

**List of affected genes, confidential preview.**

Statistics are testing for differential expression (two-sided non-null).

Ranks refer to this test.

Results are grouped by

Differentially expressed with  $q < 5\%$   $M > 0$

Differentially expressed with  $q < 5\%$   $M < 0$

Non-differentially expressed,  $q$  of 5% or higher

Up-regulation

Down-regulation

Insignificant

Orthogonal contrasts examined:

15 dpi Syncytium vs 5 dpi Syncytium

... **Table 3 & Table S3**

*up*

*down*

*non-diff*

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page 3

page 4

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Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2	AT3G15840.3   expressed protein   chr3:5356657-5358506 REVERSE   Aliases: MSJ11.24, MSJ11_24	6.4	2.3	4.0	14.9	0.65%	7.4
3	AT4G39675.1   expressed protein   chr4:18413769-18414232 FORWARD   Aliases: None	8.8	2.4	6.5	12.4	1.93%	6.1
4	AT5G54940.2   eukaryotic translation initiation factor SUI1, putative, similar to SP:P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfam profile PF01253: Translation initiation factor SUI1   chr5:22325497-22326633 REVERSE   Aliases: MBG8.21, MBG8_21	11.7	9.6	2.1	11.1	3.43%	6.3
5	AT5G50790.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr5:20673479-20675225 REVERSE   Aliases: MFB16.26, MFB16_26	8.4	3.7	4.7	10.6	3.46%	3.3
6	AT5G10040.1   expressed protein   chr5:3143724-3144158 FORWARD   Aliases: T31P16.30, T31P16_30	8.9	3.8	5.1	10.5	3.46%	4.4
7	AT1G08430.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	9.1	5.4	3.7	10.1	3.67%	3.8
9	AT1G27730.1   Symbol: ZAT10   zinc finger (C2H2 type) family protein (ZAT10) / salt-tolerance zinc finger protein (STZ), identical to salt-tolerance zinc finger protein GB:CAA64820 GI:1565227 from (Arabidopsis thaliana); contains Pfam domain, PF00096: Zinc finger, C2H2 type; identical to cDNA	9.6	5.8	3.7	9.8	3.67%	4.4
10	AT4G33560.1   expressed protein   chr4:16135403-16135917 FORWARD   Aliases: T16L1.50, T16L1_50	8.6	4.9	3.7	9.7	3.67%	4.0
11	AT5G65870.1   Symbol: ATPSK5	7.1	3.6	3.5	9.6	3.67%	4.4
12	AT1G62480.1   vacuolar calcium-binding protein-related, contains weak similarity to vacuolar calcium binding protein (Raphanus sativus) gi:9049359:dbj:BAA99394   chr1:23132370-23133424 FORWARD   Aliases: T3P18.4, T3P18_4	10.6	7.0	3.6	9.5	3.67%	3.6
13	AT3G19680.1   expressed protein   chr3:6840287-6842326 FORWARD   Aliases: MMB12.17	7.5	5.3	2.2	8.7	4.98%	4.4
14	AT5G10695.1   expressed protein   chr5:3377664-3378222 FORWARD   Aliases: None	10.7	7.8	2.9	8.7	4.98%	4.2
16	AT3G03910.1   glutamate dehydrogenase, putative, similar to glutamate dehydrogenase 1 (GDH 1) (Arabidopsis thaliana) SWISS-PROT:Q43314	9.8	5.5	4.3	8.6	4.98%	2.0
17	AT1G10010.1   Symbol: AAP8   amino acid permease, putative, similar to amino acid permease I GI:22641 from (Arabidopsis thaliana); GC splice site at position 1256 is predicted from alignment and not confirmed experimentally   chr1:3265978-3268728 FORWARD   Aliases: T27I1.3, T27I1_3	8.6	5.4	3.2	8.5	4.98%	3.3
18	AT2G18050.2   Symbol: HIS1 3	6.3	3.5	2.9	8.5	4.98%	3.8
19	AT3G48740.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr3:18063492-18065738 REVERSE   Aliases: T21J18.1	9.8	4.4	5.4	8.4	4.98%	1.9
20	AT2G22860.1   Symbol: ATPSK2	11.2	8.8	2.5	8.4	4.98%	4.1
21	AT2G17710.1   expressed protein   chr2:7700678-7701828 FORWARD   Aliases: T17A5.17, T17A5_17	8.3	3.9	4.4	8.4	4.98%	3.1
22	AT1G74880.1   Symbol: NDH O   Encodes subunit NDH-O of NAD(P)H:plastoquinone dehydrogenase complex (Ndh complex) present in the thylakoid membrane of chloroplasts. This subunit is thought to be required for Ndh complex assembly.   chr1:28133540-28134738 REVERSE   Aliases: F25A4.15, F25A4_15, NDH O	5.4	2.8	2.6	8.4	4.98%	3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1	AT3G60140.1   Symbol: DIN2   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to Cyanogenic Beta-Glucosidase (GI:1311386)(pdb:1CBG) (Trifolium Repens); identical beta-glucosidase GI:10834547   chr3:22227648-22231792 FORWARD   Aliases: DARK INDUCIBLE 2, SENESCENCE RELATED GENE 2, SRG2, T2O9.120, T2O9_120	3.0	8.6	-5.6	-20.2	0.12%	7.3
8	AT5G05340.1   peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi:5381253:dbj:BAA82306; similar to Peroxidase P7 (Brassica rapa (Turnip)) SWISS-PROT:P00434   chr5:1578952-1580876 REVERSE   Aliases: K18I23.14, K18I23_14	2.8	8.8	-6.0	-9.8	3.67%	4.9
15	AT3G50300.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr3:18654937-18656388 FORWARD   Aliases: F11C1.140	4.1	7.7	-3.5	-8.6	4.98%	3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
23	AT4G27450.1   expressed protein, similar to auxin down-regulated protein ARG10 (Vigna radiata) GI:2970051, wali7 (aluminum-induced protein) (Triticum aestivum) GI:451193   chr4:13727493-13728892 REVERSE   Aliases: F27G19.50, F27G19_50	10.9	7.7	3.2	8.3	5.3%	3.4
24	AT3G14780.1   similar to glycosyl transferase family 48 protein [Arabidopsis thaliana] (TAIR:At3g14570.1); similar to putative callose synthase 1 catalytic subunit [Oryza sativa (japonica cultivar-group)] (GB:XP_468556.1)   chr3:4961813-4963513 REVERSE   Aliases: T21E2.4	6.7	4.6	2.1	8.3	5.3%	4.0
25	AT2G35290.1   expressed protein   chr2:14868491-14869108 REVERSE   Aliases: T4C15.4, T4C15_4	7.8	2.9	4.9	8.1	5.3%	3.4
26	AT4G34410.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr4:16451880-16453264 FORWARD   Aliases: F10M10.180, F10M10_180	5.7	2.5	3.2	8.1	5.3%	3.5
27	AT4G33985.1   expressed protein   chr4:16288117-16288918 REVERSE   Aliases: None	9.0	5.6	3.4	8.1	5.3%	2.8
28	AT4G18340.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr4:10130153-10132072 REVERSE   Aliases: T9A21.190, T9A21_190	7.6	5.3	2.2	8.0	5.3%	3.4
29	AT2G41480.1   peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781334:emb:CAA71494   chr2:17303890-17305805 REVERSE   Aliases: T26J13.7, T26J13_7	7.3	4.1	3.2	8.0	5.3%	2.6
30	AT3G45970.1   Symbol: ATEXLA1   expansin family protein (EXPL1), similar to cim1 induced allergen, Glycine max, EMBL:U03860; expansin-like gene, PMID:11641069, www.bio.psu.edu/expansins   chr3:16907151-16908293 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN LIKE A1, ATEXPL1, ATHEXP BETA 2.1, EXPL1, F16L2.180, F16L2_180	10.9	9.1	1.9	7.9	5.3%	3.8
31	AT1G61340.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to late embryogenesis abundant protein GI:1350540 from (Picea glauca)	8.2	4.7	3.5	7.9	5.3%	3.2
32	AT4G10270.1   wound-responsive family protein, similar to wound induced protein (GI:19320) (Lycopersicon esculentum)   chr4:6374730-6375206 FORWARD   Aliases: T9A4.6	10.9	6.6	4.3	7.9	5.3%	2.5
33	AT1G07500.1   expressed protein, ; expression supported by MPSS   chr1:2304763-2305028 REVERSE   Aliases: F22G5.11, F22G5_11	6.6	3.2	3.4	7.9	5.3%	3.7
34	AT5G38710.1   proline oxidase, putative / osmotic stress-responsive proline dehydrogenase, putative, similar to proline oxidase, mitochondrial precursor (Osmotic stress- induced proline dehydrogenase) (Arabidopsis thaliana) SWISS-PROT:P92983   chr5:15518570-15521129 FORWARD   Aliases: MKD10.10, MKD10_10	9.0	5.6	3.4	7.8	5.3%	2.5
35	AT1G32450.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:11715130-11719935 REVERSE   Aliases: F5D14.23, F5D14_23	7.9	5.1	2.8	7.8	5.3%	3.0
36	AT1G18250.2   Symbol: ATLP 1	3.5	6.9	-3.3	-7.7	5.6%	2.3
37	AT1G20823.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:7238789-7239658 FORWARD   Aliases: F2D10.34, F2D10_34	9.4	6.0	3.4	7.5	6.8%	2.8
38	AT2G27240.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	9.6	6.0	3.6	7.5	7.0%	1.9
39	AT3G14660.1   Symbol: CYP72A13   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4924784-4927441 FORWARD   Aliases: MIE1.16	7.9	5.8	2.1	7.3	8.3%	3.2
40	AT4G37710.1   VQ motif-containing protein, contains PF05678: VQ motif   chr4:17718122-17718736 FORWARD   Aliases: T28I19.3	6.2	2.6	3.6	7.2	8.5%	3.0
41	AT4G02290.1   glycosyl hydrolase family 9 protein, similar to endo-1,4-beta glucanase; ATCEL2 GI:3132891 from (Arabidopsis thaliana)   chr4:1002446-1005202 REVERSE   Aliases: T2H3.5, T2H3_5	3.5	7.3	-3.8	-7.2	8.5%	2.4
42	AT2G11810.1   Symbol: MGDC   1,2-diacylglycerol 3-beta-galactosyltransferase, putative / monogalactosyldiacylglycerol synthase, putative / MGDG synthase, putative, identical to monogalactosyldiacylglycerol synthase type C (gi:9927295) from Arabidopsis thaliana, similar to MGDG synthase type A (gi:9884651) from Glycine max   chr2:4750448-4753859 FORWARD   Aliases: ATMGD3, F7E22.4, F7E22_4, MGD3, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE	5.4	3.2	2.2	7.1	8.5%	2.9
43	AT2G40610.1   Symbol: ATEXPA8   expansin, putative (EXP8), similar to expansin 2 GI:7025493 from (Zinnia elegans); alpha-expansin gene family, PMID:11641069   chr2:16955941-16957635 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A8, ATEXP8, ATHEXP ALPHA 1.11, EXP8, T2P4.4, T2P4_4	10.0	6.3	3.7	7.1	8.5%	2.1

