with PH domain | chr5:3924126-3930305 REVERSE LENGTH=2956
AT5G12330	UAUGCUUCUGUUGAUCCACCU	344	3.5	Translation	| Symbols: LRP1 | Lateral root primordium (LRP) protein-related | chr5:3987375-3989754 REVERSE LENGTH=1586
AT5G12370	UGCACUCGCUAGGUCUGGCAG	378	4.5	Translation	| Symbols: SEC10 | exocyst complex component sec10 | chr5:4002775-4008803 REVERSE LENGTH=2799
AT5G12420	UGUGAGUGUUUGUGAGGUCUU	178	3	Cleavage	| Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:4024314-4026741 REVERSE LENGTH=1723
AT5G12470	UGUGUAUGCAUAACUUGGGAC	106	3.5	Cleavage	| Symbols: | Protein of unknown function (DUF3411) | chr5:4044622-4047436 REVERSE LENGTH=1635
AT5G12840	UAUGCUUCUGUUGAUCCACCU	344	3.5	Cleavage	| Symbols: HAP2A, EMB2220, ATHAP2A, NF-YA1 | nuclear factor Y, subunit A1 | chr5:4050840-4053534 REVERSE LENGTH=1275

AT5G12850	AUUGAUUCUGCACUCAAGGGC	128	5	Cleavage	| Symbols: | CCCH-type zinc finger protein with ARM repeat domain | chr5:4056187-4059580 FORWARD LENGTH=2773
AT5G13000	UACGCGACCGCGGUGCUGGCC	119	5	Cleavage	| Symbols: ATGSL12, gsl12 | glucan synthase-like 12 | chr5:4110295-4121427 REVERSE LENGTH=6160
AT5G13050	UCAAGCGAUUGGAAGGAUUGUU	102	4.5	Cleavage	| Symbols: 5-FCL | 5-formyltetrahydrofolate cycloligase | chr5:4136556-4138721 REVERSE LENGTH=1196
AT5G13060	CCUGAGCCUAGUGACCGAGUA	270	3.5	Translation	| Symbols: ABAP1 | ARMADILLO BTB protein 1 | chr5:4142958-4147091 FORWARD LENGTH=2353
AT5G13180	UUCGAGGAGAUAUGACGCGCC	4887	5	Cleavage	| Symbols: ANAC083, VNI2, NAC083 | NAC domain containing protein 83 | chr5:4196572-4197848 FORWARD LENGTH=1101
AT5G13200	UUUGAUCCGAGGAUGAUGGAU	816	3	Translation	| Symbols: | GRAM domain family protein | chr5:4207004-4208289 FORWARD LENGTH=1106
AT5G13240	UUGAAAGACUUGUGGAUCACC	926	4	Cleavage	| Symbols: | transcription regulators | chr5:4225005-4227613 REVERSE LENGTH=1058
AT5G13400	UGAAGGACAAGCUCAGCUGCU	1483	2.5	Translation	| Symbols: | Major facilitator superfamily protein | chr5:4296688-4299223 REVERSE LENGTH=2185
AT5G13410	AUUGUGUAUAAUUUUGAGCCU	108	4	Cleavage	| Symbols: | FKBP-like peptidyl-prolyl cis-trans isomerase family protein | chr5:4299705-4301780 REVERSE LENGTH=970
AT5G13520	UCCACCGACUGAUGACAAUGU	1524	4.5	Cleavage	| Symbols: | peptidase M1 family protein | chr5:4341948-4344671 REVERSE LENGTH=2120
AT5G13560	UCGAACAAGAGCUGAACGUCU	423	3.5	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G37370.1); Has 12055 Blast hits to 8846 proteins in 811 species: Archae - 217; Bacteria - 1046; Metazoa - 6104; Fungi - 1115; Plants - 528; Vir
AT5G13590	UCACUGUGAAUUCCUGGAGUU	123	3.5	Cleavage	| Symbols: | unknown protein; Has 150 Blast hits to 121 proteins in 42 species: Archae - 0; Bacteria - 8; Metazoa - 80; Fungi - 5; Plants - 17; Viruses - 0; Other Eukaryotes - 40 (source: NCBI BLink). | chr5:4373239-4379356 REVERSE LENGTH=5101
AT5G13630	UACACUCACUUGAUCUAGGAG	223	4	Translation	| Symbols: GUN5, CCH, CHLH, CCH1, ABAR | magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH) | chr5:4387334-4392227 REVERSE LENGTH=4523
AT5G13640	CGUCACUGCGAAUUCCUGGAG	272	5	Cleavage	| Symbols: ATPDAT, PDAT, PDAT1 | phospholipid:diacylglycerol acyltransferase | chr5:4393062-4397541 FORWARD LENGTH=2811
AT5G13880	UAAUAAGGAGAGUCAGCUACU	298	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G47920.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT5G13920	UCAUCAAUGAACUCAUUUGGCU	103	5	Cleavage	| Symbols: | GRF zinc finger / Zinc knuckle protein | chr5:4485931-4487433 REVERSE LENGTH=1248
AT5G13980	UAACCGGGGCAUGAGAGACUC	100	5	Cleavage	| Symbols: | Glycosyl hydrolase family 38 protein | chr5:4508496-4514425 FORWARD LENGTH=3296
AT5G14050	UGAAAUAAAACUGAACCAUGCC	263	3	Translation	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:4533261-4535301 FORWARD LENGTH=1899
AT5G14060	UCUUCGACUGAGGUAAGCGCCU	355	3.5	Translation	| Symbols: CARAB-AK-LYS | Aspartate kinase family protein | chr5:4535401-4539193 FORWARD LENGTH=2229
AT5G14150	UGAGACACAACAGGGAGAUUC	244	4.5	Cleavage	| Symbols: | Protein of unknown function, DUF642 | chr5:4565172-4566988 REVERSE LENGTH=1416
AT5G14310	UACCGGAGGACGUACAACACC	302	4.5	Cleavage	| Symbols: AtCXE16, CXE16 | carboxyesterase 16 | chr5:4615318-4617615 FORWARD LENGTH=1808
AT5G14350	UCCCAACCCAUGAUCUAAGCG	236	3	Translation	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4627140-4628703 REVERSE LENGTH=726
AT5G14450	UGUGGUCGAGUAGAGCAAUCU	111	4.5	Cleavage	| Symbols: | GDSL-like Lipase/Acylhydrolase superfamily protein | chr5:4658441-4660175 FORWARD LENGTH=1358
AT5G14490	UCACCUCGCAUCUUAGAACUG	146	3	Translation	| Symbols: anac085, NAC085 | NAC domain containing protein 85 | chr5:4670779-4672072 REVERSE LENGTH=1053
AT5G14500	UACCCGUACGUCGCUUAUAAG	185	5	Translation	| Symbols: | aldose 1-epimerase family protein | chr5:4674233-4676765 REVERSE LENGTH=1329
AT5G14750	UUUAGAGAUCCCCUGUUACUG	387	4	Translation	| Symbols: WER, ATMYB66, WER1, MYB66 | myb domain protein 66 | chr5:4763452-4764738 REVERSE LENGTH=816
AT5G14760	AAACAGGACAAGUUACUCGCC	986	4	Cleavage	| Symbols: AO | L-aspartate oxidase | chr5:4768468-4772153 FORWARD LENGTH=2389
AT5G14770	UGAGCCGACAAGAGUAGUAUC	111	3	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:4772881-4775697 REVERSE LENGTH=2817
AT5G14900	UCAAGCGAUUGGAAGGAUUGUU	102	3	Cleavage	| Symbols: | helicase associated (HA2) domain-containing protein | chr5:4822676-4823581 REVERSE LENGTH=906
AT5G15280	CAUUGACUUCAAGCCUGCGCU	190	5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:4962293-4966141 FORWARD LENGTH=3849
AT5G15400	AAACACUCUAGACUCGAUCCU	123	3.5	Translation	| Symbols: | U-box domain-containing protein | chr5:4997611-5003140 REVERSE LENGTH=3503
AT5G15700	CUCAGGCUCAUACUCGACGUC	968	3	Translation	| Symbols: | DNA/RNA polymerases superfamily protein | chr5:5115300-5121840 REVERSE LENGTH=3659
AT5G15720	UGUGAGUGUUUGUGAGGUCUU	178	4	Cleavage	| Symbols: GLIP7 | GDSL-motif lipase 7 | chr5:5124525-5126181 REVERSE LENGTH=1280
AT5G15740	UGUCACCGUAGAUUUCUUCCU	123	4	Cleavage	| Symbols: | O-fucosyltransferase family protein | chr5:5134527-5137626 REVERSE LENGTH=2458
AT5G15790	UUCACAUGUCCGGGCUAGGCA	461	4.5	Cleavage	| Symbols: | RING/U-box superfamily protein | chr5:5148744-5151433 FORWARD LENGTH=1534
AT5G15802	UUUGGCGCUCAACUCUGCAAG	3787	3.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35 Blast hits to 35 proteins in 15 species: Archae - 0; Bacteria - 4; Metazoa - 0; Fu
AT5G15820	AUGGAUUUAGAUCACUUGCGUC	196	3.5	Cleavage	| Symbols: | RING/U-box superfamily protein | chr5:5161724-5163030 FORWARD LENGTH=1307
AT5G15845	UCUGUAUGCAUAACUUGGGAC	1212	3.5	Cleavage	| Symbols: | other RNA | chr5:5173185-5177889 FORWARD LENGTH=2248
AT5G15890	UCUGUACCGCUGAAUUCUUCC	275	4	Translation	| Symbols: TBL21 | TRICHOME BIREFRINGENCE-LIKE 21 | chr5:5187587-5189348 REVERSE LENGTH=1681
AT5G15920	UCUUCGACUGAGGUAAGCGCCU	355	3.5	Translation	| Symbols: SMC5 | structural maintenance of chromosomes 5 | chr5:5195683-5199559 FORWARD LENGTH=3279
AT5G16220	UCUUCGACUGAGGUAAGCGCCU	355	4	Translation	| Symbols: | Octicosapeptide/Phox/Bem1p family protein | chr5:5298303-5300610 REVERSE LENGTH=1763
AT5G16290	UUUAGAGAUCCCCUGUUACUG	387	3.5	Cleavage	| Symbols: VAT1 | VALINE-TOLERANT 1 | chr5:5333764-5337744 FORWARD LENGTH=1804
AT5G16350	UGUGAGUGUUUGUGAGGUCUU	178	3.5	Cleavage	| Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:5352626-5355070 FORWARD LENGTH=1658
AT5G16520	UUGGACGUCUCUACUAUGAGA	437	4	Translation	| Symbols: | unknown protein; Has 25 Blast hits to 25 proteins in 9 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 25; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:5394608-5397455 REVERSE LENGTH=2043
AT5G16540	UUUGAUCCGAGGAUGAUGGAU	816	3	Translation	| Symbols: ZFN3 | zinc finger nuclease 3 | chr5:5403203-5405147 FORWARD LENGTH=1454
AT5G16560	UUUAACAACUAAGGUUCCUGU	1055	4	Cleavage	| Symbols: KAN, KAN1 | Homeodomain-like superfamily protein | chr5:5406863-5411424 REVERSE LENGTH=2046
AT5G16660	UGGCAGUAGGAGUACACGACU	163	3	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast, membrane; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 14 growth stages; BEST Arab
AT5G16680	CUUCCCCUAGAAUUCUUUCCCU	192	4	Translation	| Symbols: | RING/FYVE/PHD zinc finger superfamily protein | chr5:5467373-5473506 REVERSE LENGTH=4395
AT5G16890	UUAGCACCGAGGAUGAUGGAC	291	5	Cleavage	| Symbols: | Exostosin family protein | chr5:5551629-5554917 FORWARD LENGTH=1747
AT5G16900	UAGAGUGUUCAUGUAGUUGCA	232	3.5	Cleavage	| Symbols: | Leucine-rich repeat protein kinase family protein | chr5:5555254-5559715 FORWARD LENGTH=2601
AT5G16910	UUGGUCACACAGUGGACUGUG	104	4	Cleavage	| Symbols: ATCSLD2, CSLD2 | cellulose-synthase like D2 | chr5:5561679-5565580 FORWARD LENGTH=3728
AT5G17160	UGAGAACAUUGACUUCAGACCU	158	3	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G03130.1); Has 14330 Blast hits to 10381 proteins in 896 species: Archae - 94; Bacteria - 2881; Metazoa - 4019; Fungi - 1576; Plants - 515; Vir
AT5G17270	UCUCAUGUAGUUCUAGUUCGCA	1437	4	Cleavage	| Symbols: | Protein prenyltransferase superfamily protein | chr5:5679991-5685597 FORWARD LENGTH=2704
AT5G17300	CUUGGCAUCGAAUUUGAACUC	1059	3.5	Cleavage	| Symbols: RVE1 | Homeodomain-like superfamily protein | chr5:5690227-5692902 REVERSE LENGTH=1839
AT5G17780	UCGAGUGACUUUGGAGCCAUU	244	5	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:5867283-5869050 REVERSE LENGTH=1474
AT5G17840	UGAGAACAUUGACUUCAGACCU	158	4	Cleavage	| Symbols: | DnaJ/Hsp40 cysteine-rich domain superfamily protein | chr5:5895674-5897150 REVERSE LENGTH=765
AT5G17850	UAGGCCUGAGAUUGGACGCCU	875	4	Cleavage	| Symbols: | Sodium/calcium exchanger family protein | chr5:5899253-5900932 FORWARD LENGTH=1680
AT5G17930	UAUUGAUUUUUGGCCUGAGGU	116	3.5	Cleavage	| Symbols: | MIF4G domain-containing protein / MA3 domain-containing protein | chr5:5939998-5944430 REVERSE LENGTH=2634
AT5G17970	UCUAUAGCCAAUGUACUCUACU	106	3.5	Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:5948999-5951619 REVERSE LENGTH=2343
AT5G17980	UAUUGACGUCGAGUAUGAGCC	237	4.5	Cleavage	| Symbols: | C2 calcium/lipid-binding plant phosphoribosyltransferase family protein | chr5:5953596-5956745 FORWARD LENGTH=3150
AT5G18190	UGAAGGAUUUGUGGUUAACCA	474	3	Cleavage	| Symbols: | Protein kinase family protein | chr5:6009967-6014689 REVERSE LENGTH=2674
AT5G18210	UGGCGCUCAACUCUGCGAGGU	1187	4	Translation	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:6017865-6019993 FORWARD LENGTH=1908
AT5G18350	UCAACACUCUGAUACAUCUAG	143	3.5	Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6074069-6078569 REVERSE LENGTH=3738
AT5G18360	UGGAGAUGAUAGAUUAUGCGC	126	3	Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6080049-6083027 REVERSE LENGTH=2703
AT5G18370	UUUAGGAUUGUUGCAUAUGCA	1164	3	Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:6085036-6088926 REVERSE LENGTH=3633
AT5G18390	UUAUCAACGAACUCUUGGCCC	310	3.5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:6090954-6092545 FORWARD LENGTH=1592
AT5G18490	UUCCAGCGUUCUGUAGCCAAC	156	5	Cleavage	| Symbols: | Plant protein of unknown function (DUF946) | chr5:6134152-6136765 REVERSE LENGTH=1996
AT5G18570	UCACCAUUGGCAGCUCUGUACC	187	4	Cleavage	| Symbols: EMB269, ATOBGC, CPSAR1 | GTP1/OBG family protein | chr5:6171661-6174833 REVERSE LENGTH=2234
AT5G18610	UUCGAGAACUCCCUGACCCGA	1272	4	Translation	| Symbols: | Protein kinase superfamily protein | chr5:6192443-6195753 FORWARD LENGTH=2005
AT5G18650	AAACAGGACAAGUUACUCGCC	986	3.5	Cleavage	| Symbols: | CHY-type/CTCHY-type/RING-type Zinc finger protein | chr5:6217912-6220702 FORWARD LENGTH=1480
AT5G18780	UAAGACUGAGAUACGCGUGCCU	152	4	Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr5:6264284-6266097 FORWARD LENGTH=1652
AT5G18820	UGUCACCGUAGAUUUCUUCCU	123	3.5	Cleavage	| Symbols: EMB3007 | TCP-1/cpn60 chaperonin family protein | chr5:6271489-6274327 FORWARD LENGTH=1962
AT5G18900	CUCGGGAGAAAGAAGAAGGCU	259	3.5	Cleavage	| Symbols: | 2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein | chr5:6304215-6306290 REVERSE LENGTH=1215
AT5G19090	UUUGGUUCUGAGUCCCCGCCU	669	4	Cleavage	| Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:6387489-6390024 FORWARD LENGTH=2163
AT5G19130	UGGCGCUCAACUCUGCGAGGU	1187	4.5	Cleavage	| Symbols: | GPI transamidase component family protein / Gaa1-like family protein | chr5:6415920-6419021 REVERSE LENGTH=2327
AT5G19180	UACUCCAGAAACUCACAACGA	113	4	Cleavage	| Symbols: ECR1 | E1 C-terminal related 1 | chr5:6453276-6456014 FORWARD LENGTH=1728
AT5G19260	UUUAGAGAUCCCCUGUUACUG	387	5	Cleavage	| Symbols: | Protein of unknown function (DUF3049) | chr5:6479400-6480446 REVERSE LENGTH=1047
AT5G19310	CUCAUGUAGUUCUAGUUCGCA	102	5	Cleavage	| Symbols: | Homeotic gene regulator | chr5:6498779-6503432 FORWARD LENGTH=3322
AT5G19360	UACCGGAGGACGUACAACACC	302	4.5	Translation	| Symbols: CPK34 | calcium-dependent protein kinase 34 | chr5:6521716-6523780 REVERSE LENGTH=1572
AT5G19390	UCAUCUGCAGUAAGUCCCUGA	104	4	Cleavage	| Symbols: | Rho GTPase activation protein (RhoGAP) with PH domain | chr5:6531540-6537322 FORWARD LENGTH=2690
AT5G19400	UCUGUAUGCAUAACUUGGGAC	1212	4	Cleavage	| Symbols: SMG7 | Telomerase activating protein Est1 | chr5:6540003-6544975 FORWARD LENGTH=3860
AT5G19450	UAUCGAGCACCUACGUCACUG	123	4	Translation	| Symbols: CDPK19, CPK8 | calcium-dependent protein kinase 19 | chr5:6558426-6561534 REVERSE LENGTH=1911
AT5G19530	UGAAAUAAAACUGAACCAUGCC	263	4	Cleavage	| Symbols: ACL5 | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:6588958-6591363 REVERSE LENGTH=1392
AT5G19590	UUGAGAGAUCCCCUGUUACUG	3917	5	Cleavage	| Symbols: | Protein of unknown function, DUF538 | chr5:6610730-6612103 REVERSE LENGTH=735
AT5G19620	UGGCAGUAGGAGUACACGACU	163	4	Cleavage	| Symbols: EMB213, OEP80, ATOEP80, TOC75 | outer envelope protein of 80 kDa | chr5:6623204-6627846 FORWARD LENGTH=2523
AT5G19660	UAGAUAACAAGAACUCUUUCU	107	4	Cleavage	| Symbols: ATSBT6.1, S1P, ATS1P | SITE-1 protease | chr5:6642004-6646530 REVERSE LENGTH=3343
AT5G19680	UCUUCGACUGAGGUAAGCGCCU	355	4.5	Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr5:6649605-6651935 FORWARD LENGTH=1416
AT5G19750	UUUGGCCUGAGGUUGGACGCC	367	4.5	Cleavage	| Symbols: | Peroxisomal membrane 22 kDa (Mpv17/PMP22) family protein | chr5:6677069-6679384 FORWARD LENGTH=1179
AT5G19960	UGUGAGUGUUUGUGAGGUCUU	178	3.5	Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:6743926-6746339 FORWARD LENGTH=1323