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44	AT1G48600.2   phosphoethanolamine N-methyltransferase 2, putative (NMT2), very similar to :PEM2_ARATH Putative phosphoethanolamine N-methyltransferase 2 (EC 2.1.1.103) (SP:Q944H0){Arabidopsis thaliana}; very similar to Halotolerance protein Hal3b (SP:P94063)(Arabidopsis thaliana); to similar to GB:AAF61950 from (Spinacia oleracea)   chr1:17969539-17973005 FORWARD   Aliases: T1N15.23, T1N15_23	10.9	12.2	-1.3	-7.1	8.5%	3.2
45	AT2G38870.1   protease inhibitor, putative, similar to SP:P24076 Glu S.griseus protease inhibitor (BGIA) {Momordica charantia}; contains Pfam profile PF00280: Potato inhibitor I family   chr2:16243459-16244358 REVERSE   Aliases: T7F6.4, T7F6_4	7.3	11.1	-3.8	-7.1	8.5%	2.8
46	AT2G41640.1   expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)   chr2:17367574-17369613 FORWARD   Aliases: T32G6.16, T32G6_16	8.1	4.8	3.3	7.0	9.2%	2.7
47	AT3G53450.1   hypothetical protein, contains Pfam profile PF03641: decarboxylase family protein   chr3:19823955-19826408 REVERSE   Aliases: F4P12.150	5.8	4.0	1.8	6.9	9.6%	2.9
48	AT2G40000.1   expressed protein   chr2:16707588-16709106 REVERSE   Aliases: T28M21.16, T28M21_16	9.5	7.0	2.5	6.9	10.0%	2.7
49	AT2G41540.3   similar to NAD-dependent glycerol-3-phosphate dehydrogenase family protein [Arabidopsis thaliana] (TAIR:At3g07690.1); similar to putative glycerol-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:NP_915827.1); similar to putative glycerol-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:AAU44049.1); contains InterPro domain NAD-dependent glycerol-3-phosphate dehydrogenase (InterPro:IPR006168)   chr2:17333206-17336863 FORWARD   Aliases: T32G6.6, T32G6_6	4.0	6.3	-2.3	-6.8	10.7%	2.5
50	AT1G79180.1   myb family transcription factor (MYB63), similar to myb-related protein GI:1370139 from (Lycopersicon esculentum)   chr1:29791402-29792695 FORWARD   Aliases: YUP8H12R.21, YUP8H12R_21	5.5	7.5	-2.1	-6.8	10.8%	2.5
51	AT4G34160.1   Symbol: CYCD3;1   cyclin delta-3 (CYCD3), identical to SP:P42753 Cyclin delta-3 {Arabidopsis thaliana}   chr4:16357643-16359559 FORWARD   Aliases: CYCD3, CYCD3;1, Cyclin D3;1, D3, F28A23.80, F28A23_80	3.7	6.8	-3.2	-6.7	10.8%	2.2
52	AT1G69880.1   thioredoxin, putative, similar to SP:Q38879 Thioredoxin H-type 2 (TRX-H-2) {Arabidopsis thaliana}; contains Pfam profile: PF00085 Thioredoxin   chr1:26325142-26326656 FORWARD   Aliases: T17F3.9, T17F3_9	9.0	5.3	3.7	6.7	10.8%	1.6
53	AT1G06460.1   Symbol: ACD32.1   31.2 kDa small heat shock family protein / hsp20 family protein, contains Pfam profile: PF00011 Hsp20/alpha crystallin family	7.0	4.0	3.0	6.7	11.0%	2.4
54	AT3G16150.1   L-asparaginase, putative / L-asparagine amidohydrolase, putative, similar to Swiss-Prot:P30364 L-asparaginase (EC 3.5.1.1) (L-asparagine amidohydrolase) (Lupinus angustifolius)	10.2	6.7	3.5	6.6	11.4%	1.8
55	AT4G25010.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr4:12854640-12856361 REVERSE   Aliases: F13M23.150, F13M23_150	9.8	6.2	3.6	6.6	11.4%	1.0
56	AT4G27652.1   expressed protein   chr4:13809839-13810362 FORWARD   Aliases: None	9.6	5.8	3.7	6.6	11.4%	2.2
57	AT1G02900.1   Symbol: RALFL1	4.8	7.6	-2.8	-6.6	11.4%	1.9
58	AT3G02800.1   similar to tyrosine specific protein phosphatase family protein [Arabidopsis thaliana] (TAIR:At5g16480.1); similar to putative tyrosine specific protein phosphatase protein [Oryza sativa (japonica cultivar-group)] (GB:XP_450177.1); contains InterPro domain Putative tyrosine phosphatase (InterPro:IPR004861)   chr3:606478-607893 REVERSE   Aliases: F13E7.26, F13E7_26	6.5	4.9	1.6	6.6	11.4%	2.5
59	AT4G30270.1   Symbol: MERI5B	8.9	5.8	3.1	6.5	11.4%	1.7
60	AT1G76650.1   calcium-binding EF hand family protein, similar to regulator of gene silencing calmodulin-related protein GI:12963415 from (Nicotiana tabacum); contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:28771644-28772411 REVERSE   Aliases: F28O16.2, F28O16_2	7.5	4.7	2.8	6.5	11.4%	2.2
61	AT5G17350.1   expressed protein   chr5:5718774-5719610 FORWARD   Aliases: MKP11.31, MKP11_31	6.2	3.7	2.4	6.5	11.4%	2.0
62	AT1G64700.1   expressed protein   chr1:24043473-24044258 REVERSE   Aliases: F13O11.2, F13O11_2	7.9	6.1	1.8	6.4	12.6%	2.5
63	AT1G80840.1   Symbol: WRKY40	8.7	5.5	3.2	6.3	13.4%	2.0
64	AT3G30775.1   Symbol: ERD5   proline oxidase, mitochondrial / osmotic stress-responsive proline dehydrogenase (POX) (PRO1) (ERD5), nearly identical to SP:P92983 Proline oxidase, mitochondrial precursor (EC 1.5.3.-) (Osmotic stress- induced proline dehydrogenase) (Arabidopsis thaliana); identical to cDNA proline oxidase precursor GI:1817543	11.1	8.9	2.2	6.3	13.6%	2.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
65	AT5G66110.1   similar to heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related [Arabidopsis thaliana] (TAIR:At4g38580.1); similar to Putative atfp6-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470243.1); contains InterPro domain Heavy metal binding (InterPro:IPR006191); contains InterPro domain Heavy metal transport/detoxification protein (InterPro:IPR006121)   chr5:26447428-26448138 FORWARD   Aliases: K2A18.19, K2A18_19	9.6	7.4	2.2	6.3	13.7%	2.3
66	AT1G18980.1   germin-like protein, putative, similar to germin-like protein subfamily T member 1 (SP:P92995); contains PS00725 germin family signature	6.4	10.7	-4.3	-6.3	13.7%	1.6
67	AT5G45340.2   Symbol: CYP707A3   cytochrome P450 family protein, similar to SP:Q42569:C901_ARATH Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana); contains Pfam profile: PF00067: Cytochrome P450   chr5:18385907-18388218 REVERSE   Aliases: K9E15.12, K9E15_12	8.8	6.5	2.3	6.3	13.7%	2.2
68	AT4G00880.1   auxin-responsive family protein, similar to small auxin up RNA (GI:546362) {Arabidopsis thaliana}   chr4:366373-367274 REVERSE   Aliases: A_TM018A10.6, A_TM018A10_6, T18A10.18, T18A10_18	6.7	4.9	1.8	6.2	13.7%	2.1
69	AT2G27080.2   harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, contains 1 transmembrane domain; similar to hin1 homolog (GI:13122296) (Arabidopsis thaliana); similar to hin1 (GI:22830759) (Nicotiana tabacum)   chr2:11571011-11574582 FORWARD   Aliases: T20P8.13, T20P8_13	7.2	5.5	1.7	6.2	14.1%	2.2
70	AT4G02850.1   phenazine biosynthesis PhzC/PhzF family protein, contains Pfam profile: PF02567 phenazine biosynthesis-like protein   chr4:1266463-1268612 REVERSE   Aliases: T5J8.17, T5J8_17	3.6	5.9	-2.3	-6.2	14.2%	2.0
71	AT1G22160.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana)   chr1:7823138-7823960 FORWARD   Aliases: F2E2.23, F2E2_23	5.8	3.6	2.2	6.2	14.3%	2.1
72	AT2G01530.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:20810)   chr2:239719-240492 FORWARD   Aliases: F2I9.15, F2I9_15	4.5	7.5	-3.1	-6.2	14.3%	1.1
73	AT5G26220.1   ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like protein   chr5:9162972-9164680 REVERSE   Aliases: T19G15.70, T19G15_70	6.0	9.6	-3.6	-6.1	14.4%	1.4
74	AT2G40880.1   Symbol: FL3 27	9.1	7.0	2.1	6.1	14.5%	2.0
75	AT1G43800.1   acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative, similar to Acyl-(acyl-carrier protein) desaturase from Lupinus luteus GI:4704824, Asclepias syriaca GI:1762436, Ricinus communis SP:P22337; contains Pfam profile PF03405 Fatty acid desaturase   chr1:16580056-16582162 FORWARD   Aliases: F28H19.7, F28H19_7	5.8	2.5	3.3	6.1	14.5%	2.1
76	AT5G08350.1   GRAM domain-containing protein / ABA-responsive protein-related, contains similarity to ABA-responsive protein in barley (GI:4103635) (Hordeum vulgare) (J. Exp. Bot. 50, 727-728 (1999)); FH protein interacting protein FIP1, Arabidopsis thaliana, EMBL:AF174428; contains Pfam PF02893: GRAM domain   chr5:2686246-2687250 REVERSE   Aliases: F8L15.80, F8L15_80	8.4	5.8	2.7	6.1	14.5%	1.7
77	AT5G42900.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g33980.1)   chr5:17215358-17217007 REVERSE   Aliases: MBD2.9, MBD2_9	6.8	4.6	2.2	6.1	14.5%	2.0
78	AT1G67810.1   Fe-S metabolism associated domain-containing protein, contains Pfam PF02657: Fe-S metabolism associated domain   chr1:25430151-25430968 FORWARD   Aliases: F12A21.6, F12A21_6	7.9	6.1	1.8	6.1	14.5%	2.1
79	AT3G14430.1   expressed protein   chr3:4824204-4824844 REVERSE   Aliases: MOA2.3	9.6	8.7	0.9	6.1	14.5%	2.0
80	AT2G35780.1   Symbol: SCPL26	6.9	8.3	-1.3	-6.1	14.5%	2.1
81	AT5G43150.1   expressed protein   chr5:17342246-17343126 FORWARD   Aliases: MMG4.18, MMG4_18	11.6	10.8	0.8	6.0	14.5%	2.0
82	AT4G08950.1   phosphate-responsive protein, putative (EXO), similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr4:5740294-5741521 FORWARD   Aliases: T3H13.3, T3H13_3	9.0	6.0	3.0	6.0	14.5%	1.1
83	AT1G28480.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	9.0	7.2	1.8	6.0	14.5%	2.1
84	AT1G17380.1   expressed protein   chr1:5955481-5957205 REVERSE   Aliases: F28G4.16	8.2	5.4	2.8	6.0	14.6%	1.5
85	AT2G47550.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:19516050-19519205 FORWARD   Aliases: T30B22.15	2.5	4.8	-2.3	-6.0	14.6%	1.8
86	AT5G40980.1   expressed protein   chr5:16432076-16432448 REVERSE   Aliases: MEE6.5, MEE6_5	6.8	4.2	2.6	6.0	14.6%	2.0
87	AT2G40750.1   Symbol: WRKY54	6.5	5.1	1.3	6.0	14.7%	2.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
88	AT1G07370.1   Symbol: PCNA1   proliferating cell nuclear antigen 1 (PCNA1), identical to SP:Q9M7Q7 Proliferating cellular nuclear antigen 1 (PCNA 1) {Arabidopsis thaliana}; nearly identical to SP:Q43124 Proliferating cell nuclear antigen (PCNA) {Brassica napus}; contains Pfam profiles PF00705: Proliferating cell nuclear antigen N-terminal domain, PF02747: Proliferating cell nuclear antigen C-terminal domain   chr1:2263140-2264549 FORWARD   Aliases: F22G5.29, F22G5_29, PROLIFERATING CELLULAR NUCLEAR ANTIGEN	5.2	8.6	-3.4	-6.0	14.7%	1.6
89	AT2G30750.1   Symbol: CYP71A12   cytochrome P450 71A12, putative (CYP71A12), Identical to Cytochrome P450 (SP:O49340) (Arabidopsis thaliana); contains Pfam profile: PF00067 cytochrome P450   chr2:13106475-13108490 REVERSE   Aliases: T11J7.14, T11J7_14	3.1	5.1	-2.0	-5.9	14.7%	1.7
90	AT5G67080.1   Symbol: MAPKKK19   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:26789952-26790986 FORWARD   Aliases: K21H1.4, K21H1_4	4.6	2.9	1.7	5.9	14.7%	2.0
91	AT4G23690.1   disease resistance-responsive family protein / dirigent family protein, similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669; similar to dirigent protein (Forsythia x intermedia) gi:6694693:gb:AAF25357   chr4:12338881-12339757 REVERSE   Aliases: F9D16.160, F9D16_160	2.8	7.1	-4.3	-5.9	14.7%	0.8
92	AT2G24040.1   hydrophobic protein, putative / low temperature and salt responsive protein, putative, similar to SP:Q9ZLN7 Hydrophobic protein RC12A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}; contains Pfam profile PF01679: Uncharacterized protein family   chr2:10231057-10231686 FORWARD   Aliases: T29E15.24, T29E15_24	8.2	6.7	1.4	5.9	15.3%	2.0
93	AT1G61800.1   glucose-6-phosphate/phosphate translocator, putative, similar to glucose-6-phosphate/phosphate-translocator precursor GI:2997591 from (Pisum sativum)   chr1:22828105-22830411 FORWARD   Aliases: T13M11.18, T13M11_18	5.3	3.6	1.7	5.9	15.3%	1.7
94	AT2G21820.1   expressed protein   chr2:9309965-9310327 REVERSE   Aliases: F7D8.14, F7D8_14	10.3	8.2	2.1	5.8	15.3%	1.7
95	AT4G20260.4   similar to DREPP plasma membrane polypeptide-related [Arabidopsis thaliana] (TAIR:At5g44610.1); similar to DREPP2 protein [Nicotiana tabacum] (GB:CAB91552.1); contains InterPro domain DREPP plasma membrane polypeptide (InterPro:IPR008469)   chr4:10940749-10943512 FORWARD   Aliases: F1C12.180, F1C12_180	10.9	9.5	1.4	5.8	15.3%	1.9
96	AT3G53190.1   pectate lyase family protein, similar to pectate lyase 2 GP:6606534 from (Musa acuminata)   chr3:19725019-19728568 FORWARD   Aliases: T4D2.120	6.2	7.8	-1.6	-5.8	15.3%	1.9
97	AT2G17850.1   senescence-associated family protein, contains similarity to ketoconazole resistant protein GI:928938 from (Arabidopsis thaliana) and din1 GI:2190012 from (Raphanus sativus); contains a thiosulfate sulfurtransferase domain   chr2:7767087-7767791 REVERSE   Aliases: T13L16.13, T13L16_13	6.6	3.0	3.6	5.8	15.3%	1.7
98	AT5G47240.1   MutT/nudix family protein, similar to SP:P53370 Nucleoside diphosphate-linked moiety X motif 6 {Homo sapiens}; contains Pfam profile PF00293: NUDIX domain   chr5:19200944-19202871 FORWARD   Aliases: MQL5.10, MQL5_10	6.5	4.4	2.1	5.8	15.3%	1.8
99	AT4G33420.1   peroxidase, putative, identical to class III peroxidase ATP32 (Arabidopsis thaliana) gi:17530547:gb:AAL40837; identical to cDNA class III peroxidase ATP32 GI:17530546	7.8	3.6	4.2	5.8	15.3%	1.6
100	AT4G29780.1   expressed protein   chr4:14579710-14581706 FORWARD   Aliases: F27B13.20, F27B13_20	7.4	5.2	2.2	5.8	15.8%	1.7
101	AT5G07580.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr5:2399505-2400602 FORWARD   Aliases: MBK20.1	6.6	5.2	1.4	5.8	15.8%	1.8
102	AT3G04890.1   expressed protein   chr3:1347652-1349205 FORWARD   Aliases: T9J14.16, T9J14_16	7.4	6.0	1.5	5.8	15.8%	1.8
103	AT2G47950.1   expressed protein   chr2:19631293-19631879 FORWARD   Aliases: T9J23.9, T9J23_9	7.4	4.8	2.7	5.7	16.3%	1.5
104	AT5G42200.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:16877695-16878423 FORWARD   Aliases: MJC20.31, MJC20_31	6.7	4.3	2.4	5.7	16.5%	1.7
105	AT4G24570.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr4:12686469-12687660 FORWARD   Aliases: F22K18.230, F22K18_230	8.0	5.8	2.2	5.7	16.5%	1.7
106	AT4G27654.1   expressed protein   chr4:13811651-13812132 FORWARD   Aliases: None	8.2	3.8	4.4	5.7	16.6%	1.7
107	AT1G28290.1   pollen Ole e 1 allergen and extensin family protein, similar to arabinogalactan protein (Daucus carota) GI:11322245; contains Pfam profile PF01190: Pollen proteins Ole e I family   chr1:9889112-9890980 REVERSE   Aliases: F3H9.6, F3H9_6	4.3	6.5	-2.3	-5.7	16.6%	1.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
108	AT5G07840.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:2506657-2508374 REVERSE   Aliases: F13G24.40	7.2	6.3	1.0	5.7	16.6%	1.7
109	AT3G08720.2   Symbol: ATPK19	9.2	7.8	1.4	5.7	16.6%	1.7
110	AT5G59820.1   Symbol: RHL41   zinc finger (C2H2 type) family protein (ZAT12), identical to zinc finger protein ZAT12 (Arabidopsis thaliana) gi:1418325:emb:CAA67232   chr5:24120198-24121013 FORWARD   Aliases: MMN10.11, MMN10_11, RESPONSIVE TO HIGH LIGHT 41, ZAT12	7.1	4.6	2.5	5.7	16.6%	1.3
111	AT1G67320.1   DNA primase, large subunit family, contains Pfam profile PF04104: Eukaryotic-type DNA primase, large subunit; similar to DNA primase large subunit (EC 2.7.7.-) (DNA primase 58 kDa subunit) (p58) (Swiss-Prot:P49643) (Homo sapiens)   chr1:25209055-25212635 REVERSE   Aliases: F1N21.14	4.6	7.1	-2.5	-5.7	16.6%	1.2