AT5G20040	UUGACGACCAACUCCGCUCCU	170	4	Cleavage	| Symbols: IPT9 | isopentenyltransferase 9 | chr5:6767802-6771190 REVERSE LENGTH=1757
AT5G20260	UGGGCGCUUAUACUUUGGGUU	115	5	Cleavage	| Symbols: | Exostosin family protein | chr5:6836806-6839532 REVERSE LENGTH=1377
AT5G20300	UUCCCGUUGGUGUGCGCCAC	196	4.5	Cleavage	| Symbols: | Avirulence induced gene (AIG1) family protein | chr5:6853416-6856977 REVERSE LENGTH=2654
AT5G20330	UGAAGGACAAGAUCAGCUGCU	415	3.5	Cleavage	| Symbols: BETAG4 | beta-1,3-glucanase 4 | chr5:6871561-6873112 FORWARD LENGTH=1552
AT5G20350	UUCGGUCUGGCCAUACUCGGC	147	5	Cleavage	| Symbols: TIP1 | Ankyrin repeat family protein with DHHC zinc finger domain | chr5:6876589-6881270 FORWARD LENGTH=2214
AT5G20450	UUUAAAACCGAGGACUUUUGC	115	3.5	Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Dilute (InterPro:IPR002710); BEST Arabidopsis thaliana protein match is: Myosin family protein with Dil domain (TAIR:AT5G20490.2); Has 1630 Blast hits to 1368 proteins in 340 species: Archae - 22; Ba
AT5G20490	UGACGUCGAGUAUGAGCCUGA	416	3.5	Translation	| Symbols: XIK, ATXIK, XI-17 | Myosin family protein with Dil domain | chr5:6926623-6937506 REVERSE LENGTH=5153
AT5G20600	UUUUGCUUAGACUUAGAAACU	179	3	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: rRNA processing; LOCATED IN: peribosome, small subunit precursor; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMA
AT5G20640	UGUGGUCGAGUAGAGCAAUCU	111	3	Cleavage	| Symbols: | Protein of unknown function (DUF567) | chr5:6984240-6985365 FORWARD LENGTH=947
AT5G20730	UCCUAUCCAGUCUGAAGAACGC	272	3	Cleavage	| Symbols: NPH4, MSG1, IAA21, ARF7, TIR5, BIP | Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related | chr5:7016445-7022042 REVERSE LENGTH=4292
AT5G20870	CGGAGGAAACUUAGCAGCGCC	103	3	Cleavage	| Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:7079975-7081769 REVERSE LENGTH=1598
AT5G20920	UUGGCACUCAACUCUGCAAGG	611	4	Cleavage	| Symbols: EIF2 BETA | eukaryotic translation initiation factor 2 beta subunit | chr5:7094718-7097111 REVERSE LENGTH=1188
AT5G21030	UCAACACUCUGAUACAUCUAG	143	4	Cleavage	| Symbols: | PAZ domain-containing protein / piwi domain-containing protein | chr5:7139892-7144272 REVERSE LENGTH=2553
AT5G21120	UCGGGAUCCUGCUGAAUGGUC	135	2.5	Cleavage	| Symbols: EIL2 | ETHYLENE-INSENSITIVE3-like 2 | chr5:7182621-7184342 FORWARD LENGTH=1722
AT5G22110	CAACUAACAACGAGGGCACUG	198	4.5	Translation	| Symbols: ATDPB2, CYL2, DPB2 | DNA polymerase epsilon subunit B2 | chr5:7330825-7334205 REVERSE LENGTH=1854
AT5G22250	UGAGCCGACAAGAGUAGUAUC	111	3.5	Cleavage	| Symbols: | Polynucleotidyl transferase, ribonuclease H-like superfamily protein | chr5:7365532-7366778 REVERSE LENGTH=1247
AT5G22490	UCCAGUCUGAAGAACGCGAAC	136	4	Cleavage	| Symbols: | O-acyltransferase (WSD1-like) family protein | chr5:7458943-7461049 REVERSE LENGTH=1449
AT5G22500	CUUGGCAUCGAAUUUGAACUC	1059	3.5	Cleavage	| Symbols: FAR1 | fatty acid reductase 1 | chr5:7470443-7474120 FORWARD LENGTH=1778
AT5G22590	UGAGAACAUUGACUUCAGACCU	158	4.5	Translation	| Symbols: | Leucine Rich Repeat protein family | chr5:7504536-7505838 FORWARD LENGTH=915
AT5G22600	UGAGUAGAAUUCGAUCAUAUC	114	5	Cleavage	| Symbols: | FBD / Leucine Rich Repeat domains containing protein | chr5:7510023-7511788 FORWARD LENGTH=1573
AT5G22660	UUAGCACCGAGGAUGAUGGACU	330	4.5	Translation	| Symbols: | FBD, F-box, Skp2-like and Leucine Rich Repeat domains containing protein | chr5:7536290-7537990 REVERSE LENGTH=1528
AT5G22670	UGGAGAUGAUAGAUUAUGCGC	126	3	Cleavage	| Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:7538192-7539685 REVERSE LENGTH=1332
AT5G22700	UAAGACUGAGAUACGCGUGCCU	152	3	Cleavage	| Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:7545516-7547595 REVERSE LENGTH=1583
AT5G22820	UCUGAUUGCAUGUGGUGUACC	109	4	Cleavage	| Symbols: | ARM repeat superfamily protein | chr5:7623440-7626975 REVERSE LENGTH=1902
AT5G22830	UUGAAGGAUUUGUGGUUAACCA	106	2.5	Translation	| Symbols: ATMGT10, GMN10, MGT10, MRS2-11 | magnesium (Mg) transporter 10 | chr5:7627597-7630993 FORWARD LENGTH=1736
AT5G22850	UUGUGAGUGUUUGUGAGGUCU	141	4	Cleavage	| Symbols: | Eukaryotic aspartyl protease family protein | chr5:7633437-7636567 REVERSE LENGTH=2031
AT5G22970	UUGUGGAAUCCGUAGUCUGUA	152	3.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G60000.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Ot
AT5G23090	CAUCAAGAACCGGUCAUGCCU	125	3.5	Cleavage	| Symbols: NF-YB13 | nuclear factor Y, subunit B13 | chr5:7749157-7750388 FORWARD LENGTH=755
AT5G23110	UCGAGUAUGAGCCUGAGUCAUG	250	4	Cleavage	| Symbols: | Zinc finger, C3HC4 type (RING finger) family protein | chr5:7758307-7775671 FORWARD LENGTH=14283
AT5G23150	UCAUGUAGUUCUAGUUCGCCU	245	3.5	Cleavage	| Symbols: HUA2 | Tudor/PWWP/MBT domain-containing protein | chr5:7785835-7792489 FORWARD LENGTH=4926
AT5G23190	UUGGACGUCUCUACUAUGAGA	437	4.5	Cleavage	| Symbols: CYP86B1 | cytochrome P450, family 86, subfamily B, polypeptide 1 | chr5:7803141-7805815 REVERSE LENGTH=2173
AT5G23240	AUUGAUUCUGCACUCAAGGGC	128	3	Translation	| Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:7826732-7828724 REVERSE LENGTH=1713
AT5G23270	UUUGUUAAACUCAUGGUCACCC	165	3	Cleavage	| Symbols: STP11, ATSTP11 | sugar transporter 11 | chr5:7838906-7841026 FORWARD LENGTH=1923
AT5G23390	UCCACCGACUGAUGACAAUGU	1524	4.5	Cleavage	| Symbols: | Plant protein of unknown function (DUF639) | chr5:7870513-7874505 REVERSE LENGTH=2621
AT5G23400	AUUGACGUCGAGUAUGAGCCU	2734	3.5	Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr5:7880335-7882634 FORWARD LENGTH=2300
AT5G23520	UCGACCACACUGUCAUGAUCU	174	4	Cleavage	| Symbols: | smr (Small MutS Related) domain-containing protein | chr5:7929351-7931793 REVERSE LENGTH=1799
AT5G23570	CAAACUGGACAAGCUACUGCU	324	4	Cleavage	| Symbols: SGS3, ATSGS3 | XS domain-containing protein / XS zinc finger domain-containing protein-related | chr5:7943124-7946050 FORWARD LENGTH=2145
AT5G23680	UCCUGAGUACUCUCUUCCAAG	209	4	Cleavage	| Symbols: | Sterile alpha motif (SAM) domain-containing protein | chr5:7985354-7986851 REVERSE LENGTH=1498
AT5G23770	UAGGCCUGAGAUUGGACGCCU	875	4	Cleavage	| Symbols: DUF8 | DOMAIN OF UNKNOWN FUNCTION 724 8 | chr5:8014381-8016913 REVERSE LENGTH=2027
AT5G23780	UAAGCAUUUUGAUUCACCGGA	285	3.5	Cleavage	| Symbols: DUF9, ATDUF9 | DOMAIN OF UNKNOWN FUNCTION 724 9 | chr5:8017192-8019026 REVERSE LENGTH=1380
AT5G23790	CUUGUGAGUGUUUGUGAGGUC	103	3	Cleavage	| Symbols: AtGolS5, GolS5 | galactinol synthase 5 | chr5:8020104-8021597 REVERSE LENGTH=1081
AT5G23800	UGACGCCAAUUCUGAAAGUUU	154	5	Cleavage	| Symbols: ATDUF10, DUF 10 | DOMAIN OF UNKNOWN FUNCTION 724 10 | chr5:8022216-8024689 REVERSE LENGTH=1659
AT5G23910	UACUGGAGGACGUACAGCACU	949	5	Cleavage	| Symbols: | ATP binding microtubule motor family protein | chr5:8068452-8072991 FORWARD LENGTH=2374
AT5G23950	UUUGGCCUGAGGUUGGACACC	133	4	Cleavage	| Symbols: | Calcium-dependent lipid-binding (CaLB domain) family protein | chr5:8082744-8083604 FORWARD LENGTH=861
AT5G24120	UGACGGACAAGAUAAGUUGCU	1505	4	Cleavage	| Symbols: SIGE, SIG5, ATSIG5 | sigma factor E | chr5:8157551-8160229 REVERSE LENGTH=1904
AT5G24200	UCUGGGUAGAUGGGAUCUUAUC	123	3	Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:8203003-8205793 FORWARD LENGTH=1390
AT5G24220	UUGAUCCAAGUAGCUGACUCU	4031	3.5	Cleavage	| Symbols: | Lipase class 3-related protein | chr5:8225861-8227551 FORWARD LENGTH=1131
AT5G24300	UGAAGGAUUUGUGGUUAACCA	474	4.5	Cleavage	| Symbols: SSI1, SSI, ATSS1 | Glycogen/starch synthases, ADP-glucose type | chr5:8266798-8271196 FORWARD LENGTH=2431
AT5G24450	ACAAAACUGUUGAACAAGCCU	1107	5	Cleavage	| Symbols: | Transcription factor IIIC, subunit 5 | chr5:8348242-8353303 FORWARD LENGTH=2003
AT5G24490	UAGAGUGUUCAUGUAGUUGCA	232	3	Cleavage	| Symbols: | 30S ribosomal protein, putative | chr5:8365601-8367460 FORWARD LENGTH=1298
AT5G24550	CCGAUUCUGAUUGCAUGUGGU	186	2.5	Cleavage	| Symbols: BGLU32 | beta glucosidase 32 | chr5:8392059-8395302 REVERSE LENGTH=1605
AT5G24590	UGAGCCGACAAGAGUAGUAUC	111	4	Cleavage	| Symbols: ANAC091, TIP | TCV-interacting protein | chr5:8416662-8418933 REVERSE LENGTH=1824
AT5G24740	UCUGGGUAGAUGGGAUCUUAUC	123	4.5	Cleavage	| Symbols: | Protein of unknown function (DUF1162) | chr5:8469951-8489703 REVERSE LENGTH=10517
AT5G24750	UGGCGCUCAACUCUGCAAGGU	10625	4.5	Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:8490572-8494587 REVERSE LENGTH=1863
AT5G24910	UUGGACGCCUCUACUAUGAGA	679	4.5	Cleavage	| Symbols: CYP714A1 | cytochrome P450, family 714, subfamily A, polypeptide 1 | chr5:8567581-8570358 REVERSE LENGTH=1790
AT5G25000	UGACACCGAUUCUGAUAGCUU	823	4	Cleavage	| Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:8613966-8614331 REVERSE LENG
AT5G25030	UUCUGAUUGCAUGUGGUGUACC	110	3.5	Translation	| Symbols: | Domain of unknown function (DUF2431) | chr5:8620083-8620991 REVERSE LENGTH=582
AT5G25070	UAGAGUUAAGUUGGGACAGGA	199	2.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has
AT5G25100	UUCUUCGACUGAGGUAAGCGCC	154	4.5	Translation	| Symbols: | Endomembrane protein 70 protein family | chr5:8648103-8651137 REVERSE LENGTH=2328
AT5G25110	UUGGACGCCUCUACUAUGAGA	679	4.5	Cleavage	| Symbols: CIPK25, SnRK3.25 | CBL-interacting protein kinase 25 | chr5:8657626-8659322 REVERSE LENGTH=1697
AT5G25250	UGUUGAUCCAAGUAGCUGACU	608	4	Cleavage	| Symbols: | SPFH/Band 7/PHB domain-containing membrane-associated protein family | chr5:8749727-8751636 FORWARD LENGTH=1666
AT5G25310	UCGAGUGACUUUGGAGCCAUU	244	3.5	Cleavage	| Symbols: | Exostosin family protein | chr5:8784820-8787366 FORWARD LENGTH=1574
AT5G25510	UACUUCCAGCGUUCUGUAGCC	826	4	Cleavage	| Symbols: | Protein phosphatase 2A regulatory B subunit family protein | chr5:8882468-8884834 REVERSE LENGTH=2153
AT5G25560	UGUGGAUACAAGAGCUGGGCU	215	5	Cleavage	| Symbols: | CHY-type/CTCHY-type/RING-type Zinc finger protein | chr5:8897871-8901709 FORWARD LENGTH=2735
AT5G25910	UUCUUCAGACUGGAUAGGACU	265	3	Translation	| Symbols: AtRLP52, RLP52 | receptor like protein 52 | chr5:9038860-9041377 FORWARD LENGTH=2436
AT5G25980	UAUGGAGAUGAUCGCAAUGGC	937	3	Cleavage	| Symbols: TGG2, BGLU37 | glucoside glucohydrolase 2 | chr5:9072727-9075690 FORWARD LENGTH=1857
AT5G26010	CGAGAGAUUACAGGGACUGUC	3198	3.5	Translation	| Symbols: | Protein phosphatase 2C family protein | chr5:9085393-9087372 REVERSE LENGTH=1115
AT5G26180	UCUCAUGUAGUUCUAGUUCGCG	207	3	Cleavage	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:9149227-9153502 FORWARD LENGTH=2113
AT5G26240	UGAGAGCACUCCACCGACUGA	230	4	Cleavage	| Symbols: CLC-D, ATCLC-D | chloride channel D | chr5:9189524-9194731 FORWARD LENGTH=2861
AT5G26250	UGUGGUGUACCUCUCACGUCU	112	5	Cleavage	| Symbols: | Major facilitator superfamily protein | chr5:9196758-9198801 FORWARD LENGTH=1644
AT5G26260	UUCAGGGUGAGAACAUUGACU	1291	4	Cleavage	| Symbols: | TRAF-like family protein | chr5:9200463-9202400 FORWARD LENGTH=1332
AT5G26270	CGAGAGAUUACAGGGACUGUC	3198	3.5	Cleavage	| Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:9206508-9207512 FORWARD LEN
AT5G26290	UUCAGGGUGAGAACAUUGACU	1291	4	Cleavage	| Symbols: | TRAF-like family protein | chr5:9226079-9227873 FORWARD LENGTH=1002
AT5G26310	UCGAGCACCUACGUCACUGCG	100	4.5	Cleavage	| Symbols: UGT72E3 | UDP-Glycosyltransferase superfamily protein | chr5:9234685-9236385 FORWARD LENGTH=1701
AT5G26360	UGACGGUUCAGAUUCAGGAGC	107	2.5	Cleavage	| Symbols: | TCP-1/cpn60 chaperonin family protein | chr5:9255053-9258991 REVERSE LENGTH=2276
AT5G26570	UGAGACACAACAGGGAGAUUC	244	4.5	Cleavage	| Symbols: PWD, OK1, ATGWD3 | catalytics;carbohydrate kinases;phosphoglucan, water dikinases | chr5:9261580-9267729 FORWARD LENGTH=3783
AT5G26600	UUACGAGACUCUAGCCCAACU	447	4	Cleavage	| Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr5:9377402-9379018 FORWARD LENGTH=1617
AT5G26740	UGAGAACGCUCUGCCAUUGGA	158	3	Cleavage	| Symbols: | Protein of unknown function (DUF300) | chr5:9291936-9294608 FORWARD LENGTH=1749
AT5G26920	UGUCUUACCCGUACGUCGCUU	150	4.5	Translation	| Symbols: CBP60G | Cam-binding protein 60-like G | chr5:9475682-9478751 FORWARD LENGTH=2149
AT5G26980	UAUGGAGAUGAUCGCAAUGGC	937	3.5	Cleavage	| Symbols: SYP41, ATSYP41, ATTLG2A | syntaxin of plants 41 | chr5:9488150-9490816 REVERSE LENGTH=1671
AT5G27010	UUGGCAUCGAAUUUGAACUCA	339	3.5	Cleavage	| Symbols: | ARM repeat superfamily protein | chr5:9503315-9507569 REVERSE LENGTH=2592
AT5G27060	UGGCACUCAACUCUGCAAGGU	834	4	Translation	| Symbols: AtRLP53, RLP53 | receptor like protein 53 | chr5:9522534-9525407 REVERSE LENGTH=2874
AT5G27100	CAAGAACCCGCACGACACUCG	169	4.5	Translation	| Symbols: ATGLR2.1, GLR2.1 | glutamate receptor 2.1 | chr5:9535059-9538333 REVERSE LENGTH=2829
AT5G27238	AUUGAUUCUGCACUCAAGGGC	128	4.5	Cleavage	| Symbols: | Plant self-incompatibility protein S1 family | chr5:9593904-9594434 REVERSE LENGTH=531
AT5G27240	CAAAUCCUUCAACUCUUCCCU	197	1.5	Cleavage	| Symbols: | DNAJ heat shock N-terminal domain-containing protein | chr5:9597552-9600866 FORWARD LENGTH=3315
AT5G27330	UAUCUCUGUCGUUACGAACCU	295	4	Cleavage	| Symbols: | Prefoldin chaperone subunit family protein | chr5:9632703-9634980 REVERSE LENGTH=2278
AT5G27360	UGCCUAGAUUGCUCUACUCGA	125	4.5	Translation	| Symbols: SFP2 | Major facilitator superfamily protein | chr5:9657026-9662559 FORWARD LENGTH=1664
AT5G27395	UACCCGUACGUCGCUUACAAG	3223	4	Translation	| Symbols: | Mitochondrial inner membrane translocase complex, subunit Tim44-related protein | chr5:9671496-9674119 REVERSE LENGTH=1274
AT5G27490	UUCCCCUAGAAUUCUUUCCCU	1646	4.5	Cleavage	| Symbols: | Integral membrane Yip1 family protein | chr5:9702835-9704719 REVERSE LENGTH=1210