112	AT4G02060.1   Symbol: PRL   prolifera protein (PRL) / DNA replication licensing factor Mcm7 (MCM7), identical to DNA replication licensing factor Mcm7 SP:P43299 PROLIFERA protein {Arabidopsis thaliana}; contains Pfam profile PF00493: MCM2/3/5 family   chr4:901388-905590 FORWARD   Aliases: MCM7, PROLIFERA, T10M13.7, T10M13_7	4.0	7.0	-3.0	-5.6	17.0%	1.4
113	AT2G01520.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:169000) contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr2:235928-237130 FORWARD   Aliases: F2I9.14, F2I9_14	7.3	9.4	-2.0	-5.6	17.1%	1.5
114	AT1G47410.1   expressed protein, identical to hypothetical protein GB:AAD46041 GI:5668815 from (Arabidopsis thaliana)   chr1:17397258-17397948 FORWARD   Aliases: T3F24.15	4.1	6.8	-2.7	-5.6	17.1%	1.2
115	AT5G03545.1   expressed protein, No ATG start, annotated according to PMID:11123795   chr5:894705-895399 FORWARD   Aliases: None	10.5	5.8	4.7	5.6	17.1%	-0.3
116	AT4G37490.1   Symbol: CYC1   G2/mitotic-specific cyclin (CYC1) / B-like cyclin (CYC1), identical to SP:P30183 G2/mitotic-specific cyclin (B-like cyclin) {Arabidopsis thaliana}   chr4:17621880-17624279 REVERSE   Aliases: CYCB1, CYCB1;1, CYCLIN 1, Cyclin B1;1, F6G17.140, F6G17_140	5.0	3.7	1.3	5.6	17.1%	1.6
117	AT2G19670.1   protein arginine N-methyltransferase, putative, similar to protein arginine N-methyltransferase 1-variant 1 (Homo sapiens) GI:7453577   chr2:8506199-8508232 REVERSE   Aliases: F6F22.30, F6F22_30	4.1	6.2	-2.0	-5.6	17.2%	1.5
118	AT5G19890.1   peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:1403134:emb:CAA67092   chr5:6724117-6725925 REVERSE   Aliases: F28I16.40, F28I16_40	4.5	2.2	2.3	5.5	18.5%	1.5
119	AT3G44260.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)   chr3:15963032-15964071 REVERSE   Aliases: T10D17.50	6.0	4.3	1.6	5.5	18.8%	1.5
120	AT3G48540.1   cytidine/deoxycytidylate deaminase family protein, similar to SP:P32321 Deoxycytidylate deaminase (EC 3.5.4.12) (dCMP deaminase) {Homo sapiens}; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region   chr3:18000783-18003000 REVERSE   Aliases: T8P19.50	4.0	6.0	-2.0	-5.5	18.8%	1.3
121	AT5G20150.1   SPX (SYG1/Pho81/XPR1) domain-containing protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profile PF03105: SPX domain   chr5:6802374-6803627 FORWARD   Aliases: F5O24.40, F5O24_40	5.5	3.8	1.7	5.5	18.8%	1.4
122	AT5G11930.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	6.1	4.4	1.7	5.5	18.9%	1.4
123	AT2G43620.1   chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus)   chr2:18100847-18102102 REVERSE   Aliases: F18O19.27	2.7	4.4	-1.7	-5.4	19.3%	1.5
124	AT1G72430.1   auxin-responsive protein-related, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana)   chr1:27268573-27269292 REVERSE   Aliases: T10D10.10, T10D10_10	7.4	5.4	1.9	5.4	19.8%	1.3
125	AT5G61000.1   replication protein, putative, similar to replication protein A1 (Oryza sativa) GI:2258469; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain   chr5:24566804-24569947 REVERSE   Aliases: MSL3.120, MSL3_120	5.3	8.2	-2.9	-5.4	19.8%	1.0
126	AT1G78000.2   Symbol: SULTR1;2   sulfate transporter (Sultr1;2), identical to sulfate transporter Sultr1;2 (Arabidopsis thaliana) GI:7768660; contains Pfam profiles PF00916: Sulfate transporter family and PF01740: STAS domain; contains TIGRfam profile TIGR00815: sulfate permease   chr1:29334738-29338040 FORWARD   Aliases: F28K19.22, F28K19_22, SEL1, SELENATE RESISTANT 1, SULFATE TRANSPORTER, SULFATE TRANSPORTER 1;2	6.3	8.2	-1.9	-5.4	19.8%	1.2
127	AT1G75390.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr1:28295426-28296669 FORWARD   Aliases: F1B16.8, F1B16_8	8.4	6.3	2.0	5.4	19.8%	1.4
128	AT4G37240.1   expressed protein   chr4:17524455-17525153 FORWARD   Aliases: AP22.53, AP22_53	5.4	3.7	1.7	5.4	19.8%	1.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
129	AT5G41880.1   DNA primase small subunit family, contains Pfam profile: PF01896 DNA primase small subunit   chr5:16778299-16781011 FORWARD   Aliases: K16L22.17, K16L22_17	4.3	6.8	-2.5	-5.4	19.8%	1.1
130	AT1G20920.1   DEAD box RNA helicase, putative, similar to RNA helicase (Rattus norvegicus) GI:897915; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr1:7285103-7288831 FORWARD   Aliases: F9H16.10, F9H16_10	6.6	5.5	1.1	5.4	19.8%	1.4
131	AT2G38860.2   Symbol: YLS5   protease1 (pfpl)-like protein (YLS5), contains Pfam profile PF01965: DJ-1/Pfpl family; supporting cDNA gi:13122287:dbj:AB047808.1.; identical to protease1 (pfpl)-like protein (Arabidopsis thaliana) GI:13122288, cDNA protease1 (pfpl)-like protein GI:13122287   chr2:16240522-16242309 REVERSE   Aliases: T7F6.3, T7F6_3	7.6	9.2	-1.6	-5.4	19.8%	1.4
132	AT5G63600.2   similar to flavonol synthase 1 (FLS1) [Arabidopsis thaliana] (TAIR:At5g08640.1); similar to FLS_MATIN Flavonol synthase/flavanone 3-hydroxylase (FLS) (GB:O04395); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)   chr5:25477910-25479684 REVERSE   Aliases: MBK5.7, MBK5_7	3.4	5.5	-2.1	-5.4	19.8%	1.2
133	AT5G63590.1   flavonol synthase, putative, similar to SP:Q96330 Flavonol synthase 1 (EC 1.14.11.-) (FLS 1) {Arabidopsis thaliana}; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr5:25474219-25475696 REVERSE   Aliases: MBK5.5, MBK5_5	3.5	5.2	-1.7	-5.3	19.8%	1.2
134	AT1G63640.2   kinesin motor protein-related, C-terminal region is similar to C-term region of kinesin motor protein GB:AAB51397 (Mus musculus); contains Pfam profile: PF00225 Kinesin motor domain   chr1:23592730-23599438 REVERSE   Aliases: F2K11.1, F2K11_1	4.5	6.4	-1.9	-5.3	19.8%	1.1
135	AT5G43260.1   chaperone protein dnaJ-related, similar to Chaperone protein dnaJ (SP:Q9WZV3) (Thermotoga maritima)   chr5:17374615-17375310 REVERSE   Aliases: MNL12.8, MNL12_8	9.6	7.8	1.8	5.3	19.8%	1.3
136	AT5G08020.1   replication protein, putative, similar to replication protein A1 (Oryza sativa) GI:2258469; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain   chr5:2572108-2574880 FORWARD   Aliases: F13G24.220, F13G24_220	3.2	5.0	-1.8	-5.3	19.8%	1.1
137	AT5G42290.1   transcription activator-related, contains weak similarity to beta-cell E-box transcription activator 1 gi:529197:gb:AAA65702   chr5:16928928-16929332 FORWARD   Aliases: K5J14.9, K5J14_9	6.7	4.7	2.1	5.3	19.8%	1.0
138	AT5G50800.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr5:20682303-20684530 REVERSE   Aliases: K7B16.1, K7B16_1	11.3	8.3	3.0	5.3	20.3%	1.1
139	AT2G28470.1   Symbol: BGAL8   beta-galactosidase, putative / lactase, putative, similar to Beta-galactosidase precursor SP:P48980 from (Lycopersicon esculentum)   chr2:12175930-12180647 REVERSE   Aliases: T17D12.3, T17D12_3	5.6	7.6	-2.1	-5.3	20.3%	1.3
140	AT5G12170.1   expressed protein, similar to unknown protein (pir::T09909)   chr5:3933503-3934962 FORWARD   Aliases: MXC9.13, MXC9_13	7.2	5.3	1.9	5.3	20.3%	1.0
141	AT2G22170.1   lipid-associated family protein, contains PLAT/LH2 (Polycystin-1, Lipoxygenase, Alpha-Toxin/Lipoxygenase homology) domain Pfam:PF01477   chr2:9433929-9434891 REVERSE   Aliases: T26C19.17, T26C19_17	2.5	5.0	-2.5	-5.3	20.3%	0.8
142	AT5G10010.1   expressed protein   chr5:3127907-3131721 FORWARD   Aliases: T31P16.7, T31P16_7	4.3	6.0	-1.8	-5.3	20.3%	1.2
143	AT1G52880.1   Symbol: NAM   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM (no apical meristem) GB:CAA63101 from (Petunia x hybrida); identical to cDNA NAC domain protein GI:4325285   chr1:19692625-19694210 REVERSE   Aliases: ANAC018, ATNAM, F14G24.15, F14G24_15, NAC DOMAIN PROTEIN NAM	5.4	3.7	1.6	5.3	20.3%	1.1
144	AT4G04830.1   methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein, low similarity to pilin-like transcription factor (Homo sapiens) GI:5059062, SP:P14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) {Neisseria gonorrhoeae}; contains Pfam profile PF01641: SelR domain   chr4:2445857-2447082 FORWARD   Aliases: T4B21.5, T4B21_5	12.2	13.0	-0.8	-5.3	20.3%	1.1
145	AT4G38970.2   fructose-bisphosphate aldolase, putative, strong similarity to plastidic fructose-bisphosphate aldolase (EC 4.1.2.13) from Nicotiana paniculata (NPALDP1) (GI:4827251), Oryza sativa, PIR2:T02057 (SP:Q40677)   chr4:18163490-18165734 REVERSE   Aliases: F19H22.70, F19H22_70	10.7	9.1	1.6	5.3	20.3%	1.2
146	AT1G22570.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:7976609-7978562 REVERSE   Aliases: F12K8.8, F12K8_8	7.1	5.2	1.9	5.3	20.4%	1.1
147	AT5G16570.1   Symbol: GLN1;4	10.4	8.9	1.5	5.2	20.5%	1.2
148	AT2G44460.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase 1 (GI:12043529) (Arabidopsis thaliana)   chr2:18353576-18357042 FORWARD   Aliases: F4I1.27	7.5	11.6	-4.2	-5.2	20.5%	0.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
149	AT5G16940.1   expressed protein, contains Pfam profile PF04828: Protein of unknown function (DUF636)   chr5:5571554-5572393 REVERSE   Aliases: F2K13.90, F2K13_90	6.2	4.2	2.0	5.2	20.6%	1.2
150	AT2G39350.1   ABC transporter family protein   chr2:16436774-16439635 REVERSE   Aliases: T16B24.1, T16B24_1	4.8	7.2	-2.4	-5.2	20.6%	0.9
151	AT1G70780.1   expressed protein   chr1:26698845-26700041 REVERSE   Aliases: F5A18.4, F5A18_4	10.6	9.8	0.8	5.2	20.7%	1.0
152	AT5G11840.1   expressed protein, predicted proteins in Synechococcus ,Cyanophora and other organisms   chr5:3813611-3814806 REVERSE   Aliases: F14F18.10, F14F18_10	6.2	4.6	1.6	5.2	20.8%	1.1
153	AT1G70590.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:26621984-26623946 FORWARD   Aliases: F24J13.16, F24J13_16	8.3	6.8	1.5	5.2	20.8%	1.2
154	AT1G12940.1   Symbol: ATNRT2.5   high-affinity nitrate transporter, putative, similar to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362   chr1:4416403-4418588 FORWARD   Aliases: F13K23.20, F13K23_20	5.9	3.6	2.2	5.2	20.9%	0.7
155	AT5G42650.1   Symbol: AOS   allene oxide synthase (AOS) / hydroperoxide dehydrase / cytochrome P450 74A (CYP74A), identical to Allene oxide synthase, chloroplast precursor (Hydroperoxide dehydrase) (Cytochrome P450 74A) (SP:Q96242) {Arabidopsis thaliana}   chr5:17114823-17116623 REVERSE   Aliases: ALLENE OXIDASE SYNTHASE, ALLENE OXIDE SYNTHASE, CYP74A	6.4	5.3	1.1	5.2	20.9%	1.1
156	AT1G18970.1   Symbol: GLP4   germin-like protein (GLP1) (GLP4), identical to germin-like protein subfamily T member 1 (SP:P92995)   chr1:6554559-6555331 REVERSE   Aliases: F14D16.12, F14D16_12, GERMIN LIKE PROTEIN 4	3.3	5.3	-1.9	-5.2	21.0%	1.0
157	AT5G43450.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967)   chr5:17474359-17476025 REVERSE   Aliases: MWF20.16, MWF20_16	5.2	3.8	1.4	5.2	21.2%	1.1
158	AT1G50240.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr1:18613094-18617830 FORWARD   Aliases: F14I3.25, F14I3_25	4.3	5.7	-1.4	-5.2	21.2%	1.1
159	AT1G15550.1   Symbol: GA4   gibberellin 3-beta-dioxygenase / gibberellin 3 beta-hydroxylase (GA4), identical to gibberellin 3 beta-hydroxylase (GI:2160454)   chr1:5344473-5346161 REVERSE   Aliases: ATGA3OX1, GA REQUIRING 4, GA4, GIBBERELLIN 3 BETA HYDROXYLASE, T16N11.6, T16N11_6	6.5	8.1	-1.6	-5.2	21.4%	1.1
160	AT5G34940.3   glycosyl hydrolase family 79 N-terminal domain-containing protein, similar to beta-glucuronidase precursor (Scutellaria baicalensis) GI:8918740; contains Pfam profile PF03662: Glycosyl hydrolase family 79, N-terminal domain   chr5:13253059-13255948 REVERSE   Aliases: T2L5.6	6.8	8.6	-1.9	-5.1	21.4%	1.1
161	AT3G62720.2   similar to galactosyl transferase GMA12/MNN10 family protein [Arabidopsis thaliana] (TAIR:At4g02500.1); similar to beta-6-xylosyltransferase [Gossypium raimondii] (GB:CAI11451.1); similar to beta-6-xylosyltransferase [Pinus taeda] (GB:CAI11450.1); contains InterPro domain Galactosyl transferase (InterPro:IPR008630)   chr3:23212132-23213889 FORWARD   Aliases: F26K9.150	8.2	6.3	1.9	5.1	21.6%	1.0
162	AT2G17150.2   similar to RWP-RK domain-containing protein [Arabidopsis thaliana] (TAIR:At4g35270.1); similar to Putative nodule inception protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470173.1)   chr2:7475164-7478340 REVERSE   Aliases: F6P23.15, F6P23_15	6.5	5.4	1.1	5.1	21.8%	1.1
163	AT1G16705.2   similar to TAZ zinc finger family protein / zinc finger (ZZ type) family protein [Arabidopsis thaliana] (TAIR:At1g16710.1)   chr1:5712185-5713745 FORWARD   Aliases: None	4.1	3.0	1.1	5.1	21.8%	1.1
164	AT4G39630.1   expressed protein   chr4:18397589-18399381 REVERSE   Aliases: F23K16.7	3.8	5.4	-1.6	-5.1	22.0%	1.0
165	AT4G29740.2   Symbol: CKX4   FAD-binding domain-containing protein / cytokinin oxidase family protein, similar to cytokinin oxidase, Zea mays (gi:3882018) (gi:3441978)   chr4:14566271-14569338 FORWARD   Aliases: CYTOKININ OXIDASE 4, T16L4.250, T16L4_250	5.0	3.5	1.5	5.1	22.0%	1.1
166	AT5G43170.1   Symbol: AZF3   zinc finger (C2H2 type) protein 3 (AZF3), identical to Cys2/His2-type zinc finger protein 3 (Arabidopsis thaliana) gi:6009889;dbj:BAA85109   chr5:17348173-17348874 REVERSE   Aliases: ARABIDOPSIS ZINC FINGER PROTEIN 3, MMG4.21, MMG4_21	9.1	7.7	1.4	5.1	22.0%	1.1
167	AT4G10120.2   similar to sucrose-phosphate synthase, putative [Arabidopsis thaliana] (TAIR:At1g04920.1); similar to sucrose-phosphate synthase, putative [Arabidopsis thaliana] (TAIR:At5g20280.1); similar to sucrose-phosphate synthase, putative [Arabidopsis thaliana] (TAIR:At5g11110.1); similar to sucrose-phosphate synthase [Craterostigma plantagineum] (GB:CAA72491.1); similar to sucrose-phosphate synthase [Triticum aestivum] (GB:AAQ14552.1); similar to sucrose phosphate synthase [Oryza sativa (japonica cultivar-group)] (GB:BAD87626.1); similar to Sucrose-Phosphate Synthase [Saccharum officinarum] (GB:BAA19241.1); similar to sucrose-phosphate synthase (EC 2.4.1.14) - maize (GB:JQ1329); contains InterPro domain Glycosyl transferase, group 1 (InterPro:IPR001296)   chr4:6314784-6319932 FORWARD   Aliases: F28M11.40, F28M11_40	4.7	3.0	1.7	5.1	22.2%	1.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
168	AT1G20440.1   Symbol: COR47   dehydrin (COR47), identical to dehydrin COR47 (Cold-induced COR47 protein) (Arabidopsis thaliana) SWISS-PROT:P31168   chr1:7084399-7085762 REVERSE   Aliases: F5M15.22, F5M15_22, RD17	8.9	7.2	1.8	5.1	22.6%	1.0
169	AT2G19590.1   Symbol: ACO1   1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative, similar to ACC oxidase (Cucumis melo)(GI:1183898)   chr2:8483048-8484539 REVERSE   Aliases: ACC OXIDASE 1, ACO1, F3P11.19, F3P11_19	6.8	4.4	2.4	5.1	22.6%	0.8
170	AT1G67180.1   zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein, contains Pfam domains PF00533: BRCA1 C Terminus (BRCT) domain and PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:25133762-25135832 FORWARD   Aliases: F5A8.9, F5A8_9	2.2	2.8	-0.6	-5.0	22.8%	0.6
171	AT3G03270.2   universal stress protein (USP) family protein / early nodulin ENOD18 family protein, contains Pfam profile PF00582: universal stress protein family; similar to early nodulin ENOD18 (GI:11602747) (Vicia faba)   chr3:761991-763089 REVERSE   Aliases: T17B22.4, T17B22_4	9.2	5.6	3.6	5.0	22.9%	0.6
172	AT2G30930.1   expressed protein   chr2:13169517-13170473 FORWARD   Aliases: F7F1.14, F7F1_14	10.0	7.7	2.3	5.0	22.9%	0.9
173	AT1G26840.1   similar to putative origin recognition complex subunit 6 (ORC6) containing protein [Solanum demissum] (GB:AAT39295.1); contains InterPro domain Origin recognition complex subunit 6 (InterPro:IPR008721)   chr1:9298809-9300686 FORWARD   Aliases: T2P11.3, T2P11_3	4.6	6.7	-2.1	-5.0	22.9%	0.8
174	AT3G11930.4   similar to universal stress protein (USP) family protein [Arabidopsis thaliana] (TAIR:At3g58450.1); similar to putative ethylene-responsive protein [Oryza sativa (japonica cultivar-group)] (GB:AAP53941.1); contains InterPro domain Usp domain (InterPro:IPR006016); contains InterPro domain Universal stress protein (Usp) (InterPro:IPR006015)   chr3:3776265-3777700 FORWARD   Aliases: MEC18.3	10.7	9.1	1.5	5.0	22.9%	1.0
175	AT1G19770.1   Symbol: ATPUP14   purine permease-related, low similarity to purine permease (Arabidopsis thaliana) GI:7620007; contains Pfam profile PF03151: Domain of unknown function, DUF250   chr1:6832341-6833693 FORWARD   Aliases: F14P1.13, F14P1_13	8.5	7.0	1.6	5.0	22.9%	1.0
176	AT3G18250.1   expressed protein, ; expression supported by MPSS   chr3:6258183-6258413 REVERSE   Aliases: MIE15.4	4.0	5.3	-1.3	-5.0	23.0%	0.9
177	AT1G52890.1   Symbol: ANAC019   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM (no apical meristem) GB:CAA63101 from (Petunia x hybrida)   chr1:19700672-19702140 REVERSE   Aliases: ANAC019, F14G24.16, F14G24_16	5.7	4.2	1.5	5.0	23.0%	0.9
178	AT2G37640.1   Symbol: ATEXPA3   expansin, putative (EXP3), identical to Alpha-expansin 3 precursor (At-EXP3)(Arabidopsis thaliana) SWISS-PROT:O80932; alpha-expansin gene family, PMID:11641069   chr2:15794783-15796931 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A3, ATEXP3, ATHEXP ALPHA 1.9, F13M22.14, F13M22_14	8.4	5.8	2.6	5.0	23.3%	0.5
179	AT1G04020.2   Symbol: ATBRCA1   zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein, contains Pfam domain, PF00533: BRCA1 C Terminus (BRCT) domain   chr1:1036563-1040223 FORWARD   Aliases: ATBRCA1, F21M11.4, F21M11_4	4.4	6.8	-2.4	-5.0	23.3%	0.7
180	AT5G41080.2   glycerophosphoryl diester phosphodiesterase family protein, weak similarity to SP:P37965 Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) {Bacillus subtilis}; contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family   chr5:16459036-16461213 FORWARD   Aliases: MEE6.15, MEE6_15	5.3	3.7	1.5	5.0	23.3%	0.9
181	AT4G13530.2   expressed protein, predicted protein, Arabidopsis thaliana   chr4:7866780-7868716 FORWARD   Aliases: T6G15.80, T6G15_80	9.3	7.5	1.8	5.0	23.3%	0.9
182	AT2G02560.2   Symbol: CAND1   similar to TBP-interacting protein 120A [Rattus norvegicus] (GB:NP_446456.1); similar to PREDICTED: TBP-interacting protein [Mus musculus] (GB:XP_125901.5); similar to TIP120 protein [Homo sapiens] (GB:AAH50341.1); similar to mKIAA0829 protein [Mus musculus] (GB:BAC98035.1); similar to hypothetical protein [Homo sapiens] (GB:CAB66744.1); contains InterPro domain TBP-interacting 120 (InterPro:IPR007723)   chr2:689787-697595 FORWARD   Aliases: ATCAND1, ETA2, T8K22.14, T8K22_14, TIP120	5.4	7.9	-2.5	-5.0	23.3%	0.9
183	AT5G43500.2   Symbol: ATARP9	3.3	4.4	-1.0	-5.0	23.3%	0.9
184	AT5G43440.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967)   chr5:17472461-17473885 REVERSE   Aliases: MWF20.15, MWF20_15	5.8	4.1	1.7	5.0	23.3%	0.8
185	AT5G35670.1   calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612   chr5:13873345-13875756 FORWARD   Aliases: MXH1.1, MXH1_1	2.7	4.2	-1.5	-5.0	23.4%	0.9
186	AT1G50440.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:18689479-18691575 FORWARD   Aliases: F11F12.20, F11F12_20	6.6	5.4	1.2	4.9	23.6%	0.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
187	AT2G29890.2   Symbol: VLN1   similar to villin, putative [Arabidopsis thaliana] (TAIR:At5g57320.1); similar to villin, putative [Arabidopsis thaliana] (TAIR:At4g30160.1); similar to putative villin [Oryza sativa (japonica cultivar-group)] (GB:XP_480904.1); similar to OSJNBa0041A02.24 [Oryza sativa (japonica cultivar-group)] (GB:XP_473786.1); similar to actin filament bundling protein P-115-ABP [Lilium longiflorum] (GB:BAC77209.1); contains InterPro domain Gelsolin (InterPro:IPR007122); contains InterPro domain Gelsolin region (InterPro:IPR007123)   chr2:12751227-12756663 FORWARD   Aliases: ATVLN1, F6K5.2, F6K5_2, VILLIN 1	3.7	5.3	-1.7	-4.9	23.6%	0.9
188	AT1G78290.2   serine/threonine protein kinase, putative, similar to serine-threonine protein kinase (Triticum aestivum) gi:2055374:gb:AAB58348	5.8	4.5	1.3	4.9	23.6%	0.9
189	AT3G05220.2   heavy-metal-associated domain-containing protein, similar to farnesylated protein 1 (GI:23304411) {Hordeum vulgare subsp. spontaneum}; contains Pfam profile PF00403: Heavy-metal-associated domain   chr3:1489425-1491320 FORWARD   Aliases: T12H1.19, T12H1_19	10.1	8.9	1.2	4.9	23.6%	0.7
190	AT2G06850.1   Symbol: EXGT A1   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXT) (EXGT-A1), identical to endo-xyloglucan transferase (ext) GI:469484 and endoxyloglucan transferase (EXGT-A1) GI:5533309 from (Arabidopsis thaliana)	5.7	7.5	-1.8	-4.9	23.6%	0.8
191	AT4G29520.1   expressed protein   chr4:14493920-14495735 REVERSE   Aliases: T16L4.30, T16L4_30	5.1	7.0	-1.9	-4.9	23.6%	0.8
192	AT3G51310.1   vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein, similar to vacuolar protein sorting 35 (Mus musculus) GI:11875394; contains Pfam profile PF03635: Vacuolar protein sorting-associated protein 35   chr3:19055502-19060300 REVERSE   Aliases: F24M12.350	8.2	9.5	-1.3	-4.9	23.6%	0.8
193	AT1G71450.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr1:26930750-26931618 FORWARD   Aliases: F26A9.17	3.6	2.7	0.9	4.9	23.7%	0.8
194	AT5G66400.2   Symbol: RAB18   similar to dehydrin, putative [Arabidopsis thaliana] (TAIR:At3g50980.1); similar to putative dehydrin [Helianthus hirsutus] (GB:CAC80706.1); contains InterPro domain Eggshell protein (InterPro:IPR002952); contains InterPro domain Dehydrin (InterPro:IPR000167)   chr5:26535503-26536468 REVERSE   Aliases: ARABIDOPSIS THALIANA DROUGHT INDUCED 8, ATDI8, K1F13.5, K1F13_5, RESPONSIVE TO ABA 18	6.3	3.9	2.4	4.9	23.7%	0.6
195	AT1G07280.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g29670.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAU10760.1); contains domain SER_RICH (PS50324)   chr1:2238109-2241172 FORWARD   Aliases: F22G5.38, F22G5_38	7.7	5.4	2.3	4.9	23.7%	0.8
196	AT2G02130.1   Symbol: LCR68/PDF2.3   plant defensin-fusion protein, putative (PDF2.3), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be)   chr2:540017-540615 FORWARD   Aliases: F5O4.10, F5O4_10, LCR68, Low molecular weight cysteine rich 68, PDF2.3	12.9	11.9	0.9	4.9	23.7%	0.5
197	AT2G24490.1   replication protein, putative, similar to replication protein A 30kDa (Oryza sativa (japonica cultivar-group)) GI:13516746; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain   chr2:10405484-10407568 REVERSE   Aliases: T28I24.22, T28I24_22	4.8	6.9	-2.0	-4.9	23.7%	0.7
198	AT1G12180.1   expressed protein   chr1:4130419-4131135 FORWARD   Aliases: T28K15.15, T28K15_15	3.3	5.7	-2.4	-4.9	23.7%	0.8
199	AT5G13520.1   peptidase M1 family protein, similar to SP:P09960 Leukotriene A-4 hydrolase (EC 3.3.2.6) (LTA-4 hydrolase) {Homo sapiens}; contains Pfam profile PF01433: Peptidase family M1   chr5:4341543-4344674 REVERSE   Aliases: T6I14.50, T6I14_50	8.2	10.5	-2.3	-4.9	24.5%	0.7
200	AT2G28760.2   NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family   chr2:12343268-12346104 REVERSE   Aliases: F8N16.5, F8N16_5	6.2	7.7	-1.5	-4.9	24.6%	0.8
201	AT5G38110.1   ASF1-like anti-silencing family protein, similar to SP:P32447 Anti-silencing protein 1 {Saccharomyces cerevisiae}; contains Pfam profile PF04729: Anti-silencing protein, ASF1-like   chr5:15225702-15227445 FORWARD   Aliases: F16F17.110, F16F17_110	5.5	8.2	-2.7	-4.9	24.8%	0.5
202	AT1G30500.2   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA)	8.5	6.8	1.6	4.8	24.8%	0.6
203	AT1G06650.2   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967); contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family   chr1:2035838-2037362 FORWARD   Aliases: F12K11.26, F12K11_26	7.4	5.5	1.9	4.8	24.8%	0.7
204	AT4G08850.2   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr4:5637335-5640633 REVERSE   Aliases: T32A17.160, T32A17_160	9.6	8.2	1.4	4.8	24.8%	0.7
205	AT5G57560.1   Symbol: TCH4   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (TCH4), identical to xyloglucan endotransglycosylase TCH4 protein GI:886116   chr5:23324356-23325507 REVERSE   Aliases: MUA2.13, MUA2_13, TOUCH 4, XTH22, XYLOGLUCAN ENDOTRANSGLYCOSYLASE	10.0	7.1	2.9	4.8	25.1%	0.5
206	AT4G31120.2   Skb1 methyltransferase family protein, contains Pfam profile: PF05185 Skb1 methyltransferase   chr4:15132125-15136624 REVERSE   Aliases: F6E21.40, F6E21_40	6.6	7.9	-1.3	-4.8	25.1%	0.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
207	AT1G05210.1   expressed protein   chr1:1510138-1511678 FORWARD   Aliases: YUP8H12.18, YUP8H12_18	4.8	5.8	-1.0	-4.8	25.6%	0.7
208	AT4G18470.1   Symbol: SNI1   negative regulator of systemic acquired resistance (SNI1), identical to negative regulator of systemic acquired resistance SNI1 (Arabidopsis thaliana) gi:5758933:gb:AAD50900   chr4:10192920-10195673 FORWARD   Aliases: F28J12.3, F28J12_3, SUPPRESSOR OF NPR1 1, INDUCIBLE 1	2.4	3.0	-0.6	-4.8	25.6%	0.4
209	AT3G15300.1   VQ motif-containing protein, contains PF05678: VQ motif   chr3:5147412-5148217 REVERSE   Aliases: K7L4.10	6.0	7.5	-1.6	-4.8	25.7%	0.6
210	AT2G24860.1   chaperone protein dnaJ-related, similar to Tsi1-interacting protein TSIP1 (GI:4337001) (Nicotiana tabacum)   chr2:10593854-10595408 REVERSE   Aliases: F27C12.22, F27C12_22	6.9	6.0	0.9	4.8	25.7%	0.5
211	AT2G47440.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profiles PF00226: DnaJ domain, PF00515: TPR Domain; similar to GP:2104534:AF001308 (T10M13.11)   chr2:19476789-19478956 FORWARD   Aliases: T30B22.26	8.4	6.8	1.5	4.8	25.8%	0.7
212	AT4G16146.1   expressed protein   chr4:9142445-9144588 REVERSE   Aliases: None	6.7	4.8	1.9	4.8	26.1%	0.6
213	AT1G77450.1   Symbol: ANAC032   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to GRAB1 protein GB:CAA09371, a novel member of the NAC domain family   chr1:29104848-29106155 FORWARD   Aliases: ANAC032, T5M16.4, T5M16_4	9.4	7.9	1.5	4.8	26.1%	0.6
214	AT3G25600.1   calmodulin, putative, similar to calmodulin GI:239841 from (Paramecium tetraurelia)   chr3:9308491-9309199 FORWARD   Aliases: T5M7.6	8.0	6.0	2.0	4.8	26.1%	0.7
215	AT1G43650.1   integral membrane family protein / nodulin MtN21-related, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula) similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr1:16446301-16449268 REVERSE   Aliases: F2J6.1, F2J6_1	7.1	5.0	2.1	4.8	26.1%	0.6
216	AT1G27100.1   expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569)   chr1:9407112-9411159 REVERSE   Aliases: T7N9.16, T7N9_16	6.4	5.2	1.2	4.7	26.6%	0.6
217	AT4G31290.1   ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like protein   chr4:15185997-15188490 FORWARD   Aliases: F8F16.110, F8F16_110	5.1	6.9	-1.8	-4.7	26.9%	0.6
218	AT1G64590.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily   chr1:23997196-23999172 FORWARD   Aliases: F1N19.16, F1N19_16	7.1	4.4	2.7	4.7	27.4%	0.4
219	AT3G05130.1   expressed protein, ; expression supported by MPSS   chr3:1433481-1435385 REVERSE   Aliases: T12H1.9, T12H1_9	4.2	5.9	-1.7	-4.7	27.7%	0.6
220	AT3G59350.3   similar to serine/threonine protein kinase, putative [Arabidopsis thaliana] (TAIR:At2g43230.1); similar to salt-inducible putative protein serine/threonine/tyrosine kinase [Zea mays] (GB:AAU11815.1); contains InterPro domain Tyrosine protein kinase, active site (InterPro:IPR008266); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:21943689-21946131 FORWARD   Aliases: F25L23.210	6.4	4.7	1.7	4.7	27.7%	0.6
221	AT4G11650.1   Symbol: ATOSM34   osmotin-like protein (OSM34), nearly identical to SP:P50700:OSL3_ARATH Osmotin-like protein OSM34 precursor {Arabidopsis thaliana}; contains Pfam profile PF00314: Thaumatin family   chr4:7024850-7026140 REVERSE   Aliases: T5C23.80, T5C23_80	3.0	5.5	-2.5	-4.7	27.7%	0.4
222	AT4G08780.1   peroxidase, putative, similar to peroxidase isozyme (Armoracia rusticana) gi:217932:dbj:BAA14143	3.8	5.7	-1.9	-4.7	27.7%	0.6
223	AT5G67480.2   TAZ zinc finger family protein / BTB/POZ domain-containing protein, contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 : TAZ zinc finger; similar to Chain A, Taz2 Domain Of The Transcriptional Adaptor Protein Cbp (GI:11514507) (Homo sapiens); similar to (SP:Q09472) E1A-associated protein p300 (SP:Q09472) (Homo sapiens); similar to histone acetyltransferase HAC4 (GI:21105785) (Arabidopsis thaliana)   chr5:26948166-26949982 REVERSE   Aliases: K9I9.4, K9I9_4	6.1	4.5	1.6	4.7	27.7%	0.5
224	AT1G26150.1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g38560.1); similar to putative receptor protein kinase PERK1 [Oryza sativa (japonica cultivar-group)] (GB:BAD87028.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr1:9039615-9043275 REVERSE   Aliases: F28B23.17, F28B23_17	6.0	7.6	-1.5	-4.7	27.7%	0.6
225	AT1G71692.1   Symbol: AGL12   MADS-box protein (AGL12), identical to GB:AAC49085 GI:862650 from (Arabidopsis thaliana) (Plant Cell 7 (8), 1259-1269 (1995))   chr1:26956307-26958789 REVERSE   Aliases: AGAMOUS LIKE 12, F14O23.5, F14O23_5	7.8	6.1	1.7	4.7	27.7%	0.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
226	AT5G20250.3   Symbol: DIN10   similar to alkaline alpha galactosidase, putative [Arabidopsis thaliana] (TAIR:At3g57520.2); similar to alkaline alpha galactosidase, putative [Arabidopsis thaliana] (TAIR:At3g57520.3); similar to alkaline alpha galactosidase, putative [Arabidopsis thaliana] (TAIR:At1g55740.1); similar to alkaline alpha galactosidase, putative [Arabidopsis thaliana] (TAIR:At3g57520.1); similar to putative alkaline alpha-galactosidase seed imbibition protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483143.1); similar to Sip1 protein - barley (GB:S27762); similar to putative imbibition protein [Brassica oleracea] (GB:CAA55893.1); similar to putative raffinose synthase or seed imbibition protein [Oryza sativa (japonica cultivar-group)] (GB:AAT77910.1); similar to alkaline alpha galactosidase II [Cucumis melo] (GB:AAM75140.1); contains InterPro domain Raffinose synthase (InterPro:IPR008811)   chr5:6833680-6836790 FORWARD   Aliases: DARK INDUCIBLE 10, F5O24.140, F5O24_140	8.6	7.0	1.6	4.7	27.7%	0.6