AT5G27580	UACCCGUACGUCGCUUACAAG	3223	4.5 Translation	| Symbols: AGL89 | AGAMOUS-like 89 | chr5:9736651-9737322 FORWARD LENGTH=672
AT5G27600	UCCCGGAAUGCUGAAGAAGUA	113	3 Cleavage	| Symbols: LACS7, ATLACS7 | long-chain acyl-CoA synthetase 7 | chr5:9742576-9747005 FORWARD LENGTH=2353
AT5G27620	UUCUUCAGACUGGAUAGGACU	265	4.5 Translation	| Symbols: CYCH;1 | cyclin H;1 | chr5:9771324-9774875 FORWARD LENGTH=1640
AT5G27660	UUUGCCUGUUGAACUCGAGUA	114	3.5 Cleavage	| Symbols: | Trypsin family protein with PDZ domain | chr5:9789468-9792299 REVERSE LENGTH=1718
AT5G27680	UUCCAGCGUUCUGUAGCCAAC	156	4 Cleavage	| Symbols: RECQSIM | RECQ helicase SIM | chr5:9793790-9798961 REVERSE LENGTH=3259
AT5G27800	UACCCGUACGUCGCUUAUAAG	185	4.5 Translation	| Symbols: | Class II aminoacyl-tRNA and biotin synthetases superfamily protein | chr5:9842412-9843804 FORWARD LENGTH=1029
AT5G27850	UAUAGGGCUUGAAAGAAAGUC	535	4 Cleavage	| Symbols: | Ribosomal protein L18e/L15 superfamily protein | chr5:9873152-9874598 FORWARD LENGTH=882
AT5G28080	UUCAGGGUGAGAACAUUGACU	1291	4 Cleavage	| Symbols: WNK9 | Protein kinase superfamily protein | chr5:10090070-10092386 REVERSE LENGTH=1610
AT5G28160	UUCAGGGUGAGAACAUUGACU	1291	3 Translation	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:10137926-10139013 FORWARD LENGTH=975
AT5G28230	CUAGAAUUCUUUCCCUUUCCU	235	2.5 Translation	| Symbols: | pseudogene, similar to glucose-6-phosphate/phosphate-translocator precursor, contains similarity to glucose-6-phosphate/phosphate-translocator precursors; blastp match of 78% identity and 1.6e-75 P-value to GP|2997591|gb|AA
AT5G28400	UACAAAUUCGAGCACUCCCUG	156	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28320.1); Has 2580 Blast hits to 2028 proteins in 270 species: Archae - 20; Bacteria - 158; Metazoa - 939; Fungi - 198; Plants - 144; Viruses - 1
AT5G28410	AUUGUGUAUAAUUUUGAGCCU	108	4 Cleavage	| Symbols: | unknown protein; Has 8 Blast hits to 7 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 8; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:10358373-10359438 FORWARD LENGTH=321
AT5G28510	UUCUGACGGACAAGAUAAGCU	313	3.5 Cleavage	| Symbols: BGLU24 | beta glucosidase 24 | chr5:10481041-10484022 REVERSE LENGTH=1602
AT5G28640	UCACCAUUGGCAGCUCUGUACC	187	4 Cleavage	| Symbols: AN3, GIF, GIF1, ATGIF1 | SSXT family protein | chr5:10647570-10649892 REVERSE LENGTH=1166
AT5G28730	UCAAGCGAUUGGAAGGAUUGUU	102	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G43722.1); Has 496 Blast hits to 496 proteins in 68 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 23; Plants - 470; Viruses - 0; Other Eul
AT5G28823	UAUGCUUCUGUUGAUCCACCU	344	3 Translation	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: cultured cell; BEST Arabidopsis thaliana protein match is: Zinc knuckle (CCHC-type
AT5G28840	UCACCUCGCAUCUUAGAACUG	146	4.5 Cleavage	| Symbols: GME | GDP-D-mannose 3',5'-epimerase | chr5:10862173-10864903 REVERSE LENGTH=1612
AT5G28850	UAUGAGUUGAUCGACGAAGAU	123	4 Translation	| Symbols: | Calcium-binding EF-hand family protein | chr5:10876815-10881444 REVERSE LENGTH=2413
AT5G28910	UUCGAGCACUCCCUGACCCGA	160	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G28960.1); Has 82 Blast hits to 80 proteins in 14 spe
AT5G29040	UCUAGUUCGCAUUUUUUGGAC	421	3 Cleavage	| Symbols: | pseudogene, hypothetical protein | chr5:11094905-11098337 REVERSE LENGTH=3433
AT5G32470	UAGCUAACAAGAACUCUUUCU	1828	4 Cleavage	| Symbols: | Haem oxygenase-like, multi-helical | chr5:12084899-12088603 REVERSE LENGTH=2317
AT5G34830	UUGAUCCAAGUAGCUGACUCU	4031	3.5 Cleavage	| Symbols: | unknown protein; Has 19 Blast hits to 19 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 3; Fungi - 0; Plants - 16; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:12981645-12982497 FORWARD LENGTH=468
AT5G34869	UUCGAGAACUCCCUGACCCGA	1272	4 Translation	| Symbols: | unknown protein; Has 17 Blast hits to 14 proteins in 2 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 17; Viruses - 0; Other Eukaryotes - 0 (source: NCBI BLink). | chr5:13061035-13062230 FORWARD LENGTH=1196
AT5G35180	UUGCAGAGAUGGAUGUACAAC	101	2.5 Cleavage	| Symbols: | Protein of unknown function (DUF1336) | chr5:13424418-13433018 FORWARD LENGTH=2787
AT5G35360	UUCCGCAGGGAGAGCGUCCUC	112	4 Cleavage	| Symbols: CAC2 | acetyl Co-enzyme a carboxylase biotin carboxylase subunit | chr5:13584158-13588496 FORWARD LENGTH=1984
AT5G35370	UGCACUCGCUAGGUCUGGCAG	378	5 Cleavage	| Symbols: | S-locus lectin protein kinase family protein | chr5:13588433-13591271 REVERSE LENGTH=2839
AT5G35560	UGAGAACGCUCUGCCAUUGGA	158	5 Cleavage	| Symbols: | DENN (AEX-3) domain-containing protein | chr5:13742109-13748312 REVERSE LENGTH=2923
AT5G35750	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: AHK2, HK2 | histidine kinase 2 | chr5:13911371-13916337 REVERSE LENGTH=3903
AT5G35796	UGACGGACAAGAUAAGUUGCU	1505	4.5 Cleavage	| Symbols: | pseudogene, similar to Putative protein kinase, blastp match of 29% identity and 1.6e-16 P-value to GP|21671940|gb|AAM74302.1|AC083944_20|AC083944 Putative protein kinase {Oryza sativa (japonica cultivar-group)} | chr5:13
AT5G35995	UAUUGACGUCGAGUAUGAGCCU	517	4 Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr5:14136590-14138514 REVERSE LENGTH=1536
AT5G36680	UGGGGCGUUAUACUUUGGGUU	115	3.5 Translation	| Symbols: | Protein of Unknown Function (DUF239) | chr5:14406802-14409137 REVERSE LENGTH=1002
AT5G36770	UGGGGCGUUAUACUUUGGGUU	115	3.5 Translation	| Symbols: | Protein of Unknown Function (DUF239) | chr5:14466102-14468486 REVERSE LENGTH=1051
AT5G36880	UGUCACCGUAGAUUUCUUCCU	123	3 Translation	| Symbols: ACS | acetyl-CoA synthetase | chr5:14534700-14540245 REVERSE LENGTH=2540
AT5G37017	UUAUGAGACUCUAGCCCAGCU	149	3.5 Translation	| Symbols: | Pseudogene of AT5G16486 | chr5:14628221-14628847 REVERSE LENGTH=627
AT5G37160	UUGAGAGAUCCCCUGUUACUG	3917	4 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:14705426-14708376 FORWARD LENGTH=2616
AT5G37180	UACGCUAGGGAGAUAUCUGCC	122	4.5 Cleavage	| Symbols: SUS5, ATSUS5 | sucrose synthase 5 | chr5:14718238-14722913 FORWARD LENGTH=2511
AT5G37210	UUGGCAUCGAAUUUGAACUCA	339	3.5 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:14729225-14731508 REVERSE LENGTH=2034
AT5G37260	CUUGGCAUCGAAUUUGAACUC	1059	3.5 Cleavage	| Symbols: RVE2, CIR1 | Homeodomain-like superfamily protein | chr5:14751344-14753088 REVERSE LENGTH=980
AT5G37290	UUUAACAACUAAGGUUCCUGU	1055	4 Cleavage	| Symbols: | ARM repeat superfamily protein | chr5:14762370-14764344 FORWARD LENGTH=937
AT5G37352	UCUGUAUGCAUAACUUGGGAC	1212	4 Cleavage	| Symbols: | Pseudogene of AT2G25010 | chr5:14796126-14797001 FORWARD LENGTH=790
AT5G37380	UGCAUAACUUGGGACUUACCU	413	4 Cleavage	| Symbols: | Chaperone DnaJ-domain superfamily protein | chr5:14816761-14819087 REVERSE LENGTH=1718
AT5G37420	UAACAAGAACUCUUUCUUUUCU	235	3 Cleavage	| Symbols: | Family of unknown function (DUF577) | chr5:14840143-14842070 FORWARD LENGTH=1740
AT5G37430	UACCGGAGGACGUACAUAGCU	401	4.5 Cleavage	| Symbols: | Family of unknown function (DUF577) | chr5:14842430-14844308 FORWARD LENGTH=1824
AT5G37480	UUUAACAACUAAGGUUCCUGU	1055	4.5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:14884331-1488596
AT5G37630	UCCACCGACUGAUGACAAUGU	1524	4.5 Cleavage	| Symbols: EMB2656 | ARM repeat superfamily protein | chr5:14947330-14952765 FORWARD LENGTH=3452
AT5G37732	UCACCUCGCAUCUUAGAACUG	146	4.5 Translation	| Symbols: | unknown pseudogene | chr5:14987706-14988261 REVERSE LENGTH=380
AT5G37790	UUGAUCCAAGUAGCUGACUCU	4031	4 Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:15008172-15011152 REVERSE LENGTH=2047
AT5G38000	UUUCUGACGGACAAGAUAAGU	480	3.5 Cleavage	| Symbols: | Zinc-binding dehydrogenase family protein | chr5:15141788-15143492 FORWARD LENGTH=1209
AT5G38010	UUGUGAGUGUUUGUGAGGUCU	141	4 Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:15158275-15160212 FORWARD LENGTH=1523
AT5G38110	UAGCUAACAAGAACUCUUUCU	1828	4.5 Cleavage	| Symbols: SGA1, SGA01, ASF1B | anti- silencing function 1b | chr5:15208470-15210215 FORWARD LENGTH=981
AT5G38130	UUCCAGAACUAAUGAAUGUUA	448	4.5 Cleavage	| Symbols: | HXXXD-type acyl-transferase family protein | chr5:15217910-15219372 REVERSE LENGTH=1463
AT5G38140	UAUGGCCUGGGAGCAAUCGCA	299	3.5 Cleavage	| Symbols: NF-YC12 | nuclear factor Y, subunit C12 | chr5:15220208-15222272 REVERSE LENGTH=890
AT5G38240	UACGUCACUGCGAAUUCCUGGA	271	4.5 Cleavage	| Symbols: | Protein kinase family protein | chr5:15277239-15279317 REVERSE LENGTH=1767
AT5G38300	UGAGUAGAAUUCGAUCAUAUC	114	2.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 12 plant structures; EXPRESSED DURING: 6 growth stages; BEST
AT5G38386	CAACGCUCUUGAUACAUCUAG	133	3.5 Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr5:15363178-15364815 FORWARD LENGTH=1212
AT5G38565	AAACAGGACAAGUUACUCGCC	986	4 Cleavage	| Symbols: | F-box/FBD-like domains containing protein | chr5:15444310-15446009 REVERSE LENGTH=1311
AT5G38590	UGAGUAGAAUUCGAUCAUAUC	114	4 Cleavage	| Symbols: | F-box/RNI-like/FBD-like domains-containing protein | chr5:15451933-15453885 REVERSE LENGTH=1700
AT5G38670	UUGAGAUAUCCCCUGUUACUG	106	3 Translation	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:15475786-15476871 FORWARD LENGTH=876
AT5G38740	UCUAGUUCGCGUUCUUCAGAC	300	3.5 Translation	| Symbols: AGL77 | AGAMOUS-like 77 | chr5:15513025-15514305 REVERSE LENGTH=1281
AT5G38895	UAACAAGAACUCUUUCUUUUCU	235	4.5 Cleavage	| Symbols: | RING/U-box superfamily protein | chr5:15571254-15573416 FORWARD LENGTH=1059
AT5G38940	UUUAACAACUAAGGUUCCUGU	1055	4.5 Cleavage	| Symbols: | RmlC-like cupins superfamily protein | chr5:15588757-15589666 FORWARD LENGTH=826
AT5G39210	UGAAGGACAAGCUCAGCUGCU	1483	4 Cleavage	| Symbols: CRR7 | chlororespiratory reduction 7 | chr5:15703121-15704104 FORWARD LENGTH=686
AT5G39350	UCGAGUAUGAGCCUGAGUCAUG	250	3 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:15750929-15752962 FORWARD LENGTH=2034
AT5G39380	CUUCCCCUAGAAUUCUUUCCC	401	3.5 Cleavage	| Symbols: | Plant calmodulin-binding protein-related | chr5:15758717-15760686 REVERSE LENGTH=1970
AT5G39460	UAACCGGGGCAUGAGAGACUC	100	3.5 Translation	| Symbols: | F-box family protein | chr5:15788289-15790004 REVERSE LENGTH=1716
AT5G39471	UUGAGAGAUCCCUUGUUACUG	141	4 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:15793965-15795596 REVERSE LENGTH=1632
AT5G39530	UACCGGAGGACGUACAUAGCU	401	4 Translation	| Symbols: | Protein of unknown function (DUF1997) | chr5:15826089-15828035 REVERSE LENGTH=1434
AT5G39840	UCUGAACUCAAGGCACCCAAA	493	4 Cleavage	| Symbols: | ATP-dependent RNA helicase, mitochondrial, putative | chr5:15946769-15949186 FORWARD LENGTH=2331
AT5G39865	UUGUGGAAUCCGUAGUCUGUA	152	4 Cleavage	| Symbols: | Glutaredoxin family protein | chr5:15965461-15967173 REVERSE LENGTH=1713
AT5G39880	UGAGACACAACAGGGAGAUUC	244	3.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 10 plant structures; EXPRESSED DURING: L mature pollen stage, M ge
AT5G39890	CAUCAAGAACCGGUCAUGCCU	125	3 Cleavage	| Symbols: | Protein of unknown function (DUF1637) | chr5:15974393-15976270 FORWARD LENGTH=1238
AT5G39960	UAAGCAUUUUGAUUCACCGGA	285	3 Cleavage	| Symbols: | GTP binding;GTP binding | chr5:15994021-15997058 FORWARD LENGTH=2278
AT5G39980	UAUGGCCUGGGAGCAAUCGCA	299	4.5 Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:16000712-16003072 REVERSE LENGTH=2361
AT5G39990	UACUUCCAGCGUUCUGUAGCC	826	4 Cleavage	| Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:16004281-16006740 FORWARD LENGTH=1869
AT5G40030	UAUCUCUGUCGUUACGAACCU	295	4.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:16026227-16028283 FORWARD LENGTH=1500
AT5G40070	UCUAGUUCGCGUUCUUCAGAC	300	3.5 Translation	| Symbols: | MADS-box family protein | chr5:16039179-16039747 FORWARD LENGTH=474
AT5G40100	ACAAAACUGUUGAACAAGCCU	1107	4 Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:16043929-16047355 FORWARD LENGTH=3101
AT5G40220	UCUAGUUCGCGUUCUUCAGAC	300	4 Translation	| Symbols: AGL43 | AGAMOUS-like 43 | chr5:16078390-16079364 REVERSE LENGTH=975
AT5G40300	UGCACUCGCUAGGUCUGGCAG	378	4.5 Cleavage	| Symbols: | Uncharacterised protein family (UPF0497) | chr5:16110688-16112968 FORWARD LENGTH=1170
AT5G40490	UCAUCCUCUGUAGCUUCCGUC	210	4 Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:16225376-16227709 FORWARD LENGTH=1665
AT5G40700	UAUCGAGCACCUACGUCACUGU	142	4 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G27350.1); Has 30201 Blast hits to 17322 proteins i
AT5G40820	UGAGCCGACAAGAGUAGUAUC	111	3 Cleavage	| Symbols: ATRAD3, ATR, ATATR | Ataxia telangiectasia-mutated and RAD3-related | chr5:16342745-16353898 REVERSE LENGTH=9189
AT5G40840	UCUAGUUCACAUUUUUCGGAC	427	3.5 Translation	| Symbols: SYN2 | Rad21/Rec8-like family protein | chr5:16359430-16363792 REVERSE LENGTH=2649
AT5G40890	CAACGCUCUUGAUACAUCUAG	133	3 Cleavage	| Symbols: ATCLC-A, CLC-A, CLCA, ATCLCA | chloride channel A | chr5:16381314-16384319 REVERSE LENGTH=2669
AT5G40981	UGAAUCUUGGUCAACUGGACC	197	5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:16415857-1641595
AT5G41020	UUACCCGUACGUCGCUUAUAAG	267	4.5 Cleavage	| Symbols: | myb family transcription factor | chr5:16425883-16427797 REVERSE LENGTH=1915
AT5G41030	UUGAAAGACUUGUGGAUCACC	926	4 Cleavage	| Symbols: | TCP family transcription factor | chr5:16428706-16429437 FORWARD LENGTH=732
AT5G41190	UUGACGACCAACUCCGCUCCU	170	4.5 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Nin one binding (NOB1) Zn-ribbon like (InterPro:IPR014881), D-site 20S pre-rRNA nuclease (InterPro:IPR017117); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa -
AT5G41200	UCUAGUUCGCGUUCUUCAGAC	300	3.5 Translation	| Symbols: AGL75 | AGAMOUS-like 75 | chr5:16490544-16491536 FORWARD LENGTH=993

AT5G41310	UUUUGCUUAGACUUAGAAACU	179	3 Translation	| Symbols: | P-loop nucleoside triphosphate hydrolases superfamily protein with CH (Calponin Homology) domain | chr5:16516634-16522392 REVERSE LENGTH=2886
AT5G41315	UAGUGACCGAGUAGUACCACC	461	4.5 Cleavage	| Symbols: GL3, MYC6.2 | basic helix-loop-helix (bHLH) DNA-binding superfamily protein | chr5:16529455-16532879 FORWARD LENGTH=1929
AT5G41730	UCUGUAUGCAUAACUUGGGACU	686	4.5 Cleavage	| Symbols: | Protein kinase family protein | chr5:16684914-16687145 REVERSE LENGTH=2136
AT5G41770	UCUAGUCCGAAAAAUGCGAAC	163	4 Translation	| Symbols: | crooked neck protein, putative / cell cycle protein, putative | chr5:16717996-16721222 FORWARD LENGTH=2429
AT5G41880	CUAGAAUUCUUUCCCUUUCCU	235	3.5 Cleavage	| Symbols: POLA3, POLA4 | DNA primases;DNA primases | chr5:16760908-16764276 FORWARD LENGTH=1620
AT5G42220	CCACCGACUGAUGACAACGUC	122	5 Cleavage	| Symbols: | Ubiquitin-like superfamily protein | chr5:16872342-16877666 FORWARD LENGTH=3009
AT5G42250	UAGAAUUAUCAUGUCUUGGCA	194	3 Translation	| Symbols: | Zinc-binding alcohol dehydrogenase family protein | chr5:16894009-16897620 FORWARD LENGTH=1421
AT5G42325	CUGGAGGACGUACAGCACUUA	113	3.5 Translation	| Symbols: | Transcription factor IIS protein | chr5:16924102-16924851 REVERSE LENGTH=702
AT5G42540	CAUGUCGUAUUCCAGAAACUC	192	2.5 Translation	| Symbols: XRN2, AtXRN2 | exoribonuclease 2 | chr5:17007413-17014801 FORWARD LENGTH=3406
AT5G42567	UUCUUCGACUGAGGUAAGCGCC	154	2.5 Cleavage	| Symbols: | Protein of unknown function (DUF784) | chr5:17018059-17018406 REVERSE LENGTH=348
AT5G42785	UACACUCACUUGAUCUAGGAG	223	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; M
AT5G42800	UGUCACCGUAGAUUUCUUCCU	123	4 Cleavage	| Symbols: DFR, TT3, M318 | dihydroflavonol 4-reductase | chr5:17164141-17165918 REVERSE LENGTH=1358
AT5G42825	UGAAAUAAAACUGAACCAUGCC	263	2.5 Cleavage	| Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:17171964-17172742
AT5G42870	UGACACCGAUUCUGAUUGCAU	377	4.5 Cleavage	| Symbols: ATPAH2, PAH2 | phosphatidic acid phosphohydrolase 2 | chr5:17185463-17189681 REVERSE LENGTH=3049
AT5G43180	AUAGCUAACAAGAACUCUUUCU	426	4 Translation	| Symbols: | Protein of unknown function, DUF599 | chr5:17336330-17337872 REVERSE LENGTH=871
AT5G43260	UCGAGGGCAGGAACAUUGACU	334	4 Cleavage	| Symbols: | chaperone protein dnaJ-related | chr5:17357377-17358082 REVERSE LENGTH=706
AT5G43270	UGAAGGACAAGAUCAGCUGCU	415	3.5 Cleavage	| Symbols: SPL2 | squamosa promoter binding protein-like 2 | chr5:17360287-17362975 REVERSE LENGTH=1678
AT5G43300	CUUGGCAUCGAAUUUGAACUC	1059	4 Cleavage	| Symbols: | PLC-like phosphodiesterases superfamily protein | chr5:17376734-17379277 REVERSE LENGTH=1532
AT5G43400	UAUGCUUCUGUUGAUCCACCU	344	3.5 Translation	| Symbols: | Uncharacterised conserved protein UCP015417, vWA | chr5:17425944-17428223 REVERSE LENGTH=2280
AT5G43530	UCCACCGACUGAUGACAAUGU	1524	4 Cleavage	| Symbols: | Helicase protein with RING/U-box domain | chr5:17489327-17494830 FORWARD LENGTH=3834
AT5G43620	UUCUUCCCGUUGGUGUGCGCC	170	3.5 Cleavage	| Symbols: | Pre-mRNA cleavage complex II | chr5:17522520-17524001 FORWARD LENGTH=1482
AT5G43680	UUUGAGAGCACUCCACCGACU	156	4.5 Translation	| Symbols: | unknown protein; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages. | chr5:17544029-17545752 FORWARD LENGTH=1047
AT5G43720	UCUGUACCGCUGAAUUCUUCC	275	3.5 Translation	| Symbols: | Protein of unknown function (DUF2361) | chr5:17557166-17559354 REVERSE LENGTH=1371
AT5G43810	UUGCAGAGAUGGAUGUACAAC	101	4 Cleavage	| Symbols: ZLL | Stabilizer of iron transporter SufD / Polynucleotidyl transferase | chr5:17610972-17616797 FORWARD LENGTH=3763
AT5G43860	UAGAUAACAAGAACUCUUUCU	107	3 Cleavage	| Symbols: ATCLH2, CLH2 | chlorophyllase 2 | chr5:17630450-17632312 FORWARD LENGTH=1127
AT5G43960	UAAAACUGAACCAUGCCUAGA	302	3 Cleavage	| Symbols: | Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain | chr5:17688788-17691939 REVERSE LENGTH=2005
AT5G44050	UUUAGGAUUGUUGCAUAUGCA	1164	4 Cleavage	| Symbols: | MATE efflux family protein | chr5:17722484-17726379 FORWARD LENGTH=1646
AT5G44080	CUUGGCAUCGAAUUUGAACUC	1059	3.5 Cleavage	| Symbols: | Basic-leucine zipper (bZIP) transcription factor family protein | chr5:17738652-17739873 REVERSE LENGTH=1222
AT5G44090	AUGACGAAUGUUUGACAGCCU	113	5 Cleavage	| Symbols: | Calcium-binding EF-hand family protein | chr5:17742766-17748396 REVERSE LENGTH=2463
AT5G44180	UUCUGAAGGACAAGCUCAGCU	1012	3.5 Translation	| Symbols: | Homeodomain-like transcriptional regulator | chr5:17783172-17790011 FORWARD LENGTH=4663
AT5G44265	UGUGUAUGCAUAACUUGGGAC	106	3.5 Cleavage	| Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:17832779-17833316 REVERSE LENGTH=381
AT5G44290	UUUUUCGGACUAGAUAGGACU	107	5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:17840456-17843710 REVERSE LENGTH=2480
AT5G44635	UUUAACAACUAAGGUUCCUGU	1055	4 Cleavage	| Symbols: MCM6 | minichromosome maintenance (MCM2/3/5) family protein | chr5:18006431-18010542 REVERSE LENGTH=2496
AT5G44785	CUUGUGAGUGUUUGUGAGGUC	103	4 Cleavage	| Symbols: OSB3 | organellar single-stranded DNA binding protein 3 | chr5:18070681-18073129 REVERSE LENGTH=1638
AT5G44800	UUCCAGCGUUCUGUAGCCAAC	156	4 Cleavage	| Symbols: CHR4, PKR1 | chromatin remodeling 4 | chr5:18083419-18093452 REVERSE LENGTH=7295
AT5G44830	AUCCAAGUAGCUGACUCUCCU	1104	3.5 Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr5:18100128-18101885 REVERSE LENGTH=999
AT5G44840	UUCCAGAACUAAUGAAUGUUA	448	4 Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr5:18104851-18107127 REVERSE LENGTH=1146
AT5G44970	AUCAUCCUCGGAUCAAACCCU	222	4 Cleavage	| Symbols: | Protein with RNI-like/FBD-like domains | chr5:18155837-18157340 FORWARD LENGTH=1170
AT5G45100	UAUAGGGCUUGAAAGAAAGUC	535	4 Translation	| Symbols: | SBP (S-ribonuclease binding protein) family protein | chr5:18218699-18219960 FORWARD LENGTH=1174
AT5G45180	UUGAAAGACUUGUGGAUCACC	926	4.5 Cleavage	| Symbols: | Flavin-binding monooxygenase family protein | chr5:18274179-18276586 REVERSE LENGTH=1380
AT5G45190	UCAACGAACUCUUGGCCCUAGA	152	4 Cleavage	| Symbols: | Cyclin family protein | chr5:18277620-18281875 REVERSE LENGTH=2118
AT5G45200	CUCAUGUAGUUCUAGUUCGCA	102	4 Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18283967-18290332 REVERSE LENGTH=3786
AT5G45210	UGAGUAGAAUUCGAUCAUAUC	114	3.5 Translation	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18295521-18298434 FORWARD LENGTH=2094
AT5G45230	CAAACUGGACAAGCUACUGCU	324	4.5 Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18302147-18308303 REVERSE LENGTH=3696
AT5G45260	CGUCACUGCGAAUUCCUGGAG	272	5 Translation	| Symbols: RRS1, ATWRKY52, SLH1 | Disease resistance protein (TIR-NBS-LRR class) | chr5:18326203-18332609 FORWARD LENGTH=4321
AT5G45310	UUUAAAACCGAGGACUUUUGC	115	3 Cleavage	| Symbols: | unknown protein; LOCATED IN: endomembrane system; EXPRESSED IN: stem, inflorescence meristem, root, leaf; EXPRESSED DURING: LP.04 four leaves visible; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacte
AT5G45370	UUUCUGACGGACAAGAUAAGU	480	4 Cleavage	| Symbols: | nodulin MtN21 /EamA-like transporter family protein | chr5:18388291-18390420 FORWARD LENGTH=1224
AT5G45380	UCGACCACACUGUUAGGAUCU	121	3.5 Translation	| Symbols: ATDUR3, DUR3 | solute:sodium symporters;urea transmembrane transporters | chr5:18391124-18395894 FORWARD LENGTH=2526
AT5G45440	UACGAGACUCUAGCCCAGCUU	307	4 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:18412308-18413555 REVERSE LENGTH=1248
AT5G45520	UCAACACUCUGAUACAUCUAG	143	4.5 Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr5:18449509-18453012 REVERSE LENGTH=3504
AT5G45660	CUACUCGGUCACUAGGCUCAG	311	4.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 2242
AT5G45680	UGACGCCAAUUCUGAAAGUUU	154	3.5 Cleavage	| Symbols: ATFKBP13, FKBP13 | FK506-binding protein 13 | chr5:18530880-18532337 FORWARD LENGTH=850
AT5G46040	UUCUUGUGAACUUGACCGGGA	158	3.5 Cleavage	| Symbols: | Major facilitator superfamily protein | chr5:18671397-18673551 REVERSE LENGTH=1761
AT5G46170	UAUGGAGAUGAUCGCAAUGGC	937	3.5 Cleavage	| Symbols: | F-box family protein | chr5:18714965-18716953 REVERSE LENGTH=1691
AT5G46190	UACCGGAGGACGUACAUAGCU	401	4 Cleavage	| Symbols: | RNA-binding KH domain-containing protein | chr5:18723116-18726200 REVERSE LENGTH=2414
AT5G46210	UAGAUAACAAGAACUCUUUCU	107	3 Translation	| Symbols: CUL4, ATCUL4 | cullin4 | chr5:18731418-18736810 REVERSE LENGTH=2687
AT5G46270	UCGAGUAUGAGCCUGAGUCAUG	250	4 Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18764349-18769090 REVERSE LENGTH=3904
AT5G46400	UAUUGAUUUUUGGCCUGAGGU	116	3.5 Cleavage	| Symbols: AT PRP39-2, PRP39-2 | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:18820032-18824650 FORWARD LENGTH=3239
AT5G46450	UUGAUCCAAGUAGCUGACUCU	4031	3.5 Translation	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:18835618-18839546 FORWARD LENGTH=3372
AT5G46500	UACAAAUUCGAGCACUCCCUG	156	4.5 Translation	| Symbols: | BEST Arabidopsis thaliana protein match is: disease resistance protein (TIR-NBS-LRR class) family (TAIR:AT5G46260.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 38
AT5G46580	CUUGUGAGUGUUUGUGAGGUC	103	3.5 Translation	| Symbols: | pentatricopeptide (PPR) repeat-containing protein | chr5:18897445-18899645 REVERSE LENGTH=2201
AT5G46620	UGGCAGUAGGAGUACACGACU	163	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G17960.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Ot
AT5G46680	UGGCAGUAGGAGUACACGACU	163	4 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr5:18940969-18942602 FORWARD LENGTH=1634
AT5G46760	UCCCAACCCAUGAUCUAAGCG	236	2.5 Translation	| Symbols: | Basic helix-loop-helix (bHLH) DNA-binding family protein | chr5:18974231-18976009 FORWARD LENGTH=1779
AT5G47010	UACCGGAGGACGUACAGCAUC	153	4 Cleavage	| Symbols: UPF1, LBA1, ATUPF1 | RNA helicase, putative | chr5:19072009-19079334 FORWARD LENGTH=4243
AT5G47230	UUUGAUCCGAGGAUGAUGGAU	816	3.5 Cleavage	| Symbols: ERF5, ATERF-5, ATERF5 | ethylene responsive element binding factor 5 | chr5:19179939-19181129 FORWARD LENGTH=1191
AT5G47280	UUUGAACUCAUGGAUACCCUA	227	5 Cleavage	| Symbols: ADR1-L3 | ADR1-like 3 | chr5:19193157-19195559 FORWARD LENGTH=1872
AT5G47380	UGUUGAUCCAAGUAGCUGACU	608	3 Cleavage	| Symbols: | Protein of unknown function, DUF547 | chr5:19221472-19224591 REVERSE LENGTH=1977
AT5G47400	UUGACGACCAACUCCGCUCCU	170	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1807 proteins in 277 species: A
AT5G47420	UGCAUAACUUGGGACUUACCU	413	3.5 Cleavage	| Symbols: | Tryptophan RNA-binding attenuator protein-like | chr5:19232836-19235059 FORWARD LENGTH=1247
AT5G47455	UGAAUGACAAACUGGACAAGCU	583	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: chloroplast; EXPRESSED IN: 13 plant structures; EXPRESSED DURING: 8 growth stages; BEST Arabidopsis thalia
AT5G47490	UGUUGAUCCAAGUAGCUGACU	608	3.5 Translation	| Symbols: | RGPR-related | chr5:19264675-19270800 FORWARD LENGTH=4399
AT5G47590	UGUGACACCGAUUCUGAUAGC	115	4 Cleavage	| Symbols: | Heat shock protein HSP20/alpha crystallin family | chr5:19297817-19299152 REVERSE LENGTH=976
AT5G47670	UACUUCCAGCGUUCUGUAGCC	826	4.5 Translation	| Symbols: NF-YB6, L1L | nuclear factor Y, subunit B6 | chr5:19315023-19316169 FORWARD LENGTH=937
AT5G47720	UCGACCACACUGUCAUGAUCU	174	4 Translation	| Symbols: | Thiolase family protein | chr5:19331657-19334427 FORWARD LENGTH=1782
AT5G47830	UAUGGCCUGGGAGCAAUCGCA	299	4.5 Cleavage	| Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:19372898-19374331
AT5G47940	UUUUAAUUCAAGUAGCUGACU	133	3 Cleavage	| Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:19409242-19411893 REVERSE LEI
AT5G48040	UACAGAAUAGGCUUAAGUAAC	189	3.5 Translation	| Symbols: | Ubiquitin carboxyl-terminal hydrolase family protein | chr5:19470139-19472445 FORWARD LENGTH=2134
AT5G48100	UGAAGGACAAGCUCAGCUGCU	1483	3.5 Cleavage	| Symbols: TT10, LAC15, ATLAC15 | Laccase/Diphenol oxidase family protein | chr5:19489327-19492744 REVERSE LENGTH=2063
AT5G48330	UGAAGGACAAGAUCAGCUGCU	415	4 Cleavage	| Symbols: | Regulator of chromosome condensation (RCC1) family protein | chr5:19585936-19587841 FORWARD LENGTH=1530
AT5G48412	ACAAAACUGUUGAACAAGCCU	1107	2.5 Translation	| Symbols: | | chr5:19623516-19624232 REVERSE LENGTH=717
AT5G48450	UAUCGAGCACCUACGUCACUGU	142	4 Translation	| Symbols: sks3 | SKU5 similar 3 | chr5:19632791-19635664 REVERSE LENGTH=1918
AT5G48520	CUCAUGUAGUUCUAGUUCGCA	102	3.5 Translation	| Symbols: | unknown protein; Has 609 Blast hits to 593 proteins in 129 species: Archae - 0; Bacteria - 41; Metazoa - 390; Fungi - 40; Plants - 64; Viruses - 0; Other Eukaryotes - 74 (source: NCBI BLink). | chr5:19661213-19666436 FORWARD LENG
AT5G48550	UUACCCGUACGUCGCUUAUAAG	267	5 Translation	| Symbols: | F-box associated ubiquitination effector family protein | chr5:19678917-19680560 FORWARD LENGTH=1284
AT5G48600	CUCAGGCUCAUACUCGACGUC	968	2.5 Translation	| Symbols: ATSMC3, ATCAP-C, ATSMC4, SMC3 | structural maintenance of chromosome 3 | chr5:19701877-19709130 FORWARD LENGTH=3796
AT5G48730	UACUCGACCACACUGUUAGGA	183	4 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:19763152-19765272 FORWARD LENGTH=1663
AT5G48775	AUGGAUUUAGAUCACUUGCGUC	196	3.5 Cleavage	| Symbols: | other RNA | chr5:19774170-19776460 FORWARD LENGTH=2060
AT5G48980	UGGCAGUAGGAGUACACGACU	163	4 Translation	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19860708-19862018 FORWARD LENGTH=1311
AT5G48990	UACAGAAUAGGCUUAAGUAAC	189	4 Cleavage	| Symbols: | Galactose oxidase/kelch repeat superfamily protein | chr5:19862289-19863625 FORWARD LENGTH=1337