227	AT4G02380.1   Symbol: SAG21   late embryogenesis abundant 3 family protein / LEA3 family protein, similar to several small proteins (~100 aa) that are induced by heat, auxin, ethylene and wounding such as Phaseolus aureus indole-3-acetic acid induced protein ARG (SW:32292); contains Pfam profile PF03242: Late embryogenesis abundant protein	11.5	10.8	0.7	4.7	27.7%	0.1
228	AT2G30080.1   Symbol: ZIP6   metal transporter, putative (ZIP6), identical to putative metal transporter ZIP6 (Arabidopsis thaliana) gi:17385786:gb:AAL38433; similar to zinc transporter protein ZIP1 (Glycine max) gi:15418778:gb:AAK37761; member of the Zinc (Zn <sup>2+</sup> )-Iron (Fe <sup>2+</sup> ) permease (ZIP) family, PMID:11500563   chr2:12845807-12847189 REVERSE   Aliases: T27E13.18, T27E13_18	8.0	5.6	2.3	4.7	27.7%	0.5
229	AT3G21890.1   zinc finger (B-box type) family protein, contains Pfam profile: PF01760 CONSTANS family zinc finger   chr3:7709187-7709740 REVERSE   Aliases: MZN24.1	6.7	4.0	2.6	4.7	27.7%	0.4
230	AT4G15800.1   Symbol: RALFL33   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr4:8984866-8985413 FORWARD   Aliases: DL3940C, FCAALL.206, RALF LIKE 33	7.8	6.4	1.4	4.7	27.7%	0.5
231	AT5G12030.1   Symbol: AT HSP17.6A   17.7 kDa class II heat shock protein 17.6A (HSP17.7-CII), identical to heat shock protein 17.6A GI:3256075 from (Arabidopsis thaliana)   chr5:3884108-3884738 REVERSE   Aliases: F14F18.200, F14F18_200, HSP17.6	4.6	3.4	1.2	4.7	27.7%	0.6
232	AT1G54260.1   histone H1/H5 family protein, contains Pfam domain, PF00538: linker histone H1 and H5 family   chr1:20261007-20262843 FORWARD   Aliases: F20D21.8, F20D21_8	6.9	5.2	1.7	4.6	28.0%	0.5
233	AT1G47960.1   Symbol: C/VIF1	10.8	8.8	2.0	4.6	28.0%	0.5
234	AT4G14770.1   tesmin/TSO1-like CXC domain-containing protein, similar to CXC domain containing TSO1-like protein 1 (SOL1) (Arabidopsis thaliana) GI:7767427, CXC domain protein TSO1 (Arabidopsis thaliana) GI:7767425; contains Pfam profile PF03638: Tesmin/TSO1-like CXC domain   chr4:8481369-8484820 REVERSE   Aliases: DL3425C, FCAALL.306	4.5	5.9	-1.4	-4.6	28.2%	0.5
235	AT4G32940.1   Symbol: GAMMA VPE   vacuolar processing enzyme gamma / gamma-VPE, nearly identical to SP:Q39119 Vacuolar processing enzyme, gamma-isozyme precursor (EC 3.4.22.-) (Gamma-VPE) {Arabidopsis thaliana}   chr4:15900273-15903271 REVERSE   Aliases: F26P21.60, F26P21_60, GAMMAVPE	11.4	9.6	1.8	4.6	28.2%	0.5
236	AT1G19530.1   expressed protein   chr1:6763906-6764944 FORWARD   Aliases: F18O14.29, F18O14_29	7.3	4.4	2.9	4.6	28.2%	0.4
237	AT5G53090.1   similar to oxidoreductase, forever young (FEY3) [Arabidopsis thaliana] (TAIR:At4g27760.1); similar to forever young oxidoreductase [Lycopersicon esculentum] (GB:AAL60068.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)	3.8	4.8	-1.1	-4.6	28.3%	0.5
238	AT5G54855.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr5:22300026-22301613 FORWARD   Aliases: None	10.4	9.6	0.8	4.6	28.3%	0.2
239	AT2G34710.1   Symbol: PHB   homeobox-leucine zipper transcription factor (HB-14), identical to homeodomain transcription factor (ATHB-14)GP:3132474 GB:Y11122 (Arabidopsis thaliana);	6.2	7.4	-1.3	-4.6	28.3%	0.5
240	AT3G27640.1   transducin family protein / WD-40 repeat family protein, contains seven WD-40 G-protein beta repeats; similar to RA-regulated nuclear matrix-associated protein (GI:14161320) {Homo sapiens}   chr3:10233485-10236858 FORWARD   Aliases: MGF10.5	3.1	4.1	-1.0	-4.6	28.3%	0.4
241	AT4G16690.1   esterase/lipase/thioesterase family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393, SP:Q40708 PIR7A protein {Oryza sativa}; contains Interpro entry IPR000379   chr4:9392169-9393491 REVERSE   Aliases: DL4370C, FCAALL.12	3.8	2.9	1.0	4.6	28.3%	0.5
242	AT2G35300.1   late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein, contains Pfam domain, PF03760: Late embryogenesis abundant (LEA) group 1   chr2:14869980-14870466 REVERSE   Aliases: T4C15.3, T4C15_3	3.8	2.8	1.0	4.6	28.3%	0.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
243	AT2G21330.3   similar to fructose-bisphosphate aldolase, putative [Arabidopsis thaliana] (TAIR:At4g38970.1); similar to plastidic aldolase NPALDP1 [Nicotiana paniculata] (GB:BAA77604.1); similar to latex plastidic aldolase-like protein [Hevea brasiliensis] (GB:AAM46780.1); contains InterPro domain Fructose-bisphosphate aldolase, class-I (InterPro:IPR000741)   chr2:9135228-9137293 REVERSE   Aliases: F3K23.9, F3K23_9	10.7	9.2	1.6	4.6	28.3%	0.4
244	AT5G66985.1   expressed protein   chr5:26760505-26761034 FORWARD   Aliases: None	7.2	4.4	2.7	4.6	28.3%	0.4
245	AT4G24050.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr4:12497077-12500138 FORWARD   Aliases: T19F6.40, T19F6_40	5.9	4.7	1.2	4.6	28.6%	0.4
246	AT2G23360.1   transport protein-related, contains Pfam PF05911: Plant protein of unknown function (DUF869) profile; weak similarity to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae)   chr2:9956536-9959925 FORWARD   Aliases: F26B6.1, F26B6_1	4.3	5.4	-1.1	-4.6	28.6%	0.5
247	AT3G22600.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:8006521-8007478 REVERSE   Aliases: F16J14.16	3.4	5.0	-1.6	-4.6	28.6%	0.4
248	AT3G23810.1   Symbol: SAHH2   adenosylhomocysteinase, putative / S-adenosyl-L-homocysteine hydrolase, putative / AdoHcyase, putative, strong similarity to SP:P50248:SAHH_TOBAC Adenosylhomocysteinase (EC 3.3.1.1) (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) {Nicotiana glauca}; contains Pfam profile PF00670: S-adenosyl-L-homocysteine hydrolase, NAD binding domain   chr3:8587671-8589720 REVERSE   Aliases: MYM9.17, SAHH2	3.9	7.3	-3.5	-4.6	28.6%	0.3
249	AT5G14650.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase PG1 GP:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:4724453-4726516 FORWARD   Aliases: T15N1.140, T15N1_140	2.6	3.4	-0.9	-4.6	28.6%	0.3
250	AT5G44400.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr5:17903421-17905707 REVERSE   Aliases: K9L2.20, K9L2_20	3.6	5.6	-2.0	-4.6	28.6%	0.3
251	AT1G14710.2   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:5061861-5065097 REVERSE   Aliases: F10B6.11, F10B6_11	5.2	7.1	-1.9	-4.6	28.6%	0.4
252	AT2G29570.1   Symbol: PCNA2   proliferating cell nuclear antigen 2 (PCNA2), identical to SP:Q9ZW35 Proliferating cell nuclear antigen 2 (PCNA 2) {Arabidopsis thaliana}; nearly identical to SP:Q43124 Proliferating cell nuclear antigen (PCNA) {Brassica napus}; contains Pfam profiles PF00705: Proliferating cell nuclear antigen N-terminal domain, PF02747: Proliferating cell nuclear antigen C-terminal domain   chr2:12656983-12658780 REVERSE   Aliases: F16P2.5, F16P2_5, PROLIFERATING CELL NUCLEAR 2	7.0	9.4	-2.4	-4.6	28.6%	0.4
253	AT5G19140.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g43830.1); similar to hypothetical protein ARG10 - mung bean (GB:T07820)	8.3	5.7	2.6	4.6	28.6%	0.4
254	AT3G43190.1   sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative, strong similarity to SP:P49040 Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase) {Arabidopsis thaliana} (SUS1)   chr3:15190055-15194977 REVERSE   Aliases: F7K15.40	6.0	4.2	1.9	4.6	28.6%	0.3
255	AT4G13750.1   expressed protein   chr4:7978944-7987554 FORWARD   Aliases: F18A5.140, F18A5_140	4.0	5.3	-1.4	-4.6	28.6%	0.4
256	AT4G27040.1   expressed protein   chr4:13572444-13575544 REVERSE   Aliases: F10M23.380, F10M23_380	9.3	8.2	1.1	4.6	28.9%	0.4
257	AT5G51190.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr5:20817810-20818642 REVERSE   Aliases: MWD22.13, MWD22_13	6.3	4.7	1.6	4.5	29.1%	0.4
258	AT3G20260.1   expressed protein   chr3:7064080-7066504 REVERSE   Aliases: MQC12.1	2.9	3.9	-1.1	-4.5	29.1%	0.4
259	AT4G38770.1   Symbol: PRP4   proline-rich family protein (PRP4), similar to proline-rich protein (Arabidopsis thaliana) gi:6782442:gb:AAF28388; contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:18096803-18098558 REVERSE   Aliases: ATPRP4, PROLINE RICH PROTEIN 4, T9A14.50, T9A14_50	3.0	4.0	-1.0	-4.5	29.1%	0.4
260	AT5G11070.1   expressed protein   chr5:3516218-3516996 REVERSE   Aliases: T5K6.60, T5K6_60	8.1	6.1	2.0	4.5	29.1%	0.3
261	AT4G33720.1   pathogenesis-related protein, putative, similar to SP:P33154 Pathogenesis-related protein 1 precursor (PR-1) {Arabidopsis thaliana}; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:16182755-16183536 FORWARD   Aliases: T16L1.210, T16L1_210	2.4	5.3	-2.9	-4.5	29.2%	-0.3
262	AT1G05000.1   tyrosine specific protein phosphatase family protein, contains tyrosine specific protein phosphatases active site, PROSITE:PS00383   chr1:1425592-1428781 FORWARD   Aliases: T7A14.14, T7A14_14	5.3	4.0	1.3	4.5	29.2%	0.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
263	AT3G26740.1   light responsive protein-related, similar to light regulated protein precursor SP:Q03200 ( <i>Oryza sativa</i> ) (Plant Mol. Biol. 22 (1), 165-170 (1993)), ccr protein GB:S52663 ( <i>Citrus X paradisi</i> ) (Plant Mol. Biol. 26 (1), 165-173 (1994))   chr3:9829039-9829917 FORWARD   Aliases: MLJ15.9	4.1	2.8	1.3	4.5	29.2%	0.4
264	AT5G11160.1   adenine phosphoribosyltransferase, putative, strong similarity to SP:Q42563 Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT) { <i>Arabidopsis thaliana</i> }; contains Pfam profile PF00156: Phosphoribosyl transferase domain   chr5:3550551-3552145 FORWARD   Aliases: F2I11.50, F2I11_50	6.6	5.2	1.4	4.5	29.4%	0.3
265	AT5G64900.1   expressed protein   chr5:25954396-25955302 FORWARD   Aliases: MXK3.13, MXK3_13	6.3	4.9	1.4	4.5	29.4%	0.4
266	AT4G34710.2   Symbol: ADC2   arginine decarboxylase 2 (SPE2), identical to SP:O23141 Arginine decarboxylase 2 (EC 4.1.1.19) (ARGDC 2) (ADC 2) (ADC-N) { <i>Arabidopsis thaliana</i> }   chr4:16560067-16562936 REVERSE   Aliases: ARGININE DECARBOXYLASE, ARGININE DECARBOXYLASE 2, SPE2, T4L20.290, T4L20_290	8.5	10.3	-1.8	-4.5	29.4%	0.4
267	AT1G65500.1   expressed protein   chr1:24361530-24362279 FORWARD   Aliases: F5I14.4, F5I14_4	3.7	6.6	-2.9	-4.5	29.6%	-0.0
268	AT3G15780.1   expressed protein   chr3:5341433-5342564 FORWARD   Aliases: MSJ11.18	8.6	6.8	1.9	4.5	29.8%	0.3
269	AT3G61450.1   Symbol: SYP73   syntaxin 73 (SYP73), identical to syntaxin 73 (AtSYP73) (Swiss-Prot:Q94KK5) ( <i>Arabidopsis thaliana</i> )   chr3:22749369-22750959 FORWARD   Aliases: ATSYP73, F2A19.50, SYNTAXIN OF PLANTS 73	6.2	4.4	1.7	4.5	29.8%	0.2
270	AT3G15210.1   Symbol: ATERF 4/ATERF4/ERF4/RAP2.5   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ATERF-4). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.	6.0	4.6	1.4	4.5	30.1%	0.3
271	AT1G21910.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr1:7696525-7697688 FORWARD   Aliases: T26F17.14, T26F17_14	5.3	3.7	1.6	4.5	30.1%	0.3
272	AT2G27690.1   Symbol: CYP94C1   cytochrome P450, putative, similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:O81117) { <i>Vicia sativa</i> }; contains Pfam profile: PF00067 cytochrome P450; supported by cDNA: gi_13877668   chr2:11816383-11818292 FORWARD   Aliases: F15K20.21, F15K20_21	6.4	4.8	1.6	4.5	30.1%	0.2
273	AT2G36200.1   kinesin motor protein-related   chr2:15186802-15192293 REVERSE   Aliases: F2H17.19, F2H17_19	4.1	5.5	-1.4	-4.5	30.3%	0.3
274	AT2G43290.1   Symbol: MSS3   calmodulin-like protein (MSS3), identical to calmodulin-like MSS3 from GI:9965747 ( <i>Arabidopsis thaliana</i> )	4.8	3.7	1.2	4.5	30.3%	0.3
275	AT3G55500.1   Symbol: ATEXPA16   expansin, putative (EXP16), similar to expansin GI:2828241 from ( <i>Brassica napus</i> ); alpha-expansin gene family, PMID:11641069   chr3:20586052-20587125 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A16, ATEXP16, ATHEXP ALPHA 1.7, EXP16, T22E16.160	8.5	6.0	2.5	4.5	30.3%	-0.3
276	AT1G19960.1   expressed protein   chr1:6928074-6928268 FORWARD   Aliases: T20H2.25, T20H2_25	8.2	5.2	3.0	4.5	30.3%	0.1
277	AT3G55980.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat   chr3:20787274-20789821 FORWARD   Aliases: F27K19.160	5.5	4.4	1.1	4.5	30.3%	0.3
278	AT1G09470.1   expressed protein, ; expression supported by MPSS   chr1:3055393-3056933 REVERSE   Aliases: F14J9.13, F14J9_13	3.5	5.3	-1.8	-4.5	30.3%	0.3
279	AT1G58160.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog ( <i>Arabidopsis thaliana</i> ) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	4.3	3.3	1.0	4.5	30.3%	0.2
280	AT1G21100.1   O-methyltransferase, putative, similar to GI:2781394   chr1:7386828-7388417 REVERSE   Aliases: T22I11.7, T22I11_7	4.1	3.1	1.0	4.4	30.3%	-0.0
281	AT1G69770.1   Symbol: CMT3   chromomethylase 3 (CMT3), nearly identical to chromomethylase CMT3 ( <i>Arabidopsis thaliana</i> ) GI:14583092, GI:14647157   chr1:26251990-26257248 REVERSE   Aliases: CHROMOMETHYLASE 3, T6C23.3, T6C23_3	3.7	5.4	-1.7	-4.4	30.4%	0.3
282	AT3G51920.1   Symbol: CAM9   calmodulin-9 (CAM9), identical to calmodulin 9 GI:5825602 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF00036: EF hand   chr3:19279026-19280366 REVERSE   Aliases: CALMODULIN 9, F4F15.30	10.0	8.9	1.1	4.4	30.8%	0.3
283	AT1G70900.1   expressed protein   chr1:26735523-26737537 FORWARD   Aliases: F15H11.13, F15H11_13	6.7	5.3	1.4	4.4	31.4%	0.2
284	AT3G56360.1   expressed protein, unknown protein 110K5.12 - <i>Sorghum bicolor</i> , TREMBL:AF124045_5	9.9	8.3	1.5	4.4	31.4%	0.2
285	AT5G04310.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from ( <i>Fragaria x ananassa</i> )   chr5:1203204-1207353 REVERSE   Aliases: T19N18.40, T19N18_40	8.6	7.3	1.2	4.4	31.4%	0.2
286	AT1G19730.1   Symbol: ATTRX4	6.5	5.4	1.0	4.4	31.4%	0.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
287	AT1G06000.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains similarity to UDPG glucosyltransferase GB:AAB62270 GI:2232354 from ( <i>Solanum berthaultii</i> )   chr1:1820307-1821892 REVERSE   Aliases: T21E18.5, T21E18_5	6.0	7.5	-1.5	-4.4	31.4%	0.2
288	AT5G62350.1   invertase/pectin methylesterase inhibitor family protein / DC 1.2 homolog (FL5-2I22), similar to SP:Q42534 Pectinesterase 2 precursor (EC 3.1.1.11) (Pectin methylesterase 2) (PE 2) { <i>Arabidopsis thaliana</i> }; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor; FL5-2I22 mRNA for DC 1.2 homolog, partial cds GI:11127598   chr5:25054652-25055588 FORWARD   Aliases: MMI9.21, MMI9_21	8.2	9.6	-1.4	-4.4	31.4%	0.2
289	AT3G52180.2   similar to protein phosphatase-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g10940.1); similar to unknown protein [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_482104.1); contains InterPro domain Tyrosine specific protein phosphatase and dual specificity protein phosphatase (InterPro:IPR000387); contains InterPro domain Dual specificity protein phosphatase (InterPro:IPR000340)	9.9	8.4	1.5	4.4	31.4%	0.2