AT5G49030	UUCGGUCUGGCCAUACUCGGC	147	4 Translation	| Symbols: OVA2 | tRNA synthetase class I (I, L, M and V) family protein | chr5:19876166-19882462 REVERSE LENGTH=3238
AT5G49070	UGGAUUCCGGCUGCAUACUCC	392	5 Cleavage	| Symbols: KCS21 | 3-ketoacyl-CoA synthase 21 | chr5:19888751-19890145 REVERSE LENGTH=1262
AT5G49140	UUCAGGGUGAGAACAUUGACU	1291	2 Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:19919085-19923415 REVERSE LENGTH=2943
AT5G49152	UUGAAGGAUUUGUGGUUAACCA	106	2.5 Cleavage	| Symbols: | other RNA | chr5:19928880-19929377 FORWARD LENGTH=324
AT5G49190	UCUCAUGUAGUUCUAGUUCGCA	1437	3.5 Cleavage	| Symbols: SUS2, SSA, ATSUS2 | sucrose synthase 2 | chr5:19943282-19947189 REVERSE LENGTH=2511
AT5G49300	UGUCACCGUAGAUUUCUUCCU	123	4.5 Translation	| Symbols: GATA16 | GATA transcription factor 16 | chr5:19984849-19985697 REVERSE LENGTH=642
AT5G49410	UGUUACGAGACUCUAGCCCAG	574	3.5 Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT1G73940.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; O
AT5G49448	CGAGAGAUUACAGGGACUGUC	3198	4 Cleavage	| Symbols: CPuORF4 | conserved peptide upstream open reading frame 4 | chr5:20051829-20052735 FORWARD LENGTH=907
AT5G49450	CGAGAGAUUACAGGGACUGUC	3198	4 Cleavage	| Symbols: AtbZIP1, bZIP1 | basic leucine-zipper 1 | chr5:20051829-20052735 FORWARD LENGTH=907
AT5G49470	AUUGAUUCUGCACUCAAGGGC	128	4.5 Cleavage	| Symbols: | PAS domain-containing protein tyrosine kinase family protein | chr5:20063448-20068665 FORWARD LENGTH=2757
AT5G49490	UUUUAAUUCAAGUAGCUGACU	133	3 Translation	| Symbols: AGL83 | AGAMOUS-like 83 | chr5:20075328-20076185 FORWARD LENGTH=858
AT5G49540	CUCACAAGUGAUAUAGGGCUU	208	5 Cleavage	| Symbols: | Rab5-interacting family protein | chr5:20104481-20106122 REVERSE LENGTH=822
AT5G49610	UGAGCCGACAAGAGUAGUAUC	111	3.5 Cleavage	| Symbols: | F-box family protein | chr5:20131274-20132729 REVERSE LENGTH=1456
AT5G49650	UACCCGUACGUCGCUUAUAAG	185	5 Translation	| Symbols: XK-2, XK2 | xylulose kinase-2 | chr5:20152781-20155768 FORWARD LENGTH=1983
AT5G49665	UGAAUGACAAACUGGACAAGCU	583	4 Cleavage	| Symbols: | Zinc finger (C3HC4-type RING finger) family protein | chr5:20167002-20169474 REVERSE LENGTH=2394
AT5G49680	UCAAGCGAUUGGAAGGAUUGUU	102	4 Cleavage	| Symbols: | Golgi-body localisation protein domain ;RNA pol II promoter Fmp27 protein domain | chr5:20176385-20188307 FORWARD LENGTH=7764
AT5G49720	UUGAUCCAAGUAGCUGACUCU	4031	4.5 Cleavage	| Symbols: ATGH9A1, TSD1, DEC, KOR, RSW2, IRX2, KOR1, GH9A1 | glycosyl hydrolase 9A1 | chr5:20197391-20200288 REVERSE LENGTH=2360
AT5G49890	UUGAGAGCACUCCACCGACUG	261	5 Cleavage	| Symbols: CLC-C, ATCLC-C | chloride channel C | chr5:20288119-20292350 REVERSE LENGTH=2836
AT5G50010	UCGACCACACUGUUAGGAUCU	121	4.5 Cleavage	| Symbols: | sequence-specific DNA binding transcription factors;transcription regulators | chr5:20348615-20350830 FORWARD LENGTH=1858
AT5G50011	UCGACCACACUGUUAGGAUCU	121	4.5 Cleavage	| Symbols: CPuORF37 | conserved peptide upstream open reading frame 37 | chr5:20348615-20350830 FORWARD LENGTH=1858
AT5G50012	UCGACCACACUGUUAGGAUCU	121	4.5 Cleavage	| Symbols: CPuORF36 | conserved peptide upstream open reading frame 36 | chr5:20348615-20350830 FORWARD LENGTH=1858
AT5G50335	UUGGGAGAACUAUGACACGAG	515	3.5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:20489094-2048972
AT5G50350	UCUAGUUCGCGUUCUUCAGAC	300	4 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: response to oxidative stress; LOCATED IN: chloroplast; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to
AT5G50375	UCCUAUCCAGUCUGAAGAACGC	272	3.5 Translation	| Symbols: CPI1 | cyclopropyl isomerase | chr5:20511667-20514249 FORWARD LENGTH=1212
AT5G50390	UCGAGUAUGAGCCUGAGUCAUG	250	4.5 Cleavage	| Symbols: | Pentatricopeptide repeat (PPR-like) superfamily protein | chr5:20520789-20522980 REVERSE LENGTH=2106
AT5G50520	UGCCUAGAUUGCUCUACUCGA	125	5 Cleavage	| Symbols: | Major facilitator superfamily protein | chr5:20569563-20571615 REVERSE LENGTH=1768
AT5G50590	UAGAGUUAAGUUGGGACAGGA	199	4.5 Cleavage	| Symbols: AtHSD4, HSD4 | hydroxysteroid dehydrogenase 4 | chr5:20587988-20589296 FORWARD LENGTH=900
AT5G50630	UGCCUAGAUUGCUCUACUCGA	125	5 Cleavage	| Symbols: | Major facilitator superfamily protein | chr5:20602921-20604956 REVERSE LENGTH=1751
AT5G50690	UAGAGUUAAGUUGGGACAGGA	199	4.5 Cleavage	| Symbols: AtHSD7, HSD7 | hydroxysteroid dehydrogenase 7 | chr5:20621330-20622638 FORWARD LENGTH=900
AT5G50840	UAGAUAACAAGAACUCUUUCU	107	4 Cleavage	| Symbols: | CONTAINS InterPro DOMAIN/s: Taxilin (InterPro:IPR019132); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (sour
AT5G50940	UGACGGACAAGAUAAGCUGCU	259	4 Translation	| Symbols: | RNA-binding KH domain-containing protein | chr5:20724578-20726479 FORWARD LENGTH=1101
AT5G51040	UGGCAUCGAAUUUGAACUCAU	178	3.5 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; COI
AT5G51120	CUUGUGAGUGUUUGUGAGGUC	103	3.5 Translation	| Symbols: PABN1 | polyadenylate-binding protein 1 | chr5:20779327-20781530 FORWARD LENGTH=737
AT5G51180	UUUGCCUGUUGAACUCGAGUA	114	4 Cleavage	| Symbols: | alpha/beta-Hydrolases superfamily protein | chr5:20797017-20800214 FORWARD LENGTH=1586
AT5G51190	UACACUCACUUGAUCUAGGAG	223	4 Translation	| Symbols: | Integrase-type DNA-binding superfamily protein | chr5:20800584-20801416 REVERSE LENGTH=833
AT5G51195	CCUGAGCCUAGUGACCGAGUA	270	4 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G47920.1); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT5G51370	AAACAGGACAAGUUACUCGCC	986	4 Cleavage	| Symbols: | RNI-like superfamily protein | chr5:20872762-20874284 FORWARD LENGTH=1523
AT5G51430	UUCUGACGGACAAGAUAAGCU	313	4.5 Cleavage	| Symbols: EYE | conserved oligomeric Golgi complex component-related / COG complex component-related | chr5:20886838-20890907 REVERSE LENGTH=2829
AT5G51540	UUGGCAACCGAUCUCUGAAAG	138	2.5 Translation	| Symbols: | Zincin-like metalloproteases family protein | chr5:20932031-20936413 FORWARD LENGTH=2290
AT5G51660	UCCUGAGUACUCUCUUCCAAG	209	3.5 Translation	| Symbols: CPSF160, ATCPSF160 | cleavage and polyadenylation specificity factor 160 | chr5:20980215-20989427 FORWARD LENGTH=4523
AT5G51690	UACUCCAGAAACUCACAACGA	113	3 Cleavage	| Symbols: ACS12 | 1-amino-cyclopropane-1-carboxylate synthase 12 | chr5:20997413-21001046 REVERSE LENGTH=3179
AT5G51730	UCGGCCUGAGGUUGGACGCCU	147	5 Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:21011418-21013657 FORWARD LENGTH=1246
AT5G51800	CCGAUUCUGAUUGCAUGUGGU	186	4.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:21048191-21052012 FORWARD LENGTH=3151
AT5G51820	CUUGGCAUCGAAUUUGAACUC	1059	4 Cleavage	| Symbols: PGM, ATPGMP, PGM1, STF1 | phosphoglucomutase | chr5:21063368-21068057 REVERSE LENGTH=2159
AT5G51830	UAACAAGAACUCUUUCUUUUCU	235	3.5 Cleavage	| Symbols: | pfkB-like carbohydrate kinase family protein | chr5:21069572-21071735 FORWARD LENGTH=1454
AT5G51850	CAUUGACUUCAAGCCUGCGCU	190	5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G62170.1); Has 384 Blast hits to 375 proteins in 79 species: Archae - 0; Bacteria - 14; Metazoa - 135; Fungi - 31; Plants - 92; Viruses - 0; Other E
AT5G51920	UUAUCAACGAACUCUUGGCCC	310	3.5 Cleavage	| Symbols: | Pyridoxal phosphate (PLP)-dependent transferases superfamily protein | chr5:21097106-21098959 REVERSE LENGTH=1854
AT5G51980	UUUGCCUGUUGAACUCGAGUA	114	4.5 Translation	| Symbols: | Transducin/WD40 repeat-like superfamily protein | chr5:21113650-21116197 REVERSE LENGTH=1512
AT5G52210	UUUGCUGAACAUGUACCUCCA	119	2 Cleavage	| Symbols: ATARLB1, ATGB1, GB1 | GTP-binding protein 1 | chr5:21204991-21207097 FORWARD LENGTH=992
AT5G52270	UUGAACAAGCCUGAUGAAGUU	102	5 Cleavage	| Symbols: | SNARE-like superfamily protein | chr5:21221643-21222600 REVERSE LENGTH=645
AT5G52430	UAAAACUGAACCAUGCCUAGA	302	3 Cleavage	| Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:21282750-21285271 REVERSE LENGTH=1886
AT5G52547	UAACCGGGGCAUGAGAGACUC	100	3.5 Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: cellular_component unknown; BEST Arabidopsis thaliana protein match is: DNA binding (TAIR:AT3G47680.1); Has 61 Blast hits t
AT5G52550	UCCCGGAAUGCUGAAGAAGUA	113	3.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT4G25670.2); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; V
AT5G52552	UCCCGGAAUGCUGAAGAAGUA	113	3.5 Cleavage	| Symbols: CPuORF14 | conserved peptide upstream open reading frame 14 | chr5:21327712-21330136 REVERSE LENGTH=1739
AT5G52580	UACGCGACCGCGGUGCUGGCC	119	5 Cleavage	| Symbols: | RabGAP/TBC domain-containing protein | chr5:21337861-21342985 FORWARD LENGTH=2401
AT5G52950	UUUGGCGCUCAACUCUGCAAGG	2546	4.5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:21473887-2147693
AT5G53160	UGGAGAUGAUAGAUUAUGCGC	126	3 Cleavage	| Symbols: RCAR3, PYL8 | regulatory components of ABA receptor 3 | chr5:21560718-21562260 FORWARD LENGTH=1182
AT5G53320	UUCCCGUUGGUGUGCGCCCAC	196	3.5 Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr5:21636241-21638398 REVERSE LENGTH=2079
AT5G53430	UGAAGGACAAGCUCAGCUGCU	1483	4.5 Cleavage	| Symbols: SDG29, SET29, ATX5 | SET domain group 29 | chr5:21677146-21683494 FORWARD LENGTH=3937
AT5G53570	UGGAGAUGAUAGAUUAUGCGC	126	3.5 Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:21760590-21763462 REVERSE LENGTH=2250
AT5G53750	UGAAAUAAAACUGAACCAUGCC	263	2.5 Cleavage	| Symbols: | CBS domain-containing protein | chr5:21817366-21818843 FORWARD LENGTH=1397
AT5G53760	AAACAGGACAAGUUACUCGCC	986	4 Cleavage	| Symbols: MLO11, ATMLO11 | Seven transmembrane MLO family protein | chr5:21822534-21826451 FORWARD LENGTH=2224
AT5G53910	UUUGUUAAACUCAUGGUCACCC	165	3.5 Translation	| Symbols: | RING/U-box superfamily protein | chr5:21890643-21891335 FORWARD LENGTH=693
AT5G54260	CUUCGACUGAGGUAAGCGCCU	234	4.5 Cleavage	| Symbols: MRE11, ATMRE11 | DNA repair and meiosis protein (Mre11) | chr5:22032069-22037991 FORWARD LENGTH=2574
AT5G54380	UUGAACAAGCCUGAUGAAGUU	102	2 Translation	| Symbols: THE1 | protein kinase family protein | chr5:22077092-22079880 REVERSE LENGTH=2789
AT5G54490	UCGAGCACCUACGUCACUGCG	100	4 Translation	| Symbols: PBP1 | pinoid-binding protein 1 | chr5:22121404-22121931 FORWARD LENGTH=528
AT5G54540	UUGAGAAGAUACAUUGACGGU	731	3.5 Translation	| Symbols: | Uncharacterised conserved protein (UCP012943) | chr5:22156498-22158054 FORWARD LENGTH=1197
AT5G54630	UUAUGAGACUCUAGCCCAGCU	149	4.5 Cleavage	| Symbols: | zinc finger protein-related | chr5:22192499-22194308 REVERSE LENGTH=1575
AT5G54670	UUCUUGUGAACUUGACCGGGA	158	3 Cleavage	| Symbols: ATK3, KATC | kinesin 3 | chr5:22209472-22214134 FORWARD LENGTH=2835
AT5G54690	UGAAGGACAAGCUCAGCUGCU	1483	5 Cleavage	| Symbols: GAUT12, LGT6, IRX8 | galacturonosyltransferase 12 | chr5:22219224-22221840 REVERSE LENGTH=1890
AT5G54840	UACUCGACCACACUGUUAGGA	183	3.5 Translation	| Symbols: ATSGP1, SGP1 | Ras-related small GTP-binding family protein | chr5:22276513-22278423 REVERSE LENGTH=1060
AT5G54860	CAACUAACAACGAGGGCACUG	198	3 Cleavage	| Symbols: | Major facilitator superfamily protein | chr5:22284581-22287206 FORWARD LENGTH=1797
AT5G54870	UUACGAGACUCUAGCCCAGCU	3733	3.5 Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: vacuole; EXPRESSED IN: 24 plant structures; EXPRESSED DURING: 15 growth stages; BEST Arabidopsis thaliana
AT5G55430	UUUUGCUUAGACUUAGAAACU	179	3.5 Cleavage	| Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:22464589-22465218 FORWARD L
AT5G55550	CUUGGCAUCGAAUUUGAACUC	1059	4.5 Cleavage	| Symbols: | RNA-binding (RRM/RBD/RNP motifs) family protein | chr5:22501535-22504011 REVERSE LENGTH=2075
AT5G55600	UAGUGACCGAGUAGUACCACC	461	3.5 Cleavage	| Symbols: | agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein | chr5:22521849-22525645 REVERSE LENGTH=3224
AT5G55720	UAAGCAUUUUGAUUCACCGGA	285	4 Cleavage	| Symbols: | Pectin lyase-like superfamily protein | chr5:22556047-22557725 FORWARD LENGTH=1408
AT5G55800	UGAAUGACAAACUGGACAAGCU	583	5 Cleavage	| Symbols: | Cysteine/Histidine-rich C1 domain family protein | chr5:22581694-22583430 FORWARD LENGTH=1737
AT5G55860	UACCGGAGGACGUACAUAGCU	401	4.5 Translation	| Symbols: | Plant protein of unknown function (DUF827) | chr5:22609532-22612393 FORWARD LENGTH=2469
AT5G55950	GCAAGUGAUGAUAAAAAGACA	100	3.5 Cleavage	| Symbols: | Nucleotide/sugar transporter family protein | chr5:22658112-22660434 REVERSE LENGTH=1677
AT5G55960	UUAAUCCAAGUAGCUGACUCU	2805	3 Cleavage	| Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Uncharacterised protein family UPF0118 (InterPro:IPR002549); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Pla
AT5G55970	UCACUUUGCUGAACAUGUACC	138	4 Cleavage	| Symbols: | RING/U-box superfamily protein | chr5:22667906-22669545 FORWARD LENGTH=1378
AT5G56000	UUCGGUCUGGCCAUACUCGGC	147	4 Cleavage	| Symbols: Hsp81.4, AtHsp90.4 | HEAT SHOCK PROTEIN 81.4 | chr5:22677451-22680152 REVERSE LENGTH=2336
AT5G56010	CUCACAAGUGAUAUAGGGCUU	208	4.5 Cleavage	| Symbols: HSP81-3, Hsp81.3, AtHsp90-3, AtHsp90.3 | heat shock protein 81-3 | chr5:22681305-22684129 FORWARD LENGTH=2423
AT5G56110	UUGAAAGACUUGUGGAUCACC	926	4.5 Cleavage	| Symbols: AtMYB103, ATMYB80, MYB103, MS188 | myb domain protein 103 | chr5:22719191-22720664 FORWARD LENGTH=963
AT5G56160	UCUAGUUCGCGUUCUUCAGAC	300	3.5 Translation	| Symbols: | Sec14p-like phosphatidylinositol transfer family protein | chr5:22731974-22735590 FORWARD LENGTH=2191
AT5G56200	UGACGGACAAGAUAAGCUGCU	259	4.5 Translation	| Symbols: | C2H2 type zinc finger transcription factor family | chr5:22747768-22749249 FORWARD LENGTH=1482
AT5G56290	UUUGAGCACUCCUUGACCCGA	154	4 Cleavage	| Symbols: PEX5, ATPEX5 | peroxin 5 | chr5:22786506-22792161 FORWARD LENGTH=2525
AT5G56510	AUUGAUUCUGCACUCAAGGGC	128	4 Cleavage	| Symbols: APUM12, PUM12 | pumilio 12 | chr5:22881721-22883842 FORWARD LENGTH=1791

AT5G56610	UUCCCCUAGAAUUCUUUCCCU	1646	4.5	Cleavage	| Symbols: | Phosphotyrosine protein phosphatases superfamily protein | chr5:22916731-22918338 FORWARD LENGTH=772
AT5G56620	UGACACCGAUUCUGAUUGCAU	377	3.5	Cleavage	| Symbols: anac099, NAC099 | NAC domain containing protein 99 | chr5:22918521-22921139 REVERSE LENGTH=1161
AT5G56630	UUUUUCGGACUAGAUAGGACU	107	3	Cleavage	| Symbols: PFK7 | phosphofructokinase 7 | chr5:22923922-22926963 FORWARD LENGTH=2082
AT5G56800	UGAAGGACAAGCUCAGCUGCU	1483	4	Cleavage	| Symbols: | Protein with RNI-like/FBD-like domains | chr5:22972989-22974308 FORWARD LENGTH=1135
AT5G56870	UUUGGGUUUGGGUUAACUGCU	225	3.5	Cleavage	| Symbols: BGAL4 | beta-galactosidase 4 | chr5:23004196-23008649 FORWARD LENGTH=2502
AT5G56970	UUGAGAGCACUCCACCGACUG	261	4.5	Translation	| Symbols: CKX3, ATCKX3 | cytokinin oxidase 3 | chr5:23044944-23048268 REVERSE LENGTH=1595
AT5G57030	UUAAUCCAAGUAGCUGACUCU	2805	5	Translation	| Symbols: LUT2 | Lycopene beta/epsilon cyclase protein | chr5:23077265-23080053 FORWARD LENGTH=1943
AT5G57120	UCAUCCUCUGUAGCUUCCGUC	210	3.5	Cleavage	| Symbols: | FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 21 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPro DOMAIN/s: LisH dimer
AT5G57180	AUUGUGUAUAAUUUUGAGCCU	108	3.5	Cleavage	| Symbols: CIA2 | chloroplast import apparatus 2 | chr5:23167842-23169739 FORWARD LENGTH=1898
AT5G57210	UGAGAUUGCUAGAGGAAAGAG	101	3.5	Cleavage	| Symbols: | Ypt/Rab-GAP domain of gyp1p superfamily protein | chr5:23180833-23183811 REVERSE LENGTH=2575
AT5G57270	UACUGGAGGACGUACAACACU	176	4	Cleavage	| Symbols: | Core-2/I-branching beta-1,6-N-acetylglucosaminyltransferase family protein | chr5:23200614-23203792 REVERSE LENGTH=1907
AT5G57350	UUAGAAUUAUCAUGUCUUGGC	138	4	Cleavage	| Symbols: HA3 | H(+)-ATPase 3 | chr5:23230879-23236572 REVERSE LENGTH=3220
AT5G57370	UCUAGUUCGCAUUUUUUGGAC	421	3.5	Translation	| Symbols: | unknown protein; CONTAINS InterPro DOMAIN/s: Protein of unknown function DUF1777 (InterPro:IPR013957); Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plant
AT5G57565	UUGUGGAAUCCGUAGUCUGUA	152	3.5	Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:23310346-23311564 FORWARD LENGTH=1028
AT5G57580	UUUAACAACUAAGGUUCCUGU	1055	4	Translation	| Symbols: | Calmodulin-binding protein | chr5:23314716-23318125 REVERSE LENGTH=2434
AT5G57610	UACUCGACCACACUGUUAGGA	183	5	Cleavage	| Symbols: | Protein kinase superfamily protein with octicosapeptide/Phox/Bem1p domain | chr5:23324791-23329347 FORWARD LENGTH=3846
AT5G57740	UCGGCUCAAACCUAACACGUU	129	4	Translation	| Symbols: XBAT32 | XB3 ortholog 2 in Arabidopsis thaliana | chr5:23394585-23397650 REVERSE LENGTH=2236
AT5G57800	UCUAGUUCGCAUUUUUUGGAC	421	3.5	Cleavage	| Symbols: FLP1, YRE, CER3, WAX2 | Fatty acid hydroxylase superfamily | chr5:23420209-23424052 FORWARD LENGTH=2499
AT5G57980	ACAAAACUGUUGAACAAGCCU	1107	3.5	Translation	| Symbols: RPB5C | RNA polymerase II fifth largest subunit, C | chr5:23469050-23469768 REVERSE LENGTH=633
AT5G58120	UCUGUAUGCAUAACUUGGGAC	1212	5	Cleavage	| Symbols: | Disease resistance protein (TIR-NBS-LRR class) family | chr5:23517492-23521067 FORWARD LENGTH=3281
AT5G58170	UCAACACUCUGAUACAUCUAG	143	3.5	Cleavage	| Symbols: SVL5 | SHV3-like 5 | chr5:23540049-23543345 REVERSE LENGTH=2622
AT5G58190	UUGGGAGAACUAUGACACGAG	515	3.5	Cleavage	| Symbols: ECT10 | evolutionarily conserved C-terminal region 10 | chr5:23546329-23549605 FORWARD LENGTH=1931
AT5G58210	UACGUCACUGCGAAUUCCUGGA	271	3.5	Cleavage	| Symbols: | hydroxyproline-rich glycoprotein family protein | chr5:23552094-23554402 FORWARD LENGTH=1736
AT5G58240	UAACCGGGGCAUGAGAGACUC	100	4.5	Cleavage	| Symbols: FHIT | FRAGILE HISTIDINE TRIAD | chr5:23558114-23559201 REVERSE LENGTH=748
AT5G58320	UAUCGAGCACCUACGUCACUG	123	4	Translation	| Symbols: | Kinase interacting (KIP1-like) family protein | chr5:23577512-23579786 FORWARD LENGTH=1939
AT5G58380	UUAGCCUGAGGUUGGACGCCU	231	4.5	Cleavage	| Symbols: CIPK10, PKS2, SIP1, SNRK3.8 | SOS3-interacting protein 1 | chr5:23596962-23599242 REVERSE LENGTH=1963
AT5G58410	CAAACUGGACAAGCUACUGCU	324	4	Translation	| Symbols: | HEAT/U-box domain-containing protein | chr5:23609663-23617386 FORWARD LENGTH=5665
AT5G58450	UUCUGAAGGACAAGCUCAGCU	1012	3.5	Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:23626826-23632223 FORWARD LENGTH=3350
AT5G58500	UAGUGACCGAGUAGUACCACC	461	4.5	Translation	| Symbols: LSH5 | Protein of unknown function (DUF640) | chr5:23645535-23646083 REVERSE LENGTH=549
AT5G58540	UUGAGAGCACUCCACCGACUG	261	4	Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:23663136-23665316 FORWARD LENGTH=1930
AT5G58550	UACCGGAGGACGUACAUAGCU	401	4.5	Cleavage	| Symbols: EOL2 | ETO1-like 2 | chr5:23665182-23668226 REVERSE LENGTH=2568
AT5G58750	UGAGACACAACAGGGAGAUUC	244	4.5	Translation	| Symbols: | NAD(P)-binding Rossmann-fold superfamily protein | chr5:23728788-23730122 FORWARD LENGTH=1335
AT5G58800	UAGAUAACAAGAACUCUUUCU	107	4.5	Cleavage	| Symbols: | Quinone reductase family protein | chr5:23745891-23747274 REVERSE LENGTH=900
AT5G58880	UCGACCACACUGUCAUGAUCU	174	4	Translation	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT2G29620.1); Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; O
AT5G58920	UCGAGGGCAGGAACAUUGACU	334	3	Cleavage	| Symbols: | unknown protein; Has 1807 Blast hits to 1807 proteins in 277 species: Archae - 0; Bacteria - 0; Metazoa - 736; Fungi - 347; Plants - 385; Viruses - 0; Other Eukaryotes - 339 (source: NCBI BLink). | chr5:23793129-23794245 FORWARD L
AT5G58930	UUGACGACCAACUCCGCUCCU	170	4	Cleavage	| Symbols: | Protein of unknown function (DUF740) | chr5:23794315-23796461 REVERSE LENGTH=2147
AT5G58950	AUGGAUUUAGAUCACUUGCGUC	196	4	Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:23800928-23803673 REVERSE LENGTH=2310
AT5G59210	UCUAGUUCGCGUUUUUCAGAC	163	3	Translation	| Symbols: | myosin heavy chain-related | chr5:23890636-23893665 REVERSE LENGTH=1514
AT5G59260	UUGAUCCAAGUAGCUGACUCU	4031	3.5	Cleavage	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:23907901-23909925 REVERSE LENGTH=2025
AT5G59270	UUGAUCCAAGUAGCUGACUCU	4031	4	Cleavage	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:23911151-23913235 REVERSE LENGTH=2007
AT5G59350	UUUGUUAAACUCAUGGUCACCC	165	2.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807
AT5G59490	UAGAGUUAAGUUGGGACAGGA	199	3	Cleavage	| Symbols: | Haloacid dehalogenase-like hydrolase (HAD) superfamily protein | chr5:23982724-23984617 REVERSE LENGTH=1089
AT5G59600	UCGAGUAUGAGCCUGAGUCAUG	250	3.5	Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:24011000-24013025 REVERSE LENGTH=2026
AT5G59630	UUAAUCCAAGUAGCUGACUCU	2805	4.5	Cleavage	| Symbols: | pseudogene, glycine-rich protein, blastp match of 53% identity and 5.4e-10 P-value to GP|9837280|gb|AAG00510.1||AF285172 leaf senescence-associated receptor-like protein kinase {Phaseolus vulgaris} | chr5:24021433-240239
AT5G59650	CUUCCCCUAGAAUUCUUUCCC	401	3.5	Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24031346-24035100 FORWARD LENGTH=2679
AT5G59680	CUUCCCCUAGAAUUCUUUCCC	401	3	Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr5:24046792-24050801 FORWARD LENGTH=2664
AT5G59830	UGACGCCAAUUCUGAAAGUUU	154	4.5	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G13660.2); Has 174 Blast hits to 139 proteins in 16 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 172; Viruses - 0; Other Euka
AT5G59900	CUUCGACUGAGGUAAGCGCCU	234	5	Cleavage	| Symbols: | Pentatricopeptide repeat (PPR) superfamily protein | chr5:24123983-24126706 REVERSE LENGTH=2724
AT5G60020	CAUCAAGAACCGGUCAUGCCU	125	3	Translation	| Symbols: LAC17, ATLAC17 | laccase 17 | chr5:24167996-24170462 FORWARD LENGTH=2049
AT5G60022	UCCAAGUAGCUGACUCUCCUU	596	5	Translation	| Symbols: | other RNA | chr5:24167141-24170261 REVERSE LENGTH=1247
AT5G60040	UUUGAGCACUCUACAGACAGG	162	3.5	Cleavage	| Symbols: NRPC1 | nuclear RNA polymerase C1 | chr5:24173403-24183641 FORWARD LENGTH=4582
AT5G60100	UAUUGAUUUUUGGCCUGAGGU	116	3.5	Cleavage	| Symbols: APRR3, PRR3 | pseudo-response regulator 3 | chr5:24197999-24201364 REVERSE LENGTH=2100
AT5G60210	UACAGAAUAGGCUUAAGUAAC	189	4	Translation	| Symbols: RIP5 | ROP interactive partner 5 | chr5:24243083-24245968 REVERSE LENGTH=2130
AT5G60280	AUUGAUUCUGCACUCAAGGGC	128	3	Translation	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:24260563-24262536 FORWARD LENGTH=1974
AT5G60330	UUGAACAAGCCUGAUGAAGUU	102	3.5	Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: endomembrane system; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G45320.1); H
AT5G60380	UACGUCACUGCGAAUUCCUGGA	271	5	Translation	| Symbols: | Protein of Unknown Function (DUF239) | chr5:24285920-24287808 FORWARD LENGTH=1122
AT5G60610	UUACCCGUACGUCGCUUAUAAG	267	4.5	Cleavage	| Symbols: | F-box/RNI-like superfamily protein | chr5:24363591-24365528 FORWARD LENGTH=1441
AT5G60790	UGCAUAACUUGGGACUUACCU	413	4	Cleavage	| Symbols: ATGCN1, GCN1 | ABC transporter family protein | chr5:24453258-24455970 REVERSE LENGTH=2387
AT5G60800	UUUGCCUGUUGAACUCGAGUA	114	3	Translation	| Symbols: | Heavy metal transport/detoxification superfamily protein | chr5:24460887-24462536 REVERSE LENGTH=1153
AT5G60950	UUUGAGAGAUCCCCUGUUACUG	632	4	Cleavage	| Symbols: COBL5 | COBRA-like protein 5 precursor | chr5:24526847-24528084 REVERSE LENGTH=1004
AT5G61010	UAUAGGGCUUGAAAGAAAGUC	535	3.5	Cleavage	| Symbols: ATEXO70E2, EXO70E2 | exocyst subunit exo70 family protein E2 | chr5:24553841-24556749 FORWARD LENGTH=2805
AT5G61228	UUACGAGACUCUAGCCCAGCU	3733	4	Translation	| Symbols: CPuORF15 | conserved peptide upstream open reading frame 15 | chr5:24627187-24628968 FORWARD LENGTH=1335
AT5G61230	UUACGAGACUCUAGCCCAGCU	3733	4	Translation	| Symbols: | Ankyrin repeat family protein | chr5:24627187-24628968 FORWARD LENGTH=1335
AT5G61250	UGGCAGUAGGAGUACACGACU	163	5	Cleavage	| Symbols: AtGUS1, GUS1 | glucuronidase 1 | chr5:24632154-24634805 REVERSE LENGTH=1841
AT5G61280	UCCCAACCCAUGAUCUAAGCG	236	3	Cleavage	| Symbols: | Remorin family protein | chr5:24643625-24644910 REVERSE LENGTH=792
AT5G61440	CCACCGACUGAUGACAAUGUC	446	4.5	Cleavage	| Symbols: ACHT5 | atypical CYS HIS rich thioredoxin 5 | chr5:24707500-24708893 FORWARD LENGTH=1105
AT5G61470	CUGGAGGACGUACAGCACUUA	113	4	Cleavage	| Symbols: | C2H2-like zinc finger protein | chr5:24722870-24723983 FORWARD LENGTH=1114
AT5G61550	UACCGGAGGACGUACAUAGCU	401	4.5	Cleavage	| Symbols: | U-box domain-containing protein kinase family protein | chr5:24748102-24751871 FORWARD LENGTH=2715
AT5G61670	UGUGGUGUACCUCUUACGUCU	106	4	Cleavage	| Symbols: | Encodes a close homolog of the Cauliflower OR (Orange) protein. The function of OR is to induce the differentiation of proplastids or other noncolored plastids into chromoplasts for carotenoid accumulation. Both proteins contain a
AT5G61740	UUGGACGUCUCUACUAUGAGA	437	5	Cleavage	| Symbols: ATATH14, ATH14 | ABC2 homolog 14 | chr5:24808484-24812597 FORWARD LENGTH=2547
AT5G61790	UCUUGGCAUCGAAUUUGAACU	154	3.5	Cleavage	| Symbols: CNX1, ATCNX1 | calnexin 1 | chr5:24827102-24829791 REVERSE LENGTH=2034
AT5G61930	UCUGUAUGCAUAACUUGGGAC	1212	3	Cleavage	| Symbols: APO3 | Arabidopsis thaliana protein of unknown function (DUF794) | chr5:24866075-24867821 REVERSE LENGTH=1520
AT5G61960	UGAAGGAUUUGUGGUUAACCA	474	4	Cleavage	| Symbols: AML1, ML1 | MEI2-like protein 1 | chr5:24878521-24884720 REVERSE LENGTH=3886
AT5G61970	CCUGAGCCUAGUGACCGAGUA	270	4.5	Translation	| Symbols: | signal recognition particle-related / SRP-related | chr5:24888617-24893328 FORWARD LENGTH=2265
AT5G62170	CUUUGCACUCAUGAAUCUUUC	119	4	Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G51850.1); Has 381 Blast hits to 359 proteins in 81 species: Archae - 0; Bacteria - 16; Metazoa - 101; Fungi - 21; Plants - 99; Viruses - 3; Other E
AT5G62190	CAACGCUCUUGAUACAUCUAG	133	3	Cleavage	| Symbols: PRH75 | DEAD box RNA helicase (PRH75) | chr5:24980268-24983973 REVERSE LENGTH=2384
AT5G62220	UGACGGACAAGAUAAGCUGCU	259	4	Translation	| Symbols: ATGT18, GT18 | glycosyltransferase 18 | chr5:24988456-24990009 REVERSE LENGTH=1554
AT5G62310	UUCGAGAACUCCCUGACCCGA	1272	4	Cleavage	| Symbols: IRE | AGC (cAMP-dependent, cGMP-dependent and protein kinase C) kinase family protein | chr5:25023355-25028414 FORWARD LENGTH=3557
AT5G62600	UGACGCCAAUUCUGAAAGUUU	154	3	Cleavage	| Symbols: | ARM repeat superfamily protein | chr5:25123051-25132676 REVERSE LENGTH=3366
AT5G62700	UUCUUCCCGUUGGUGUGCGCC	170	3	Cleavage	| Symbols: TUB3 | tubulin beta chain 3 | chr5:25184397-25186711 FORWARD LENGTH=1742
AT5G63150	UCCACCGACUGAUGACAAUGU	1524	4.5	Cleavage	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: mitochondrion; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; CONTAINS InterPr
AT5G63320	CUCGGGAGAAAGAAGAAGGCU	259	3.5	Translation	| Symbols: NPX1 | nuclear protein X1 | chr5:25377096-25379246 REVERSE LENGTH=1981
AT5G63370	UCACUUUGCUGAACAUGUACC	138	3.5	Translation	| Symbols: | Protein kinase superfamily protein | chr5:25384172-25387252 REVERSE LENGTH=2943
AT5G63410	UCUUCGACUGAGGUAAGCGCCU	355	4	Translation	| Symbols: | Leucine-rich repeat protein kinase family protein | chr5:25394984-25398153 REVERSE LENGTH=2492
AT5G63460	UCUAGUUCGCGUUCUUCAGAC	300	4	Cleavage	| Symbols: | SAP domain-containing protein | chr5:25413356-25415592 REVERSE LENGTH=742
AT5G63510	AUGACGAAUGUUUGACAGCCU	113	3.5	Cleavage	| Symbols: GAMMA CAL1 | gamma carbonic anhydrase like 1 | chr5:25423984-25425841 FORWARD LENGTH=1058
AT5G63580	UUCUGAUUGCAUGUGGUGUACC	110	3.5	Cleavage	| Symbols: FLS2, ATFLS2 | flavonol synthase 2 | chr5:25454730-25456476 FORWARD LENGTH=1137
AT5G63600	UUGGACGUCUCUACUAUGAGA	437	4	Translation	| Symbols: FLS5, ATFLS5 | flavonol synthase 5 | chr5:25460684-25462458 REVERSE LENGTH=1567
AT5G63610	UGACGGAAGCUACAGAGGAUG	108	4.5	Cleavage	| Symbols: HEN3, CDKE;1, ATCDK8 | cyclin-dependent kinase E;1 | chr5:25463437-25465897 REVERSE LENGTH=1901