290	AT2G38465.1   expressed protein   chr2:16113341-16113978 REVERSE   Aliases: None	7.2	5.9	1.3	4.4	31.4%	0.2
291	AT5G66710.1   protein kinase, putative, similar to protein kinase ATN1 GP:1054633 ( <i>Arabidopsis thaliana</i> )   chr5:26653835-26655790 FORWARD   Aliases: MSN2.10, MSN2_10	3.5	4.5	-1.1	-4.4	31.4%	0.2
292	AT2G22420.1   peroxidase 17 (PER17) (P17), identical to SP:Q9SJZ2 Peroxidase 17 precursor (EC 1.11.1.7) (Atperox P17) (ATP25a) { <i>Arabidopsis thaliana</i> }   chr2:9520299-9521615 FORWARD   Aliases: F14M13.18, F14M13_18	6.4	7.7	-1.4	-4.4	31.4%	0.1
293	AT5G05960.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:1790232-1790834 FORWARD   Aliases: K18J17.13, K18J17_13	3.9	6.1	-2.2	-4.4	31.4%	-0.2
294	AT2G31110.1   expressed protein   chr2:13265406-13266629 REVERSE   Aliases: T16B12.8, T16B12_8	7.5	6.4	1.2	4.4	31.4%	0.2
295	AT5G23240.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:O34136 Chaperone protein dnaJ (40 kDa heat shock chaperone protein) (HSP40) { <i>Deinococcus proteolyticus</i> }; contains Pfam profile PF00226: DnaJ domain   chr5:7826737-7828727 REVERSE   Aliases: MKD15.10, MKD15_10	6.0	4.0	2.0	4.4	31.4%	0.2
296	AT5G24800.1   Symbol: BZO2H2	11.1	9.5	1.6	4.4	31.4%	0.2
297	AT5G62630.1   expressed protein   chr5:25160821-25163685 REVERSE   Aliases: MRG21.5, MRG21_5	8.0	9.8	-1.8	-4.4	31.8%	0.2
298	AT3G22890.1   Symbol: APS1   sulfate adenylyltransferase 1 / ATP-sulfurylase 1 (APS1), nearly identical to ATP sulfurylase (APS1) ( <i>Arabidopsis thaliana</i> ) GI:6606509   chr3:8112730-8114996 FORWARD   Aliases: F5N5.7	7.6	10.3	-2.7	-4.4	31.8%	0.2
299	AT3G27220.1   kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (4 repeats); contains Prosite PS00334: Myb DNA-binding domain repeat signature 2; similar to Male enhanced Antigen-1 (peas) (GI:20513270) ( <i>Mus musculus</i> )   chr3:10052849-10054915 REVERSE   Aliases: K17E12.4	6.7	4.3	2.4	4.4	31.8%	0.1
300	AT1G72230.1   plastocyanin-like domain-containing protein, similar to blue copper protein SP:Q41001 from ( <i>Pisum sativum</i> )   chr1:27191728-27192906 FORWARD   Aliases: T9N14.17, T9N14_17	4.3	7.3	-3.0	-4.4	31.8%	-0.0
301	AT3G08030.2   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr3:2564159-2566008 FORWARD   Aliases: F17A17.37	6.9	9.6	-2.7	-4.4	31.8%	0.0
302	AT5G13200.1   GRAM domain-containing protein / ABA-responsive protein-related, similar to ABA-responsive protein ( <i>Hordeum vulgare</i> ) GI:4103635; contains Pfam profile PF02893: GRAM domain   chr5:4207007-4208292 FORWARD   Aliases: T19L5.4	5.0	3.9	1.1	4.4	31.8%	0.2
303	AT2G01400.1   expressed protein   chr2:174270-175616 FORWARD   Aliases: F10A8.4	4.8	3.5	1.3	4.4	31.8%	0.2
304	AT4G27280.1   calcium-binding EF hand family protein, similar to EF-hand Ca <sup>2+</sup> -binding protein CCD1 ( <i>Triticum aestivum</i> ) GI:9255753; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:13663582-13664246 REVERSE   Aliases: M4I22.90, M4I22_90	8.9	7.5	1.4	4.4	31.8%	0.1
305	AT5G53420.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g27900.1); similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g27900.2); similar to zinc finger CONSTANS-like protein [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:BAD73395.1)   chr5:21691615-21692959 FORWARD   Aliases: MYN8.3, MYN8_3	9.4	7.9	1.5	4.3	31.9%	0.2
306	AT1G18740.1   expressed protein   chr1:6463985-6466445 FORWARD   Aliases: F6A14.15, F6A14_15	4.7	3.5	1.3	4.3	32.2%	0.2
307	AT5G65280.1   lanthionine synthetase C-like family protein, contains Pfam domain, PF05147: Lanthionine synthetase C-like protein   chr5:26103199-26105370 REVERSE   Aliases: MQN23.23, MQN23_23	7.9	6.3	1.6	4.3	32.2%	0.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
308	AT4G25790.1   allergen V5/Tpx-1-related family protein, similar to SP:Q40374 Pathogenesis-related protein PR-1 precursor {Medicago truncatula}; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:13122257-13123299 REVERSE   Aliases: F14M19.70, F14M19_70	8.5	6.8	1.7	4.3	32.2%	0.1
309	AT5G58150.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:23547307-23550066 REVERSE   Aliases: MCK7.2, MCK7_2	5.2	6.2	-0.9	-4.3	32.2%	-0.0
310	AT1G48520.3   Symbol: GATB   glutamyl-tRNA(Gln) amidotransferase B family protein, contains Pfam profiles: PF02934 PET112 family, N terminal region, PF02637 GatB/Yqey domain, PF01162 PET112 family, C terminal region   chr1:17943756-17946490 FORWARD   Aliases: GLU ADT SUBUNIT B, GLU TRNA(GLN) AMIDOTRANSFERASE SUBUNIT B	4.6	5.7	-1.2	-4.3	32.2%	0.1
311	AT5G54080.2   Symbol: HGO   homogentisate 1,2-dioxygenase / homogentisicase/homogentisate oxygenase / homogentisic acid oxidase (HGO), identical to SP:Q9ZRA2 Homogentisate 1,2-dioxygenase (EC 1.13.11.5) (Homogentisicase) (Homogentisate oxygenase) (Homogentisic acid oxidase) {Arabidopsis thaliana}; contains Pfam profile PF04209: homogentisate 1,2-dioxygenase   chr5:21963095-21966139 FORWARD   Aliases: HOMOGENTISATE 1,2 DIOXYGENASE, MJP23.6, MJP23_6	8.7	7.6	1.1	4.3	32.2%	-0.0
312	AT5G53250.1   arabinogalactan-protein, putative (AGP22), similar to arabinogalactan protein (Arabidopsis thaliana) gi:10880509:gb:AAG24284   chr5:21620846-21621457 FORWARD   Aliases: K19E1.5, K19E1_5	7.1	4.7	2.4	4.3	32.2%	0.1
313	AT3G24495.1   DNA mismatch repair protein MSH6-2 (MSH7), identical to SP:Q9SMV7 DNA mismatch repair protein MSH6-2 (AtMsh6-2) (MutS homolog 7) {Arabidopsis thaliana}; GC donor splice site at exon 11	4.0	5.5	-1.5	-4.3	32.2%	0.1
314	AT3G54810.2   zinc finger (GATA type) family protein, GATA transcription factor 3, Arabidopsis thaliana, Y13650   chr3:20307246-20309669 FORWARD   Aliases: T5N23.3	5.3	3.9	1.3	4.3	32.2%	0.1
315	AT4G34600.1   expressed protein   chr4:16529230-16530191 FORWARD   Aliases: T4L20.180, T4L20_180	7.4	5.8	1.6	4.3	32.2%	0.1
316	AT2G02120.1   Symbol: LCR70/PDF2.1   plant defensin-fusion protein, putative (PDF2.1), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains a gamma-thionin family signature (PDOC00725)   chr2:538254-539054 FORWARD   Aliases: F5O4.11, F5O4_11, LCR70, Low molecular weight cysteine rich 70, PDF2.1	11.7	10.4	1.3	4.3	32.2%	0.1
317	AT3G22240.1   expressed protein   chr3:7863684-7864586 REVERSE   Aliases: MMP21.2	8.4	10.2	-1.8	-4.3	32.2%	0.1
318	AT3G55040.1   In2-1 protein, putative, similar to In2-1 protein, Zea mays, P49248   chr3:20409695-20411282 REVERSE   Aliases: T15C9.60	5.8	4.6	1.2	4.3	32.2%	0.1
319	AT2G43510.1   Symbol: ATTI1   Encodes a defensin-like (DEFL) family protein.   chr2:18074251-18074877 FORWARD   Aliases: T1O24.25, TRYPSIN INHIBITOR	3.6	4.8	-1.2	-4.3	32.2%	0.1
320	AT1G61160.1   expressed protein   chr1:22548684-22550022 REVERSE   Aliases: F11P17.19, F11P17_19	5.3	4.0	1.2	4.3	32.2%	0.1
321	AT5G56580.1   Symbol: ATMKK6	3.5	5.0	-1.5	-4.3	32.6%	0.1
322	AT2G41010.1   VQ motif-containing protein, contains PF05678: VQ motif   chr2:17120944-17121882 REVERSE   Aliases: T3K9.22, T3K9_22	7.3	5.7	1.6	4.3	32.6%	0.1
323	AT3G25130.1   expressed protein   chr3:9152411-9153878 FORWARD   Aliases: MJL12.7	3.0	4.7	-1.7	-4.3	32.7%	0.1
324	AT2G45730.1   eukaryotic initiation factor 3 gamma subunit family protein, contains Pfam profile PF04189: Eukaryotic initiation factor 3, gamma subunit   chr2:18843459-18846234 REVERSE   Aliases: F4I18.29	6.3	7.6	-1.3	-4.3	32.7%	0.1
325	AT3G15500.1   Symbol: ATNAC3	4.8	3.8	1.1	4.3	32.7%	0.1
326	AT2G31400.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587, post-transcriptional control of chloroplast gene expression CRP1 (Zea mays) GI:3289002; contains Pfam profile PF01535: PPR repeat   chr2:13394081-13397783 REVERSE   Aliases: T28P16.11, T28P16_11	9.0	10.1	-1.1	-4.3	32.8%	-0.0
327	AT3G42660.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); AND-1 protein - Homo sapiens, EMBL:AJ006266	5.9	8.5	-2.6	-4.3	33.0%	-0.0
328	AT3G53900.2   uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative, similar to SP:P50926 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Lactococcus lactis}; contains Pfam profile PF00156: Phosphoribosyl transferase domain   chr3:19967634-19970019 REVERSE   Aliases: F5K20.200	4.8	6.7	-1.9	-4.3	33.1%	0.0
329	AT1G15660.1   expressed protein, similar to CENPCA protein (GI:11863170) {Zea mays}   chr1:5381165-5385249 FORWARD   Aliases: T16N11.16, T16N11_16	5.7	7.3	-1.7	-4.3	33.3%	0.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
330	AT4G13660.1   pinorexinol-lariciresinol reductase, putative, similar to pinorexinol-lariciresinol reductase TH1 (Tsuga heterophylla)(GI:7578915); contains isoflavone reductase domain PF02716	7.7	9.7	-2.0	-4.3	33.3%	0.0
331	AT1G71880.1   Symbol: SUC1   sucrose transporter / sucrose-proton symporter (SUC1), identical to sucrose-proton symporter SUC1 (Arabidopsis thaliana) GI:407094   chr1:27057842-27060001 FORWARD   Aliases: ATSUC1, F17M19.3, F17M19_3, SUCROSE H+ SYMPORTER	6.3	5.1	1.1	4.2	33.6%	0.0
332	AT4G19370.1   expressed protein   chr4:10566274-10567546 REVERSE   Aliases: T5K18.150, T5K18_150	5.2	4.0	1.2	4.2	33.6%	0.0
333	AT4G35800.1   Symbol: NRPB1   DNA-directed RNA polymerase II largest subunit (RPB205) (RPII) (RPB1), nearly identical to P:P18616 DNA-directed RNA polymerase II largest subunit (EC 2.7.7.6) {Arabidopsis thaliana}   chr4:16960661-16967896 REVERSE   Aliases: F4B14.70, F4B14_70, RNA POLYMERASE II LARGE SUBUNIT, RNA_POL_II_LS, RNA_POL_II_LSRNA_POL_II_LS, RPB1	3.4	4.6	-1.2	-4.2	33.6%	0.0
334	AT5G11780.1   expressed protein   chr5:3793929-3796142 FORWARD   Aliases: T22P22.170, T22P22_170	2.9	3.7	-0.8	-4.2	34.2%	-0.1
335	AT1G68585.1   expressed protein   chr1:25760521-25761532 FORWARD   Aliases: None	8.1	6.8	1.3	4.2	34.2%	0.0
336	AT1G75030.1   Symbol: ATLP 3	3.7	5.3	-1.6	-4.2	34.6%	-0.0
337	AT5G65420.1   Symbol: CYCD4;1   cyclin, putative, similar to cyclin D2.1 protein (Nicotiana tabacum) GI:4160298; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr5:26158699-26161219 REVERSE   Aliases: CYCD4;1, Cyclin D4;1, MNA5.15, MNA5_15	5.4	6.3	-0.9	-4.2	34.8%	-0.0
338	AT5G40990.1   GDSL-motif lipase/hydrolase family protein, similar to lipase (Arabidopsis thaliana) GI:1145627; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:16436148-16437628 FORWARD   Aliases: MEE6.6, MEE6_6	2.8	4.9	-2.1	-4.2	34.9%	-0.4
339	AT5G04760.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:1373531-1374736 REVERSE   Aliases: MUK11.7	7.5	6.0	1.5	4.2	35.0%	-0.0
340	AT2G37790.1   aldo/keto reductase family protein, similar to chalcone reductase (Sesbania rostrata)(GI:2792155), and aldose reductase ALDRXV4 (Xerophyta viscosa)(GI:4539944),	7.7	9.5	-1.7	-4.2	35.0%	-0.0
341	AT4G25170.1   expressed protein   chr4:12909585-12911590 FORWARD   Aliases: F24A6.10, F24A6_10	7.6	5.7	1.9	4.2	35.1%	-0.0
342	AT1G76570.1   chlorophyll A-B binding family protein, similar to chlorophyll A-B binding protein GB:P12470 (Nicotiana plumbaginifolia); contains Pfam profile: PF00504 Chlorophyll A-B binding proteins   chr1:28734026-28735719 FORWARD   Aliases: F14G6.17, F14G6_17	6.2	5.4	0.9	4.2	35.1%	-0.1
343	AT3G02550.1   LOB domain protein 41 / lateral organ boundaries domain protein 41 (LBD41), identical to LOB DOMAIN 41 (Arabidopsis thaliana) GI:17227172   chr3:536512-538005 REVERSE   Aliases: F16B3.18, F16B3_18	8.8	6.6	2.2	4.2	35.3%	-0.0
344	AT5G53460.1   Symbol: GLT1   glutamate synthase (NADH), chloroplast, putative, similar to SP:Q03460 Glutamate synthase (NADH), chloroplast precursor (EC 1.4.1.14) (NADH- GOGAT) {Medicago sativa}   chr5:21717744-21726855 FORWARD   Aliases: MYN8.7, MYN8_7, NADH GOGAT	7.3	8.5	-1.3	-4.2	35.3%	-0.1
345	AT3G61790.1   seven in absentia (SINA) family protein, similar to siah-1A protein (Mus musculus) GI:297035; contains Pfam profile PF03145: Seven in absentia protein family   chr3:22882768-22884665 REVERSE   Aliases: F21F14.2	6.7	5.3	1.4	4.2	35.3%	-0.0
346	AT5G18130.2   expressed protein, similar to unknown protein (gb:AAF00631.1)   chr5:5995482-5997400 FORWARD   Aliases: MRG7.9, MRG7_9	6.3	5.2	1.1	4.2	35.3%	-0.1
347	AT3G50980.1   dehydrin, putative, similar to dehydrin Xero 1 (Arabidopsis thaliana) SWISS-PROT:P25863   chr3:18952957-18953846 FORWARD   Aliases: F24M12.20	6.3	4.6	1.7	4.2	35.3%	-0.1
348	AT1G18730.1   expressed protein   chr1:6460590-6462212 FORWARD   Aliases: F6A14.16, F6A14_16	6.9	5.1	1.7	4.2	35.5%	-0.1
349	AT3G55470.1   C2 domain-containing protein, similar to phloem protein GI:4164539 from (Cucurbita maxima)   chr3:20575222-20577665 FORWARD   Aliases: T2E16.130	5.7	4.2	1.4	4.2	35.6%	-0.1
350	AT1G73780.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family   chr1:27747533-27747829 FORWARD   Aliases: F25P22.20, F25P22_20	2.1	2.4	-0.3	-4.2	35.9%	-0.9
351	AT2G39310.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.8	5.3	-1.5	-4.2	36.0%	-0.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
352	AT2G22470.1   Symbol: AGP2   arabinogalactan-protein (AGP2), identical to gi:3883122:gb:AAC77824; supported by cDNA gi:3883121:gb:AF082299   chr2:9545277-9545959 REVERSE   Aliases: ARABINO GALACTAN PROTEIN 2, F14M13.13, F14M13_13	7.5	6.3	1.3	4.2	36.1%	-0.1
353	AT1G08090.1   Symbol: ATNRT2:1   high-affinity nitrate transporter (ACH1), identical to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362   chr1:2524073-2526161 FORWARD   Aliases: ACH1, ATNRT2.1, LATERAL ROOT INITIATION 1, LIN1, NITRATE TRANSPORTER 1, NRT2, NRT2;1AT, T6D22.17, T6D22_17, TRANS MEMBRANE NITRATE TRANSPORTER PROTEIN ATNRT2:1	5.4	7.4	-2.0	-4.2	36.1%	-0.3
354	AT1G76600.1   expressed protein   chr1:28751782-28752739 FORWARD   Aliases: F14G6.20, F14G6_20	6.8	5.7	1.2	4.2	36.1%	-0.1
355	AT1G29060.1   expressed protein   chr1:10147679-10149667 FORWARD   Aliases: F28N24.23, F28N24_23	5.9	4.7	1.2	4.1	36.1%	-0.1
356	AT1G01990.1   expressed protein   chr1:343166-344319 REVERSE   Aliases: F22M8.12, F22M8_12	5.9	5.2	0.7	4.1	36.1%	-0.3
357	AT2G20290.1   Symbol: XIG   myosin, putative, similar to myosin (GI:499047) (Arabidopsis thaliana)   chr2:8750356-8758959 REVERSE   Aliases: ATXIG, F11A3.16, F11A3_16	3.4	4.7	-1.4	-4.1	36.1%	-0.1
358	AT1G78490.1   Symbol: CYP708A3   cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana)   chr1:29533169-29535558 FORWARD   Aliases: T30F21.17, T30F21_17	5.7	4.2	1.4	4.1	36.1%	-0.1
359	AT1G73500.1   Symbol: ATMKK9	7.3	6.2	1.1	4.1	36.1%	-0.1
360	AT4G36430.1   peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:6822093:emb:CAB71009; identical to cDNA class III peroxidase ATP31, GI:17530561	5.0	8.8	-3.8	-4.1	36.2%	-0.4
361	AT3G22790.1   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia)   chr3:8052453-8057895 REVERSE   Aliases: MWI23.16	3.7	4.6	-0.9	-4.1	36.2%	-0.1
362	AT5G49160.1   Symbol: MET1   DNA (cytosine-5-)-methyltransferase (ATHIM), identical to SP:P34881 DNA (cytosine-5)-methyltransferase AthI (EC 2.1.1.37) {Arabidopsis thaliana}	5.2	7.2	-2.0	-4.1	36.2%	-0.1
363	AT3G23170.1   expressed protein   chr3:8267949-8268742 REVERSE   Aliases: K14B15.6	5.4	3.8	1.6	4.1	36.4%	-0.1
364	AT1G32900.1   starch synthase, putative, similar to starch synthase SP:Q42857 from (Ipomoea batatas)   chr1:11920371-11923746 REVERSE   Aliases: F9L11.8, F9L11_8	9.2	7.5	1.7	4.1	36.7%	-0.1
365	AT1G04610.1   flavin-containing monooxygenase / FMO (YUCCA3), identical to gi:16555356	5.3	7.7	-2.4	-4.1	36.8%	-0.2
366	AT1G18090.2   exonuclease, putative, similar to Swiss-Prot:P53695 exonuclease I (EXO I) (Schizosaccharomyces pombe)   chr1:6224497-6228233 FORWARD   Aliases: T10F20.10	3.3	4.3	-1.0	-4.1	36.8%	-0.2
367	AT3G01970.1   Symbol: WRKY45	6.1	4.6	1.5	4.1	36.8%	-0.1
368	AT5G49650.2   xylulose kinase, putative, similar to D-xylulokinase (Pichia stipitis) gi:8100400:gb:AAF72328   chr5:20170007-20172994 FORWARD   Aliases: MNI5.3, MNI5_3	6.8	9.3	-2.4	-4.1	36.8%	-0.1
369	AT1G15380.2   similar to lactoylglutathione lyase family protein / glyoxalase I family protein [Arabidopsis thaliana] (TAIR:At1g80160.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_916470.1); contains InterPro domain Glyoxalase I (InterPro:IPR004361); contains InterPro domain Glyoxalase/Bleomycin resistance protein/dioxygenase domain (InterPro:IPR004360)   chr1:5290742-5292529 FORWARD   Aliases: F9L1.33, F9L1_33	6.3	4.3	2.0	4.1	36.9%	-0.3
370	AT3G24660.1   Symbol: TMKL1   leucine-rich repeat transmembrane protein kinase, putative, identical to putative kinase-like protein TMKL1 precursor GB:P33543 from (Arabidopsis thaliana), (Plant Mol. Biol. 23 (2), 415-421 (1993))   chr3:9003583-9005950 FORWARD   Aliases: MSD24.6, TRANSMEMBRANE KINASE LIKE 1	5.4	6.1	-0.7	-4.1	37.0%	-0.3
371	AT2G15580.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:6804723-6806021 FORWARD   Aliases: F9O13.13	7.0	5.4	1.5	4.1	37.1%	-0.2
372	AT1G67940.1   Symbol: ATNAP3	8.7	7.8	0.9	4.1	37.1%	-0.3
373	AT4G16190.1   cysteine proteinase, putative, contains similarity to papain-like cysteine proteinase isoform I GI:7381219 from (Ipomoea batatas)   chr4:9171482-9173120 FORWARD   Aliases: DL4135W, FCAALL.298	8.4	5.3	3.1	4.1	37.1%	-0.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
374	AT1G42990.1   Symbol: ATBZIP60   AtbZIP60 consists of a bZIP DNA binding domain followed by a putative transmembrane domain. GFP fusions containing the first 260 amino acids (AtbZIP60deltaC) are nuclear-localized. AtbZIP60 is upregulated by the addition of tunicamycin (ER stress response inducer), DTT (inhibitor of disulfide bond formation) and azetin-2-carboxylate (proline analog perturbing protein structure). It is hypothesized that upon ER stress the protein is proteolyzed and the soluble part translocated into the nucleus. AtbZIP60deltaC can activate the promoters of the ER chaperones BiP1, BiP2 and BiP3 and CNX1 and CNX2 via binding to the ER stress response element (ERSE) and the plant unfolded protein response element(P-UPRE). It can also activate its own transcription.   chr1:16138292-16139903 REVERSE   Aliases: ATBZIP60, F13A11.5, F13A11_5	9.1	7.9	1.2	4.1	37.1%	-0.2
375	AT5G53320.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:21653295-21655622 REVERSE   Aliases: K19E1.12, K19E1_12	5.5	6.6	-1.1	-4.1	37.3%	-0.2
376	AT1G56300.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9QYI7 DnaJ homolog subfamily B member 8 Mus musculus; contains Pfam profile: PF00226: DnaJ domain   chr1:21082485-21083991 REVERSE   Aliases: F14G9.9, F14G9_9	8.1	6.7	1.3	4.1	37.3%	-0.2
377	AT1G77720.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:29215415-29218973 FORWARD   Aliases: T32E8.5, T32E8_5	2.5	3.0	-0.5	-4.1	37.4%	-0.6
378	AT1G16490.1   myb family transcription factor (MYB58), contains PFAM profile: myb DNA binding domain PF00249   chr1:5629648-5630988 REVERSE   Aliases: F309.29, F309_29	3.4	4.7	-1.2	-4.1	37.5%	-0.2
379	AT1G72450.1   expressed protein   chr1:27277727-27279950 REVERSE   Aliases: T10D10.8, T10D10_8	7.1	5.5	1.7	4.1	37.9%	-0.3
380	AT2G07690.1   minichromosome maintenance family protein / MCM family protein, similar to SP:P55862 DNA replication licensing factor MCM5 (CDC46 homolog) {Xenopus laevis}; contains Pfam profile PF00493: MCM2/3/5 family   chr2:3523243-3527428 REVERSE   Aliases: T12J2.1	4.9	5.7	-0.9	-4.1	37.9%	-0.3
381	AT2G38720.1   microtubule associated protein (MAP65/ASE1) family protein, low similarity to myosin (Schistosoma japonicum) GI:3941320; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr2:16195125-16199180 FORWARD   Aliases: T6A23.8, T6A23_8	3.7	5.9	-2.1	-4.1	38.3%	-0.4
382	AT1G27590.1   expressed protein, similar to hypothetical protein GB:AAD45997 GI:5668770 from (Arabidopsis thaliana)   chr1:9592149-9593949 FORWARD   Aliases: T22C5.2	3.6	2.9	0.7	4.1	38.4%	-0.3
383	AT3G59550.1   Symbol: SYN3   cohesion family protein SYN3 (SYN3), nearly identical to cohesion family protein SYN3 (Arabidopsis thaliana) GI:12006362; supporting cDNA gi:12006361:gb:AF281155.1:AF281155   chr3:22008031-22011655 FORWARD   Aliases: T16L24.100	3.3	5.1	-1.8	-4.0	38.5%	-0.3
384	AT3G05490.1   Symbol: RALFL22   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr3:1591283-1591989 FORWARD   Aliases: F22F7.6, F22F7_6, RALF LIKE 22	7.7	5.9	1.7	4.0	38.5%	-0.2
385	AT3G18940.1   clast3-related, contains Prosite PS00626: Regulator of chromosome condensation (RCC1) signature 2; similar to Clast3 protein (GI:9857631) (Mus musculus)	5.7	7.0	-1.2	-4.0	38.5%	-0.2
386	AT4G27800.3   protein phosphatase 2C PPH1 / PP2C PPH1 (PPH1), identical to SP:P49599:P2C3_ARATH Protein phosphatase 2C PPH1 (EC 3.1.3.16) (PP2C) {Arabidopsis thaliana}; similar to protein phosphatase-2C; PP2C (GI:3643090) (Mesembryanthemum crystallinum)   chr4:13851876-13854197 REVERSE   Aliases: T27E11.40, T27E11_40	9.2	8.3	0.9	4.0	38.5%	-0.3
387	AT4G19830.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, similar to 70 kDa peptidylprolyl isomerase (Peptidylprolyl cis-trans isomerase) (PPIase) (Rotamase) (SP:Q43207) (Triticum aestivum); FKBP-type peptidyl-prolyl cis-trans isomerase, Synechocystis sp., PIR2:S75144; contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr4:10772441-10774033 REVERSE   Aliases: T16H5.190, T16H5_190	6.1	4.8	1.3	4.0	38.7%	-0.2
388	AT5G05470.1   Symbol: EIF2 ALPHA   eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative, similar to SWISS-PROT:P20459 eukaryotic translation initiation factor 2 alpha subunit (eIF-2- alpha) (Saccharomyces cerevisiae); identical to cDNA cohesin GI:6682280   chr5:1620459-1622777 FORWARD   Aliases: ATEIF2 A2, EIF2 A2, K18I23.28, K18I23_28	5.1	6.5	-1.4	-4.0	38.7%	-0.3
389	AT4G12580.1   expressed protein, predicted protein   chr4:7449371-7449676 REVERSE   Aliases: T1P17.170, T1P17_170	5.9	4.5	1.5	4.0	39.1%	-0.2
390	AT1G04730.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family ('A'TPases 'A'ssociated with diverse cellular 'A'ctivities)   chr1:1325384-1331085 REVERSE   Aliases: T1G11.3, T1G11_3	3.2	4.1	-0.9	-4.0	39.4%	-0.3
391	AT4G30430.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr4:14878789-14880337 REVERSE   Aliases: F17I23.230, F17I23_230	6.1	4.6	1.6	4.0	39.4%	-0.3
392	AT5G27280.1   zinc finger (DNL type) family protein, contains Pfam profile PF05180: DNL zinc finger   chr5:9617489-9618484 FORWARD   Aliases: F21A20.2	6.7	5.9	0.9	4.0	39.4%	-0.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
393	AT5G07660.1   structural maintenance of chromosomes (SMC) family protein, similar to SMC-like protein (MIM) (Arabidopsis thaliana) GI:5880614; contains Pfam profile PF02463: RecF/RecN/SMC N terminal domain   chr5:2422840-2429913 FORWARD   Aliases: MBK20.10, MBK20_10	3.5	4.6	-1.1	-4.0	39.4%	-0.3
394	AT2G15000.2   expressed protein   chr2:6488440-6489469 REVERSE   Aliases: T15J14.4, T15J14_4	5.8	7.5	-1.7	-4.0	39.4%	-0.3
395	AT2G21790.1   Symbol: R1   ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative, similar to ribonucleotide reductase GI:4151068 from (Nicotiana tabacum)   chr2:9300435-9304922 FORWARD   Aliases: F7D8.11, F7D8_11, R1	5.4	7.6	-2.1	-4.0	39.6%	-0.3
396	AT5G20220.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr5:6821992-6825983 FORWARD   Aliases: F5O24.110, F5O24_110	5.1	4.3	0.8	4.0	39.7%	-0.3
397	AT3G11230.1   yippee family protein, similar to qdgl-1 (Coturnix coturnix) GI:10441650, Yippee protein (Homo sapiens) GI:5713281; contains Pfam profile PF03226: Yippee putative zinc-binding protein   chr3:3516583-3518377 FORWARD   Aliases: F11B9.15	9.4	8.8	0.6	4.0	39.7%	-0.5
398	AT3G14450.1   Symbol: CID9   RNA-binding protein, putative, contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain) (2 copies). Contains PAM PABC binding domain.   chr3:4849795-4851608 FORWARD   Aliases: CID9, MOA2.5	4.0	3.3	0.7	4.0	39.7%	-0.6
399	AT1G52550.1   expressed protein   chr1:19576596-19577699 REVERSE   Aliases: F6D8.23, F6D8_23	4.4	3.2	1.2	4.0	40.3%	-0.3
400	AT5G52910.1   Symbol: ATIM   timeless family protein, contains Pfam domains PF05029: Timeless protein C terminal region and PF04821: Timeless protein	3.8	4.7	-0.8	-4.0	40.4%	-0.4
401	AT4G01250.1   Symbol: WRKY22	4.6	3.2	1.3	4.0	40.4%	-0.3
402	AT5G40960.1   expressed protein   chr5:16429973-16430179 REVERSE   Aliases: MEE6.3, MEE6_3	9.6	7.7	1.9	4.0	40.4%	-0.3
403	AT1G07135.1   glycine-rich protein   chr1:2189927-2190623 REVERSE   Aliases: None	8.9	5.8	3.1	4.0	40.4%	-0.6
404	AT5G18620.2   DNA-dependent ATPase, putative, similar to DNA-dependent ATPase SNF2H (Mus musculus) GI:14028669; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00249: Myb-like DNA-binding domain   chr5:6195919-6202168 REVERSE   Aliases: T1A4.2	6.7	9.2	-2.5	-4.0	40.4%	-0.3
405	AT2G18600.1   RUB1-conjugating enzyme, putative, strong similarity to gi:6635457 RUB1 conjugating enzyme (Arabidopsis thaliana); contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr2:8080282-8082030 REVERSE   Aliases: F24H14.5, F24H14_5	8.3	6.9	1.4	4.0	40.4%	-0.3
406	AT3G59480.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr3:21993998-21995572 FORWARD   Aliases: T16L24.30	4.1	5.8	-1.7	-4.0	40.4%	-0.3
407	AT5G37990.1   similar to S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis thaliana] (TAIR:At5g37970.1); similar to AtPP homologue [Brassica napus] (GB:CAC80637.1); contains InterPro domain SAM dependent carboxyl methyltransferase (InterPro:IPR005299)   chr5:15150967-15152730 REVERSE   Aliases: K18L3.150, K18L3_150	3.4	4.5	-1.2	-4.0	40.4%	-0.3
408	AT5G16480.1   tyrosine specific protein phosphatase family protein, contains tyrosine specific protein phosphatases active site, PROSITE:PS00383   chr5:5381116-5382900 REVERSE   Aliases: MQK4.21, MQK4_21	7.2	5.5	1.7	4.0	40.4%	-0.3
409	AT1G64660.1   Cys/Met metabolism pyridoxal-phosphate-dependent enzyme family protein, similar to SP:P13254 Methionine gamma-lyase (EC 4.4.1.11) (L-methioninase) {Pseudomonas putida}; contains Pfam profile PF01053: Cys/Met metabolism PLP-dependent enzyme   chr1:24032581-24034443 FORWARD   Aliases: F1N19.23, F1N19_23	4.7	6.3	-1.6	-4.0	40.4%	-0.3
410	AT2G48010.1   Symbol: RKF3   serine/threonine protein kinase (RKF3), identical to receptor-like serine/threonine kinase (Arabidopsis thaliana) gi:2465927:qb:AAC50045	8.0	6.9	1.1	4.0	40.4%	-0.5
411	AT3G27360.1   histone H3, identical to histone H3 from Zea mays SP:P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP:P08903, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr3:10130520-10131174 REVERSE   Aliases: K1G2.15	5.6	7.5	-1.9	-4.0	40.5%	-0.3
412	AT1G19020.1   expressed protein   chr1:6568064-6568569 FORWARD   Aliases: F14D16.17, F14D16_17	7.6	6.2	1.5	4.0	41.1%	-0.4
413	AT1G77230.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr1:29021023-29022858 FORWARD   Aliases: T14N5.9, T14N5_9	6.5	4.7	1.8	3.9	41.2%	-0.4
414	AT4G33940.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:16266035-16267786 FORWARD   Aliases: F17I5.1	6.4	5.3	1.1	3.9	41.2%	-0.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
415	AT3G48110.1   Symbol: EDD1   similar to glycyl-tRNA synthetase alpha chain and beta chain [Tropheryma whipplei str. Twist] (GB:AAO44597.1); similar to probable glycyl-tRNA synthetase [Parachlamydia sp. UWE25] (GB:YP_007692.1); similar to putative glycine--tRNA ligase [Oryza sativa (japonica cultivar-group)] (GB:XP_476283.1); similar to glycyl-tRNA synthetase [Tropheryma whipplei TW08/27] (GB:NP_789201.1); contains InterPro domain Glycyl-tRNA synthetase, beta subunit (InterPro:IPR002311); contains InterPro domain Heterodimeric glycyl-transfer RNA synthetase (InterPro:IPR006194); contains InterPro domain Glycyl-tRNA synthetase, alpha subunit (InterPro:IPR002310)   chr3:17773986-17782131 FORWARD   Aliases: EDD, EMBRYO DEFECTIVE DEVELOPMENT 1, GLYCYL TRNA SYNTHETASE, T17F15.20	4.3	5.6	-1.3	-3.9	41.3%	-0.3
416	AT4G32240.1   expressed protein   chr4:15568306-15569194 FORWARD   Aliases: F10M6.120, F10M6_120	11.7	10.8	0.8	3.9	41.4%	-0.9
417	AT1G27120.1   galactosyltransferase family protein, contains Pfam profile:PF01762 galactosyltransferase   chr1:9421164-9424054 FORWARD   Aliases: T7N9.18, T7N9_18	5.1	7.0	-1.9	-3.9	41.4%	-0.5
418	AT1G18030.1   protein phosphatase 2C, putative / PP2C, putative, contains similarity to protein phosphatase 2C GI:3777604 from (Rattus norvegicus)   chr1:6204336-6206981 FORWARD   Aliases: T10F20.4, T10F20_4	5.5	4.8	0.7	3.9	41.5%	-0.5
419	AT1G29050.1   expressed protein, similar to hypothetical protein GB:AAB67625 GI:2342727 from (Arabidopsis thaliana)   chr1:10136217-10139194 REVERSE   Aliases: F28N24.24, F28N24_24	8.0	7.1	0.9	3.9	41.5%	-0.5
420	AT4G18910.1   aquaglyceroporin / NOD26-like major intrinsic protein 2 (NLM2), contains Pfam profile: MIP PF00230; similar to SP:P08995 {Glycine max} Nodulin-26 (N-26); identical to cDNA aquaglyceroporin (nlm2 gene) GI:11071655, aquaglyceroporin (Arabidopsis thaliana) GI:11071656   chr4:10366070-10368392 FORWARD   Aliases: F13C5.80, F13C5_80	4.6	6.8	-2.1	-3.9	41.6%	-0.4
421	AT5G46280.1   DNA replication licensing factor, putative, similar to SP:Q43704 DNA replication licensing factor MCM3 homolog (Replication origin activator) (ROA protein) {Zea mays}; contains Pfam profile PF00493: MCM2/3/5 family   chr5:18786924-18790885 REVERSE   Aliases: MPL12.6, MPL12_6	5.3	7.7	-2.4	-3.9	41.6%	-0.4
422	AT2G01120.1   origin recognition complex subunit 4, putative (ORC4), similar to origin recognition complex subunit 4 (GI:15866782) (Zea mays)   chr2:87317-88122 FORWARD   Aliases: F23H14.9, F23H14_9	4.1	5.8	-1.6	-3.9	42.0%	-0.4
423	AT1G20070.1   expressed protein   chr1:6958001-6959114 REVERSE   Aliases: T20H2.15, T20H2_15	6.4	4.3	2.1	3.9	42.5%	-0.5
424	AT2G38640.1   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr2:16164682-16165632 REVERSE   Aliases: T6A23.16, T6A23_16	5.7	4.2	1.5	3.9	42.5%	-0.4