AT5G63630	UGUUACGAGACUCUAGCCCAG	574	3.5 Translation	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:25472598-25476511 REVERSE LENGTH=2476
AT5G63770	UAUCGAGCACCUACGUCACUGU	142	4 Cleavage	| Symbols: ATDGK2, DGK2 | diacylglycerol kinase 2 | chr5:25518641-25523621 FORWARD LENGTH=3580
AT5G63790	UGACGCCAAUUCUGAAAGUUU	154	3.5 Translation	| Symbols: ANAC102, NAC102 | NAC domain containing protein 102 | chr5:25526509-25528013 REVERSE LENGTH=1317
AT5G63870	UCUUGGCAUCGAAUUUGAACU	154	3.5 Cleavage	| Symbols: PP7 | serine/threonine phosphatase 7 | chr5:25561172-25563274 REVERSE LENGTH=1615
AT5G63950	CUUCGACUGAGGUAAGCGCCU	234	3.5 Cleavage	| Symbols: CHR24 | chromatin remodeling 24 | chr5:25591956-25598505 REVERSE LENGTH=3577
AT5G64080	UUUGAGCACUCUACAGACAGG	162	4 Translation	| Symbols: | Bifunctional inhibitor/lipid-transfer protein/seed storage 2S albumin superfamily protein | chr5:25645263-25646728 REVERSE LENGTH=839
AT5G64170	UUUGCUGAACAUGUACCUCCA	119	4 Cleavage	| Symbols: | dentin sialophosphoprotein-related | chr5:25672466-25676746 REVERSE LENGTH=2590
AT5G64310	UCAACACUCUGAUACAUCUAG	143	4 Cleavage	| Symbols: AGP1, ATAGP1 | arabinogalactan protein 1 | chr5:25721933-25722646 FORWARD LENGTH=714
AT5G64390	CUCACAAGUGAUAUAGGGCUU	208	4 Cleavage	| Symbols: HEN4 | RNA-binding KH domain-containing protein | chr5:25743344-25747548 FORWARD LENGTH=2840
AT5G64440	UCUAGUUCGCAUUUUUUGGAC	421	3.5 Cleavage	| Symbols: AtFAAH, FAAH | fatty acid amide hydrolase | chr5:25765750-25770500 FORWARD LENGTH=2227
AT5G64480	UUAUCAACGAACUCUUGGCCC	310	4 Cleavage	| Symbols: | unknown protein; Has 35333 Blast hits to 34131 proteins in 2444 species: Archae - 798; Bacteria - 22429; Metazoa - 974; Fungi - 991; Plants - 531; Viruses - 0; Other Eukaryotes - 9610 (source: NCBI BLink). | chr5:25778169-25778922
AT5G64500	AAACAGGACAAGUUACUCGCC	986	4 Translation	| Symbols: | Major facilitator superfamily protein | chr5:25780382-25783654 FORWARD LENGTH=1764
AT5G64560	UUUGCCUGUUGAACUCGAGUA	114	3 Cleavage	| Symbols: MGT9, MRS2-2, ATMGT9 | magnesium transporter 9 | chr5:25807121-25809595 REVERSE LENGTH=1299
AT5G64680	AACAAAACUGUUGAACAAGCCU	111	3 Translation	| Symbols: | unknown protein; FUNCTIONS IN: molecular_function unknown; INVOLVED IN: biological_process unknown; LOCATED IN: nucleolus; EXPRESSED IN: 23 plant structures; EXPRESSED DURING: 13 growth stages; Has 1807 Blast hits to 1
AT5G64790	GCAAGUGAUGAUAAAAAGACA	100	4.5 Cleavage	| Symbols: | O-Glycosyl hydrolases family 17 protein | chr5:25902641-25904701 FORWARD LENGTH=1672
AT5G64880	UUUAAAACCGAGGACUUUUGC	115	3.5 Cleavage	| Symbols: | unknown protein; Has 30201 Blast hits to 17322 proteins in 780 species: Archae - 12; Bacteria - 1396; Metazoa - 17338; Fungi - 3422; Plants - 5037; Viruses - 0; Other Eukaryotes - 2996 (source: NCBI BLink). | chr5:25932290-2593415
AT5G64905	GCAAGUGAUGAUAAAAAGACA	100	3 Translation	| Symbols: PROPEP3 | elicitor peptide 3 precursor | chr5:25939574-25940059 FORWARD LENGTH=486
AT5G64950	UUCGAGGAGAUAUGACGCGCC	4887	4 Translation	| Symbols: | Mitochondrial transcription termination factor family protein | chr5:25953844-25955160 FORWARD LENGTH=1317
AT5G65090	UCCUGAGGACGCUCUCCCUGC	106	3.5 Translation	| Symbols: MRH3, BST1, DER4 | DNAse I-like superfamily protein | chr5:26004724-26006851 FORWARD LENGTH=1709
AT5G65158	UGCCUAGAUUGCUCUACUCGA	125	5 Cleavage	| Symbols: | Lipase/lipooxygenase, PLAT/LH2 family protein | chr5:26030100-26031003 FORWARD LENGTH=809
AT5G65160	UUUGAUUCACCGGAUAAACUC	175	3.5 Cleavage	| Symbols: TPR14 | tetratricopeptide repeat (TPR)-containing protein | chr5:26031184-26033889 REVERSE LENGTH=2276
AT5G65350	UCUCAUGUAGUUCUAGUUCGCA	1437	4 Cleavage	| Symbols: HTR11 | histone 3 11 | chr5:26119211-26119825 REVERSE LENGTH=615
AT5G65380	UUCAGGGUGAGAACAUUGACU	1291	4 Cleavage	| Symbols: | MATE efflux family protein | chr5:26122989-26126439 REVERSE LENGTH=1800
AT5G65500	CUCACAAGUGAUAUAGGGCUUG	110	4.5 Translation	| Symbols: | U-box domain-containing protein kinase family protein | chr5:26181093-26183997 REVERSE LENGTH=2376
AT5G65550	UCCCAACCCAUGAUCUAAGCG	236	4 Cleavage	| Symbols: | UDP-Glycosyltransferase superfamily protein | chr5:26198304-26199827 REVERSE LENGTH=1524
AT5G65570	AUUCGAGAACUCCCUGACCCG	350	4.5 Cleavage	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:26203968-26206184 FORWARD LENGTH=2217
AT5G65600	CAAAUUCGAGAACUCCCUGAC	283	4 Cleavage	| Symbols: | Concanavalin A-like lectin protein kinase family protein | chr5:26216126-26218153 REVERSE LENGTH=2028
AT5G65620	UGACGGAAGCUACAGAGGAUG	108	3 Cleavage	| Symbols: | Zincin-like metalloproteases family protein | chr5:26221932-26225903 FORWARD LENGTH=2514
AT5G65670	UAGAGUGUUCAUGUAGUUGCA	232	3 Translation	| Symbols: IAA9 | indole-3-acetic acid inducible 9 | chr5:26253658-26256381 FORWARD LENGTH=1531
AT5G65687	ACAAAACUGUUGAACAAGCCU	1107	3 Cleavage	| Symbols: | Major facilitator superfamily protein | chr5:26269856-26272899 REVERSE LENGTH=1773
AT5G65700	UUUUGAGAGCCUUGUAGUAGU	118	2.5 Translation	| Symbols: BAM1 | Leucine-rich receptor-like protein kinase family protein | chr5:26281757-26285247 FORWARD LENGTH=3383
AT5G65770	UUAACUCUACCCUUUGCACUC	380	3 Translation	| Symbols: LINC4 | little nuclei4 | chr5:26311587-26315544 FORWARD LENGTH=3129
AT5G65780	UUAACUCUACCCUUUGCACUC	380	3 Translation	| Symbols: ATBCAT-5 | branched-chain amino acid aminotransferase 5 / branched-chain amino acid transaminase 5 (BCAT5) | chr5:26311311-26316025 FORWARD LENGTH=3579
AT5G65790	UAGAGUUAAGUUGGGACAGGA	199	4 Cleavage	| Symbols: ATMYB68, MYB68 | myb domain protein 68 | chr5:26322948-26324578 FORWARD LENGTH=1405
AT5G65870	UGUUGAUCCAAGUAGCUGACU	608	3.5 Cleavage	| Symbols: ATPSK5, PSK5 | phytosulfokine 5 precursor | chr5:26351508-26352269 FORWARD LENGTH=533
AT5G65925	UGCCAUGAUCGAGAGCUGCCU	164	4.5 Cleavage	| Symbols: | unknown protein; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT3G49820.1); Has 45 Blast hits to 45 proteins in 6 species: Archae - 0; Bacteria - 0; Metazoa - 0; Fungi - 0; Plants - 45; Viruses - 0; Other Eukaryot
AT5G66180	UUGGACGCCUCUACUAUGAGA	679	3.5 Translation	| Symbols: | S-adenosyl-L-methionine-dependent methyltransferases superfamily protein | chr5:26448938-26451154 FORWARD LENGTH=1437
AT5G66190	UACAGGAAGUGGGCGCACACC	102	4 Translation	| Symbols: ATLFNR1, FNR1 | ferredoxin-NADP(+)-oxidoreductase 1 | chr5:26450964-26453199 REVERSE LENGTH=1509
AT5G66220	UUCGAGAACUCCCUGACCCGA	1272	3.5 Translation	| Symbols: | Chalcone-flavanone isomerase family protein | chr5:26461177-26462174 FORWARD LENGTH=696
AT5G66230	UUCGAGAACUCCCUGACCCGA	1272	3.5 Translation	| Symbols: | Chalcone-flavanone isomerase family protein | chr5:26461152-26463916 FORWARD LENGTH=1706
AT5G66455	UGCCAUGAUCGAGAGCUGCCU	164	3.5 Cleavage	| Symbols: | pseudogene of pentatricopeptide (PPR) repeat-containing protein | chr5:26535980-26538011 REVERSE LENGTH=1449
AT5G66520	UAUCCUGAGAGCGGUGCUGGCC	101	4.5 Translation	| Symbols: | Tetratricopeptide repeat (TPR)-like superfamily protein | chr5:26551879-26553741 FORWARD LENGTH=1863
AT5G66710	UUCGAGAACUCCCUGACCCGA	1272	3.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:26636609-26638794 FORWARD LENGTH=1448
AT5G66790	UCUGUACCGCUGAAUUCUUCC	275	3.5 Cleavage	| Symbols: | Protein kinase superfamily protein | chr5:26665142-26667531 FORWARD LENGTH=2052
AT5G66890	AAACAGGACAAGUUACUCGCC	986	4.5 Cleavage	| Symbols: | Leucine-rich repeat (LRR) family protein | chr5:26712944-26714383 REVERSE LENGTH=1248
AT5G67170	UGACGGACAAGAUAAGCUGCU	259	4.5 Cleavage	| Symbols: | SEC-C motif-containing protein / OTU-like cysteine protease family protein | chr5:26799771-26802067 FORWARD LENGTH=1407
AT5G67220	UUCCGCAGGGAGAGCGUCCUC	112	3.5 Cleavage	| Symbols: | FMN-linked oxidoreductases superfamily protein | chr5:26820121-26821964 REVERSE LENGTH=1465
AT5G67270	UUUUGAUUCACCGGAUAAACUC	104	4 Cleavage	| Symbols: ATEB1C, EB1C, ATEB1H1 | end binding protein 1C | chr5:26840070-26842081 REVERSE LENGTH=1265
AT5G67310	UACCGGAGGACGUACAGCAUC	153	3.5 Cleavage	| Symbols: CYP81G1 | cytochrome P450, family 81, subfamily G, polypeptide 1 | chr5:26855216-26856941 REVERSE LENGTH=1638
AT5G67630	UCACCUCGCAUCUUAGAACUG	146	4.5 Cleavage	| Symbols: | P-loop containing nucleoside triphosphate hydrolases superfamily protein | chr5:26967381-26969394 REVERSE LENGTH=1652
ATCG00300	UACUCGACCACACUGUUAGGA	183	3.5 Translation	| Symbols: YCF9 | YCF9 | chrC:35751-35939 FORWARD LENGTH=189
ATCG00590	UUUUGCUUAGACUUAGAAACU	179	2.5 Cleavage	| Symbols: ORF31 | electron carriers | chrC:65712-65807 FORWARD LENGTH=96
ATCG00800	UUCGGACUGGAUAGGACUAGG	101	3.5 Translation	| Symbols: | structural constituent of ribosome | chrC:82826-83482 REVERSE LENGTH=657
ATCG00830	UACAAAUUCGAGCACUCCCUG	156	3.5 Translation	| Symbols: RPL2.1 | ribosomal protein L2 | chrC:84337-85843 REVERSE LENGTH=825
ATCG01310	UACAAAUUCGAGCACUCCCUG	156	3.5 Translation	| Symbols: RPL2.2 | ribosomal protein L2 | chrC:152806-154312 FORWARD LENGTH=825
ATMG00260	UAUGAGUUGAUCGACGAAGAU	123	3.5 Cleavage	| Symbols: ORF101A | hypothetical protein | chrM:76132-76437 FORWARD LENGTH=306
ATMG00570	CUUCCCCUAGAAUUCUUUCCC	401	3 Cleavage	| Symbols: ORFX | Sec-independent periplasmic protein translocase | chrM:157491-158351 FORWARD LENGTH=861
ATMG00730	UAACUCUACCCUUUGCACUCG	727	4.5 Cleavage	| Symbols: COX3 | cytochrome c oxidase subunit 3 | chrM:217631-219077 FORWARD LENGTH=1447
ATMG01130	UUCGGACUGGAUAGGACUAGG	101	4 Cleavage	| Symbols: ORF106F | hypothetical protein | chrM:289197-289517 REVERSE LENGTH=321
ATMG01210	UGAGAACAUUGACUUCAGACCU	158	5 Cleavage	| Symbols: ORF101B | hypothetical protein | chrM:304779-305084 REVERSE LENGTH=306

total=3102

Supplemental Table 3

Genes decreased at least 2-fold at p<0.05 in *ddm1* F6 vs wt Col

Probe Set ID	Gene	Value in *ddm1* F6	Value in wt Col	Fold change (*ddm1* F6 / wt Col)	p-value	TE in gene space?
251252_at	AT3G62230	260.10	10.06	25.79982	4.05E-04	no
266665_at	AT2G29790	196.68	12.29	17.02106	2.58E-04	yes
255008_at	AT4G10060	450.46	33.95	13.502051	4.62E-06	yes
260100_at	AT1G73177	227.50	18.23	12.684839	1.93E-06	no
247424_at	AT5G62850	634.59	55.62	12.237515	7.84E-04	no
261943_at	AT1G80660	888.62	90.53	11.330644	0.001402831	no
260557_at	AT2G43610	118.99	11.59	10.145937	6.50E-05	no
246789_at	AT5G27600	70.30	7.41	9.469623	4.85E-05	yes
249226_at	AT5G42170	216.04	23.04	9.305346	7.42E-04	yes
257256_at	AT3G21970	309.66	42.54	7.9923186	5.60E-04	no
258561_at	AT3G05960	132.33	16.78	7.9372573	8.09E-05	no
258408_at	AT3G17630	120.66	15.91	7.892432	1.27E-04	yes
261532_at	AT1G71680	176.72	23.79	7.6151543	1.55E-04	yes
265405_at	AT2G16750	415.86	58.19	7.486453	2.26E-04	no
254972_at	AT4G10440	124.67	18.05	7.3581605	6.33E-04	no
267317_at	AT2G34700	48.08	6.44	7.329497	1.40E-04	yes
265080_at	AT1G55570	1050.12	153.85	7.036429	3.09E-04	no
264112_at	AT2G13680	139.55	20.38	6.9105945	9.90E-05	no
257726_at	AT3G18360	180.41	27.56	6.8825173	0.001930365	no
265053_at	AT1G52000	216.96	31.63	6.651175	2.68E-05	yes
258671_at	AT3G08560	234.78	37.69	6.648874	0.00118247	yes
259189_at	AT3G01700	404.46	63.62	6.5997653	0.001071539	no
249245_at	AT5G42280	69.60	10.90	6.4735227	0.001490637	yes
256638_at	AT3G19090	70.74	10.98	6.4475327	0.001144193	no
265280_at	AT2G28355	1046.74	177.99	6.2346315	0.001068629	yes
262463_at	AT1G50310	738.61	122.18	6.15808	3.38E-04	no
261015_at	AT1G26480	142.57	23.23	6.105908	3.18E-04	no
253226_at	AT4G35010	498.95	83.36	6.0371876	3.73E-04	no
257059_at	AT3G15280	88.33	14.97	6.0081296	8.54E-04	no
249048_at	AT5G44300	1686.73	284.78	5.981856	3.63E-04	yes
253151_at	AT4G35670	82.58	14.05	5.8549027	2.74E-04	no
247056_at	AT5G66750	195.42	33.70	5.802461	9.58E-06	no
254961_at	AT4G11030	55.79	10.00	5.696744	7.75E-04	no
250631_at	AT5G07430	888.42	161.63	5.6322875	0.001733625	yes
254886_at	AT4G11760	1680.54	303.20	5.6253586	7.14E-04	yes
258639_at	AT3G07820	2108.48	394.78	5.443635	5.36E-04	no
256587_at	AT3G28780	747.03	137.62	5.417619	3.02E-04	yes
258465_at	AT3G17220	109.71	20.24	5.383513	6.05E-04	no
254033_at	AT4G25950	147.19	28.13	5.356676	0.001304095	no
267178_at	AT2G37750	98.02	18.24	5.3214355	1.15E-04	no
256581_at	AT3G28830	2820.30	532.00	5.318562	2.00E-04	yes
262022_at	AT1G35490	105.67	21.52	5.2948923	0.00151673	yes
263950_at	AT2G36020	72.93	14.22	5.2909064	0.001208057	no
245912_at	AT5G19600	64.65	12.80	5.210883	0.001921586	no
259269_at	AT3G01270	1436.81	276.57	5.180692	8.64E-04	yes
260888_at	AT1G29140	463.45	95.79	5.144302	0.00143741	no
267643_at	AT2G32890	265.05	53.03	5.098985	5.89E-04	yes
266654_at	AT2G25890	88.02	18.19	5.08119	0.001135627	no
247253_at	AT5G64790	46.25	9.10	5.0729113	0.002048545	yes
257158_at	AT3G24360	50.70	9.87	5.068173	0.007479937	yes
247512_at	AT5G61720	896.02	179.70	5.012007	4.11E-04	no
264208_at	AT1G22760	553.76	109.02	4.992296	1.36E-04	no
256588_at	AT3G28790	2739.01	549.49	4.9804993	1.51E-04	yes
255717_at	AT4G00350	55.69	10.79	4.966897	6.16E-04	yes
265473_at	AT2G15535	89.81	18.66	4.9483733	0.004093149	yes
245946_at	AT5G19580	1019.88	206.34	4.938102	9.06E-04	no

265552_at	AT2G07560	1292.17	266.27	4.9360094	1.50E-04	yes
254104_at	AT4G25040	501.20	126.38	4.9297276	0.007975142	yes
256584_at	AT3G28750	1593.51	326.27	4.921364	5.11E-04	no
250174_at	AT5G14380	1750.30	358.53	4.9080043	9.21E-04	yes
248822_at	AT5G47000	150.46	35.95	4.8835526	0.00495313	yes
266765_at	AT2G46860	261.37	62.56	4.856438	0.00736629	no
245335_at	AT4G16160	80.84	16.95	4.765691	5.01E-04	no
251258_at	AT3G62170	2729.78	575.89	4.76068	4.94E-04	no
267449_at	AT2G33690	89.31	19.03	4.7399125	7.58E-04	no
257313_at	AT3G26520	5571.85	1170.56	4.7342634	2.52E-05	yes
256647_at	AT3G13610	91.52	20.58	4.6766973	0.003796151	no
265031_at	AT1G61590	35.51	7.12	4.643443	0.003148268	no
262664_at	AT1G13970	70.88	17.00	4.6249847	0.005786907	no
262156_at	AT1G52680	649.07	142.20	4.6138635	0.00207021	yes
256966_at	AT3G13400	2258.67	494.55	4.573046	4.39E-04	no
255515_at	AT4G02250	295.23	65.92	4.5691	0.002159848	yes
262147_at	AT1G52570	184.70	40.57	4.5664897	8.46E-05	no
264235_at	AT1G54560	139.73	31.37	4.431889	6.49E-05	no
265176_at	AT1G23520	206.19	47.68	4.3684716	6.29E-04	no
264580_at	AT1G05340	53.53	12.25	4.3423533	0.00740631	no
250904_at	AT5G03620	159.85	36.24	4.340688	5.52E-04	no
254716_at	AT4G13560	4536.98	1078.17	4.331763	7.23E-04	no
253725_at	AT4G29340	480.56	112.44	4.3113494	2.01E-04	yes
254762_at	AT4G13230	884.60	210.62	4.293254	0.001257119	yes
248824_at	AT5G46940	162.99	42.72	4.278178	0.017119208	yes
249536_at	AT5G38760	2466.93	579.66	4.252036	2.94E-04	yes
248227_at	AT5G53820	2700.54	640.43	4.2221837	1.25E-04	no
255530_at	AT4G02140	378.60	90.61	4.2041316	5.89E-04	no
254415_at	AT4G21326	35.33	8.42	4.183755	5.21E-05	no
257986_at	AT3G20865	1175.93	284.33	4.1754913	4.03E-04	no
254287_at	AT4G22960	218.59	57.35	4.1476974	0.004939083	no
262122_at	AT1G02790	3477.93	839.27	4.1470613	2.88E-04	no
250514_at	AT5G09550	736.96	182.11	4.1369324	0.001113325	no
258058_at	AT3G28980	3029.94	735.56	4.1324463	0.001344193	no
255276_at	AT4G04930	67.36	16.35	4.1294913	0.001079603	yes
265179_at	AT1G23650	104.67	26.33	4.1070952	0.001645239	no
258851_at	AT3G03190	40.77	10.15	4.075465	0.033683732	no
251180_at	AT3G62640	65.24	16.33	4.0702353	0.003551517	no
246915_at	AT5G25880	122.99	30.81	4.033137	5.40E-04	yes
259793_at	AT1G64380	39.41	9.81	4.0330153	8.69E-05	no
258498_at	AT3G02480	2087.01	523.30	3.9992898	0.00179056	no
256354_at	AT1G54870	82.72	21.32	3.94937	0.004229826	yes
266697_at	AT2G19770	712.32	182.84	3.9177396	7.33E-04	yes
259044_at	AT3G03430	535.47	142.96	3.9152694	0.001368067	no
255861_at	AT2G30290	36.24	9.14	3.8725908	0.013892815	no
259265_at	AT3G01250	349.21	91.83	3.8630598	0.007785429	no
246431_at	AT5G17480	1139.05	303.57	3.8623755	0.001564621	yes
266764_at	AT2G47050	1996.59	535.23	3.827247	0.001432283	no
263753_at	AT2G21490	484.46	127.21	3.814271	0.001892292	no
248926_at	AT5G45880	1696.71	447.67	3.8024123	5.80E-04	no
246878_at	AT5G26060	47.84	12.68	3.7851985	0.008195365	no
245036_at	AT2G26410	21.97	5.62	3.7581515	0.012612021	yes
248714_at	AT5G48140	109.98	29.62	3.7514598	0.001812005	yes
248484_at	AT5G51030	99.29	27.81	3.7455623	0.00222101	yes
250608_at	AT5G07420	222.58	61.19	3.738575	0.002591189	yes
263909_at	AT2G36490	145.30	40.77	3.696608	3.87E-04	yes
259266_at	AT3G01240	925.14	252.09	3.6842976	0.003343268	no
264395_at	AT1G12070	104.96	31.48	3.6799912	0.012735958	no
245658_at	AT1G28270	894.90	247.11	3.6355426	0.001051357	no
265115_at	AT1G62450	51.22	14.21	3.625685	1.80E-04	yes

256955_at	AT3G13390	438.16	124.96	3.6117435	7.10E-04	no
247122_at	AT5G66020	55.77	16.02	3.565601	1.65E-04	no
264603_at	AT1G04670	320.69	89.83	3.5651546	0.002010378	no
261942_at	AT1G22590	220.83	62.14	3.5470347	9.71E-05	no
250957_at	AT5G03250	83.62	23.98	3.54573	8.31E-04	no
263754_at	AT2G21510	54.41	15.44	3.544004	0.017452165	no
265188_at	AT1G23800	390.33	113.86	3.5097258	3.28E-04	no
265923_at	AT2G18470	59.06	16.92	3.5027149	6.18E-04	yes
262760_at	AT1G10770	932.10	273.40	3.4457767	0.001644095	no
258748_at	AT3G05930	62.90	18.99	3.445511	0.007476477	no
251590_at	AT3G57690	1972.45	575.47	3.4413326	1.28E-04	no
252531_at	AT3G46520	85.54	24.87	3.4368322	5.47E-04	no
258685_at	AT3G07830	43.10	12.36	3.4361675	0.009527023	no
261511_at	AT1G71770	459.33	132.83	3.4310496	6.04E-04	yes
265002_at	AT1G24400	264.77	77.78	3.392483	6.17E-04	no
247736_at	AT5G59370	92.22	27.37	3.3895378	8.06E-04	no
245232_at	AT4G25590	223.21	66.48	3.3650608	0.002626282	no
252102_at	AT3G50970	463.20	141.80	3.3537579	0.021862911	no
247055_at	AT5G66740	46.79	13.98	3.3505068	0.00108267	no
256307_at	AT1G30350	308.83	92.85	3.348251	2.50E-04	no
252820_at	AT3G42640	386.65	117.49	3.3208952	0.001712484	no
264151_at	AT1G02070	57.68	18.05	3.3098695	0.002237665	no
252107_at	AT3G51490	140.48	42.80	3.2976906	1.63E-04	no
249375_at	AT5G40730	1056.79	321.43	3.2869718	2.96E-04	no
247546_at	AT5G61605	1366.07	432.08	3.2599456	0.001638986	yes
265205_at	AT2G36660	154.44	50.00	3.2502065	0.00182947	no
246896_at	AT5G25550	63.40	19.21	3.2454767	0.001454356	yes
245820_at	AT1G26320	195.25	60.21	3.2239423	0.002250842	no
264798_at	AT1G08730	63.73	19.88	3.2060525	4.01E-05	no
246551_at	AT5G15070	24.14	7.52	3.199446	2.83E-04	no
263003_at	AT1G54450	94.27	29.65	3.1871872	8.83E-05	no
249277_at	AT5G41890	37.68	12.42	3.1683602	0.004104161	yes
266453_at	AT2G43230	35.48	11.19	3.1661491	0.004986311	no
260997_at	AT1G26610	106.84	33.74	3.162287	1.66E-04	no
252140_at	AT3G51070	61.67	19.91	3.1581423	0.017062964	no
248168_at	AT5G54570	86.68	29.52	3.137777	0.017452022	yes
247897_at	AT5G57810	154.63	48.89	3.137519	7.95E-04	no
253641_at	AT4G29980	790.07	256.84	3.1068714	1.55E-04	no
250269_at	AT5G12970	32.71	10.70	3.097592	8.68E-04	no
261673_at	AT1G18280	1159.19	373.89	3.0912645	5.61E-04	no
259693_at	AT1G63060	193.31	62.98	3.0911534	0.001507254	no
246963_at	AT5G24820	136.35	46.05	3.0857022	0.005012851	no
257399_at	AT1G23690	81.20	25.99	3.0775673	9.78E-04	no
248367_at	AT5G52360	259.39	84.79	3.0763881	0.001010569	no
255081_at	AT4G09140	54.56	18.11	3.075739	0.003755624	no
258840_at	AT3G04620	375.84	123.22	3.0725377	0.001211365	no
245577_at	AT4G14780	154.83	50.95	3.0485573	4.99E-04	yes
245970_at	AT5G20710	851.20	277.47	3.0470812	3.81E-04	yes
261499_at	AT1G28430	496.92	167.87	3.0176651	0.003044215	no
265170_at	AT1G23730	309.41	105.45	3.0110934	0.006069331	no
262393_at	AT1G49490	27.96	9.37	3.0098157	0.015442135	no
258001_at	AT3G28950	92.01	31.22	3.002913	6.00E-04	yes
252733_at	AT3G43120	74.49	24.94	2.9957993	0.003818771	yes
248534_at	AT5G50030	262.46	88.60	2.9941647	0.001035591	yes
249429_at	AT5G39880	72.45	24.69	2.9865193	0.00245141	yes
255101_at	AT4G08670	1251.59	416.61	2.9840956	0.001293561	yes
260621_at	AT1G08065	67.81	23.13	2.9809265	0.005316635	no
254301_at	AT4G22790	84.91	28.64	2.9764225	4.18E-05	yes
258940_at	AT3G09930	14.22	4.62	2.9671555	0.03026893	no
251981_at	AT3G53080	10.20	3.42	2.963246	0.020234704	no

254520_at	AT4G19960	81.32	28.34	2.955541	0.006909187	no
257183_at	AT3G13220	380.49	129.50	2.9446557	2.87E-05	no
262385_at	AT1G72960	16.24	5.78	2.9348474	0.007159626	no
265163_at	AT1G23580	328.07	113.69	2.9334447	0.001762001	no
263718_at	AT2G13570	247.14	86.13	2.923781	0.004305918	yes
260059_at	AT1G78090	25.40	8.71	2.9147358	0.001603415	no
267295_at	AT2G23800	1001.88	343.08	2.9125767	5.59E-04	no
252061_at	AT3G52620	191.76	66.37	2.9102492	0.002177592	no
245151_at	AT2G47550	28.84	9.87	2.9084165	0.002713474	no
259346_at	AT3G03910	443.88	154.08	2.9032545	0.001426009	no
260773_at	AT1G78440	211.31	74.99	2.8983023	0.019844882	no
255175_at	AT4G07960	50.95	17.90	2.8946047	0.003433484	yes
266143_at	AT2G38905	337.59	118.13	2.8802803	4.96E-04	no
259527_at	AT1G12600	62.54	21.55	2.872524	0.002062767	no
264187_at	AT1G54860	301.22	107.00	2.8505664	0.002318854	no
260158_at	AT1G79910	22.26	8.41	2.8500447	0.008281982	no
264482_at	AT1G77210	127.36	45.60	2.8494399	0.003249186	no
256128_at	AT1G18140	154.30	57.07	2.8453195	0.004144106	no
255806_at	AT4G10260	358.22	126.75	2.8330023	3.16E-04	no
246545_at	AT5G15110	40.60	14.77	2.8303041	0.002768278	yes
250476_at	AT5G10140	31.98	11.74	2.8272328	0.008290174	no
257255_at	AT3G21960	26.76	9.51	2.8261535	0.002275632	no
265180_at	AT1G23590	100.64	35.74	2.8200562	1.85E-04	no
259975_at	AT1G76470	1016.63	363.87	2.810662	0.00558342	no
253934_at	AT4G26830	117.41	42.21	2.8104222	2.70E-04	yes
265672_at	AT2G31980	9103.72	3281.14	2.7986882	0.001294095	no
255580_at	AT4G01470	355.54	129.42	2.7895436	0.002551445	no
245830_at	AT1G57790	32.68	11.67	2.7886803	8.88E-05	no
257349_at	AT2G30630	16.37	5.93	2.7801325	0.002683393	yes
256598_at	AT3G30180	349.26	125.99	2.7708561	8.53E-04	yes
265185_at	AT1G23670	396.58	142.91	2.768346	3.63E-04	no
252090_at	AT3G52130	2625.37	962.45	2.7441087	1.45E-05	no
267322_at	AT2G19330	19.07	6.93	2.7417116	0.004294978	no
266481_at	AT2G31070	281.12	107.30	2.7396438	0.004683437	yes
251743_at	AT3G55890	36.36	13.58	2.7313235	0.002761965	no
248964_at	AT5G45340	94.12	34.47	2.7233236	0.039089344	yes
260097_at	AT1G73220	444.37	170.33	2.7173486	0.007653333	no
261305_at	AT1G48470	300.38	110.86	2.713855	2.02E-04	no
248245_at	AT5G53190	895.09	333.93	2.7044272	0.001707063	yes
249542_at	AT5G38140	102.71	37.95	2.7040215	1.37E-04	yes
263028_at	AT1G24030	38.18	15.21	2.6950645	0.022177372	no
254933_at	AT4G11130	52.51	20.52	2.6946614	0.005648575	yes
254453_at	AT4G21120	73.24	27.33	2.6807127	1.00E-04	no
258035_at	AT3G21180	27.79	10.44	2.6672568	0.002283316	no
266799_at	AT2G22860	52.24	20.40	2.661277	0.009238644	yes
247519_at	AT5G61430	137.29	52.46	2.6557953	0.003082249	yes
261396_at	AT1G79800	50.46	18.97	2.654841	8.28E-04	no
263360_at	AT2G03830	49.84	18.49	2.654561	0.007107353	no
251358_at	AT3G61160	81.25	31.27	2.651964	0.006749032	no
262987_at	AT1G23240	2675.61	1014.07	2.6493645	7.35E-04	no
250638_at	AT5G07540	1818.91	690.78	2.6434789	0.003225475	no
262358_at	AT1G73050	29.26	10.43	2.6342878	0.015482771	no
256578_at	AT3G28200	43.12	16.26	2.6333697	0.024021802	yes
252005_at	AT3G52810	687.77	265.37	2.6308815	0.001780303	no
264610_at	AT1G04645	47.89	18.67	2.6186287	0.009615727	no
250636_at	AT5G07520	801.25	308.23	2.617712	0.001031331	no
246841_at	AT5G26700	222.26	86.86	2.6081374	0.002867362	no
257491_at	AT1G06170	375.88	144.96	2.6075747	3.96E-05	no
257841_at	AT3G25260	53.64	20.31	2.6060078	9.41E-04	no
246344_at	AT3G56730	45.05	17.48	2.597431	0.007438321	no

246592_at	AT5G14890	20.74	7.95	2.5918186	0.020266501	no
257102_at	AT3G25050	5563.43	2215.68	2.5906463	0.004485958	no
266353_at	AT2G01520	1025.28	408.35	2.58214	0.002019035	no
254468_at	AT4G20460	329.37	135.16	2.5761354	0.014921484	yes
266708_at	AT2G03200	417.12	163.91	2.5756876	0.001224869	no
257402_at	AT1G23570	1284.69	503.79	2.5720782	0.003179174	no
249920_at	AT5G19260	138.88	57.11	2.5602443	0.045878716	no
265127_at	AT1G55560	298.79	116.47	2.5602136	0.001496798	no
262949_at	AT1G75790	624.75	247.15	2.5599334	0.001262055	no
254956_at	AT4G10850	386.34	153.10	2.5581117	0.002927222	yes
257951_at	AT3G21700	136.56	53.23	2.555616	0.004526666	yes
258322_at	AT3G22740	106.20	43.98	2.5552933	0.02291038	no
264710_at	AT1G09790	51.99	19.90	2.5524142	0.018209817	no
245499_at	AT4G16480	287.71	112.28	2.5519614	2.45E-04	no
260914_at	AT1G02640	534.82	208.78	2.5511124	1.12E-04	no
260032_at	AT1G68750	32.03	12.80	2.5473082	0.003957294	no
246377_at	AT1G57550	58.39	23.25	2.5434499	0.011072521	no
252440_at	AT3G47440	130.07	51.76	2.524004	0.01465098	no
265967_at	AT2G37450	323.10	128.70	2.5183892	8.25E-05	no
256059_at	AT1G06990	441.26	175.97	2.513862	3.21E-04	no
247719_at	AT5G59305	82.72	32.23	2.5053816	0.012130296	no
252769_at	AT3G42850	277.39	111.99	2.4790049	6.36E-05	yes
247561_at	AT5G61110	11.76	4.74	2.4778419	2.95E-04	no
253590_at	AT4G30850	208.61	84.96	2.465916	7.23E-04	no
245086_at	AT2G39820	53.03	22.01	2.4642994	0.011418066	no
260461_at	AT1G10980	254.80	103.66	2.4640708	0.001209544	no
264039_at	AT2G03740	1501.15	615.37	2.4489725	0.001125879	no
262917_at	AT1G64800	21.56	8.81	2.4446428	0.04042506	no
260788_at	AT1G06260	1976.14	827.65	2.4427552	0.002843642	no
248350_at	AT5G52160	340.92	139.67	2.4394693	0.004866162	yes
263020_at	AT1G23880	61.68	26.20	2.4365895	0.007215359	no
266115_at	AT2G02140	140.82	59.61	2.4311852	0.00247788	no
254494_at	AT4G20050	2026.05	847.76	2.4201732	0.001314773	no
255956_at	AT1G22015	380.31	160.33	2.4129035	0.002764732	no
262683_at	AT1G75920	1601.14	672.90	2.4119587	0.002206837	no
246859_at	AT5G25950	14.31	5.58	2.4070065	0.030912556	yes
255345_at	AT4G04460	7067.66	2931.92	2.4066112	0.001444061	yes
259063_at	AT3G07450	1769.64	736.00	2.4042096	1.43E-05	no
248919_at	AT5G45920	45.14	18.62	2.4011075	0.002198515	yes
265331_at	AT2G18420	157.84	66.66	2.3968756	0.001840307	no
253850_at	AT4G28090	41.53	17.52	2.3888187	0.005305177	no
261069_at	AT1G07410	102.39	43.69	2.3867562	0.003598909	no
254904_at	AT4G11160	572.73	240.32	2.3840218	1.34E-06	yes
246208_at	AT4G36490	66.26	28.57	2.3738394	0.002151529	no
251250_at	AT3G62180	122.67	52.21	2.3721924	0.007243713	no
245228_at	AT3G29810	15.17	6.27	2.3712816	0.04880642	yes
266118_at	AT2G02130	4469.03	1893.70	2.3679209	1.46E-04	no
248040_at	AT5G55970	196.08	82.96	2.3659494	4.38E-04	no
263011_at	AT1G23250	130.07	57.37	2.3646946	0.02090834	no
257107_at	AT3G29070	19.95	8.46	2.3556914	0.005916068	yes
257904_at	AT3G28470	13.26	5.70	2.3552413	0.013052155	no
266530_at	AT2G16910	850.90	362.67	2.3523662	2.90E-04	no
261264_at	AT1G26710	358.18	158.88	2.3510058	0.005153147	no
266494_at	AT2G07040	46.64	20.24	2.3419018	0.006343479	no
266866_at	AT2G29940	88.03	38.82	2.326367	0.001530079	no
249527_at	AT5G38710	70.70	30.41	2.3244395	0.028316176	yes
266462_at	AT2G47770	65.05	28.12	2.320686	0.005099452	no
264117_at	AT2G31210	36.29	15.53	2.319421	0.017627252	no
257275_at	AT3G14450	101.87	44.42	2.3114698	4.50E-04	no
256416_at	AT3G11050	78.88	33.73	2.30996	0.013630518	no

249046_at	AT5G44400	613.87	266.01	2.3098233	2.37E-04	yes
250509_at	AT5G09970	55.21	24.05	2.3087308	0.021906197	yes
262674_at	AT1G75910	5444.71	2404.32	2.307473	0.00313648	no
262675_at	AT1G75930	7556.33	3312.00	2.3034918	0.001909436	no
261302_at	AT1G48580	75.28	33.22	2.2959292	0.004611112	no
267150_at	AT2G23510	166.96	74.20	2.295831	0.001617308	no
247657_at	AT5G59845	2113.44	943.14	2.2887785	0.004644582	yes
250635_at	AT5G07510	1505.58	674.00	2.288495	0.002925841	yes
248499_at	AT5G50400	559.07	246.76	2.285179	7.90E-04	yes
249687_at	AT5G36150	40.17	17.39	2.2847648	3.43E-04	yes
263599_at	AT2G01830	165.28	71.63	2.2802174	0.007600582	no
245674_at	AT1G56680	24.17	10.60	2.2755013	0.006705329	no
259744_at	AT1G71160	1228.04	541.46	2.272846	4.75E-04	no
265164_at	AT1G23600	168.00	76.45	2.2687294	0.017416866	no
245982_at	AT5G13170	145.75	63.34	2.2646103	0.006028885	no
259377_at	AT3G16380	60.77	26.74	2.2637517	1.86E-05	no
249540_at	AT5G38120	292.22	132.11	2.2632883	0.011114489	yes
264835_at	AT1G03550	50.78	22.33	2.262646	0.001649815	no
251595_at	AT3G57620	273.52	130.53	2.2611506	0.029868439	no
261670_at	AT1G18520	135.90	60.69	2.2600834	0.012488171	no
257348_at	AT2G42140	17.51	7.69	2.2589464	0.011257623	no
264577_at	AT1G05260	41.35	17.82	2.2550485	0.010892336	no
260355_at	AT1G69180	398.78	177.19	2.2547572	5.77E-05	no
265263_at	AT2G42940	527.59	230.33	2.2464535	0.017501118	no
257405_at	AT1G24620	62.48	28.16	2.2387059	0.003920351	no
261392_at	AT1G79780	173.10	77.41	2.2370272	7.62E-05	no
251277_at	AT3G61760	69.01	31.09	2.2288997	0.001229496	no
247567_at	AT5G61190	179.82	80.56	2.2263343	9.98E-05	no
260627_at	AT1G62310	46.75	21.26	2.2231903	4.09E-04	no
254809_at	AT4G12410	122.63	58.44	2.2153375	0.013289147	yes
254487_at	AT4G20780	33.33	15.05	2.2088547	0.028817577	no
254683_at	AT4G13800	50.30	22.94	2.202764	0.012466529	no
262213_at	AT1G74870	108.68	49.74	2.202728	0.001805092	no
249767_at	AT5G24090	34.37	15.21	2.1984086	0.015481235	no
251441_at	AT3G60020	18.00	8.42	2.1932404	0.022780076	no
246533_at	AT5G15880	287.36	131.75	2.187005	4.03E-05	no
245322_at	AT4G14815	1852.13	847.28	2.181359	0.002817046	no
262925_at	AT1G65730	165.55	76.11	2.180504	0.007037075	no
249381_at	AT5G40040	594.95	275.12	2.1723444	5.56E-04	yes
249732_at	AT5G24420	2322.90	1064.69	2.1723216	0.001860342	no
245699_at	AT5G04250	397.78	185.78	2.1709194	0.001806819	no
248872_at	AT5G46795	98.76	46.04	2.1691184	0.010330169	yes
260233_at	AT1G74550	624.67	289.74	2.164311	9.62E-04	no
263363_at	AT2G03850	3308.34	1548.93	2.1580024	0.002243994	no
260791_at	AT1G06250	157.19	73.82	2.1565793	0.001196704	no
250479_at	AT5G10260	67.62	30.99	2.1554556	0.025270592	no
250997_at	AT5G02570	77.24	35.97	2.1541576	0.003565648	no
267255_at	AT2G22950	40.49	19.09	2.1506844	0.001766285	no
252571_at	AT3G45280	60.26	28.38	2.145433	0.007139439	yes
254946_at	AT4G10950	9.82	4.54	2.1391761	6.49E-04	no
245883_at	AT5G09500	563.43	278.58	2.1343565	0.011803113	yes
256481_at	AT1G33430	3657.56	1729.44	2.1322849	0.001353877	no
248581_at	AT5G49900	311.31	148.69	2.131304	0.005098539	yes
261051_at	AT1G01280	829.25	393.71	2.1289382	0.002925493	no
265387_at	AT2G20670	100.01	46.34	2.1284664	0.0270081	no
250619_at	AT5G07230	3304.96	1567.07	2.1213615	5.65E-04	no
261222_at	AT1G20120	1754.54	838.37	2.1190326	0.009754958	no
253963_at	AT4G26470	13.47	6.44	2.1119611	0.03803137	yes
255703_at	AT4G00040	788.07	374.86	2.1096938	5.94E-04	yes
262637_at	AT1G06640	663.79	314.95	2.1078408	0.005557725	no

258385_at	AT3G15510	120.47	58.62	2.1013768	0.00144159	no
266015_at	AT2G24190	73.93	35.67	2.1013253	0.002434236	no
246386_at	AT1G77410	53.49	25.84	2.1010628	0.001612896	no
250872_at	AT5G03960	117.72	55.66	2.1005015	0.010665043	yes
253012_at	AT4G37900	1553.43	739.57	2.0964906	2.48E-04	yes
253863_at	AT4G27420	102.60	49.72	2.0941036	0.002111907	yes
262765_at	AT1G13150	414.68	202.13	2.0866454	0.002374353	no
247582_at	AT5G60760	117.71	56.67	2.084815	0.030722763	no
247759_at	AT5G59040	89.84	43.70	2.0776815	4.66E-04	no
248638_at	AT5G49070	121.22	58.16	2.077253	0.041356646	no
256419_at	AT1G33470	105.90	51.35	2.074363	6.12E-04	no
263368_at	AT2G20470	73.42	35.47	2.074313	9.57E-04	no
260022_at	AT1G30020	645.75	311.76	2.071682	0.002724563	no
248371_at	AT5G51810	24.11	12.02	2.0704272	0.006678246	no
266078_at	AT2G40670	559.63	272.66	2.0658307	0.012825166	no
250860_at	AT5G04770	114.64	55.74	2.060856	0.002987884	no
250639_at	AT5G07560	4752.25	2322.05	2.0596669	0.001550682	no
249865_at	AT5G22820	81.82	40.14	2.0571916	0.012160042	no
251361_at	AT3G61230	36.53	20.11	2.0571735	0.040686645	no
247462_at	AT5G62080	8094.70	3939.76	2.056002	7.79E-06	no
250637_at	AT5G07530	24174.00	11837.39	2.055867	5.63E-04	no
248296_at	AT5G53090	136.21	67.26	2.053872	0.005764713	no
254175_at	AT4G24050	90.53	44.91	2.053023	0.001748134	no
251356_at	AT3G61060	125.78	62.14	2.0484092	7.70E-04	no
256297_at	AT1G69500	2903.12	1435.01	2.0445437	8.75E-04	no
265186_at	AT1G23560	448.05	219.41	2.0398157	0.001424264	no
250471_at	AT5G10170	165.11	80.67	2.0377858	0.004595071	no
261559_at	AT1G01780	161.56	79.17	2.0363097	0.015372991	no
267127_at	AT2G23610	123.34	61.25	2.0360088	0.01632749	no
251825_at	AT3G55100	12.56	6.12	2.033751	0.029315587	yes
263453_at	AT2G22180	24.01	11.76	2.032304	0.017392747	no
263406_at	AT2G04160	44.58	22.28	2.0315905	0.033211783	no
263905_at	AT2G36190	263.29	128.90	2.031369	0.007802574	no
250648_at	AT5G06760	8.75	4.31	2.0283942	4.76E-04	no
257476_at	AT1G80960	55.13	27.82	2.02422	0.010876722	no
247956_at	AT5G56970	250.38	124.61	2.0219152	0.030805903	no
261171_at	AT1G04880	207.79	103.85	2.018744	0.002204213	no
250907_at	AT5G03670	244.61	122.54	2.0135083	4.89E-04	no
263513_at	AT2G12400	439.99	218.94	2.013043	1.81E-04	no
266666_at	AT2G29780	10.93	5.16	2.009186	0.032963917	no
261109_at	AT1G75450	87.60	41.72	2.006382	0.04030508	no
262115_at	AT1G02813	2084.22	1070.93	2.0050085	0.019345041	no
259461_at	AT1G18900	137.26	69.45	2.0035214	0.006289406	no
246075_at	AT5G20410	103.22	51.89	2.0034378	0.001624272	no
250576_at	AT5G08250	63.56	31.70	2.0021982	0.003285957	no
264225_at	AT1G67420	46.12	23.54	2.0020037	0.020862415	no
262942_at	AT1G79450	28.60	14.42	2.0000415	0.020962957	no

Supplemental Table 4

Genes both predicted to be cleaved by TE siRNAs and decreased 2-fold in *ddm1* F6 p<0.05, with no TE in gene space

siRNA sequence	siRNA RPM in *ddm1* F6 AGO1-IP	small RNA length	predicted target gene	E-value	Gene expression fold-change in *ddm1* F6	gene annotation
UUCCAGAACUAAUGAAUGUUA	448	21	AT4G35670	4	5.85	Pectin lyase-like superfamily protein
UCGGCUCAAACCUAACACGUU	129	21	AT3G13610	5	4.68	2-oxoglutarate (2OG) and Fe(II)-dependent oxygenase superfamily protein
UUCUGAAGGACAAGAUCAGCU	351	21	AT3G20865	4	4.18	AGP40, arabinogalactan protein 40
UUCAGGGUGAGAACAUUGACU	1291	21	AT4G22960	4	4.15	Protein of unknown function (DUF544)
CUUCCCCUAGAAUUCUUUCCC	401	21	AT5G09550	3.5	4.14	GDP dissociation inhibitor family protein / Rab GTPase activator family protein
UUUGGGUUUGGGUUAACUGCU	225	21	AT5G03250	3	3.55	Phototropic-responsive NPH3 family protein
CAAGAACCCGCACGACACUCG	169	21	AT3G51490	5	3.30	TMT3, tonoplast monosaccharide transporter3
UACUCGACCACACUGUUAGGA	183	21	AT3G51070	4.5	3.16	S-adenosyl-L-methionine-dependent methyltransferases superfamily protein
AUACCCAAACCUGAACUUUCU	127	21	AT1G08065	4	2.98	ATACA5, ACA5, alpha carbonic anhydrase 5
UACUCCAGAAACUCACAACGA	113	21	AT1G79910	3.5	2.85	Regulator of Vps4 activity in the MVB pathway protein
UGCACUCGCUAGGUCUGGCAG	378	21	AT1G57790	4.5	2.79	F-box family protein
CCUGAGCCUAGUGACCGAGUA	270	21	AT4G21120	4	2.68	AAT1, CAT1, amino acid transporter 1
UUUAGAGAUCCCCUGUUACUG	387	21	AT5G19260	5	2.56	FAF3, Fantasic four protein #3, regulates shoot apical meristem size
UCACCUCGCAUCUUAGAACUG	146	21	AT1G68750	3	2.55	ATPPC4, PPC4, phosphoenolpyruvate carboxylase 4
UGUCACCGUAGAUUUCUUCCU	123	21	AT4G30850	3	2.47	HHP2, heptahelical transmembrane protein2
AAUUCGAGAACUCCCUGACCC	255	21	AT1G64800	4	2.44	DNA binding;sequence-specific DNA binding transcription factors
UCACUUUGCUGAACAUGUACC	138	21	AT5G55970	4	2.37	RING/U-box superfamily protein
UUUGAUCCGAGGAUGAUGGAU	816	21	AT2G16910	2	2.35	AMS, basic helix-loop-helix (bHLH) DNA-binding superfamily protein
UGAGCCGACAAGAGUAGUAUC	111	21	AT2G29940	4.5	2.33	PDR3, ATPDR3, pleiotropic drug resistance 3
UUGACUUCAGACCUGCGCGUG	131	21	AT2G47770	4	2.32	ATTSPO, TSPO, outer membrane tryptophan-rich sensory protein-related
UGUCCCAACUUAACUCUACCCU	279	22	AT1G18520	3.5	2.26	TET11, tetraspanin11
UACGCGACCGCGGUGCUGGCC	119	21	AT2G20670	4.5	2.13	Protein of unknown function (DUF506)
UGGAUUCCGGCUGCAUACUCC	392	21	AT5G49070	5	2.08	KCS21, 3-ketoacyl-CoA synthase 21
UGUGGAUACAAGAGCUGGGCU	215	21	AT5G07560	4	2.06	GRP20, ATGRP20, glycine-rich protein 20
UCUGAUUGCAUGUGGUGUACC	109	21	AT5G22820	4	2.06	ARM repeat superfamily protein
UAUGAGUUGAUCGACGAAGAU	123	21	AT3G61060	4.5	2.05	AtPP2-A13, PP2-A13, phloem protein 2-A13, carbohydrate binding
GCAAGUGAUGAUAAAAAGACA	100	21	AT2G36190	3	2.03	AtcwINV4, cwINV4, cell wall invertase 4
average	278.828			3.963	2.901	
			total=27			

Supplemental Table 5
Mutant alleles and primer sequences used in this report

Mutant Allele	Original background
ddm1-2	Col
rdr6-15	Col
ubp1b (FLAG_298B04)	Ws

Target	Experiment	Figure	Forward primer sequence	Reverse primer sequence 1	Reverse primer sequence 2
Athila6	probe for Northern blot	Figure 1	TCACTTGCGTCGTTGTGAGTTT	TCAGAAACGTGATGGCTTTGAA	
MiR166a	probe for Northern blot	Figure 1	GGGGAATGAAGCCTGGTCCGA		
MiR161	probe for Northern blot	Figure 1	TAGTCACTTTCAATGCATTGA		
At2g16910 (*AMS*)	qRT-PCR	Figure 4	AGCGGAGAATGGAACAGAAGAG	CCGGAATCAAGAGGTATGGAAG	
AT4G30850 (*HHP2*)	qRT-PCR	Figure 4	GATTCGCCGGAGTTCAATTTC	CTTCACCGTTCTCCGTTTCTG	
AT1G57790	qRT-PCR	Figure 4	AGCCTTGCCTTTTCTTCACTTG	GGCCTGGATCATAATCCTTGATAG	
AT4G07960 (*AtCLSC12*)	qRT-PCR	Figure 4	CCCGCGGTCATTAAATCAAAG	TCGGGTACAAACATAGTCATTGG	
AT5G27600 (*ATLACS7*)	qRT-PCR	Figure 4	CAAGTGCCGTAAAATCATCTGG	TCAGGTGACAAAGGAGAAGCAC	
AT4G17610	qRT-PCR	Figure 4	CGACAGAGTTTGATCCTTGTGG	CTTGCATCTGCAACAGCAAGAC	
AT4G30850 (*HHP2*)	modified 5' RACE	Figure 4		ATCTCTTCTTTTCGCCGGAATC	GTTCTCCGTTTCTGCATGATTC
DCP2	RFP fusion	Figure 5	CACCATGTCGGGCCTCCATCG	AGCTGAATTACCAGATTCCAACGCCTG	
G3PB	RFP fusion	Figure 5	CACCATGGCACAGCAGGAAGC	AGATGAACCACCACCTCGAGCTC	
MiR156	probe for Northern blot	Supplemental Figure 1	GTGCTCACTCTCTTCTGTCA		
MiR166	probe for Northern blot	Supplemental Figure 1	GGGGAATGAAGCCTGGTCCGA		
AGO1	qRT-PCR	Supplemental Figure 2	GGAGGTGGACCTTCTTCTGGAC	CCTCAGACAGTGTAGGCTGAGAAG	
AGO1	modified 5' RACE	Supplemental Figure 2		TTGTTTCATCACAGCACGATTG	CAGGCAGTTCAGCAAAGAAATG
ATHB-15	qRT-PCR	Supplemental Figure 3	ACAAAGGAAAGAGGCTTCACG	TCTGCAACCTGTCATTCTCCTC	
ATHB-15	modified 5' RACE	Supplemental Figure 3		GAGATCTCTCGCACACCACAAG	GGCCAATGTAGTTGGTGCATAG
MYB33	qRT-PCR	Supplemental Figure 3	GCCCATCTATTACCCATCTTGG	GCCCATCTATTACCCATCTTGG	
MYB33	modified 5' RACE	Supplemental Figure 3		CAGTAACCTGGCCAAGATCAGC	CCAGAAGCAACATATCGAGCAG
DCL1	qRT-PCR	Supplemental Figure 3	TATCTCACGCAGCGTTCCTAAG	AGCTAACCATGGCACCAGTTG	
DCL1	modified 5' RACE	Supplemental Figure 3		TCCCAGTTGATCCCTTTTATGG	ACAAACAGGTAGGCCTTTGCAG