425	AT5G59400.2   expressed protein, predicted protein, Arabidopsis thaliana   chr5:23974971-23976858 FORWARD   Aliases: F2O15.8, F2O15_8	5.1	4.1	1.1	3.9	42.5%	-0.4
426	AT1G26730.1   EXS family protein / ERD1/XPR1/SYG1 family protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family	7.9	6.4	1.5	3.9	42.5%	-0.4
427	AT4G16520.2   autophagy 8f (APG8f), identical to autophagy 8f (Arabidopsis thaliana) GI:19912161; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3   chr4:9306708-9308465 REVERSE   Aliases: DL4285C, FCAALL.383	11.9	11.2	0.7	3.9	42.5%	-0.7
428	AT3G04980.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain   chr3:1378690-1382187 REVERSE   Aliases: T9J14.7, T9J14_7	3.5	4.6	-1.1	-3.9	42.5%	-0.4
429	AT2G01110.1   Symbol: APG2   thylakoid membrane formation protein / cpTatC (APG2), identical to thylakoid membrane formation protein (cpTatC) GI:15004994 from (Arabidopsis thaliana); contains Pfam profile PF00902:	5.7	4.4	1.3	3.9	42.5%	-0.4
430	AT1G16240.2   Symbol: SYP51   similar to syntaxin 52 (SYP52) [Arabidopsis thaliana] (TAIR:At1g79590.1); similar to putative syntaxin of plants 52 [Oryza sativa (japonica cultivar-group)] (GB:XP_463898.1); contains InterPro domain Target SNARE coiled-coil domain (InterPro:IPR000727)   chr1:5555001-5556797 REVERSE   Aliases: ATSYP51, F3O9.4, F3O9_4, SYNTAXIN OF PLANTS 51	10.5	9.7	0.8	3.9	42.5%	-0.6
431	AT1G45474.2   Symbol: LHCA5   chlorophyll A-B binding protein, putative (LHCA5), identical to Lhca5 protein (Arabidopsis thaliana) GI:4741942; contains Pfam profile: PF00504 chlorophyll A-B binding protein; similar to light-harvesting complex protein GI:22752 from (Pinus sylvestris)   chr1:17181742-17183246 FORWARD   Aliases: F2G19.4, F2G19_4	7.3	5.3	2.0	3.9	42.8%	-0.4
432	AT3G12080.1   Symbol: EMB2738   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function	5.8	7.0	-1.2	-3.9	42.8%	-0.4
433	AT4G00010.1   expressed protein   chr4:3894-5908 REVERSE   Aliases: T15P10.10, T15P10_10	3.5	4.8	-1.3	-3.9	42.8%	-0.4
434	AT5G62410.1   Symbol: SMC2   SMC2-like condensin, putative (SMC2) (TITAN3), very strong similarity to SMC2-like condensin (TITAN3) (Arabidopsis thaliana) GI:14279543; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain	4.7	6.3	-1.6	-3.9	43.2%	-0.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
435	AT4G26760.1   microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr4:13478598-13481757 REVERSE   Aliases: F10M23.100, F10M23_100	3.7	5.1	-1.4	-3.9	43.2%	-0.5
436	AT5G05110.1   cysteine protease inhibitor, putative / cystatin, putative, similar to cysteine proteinase inhibitor (Glycine max) GI:1944342; contains Pfam profile PF00031: Cystatin domain   chr5:1507420-1508868 REVERSE   Aliases: MUG13.3, MUG13_3	8.4	5.6	2.8	3.9	43.6%	-0.4
437	AT1G01670.1   U-box domain-containing protein   chr1:242844-245988 REVERSE   Aliases: T1N6.28, T1N6_28	5.4	4.1	1.3	3.9	43.6%	-0.5
438	AT3G54430.1   lateral root primordium (LRP) protein-related, similar to lateral root primordium 1 (LRP1) (Arabidopsis thaliana) GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702)   chr3:20158079-20159105 REVERSE   Aliases: T14E10.2	6.5	5.4	1.1	3.9	43.6%	-0.4
439	AT1G63660.2   GMP synthase (glutamine-hydrolyzing), putative / glutamine amidotransferase, putative, similar to SP:P38625 GMP synthase (glutamine-hydrolyzing) (EC 6.3.5.2) (Glutamine amidotransferase) (GMP synthetase) {Saccharomyces cerevisiae}; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr1:23607602-23610938 REVERSE   Aliases: F24D7.15, F24D7_15	7.3	8.7	-1.4	-3.9	43.6%	-0.4
440	AT5G56030.1   Symbol: HSP81 2   heat shock protein 81-2 (HSP81-2), nearly identical to SP:P55737 Heat shock protein 81-2 (HSP81-2) {Arabidopsis thaliana}   chr5:22704058-22706876 FORWARD   Aliases: HEAT SHOCK PROTEIN 81 2, MDA7.7, MDA7_7	9.3	10.2	-0.9	-3.9	43.6%	-0.6
441	AT5G23380.1   expressed protein   chr5:7866745-7870135 FORWARD   Aliases: T32G24.1, T32G24_1	4.2	3.4	0.8	3.9	43.6%	-0.6
442	AT1G16500.1   expressed protein   chr1:5639025-5640166 FORWARD   Aliases: F3O9.30, F3O9_30	6.7	5.3	1.5	3.9	43.7%	-0.5
443	AT1G20640.2   RWP-RK domain-containing protein, similar to nodule inception protein GI:6448579 from (Lotus japonicus); contains Pfam profile: PF02042 RWP-RK domain   chr1:7154400-7158208 FORWARD   Aliases: F5M15.4	8.9	7.2	1.7	3.9	43.7%	-0.5
444	AT5G22250.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, (CAF1) (Mus musculus)   chr5:7365535-7366781 REVERSE   Aliases: T6G21.2	4.8	4.2	0.7	3.9	43.7%	-0.7
445	AT5G67520.1   adenylylsulfate kinase, putative, similar to adenylylsulfate kinase, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Catharanthus roseus) SWISS-PROT:O49204   chr5:26956385-26958172 FORWARD   Aliases: K9I9.8, K9I9_8	6.0	4.6	1.3	3.9	43.8%	-0.5
446	AT5G15530.1   Symbol: BCCP2   biotin carboxyl carrier protein 2 (BCCP2), identical to biotin carboxyl carrier protein isoform 2 (Arabidopsis thaliana) gi:8886869:gb:AAF80592	4.1	5.6	-1.5	-3.9	43.8%	-0.5
447	AT1G31290.1   PAZ domain-containing protein / piwi domain-containing protein, contains Pfam profiles PF02170: PAZ domain, PF02171: Piwi domain	5.3	3.7	1.6	3.8	43.9%	-0.5
448	AT4G11480.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:6971403-6973794 FORWARD   Aliases: F25E4.100, F25E4_100	2.8	3.5	-0.7	-3.8	43.9%	-0.6
449	AT5G24090.1   acidic endochitinase (CHIB1), identical to SP:P19172 Acidic endochitinase precursor (EC 3.2.1.14) {Arabidopsis thaliana}	7.8	6.8	1.0	3.8	43.9%	-0.6
450	AT3G54750.2   expressed protein   chr3:20275683-20279726 REVERSE   Aliases: T5N23.110	5.5	7.7	-2.2	-3.8	44.1%	-0.5
451	AT4G11960.1   expressed protein, hypothetical protein F7H19.70 - Arabidopsis thaliana, PID:e1310057   chr4:7174880-7177752 REVERSE   Aliases: F16J13.30, F16J13_30	7.5	6.0	1.5	3.8	44.3%	-0.5
452	AT4G23670.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr4:12332570-12333814 REVERSE   Aliases: F9D16.140, F9D16_140	4.9	7.4	-2.5	-3.8	44.3%	-0.6
453	AT1G57820.2   zinc finger (C3HC4-type RING finger) family protein, low similarity to nuclear protein np95 (Mus musculus) GI:4220590; contains Pfam profiles PF02182: YDG/SRA domain, PF00097: Zinc finger, C3HC4 type (RING finger), PF00628: PHD-finger   chr1:21417876-21421602 REVERSE   Aliases: F12K22.14, F12K22_14	4.8	6.3	-1.5	-3.8	44.3%	-0.5
454	AT3G02480.1   ABA-responsive protein-related, similar to ABA-inducible protein (Fagus sylvatica) GI:3901016, cold-induced protein kin1 (Brassica napus) GI:167146   chr3:512321-513034 FORWARD   Aliases: F16B3.11, F16B3_11	7.2	10.0	-2.8	-3.8	44.3%	-0.5
455	AT1G70790.2   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr1:26704077-26706002 FORWARD   Aliases: F15H11.4, F15H11_4	7.9	6.6	1.2	3.8	44.3%	-0.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
456	AT2G34770.1   Symbol: FAH1   fatty acid hydroxylase (FAH1), identical to fatty acid hydroxylase Fah1p GB:AF021804 GI:2736147 from (Arabidopsis thaliana)   chr2:14672746-14675329 FORWARD   Aliases: FAH1P, FATTY ACID HYDROXYLASE 1, T29F13.2, T29F13_2	8.7	6.6	2.1	3.8	44.6%	-0.5
457	AT4G30460.1   glycine-rich protein   chr4:14888986-14889808 REVERSE   Aliases: F17I23.200, F17I23_200	7.3	5.4	1.9	3.8	44.6%	-0.5
458	AT5G49520.1   Symbol: WRKY48	5.2	3.2	2.0	3.8	44.7%	-0.5
459	AT5G45920.1   similar to GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] (TAIR:At5g62930.1); similar to OSJNBa0038J17.19 [Oryza sativa (japonica cultivar-group)] (GB:NP_913321.1); contains InterPro domain Lipolytic enzyme, G-D-S-L family (InterPro:IPR001087)   chr5:18639992-18642012 FORWARD   Aliases: K15I22.12, K15I22_12	5.9	4.6	1.2	3.8	44.7%	-0.5
460	AT1G75290.1   isoflavone reductase, putative, similar to SP:P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains Pfam profile PF02716: Isoflavone reductase   chr1:28257496-28258947 FORWARD   Aliases: F22H5.18, F22H5_18	5.3	7.3	-2.0	-3.8	44.7%	-0.6
461	AT2G22880.1   VQ motif-containing protein, contains PF05678: VQ motif   chr2:9748199-9748543 REVERSE   Aliases: T20K9.9, T20K9_9	4.5	3.2	1.2	3.8	44.7%	-0.5
462	AT5G62430.1   Symbol: CDF1   Dof-type zinc finger domain-containing protein, similar to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana)   chr5:25086321-25087403 REVERSE   Aliases: CYCLING DOF FACTOR 1, K19B1.4, K19B1_4	5.9	4.6	1.3	3.8	44.7%	-0.5
463	AT4G39800.1   Symbol: MI 1 P SYNTHASE   inositol-3-phosphate synthase isozyme 1 / myo-inositol-1-phosphate synthase 1 / MI-1-P synthase 1 / IPS 1, identical to SP:P42801 Inositol-3-phosphate synthase isozyme 1 (EC 5.5.1.4) (Myo-inositol-1-phosphate synthase 1) (MI-1-P synthase 1) (IPS 1) {Arabidopsis thaliana}   chr4:18469342-18471958 REVERSE   Aliases: MYO INOSITOL 1 PHOSPHATE SYNTHASE, T19P19.190, T19P19_190, T5J17.3	5.2	7.0	-1.7	-3.8	44.7%	-0.5
464	AT4G18280.1   glycine-rich cell wall protein-related, glycine-rich protein 1.0 precursor, Phaseolus vulgaris, PIR1:S01821   chr4:10104007-10104735 FORWARD   Aliases: T9A21.130, T9A21_130	11.9	10.3	1.5	3.8	44.7%	-0.5
465	AT2G04410.1   expressed protein   chr2:1533838-1535165 REVERSE   Aliases: T1O3.18, T1O3_18	8.2	7.0	1.2	3.8	44.8%	-0.5
466	AT2G04780.2   Symbol: FLA7   fasciclin-like arabinogalactan-protein (FLA7), identical to gi_13377782_gb_AAK20860   chr2:1676996-1678452 FORWARD   Aliases: F28I8.18, F28I8_18, fasciclin like arabinogalactan protein 7	5.9	7.9	-2.0	-3.8	44.8%	-0.5
467	AT5G52750.1   heavy-metal-associated domain-containing protein, Pfam profile PF00403: Heavy-metal-associated domain   chr5:21401269-21402150 FORWARD   Aliases: F6N7.24, F6N7_24	2.8	3.4	-0.6	-3.8	44.8%	-0.8
468	AT2G39830.1   LIM domain-containing protein, contains Pfam profile PF00412: LIM domain	5.5	4.6	0.9	3.8	44.8%	-0.6
469	AT1G52590.1   expressed protein   chr1:19592678-19593942 REVERSE   Aliases: F6D8.19, F6D8_19	7.6	6.4	1.2	3.8	44.8%	-0.5
470	AT1G05160.1   Symbol: CYP88A3   ent-kaurenoic acid hydroxylase (KAO1) / cytochrome P450 88A3, putative (CYP88A3), identical to Cytochrome P450 88A3 (SP:O23051) (Arabidopsis thaliana); nearly identical to ent-kaurenoic acid hydroxylase (KAO1) GI:13021852 from (Arabidopsis thaliana)   chr1:1487377-1490946 REVERSE   Aliases: ATKAO1, ENT KAURENOIC ACID HYDROXYLASE 1, KAO1, YUP8H12.23, YUP8H12_23	5.3	4.2	1.1	3.8	44.8%	-0.6
471	AT3G48520.1   Symbol: CYP94B3   cytochrome P450 family protein, similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:O81117) {Vicia sativa}; contains Pfam profile: PF00067 cytochrome P450   chr3:17985962-17987655 REVERSE   Aliases: T8P19.30	6.1	4.7	1.3	3.8	44.8%	-0.5
472	AT3G01060.3   expressed protein   chr3:16650-18847 REVERSE   Aliases: T4P13.26, T4P13_26	5.3	4.4	0.9	3.8	44.9%	-0.6
473	AT5G53360.1   seven in absentia (SINA) family protein, low similarity to siah-1A protein (Mus musculus) GI:297035; contains Pfam profile PF03145: Seven in absentia protein family   chr5:21665186-21666801 FORWARD   Aliases: K19E1.16, K19E1_16	8.7	7.8	0.9	3.8	44.9%	-0.6
474	AT1G78020.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana)   chr1:29343587-29344649 FORWARD   Aliases: F28K19.24, F28K19_24	6.3	4.7	1.5	3.8	44.9%	-0.5
475	AT5G05410.2   Symbol: DREB2A	7.5	5.4	2.1	3.8	45.3%	-0.6
476	AT2G45560.2   Symbol: CYP76C1   cytochrome P450 family protein   chr2:18784299-18785448 REVERSE   Aliases: F17K2.9	3.1	2.6	0.5	3.8	45.3%	-1.0
477	AT2G47720.1   expressed protein   chr2:19563694-19564209 FORWARD   Aliases: F17A22.11	4.9	3.9	1.1	3.8	45.4%	-0.6
478	AT5G37070.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:14668321-14669377 FORWARD   Aliases: MJG14.7, MJG14_7	7.2	6.4	0.8	3.8	45.4%	-0.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
479	AT4G28270.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:14007545-14009025 REVERSE   Aliases: F26K10.150, F26K10_150	6.8	6.0	0.9	3.8	45.4%	-0.6
480	AT1G62690.1   expressed protein   chr1:23214109-23215054 REVERSE   Aliases: F23N19.23, F23N19_23	4.5	3.5	1.0	3.8	45.4%	-0.6
481	AT2G20800.1   pyridine nucleotide-disulphide oxidoreductase family protein, similar to GI:3718005 alternative NADH-dehydrogenase {Yarrowia lipolytica} ; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr2:8960333-8962780 REVERSE   Aliases: F5H14.23, F5H14_23	3.0	4.7	-1.7	-3.8	45.4%	-0.6
482	AT1G62990.1   Symbol: KNAT7   homeodomain transcription factor (KNAT7), contains Pfam profiles: PF03789 ELK domain, PF03790 KNOX1 domain, PF03791 KNOX2 domain; similar to homeobox protein HD1 SP:P46606 from (Brassica napus); identical to cDNA homeodomain transcription factor KNAT7 (KNAT7) GI:11878229   chr1:23341030-23344353 FORWARD   Aliases: F16P17.16, F16P17_16, IXR11, TRANSCRIPTION FACTOR KNAT7	6.2	4.9	1.4	3.8	45.4%	-0.6
483	AT5G17850.1   cation exchanger, putative (CAX8), similar to sodium/calcium exchanger protein (Mus musculus) gi:13925661:gb:AAK49407; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563	7.4	6.2	1.2	3.8	45.4%	-0.6
484	AT1G08080.1   carbonic anhydrase family protein, similar to storage protein (dioscorin) (Dioscorea cayenensis) GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase   chr1:2516988-2518543 REVERSE   Aliases: T6D22.16, T6D22_16	2.7	3.9	-1.2	-3.8	45.5%	-0.6
485	AT2G37560.2   Symbol: ATORC2	3.3	4.4	-1.1	-3.8	45.5%	-0.6
486	AT2G44480.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) (Prunus serotina)   chr2:18366810-18370164 FORWARD   Aliases: F4I1.29	3.1	4.6	-1.5	-3.8	45.5%	-0.6
487	AT5G25160.1   Symbol: ZFP3   zinc finger (C2H2 type) family protein (ZFP3), identical to zinc finger protein, ZFP3 gi:790677:gb:AAA87299; contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:8687473-8688418 FORWARD   Aliases: F21J6.6, F21J6_6, ZFP3, ZINC FINGER PROTEIN 3	5.9	5.0	0.9	3.8	45.5%	-0.6
488	AT5G40630.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr5:16288368-16289698 REVERSE   Aliases: MNF13.18, MNF13_18	4.7	3.8	0.9	3.8	45.5%	-0.7
489	AT3G24310.1   Symbol: MYB305	9.0	7.4	1.6	3.8	45.6%	-0.6
490	AT5G13980.3   similar to glycosyl hydrolase family 38 protein [Arabidopsis thaliana] (TAIR:At3g26720.1); similar to glycosyl hydrolase family 38 protein [Arabidopsis thaliana] (TAIR:At5g66150.1); similar to MA2B1_MACFA Lysosomal alpha-mannosidase precursor (Mannosidase, alpha B) (Lysosomal acid alpha-mannosidase) (Laman) (Mannosidase alpha class 2B member 1) (GB:Q60HE9); similar to hypothetical protein [Pongo pygmaeus] (GB:CAH91346.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG12505.1); similar to mannosidase, alpha, class 2B, member 1 precursor variant [Homo sapiens] (GB:BAD93158.1); similar to hypothetical protein LOC541519 [Danio rerio] (GB:NP_001014354.1); contains InterPro domain Glycoside hydrolase, family 38 (InterPro:IPR000602)   chr5:4508498-4514427 FORWARD   Aliases: MAC12.38, MAC12_38	6.5	7.6	-1.1	-3.8	45.6%	-0.6
491	AT5G13720.1   expressed protein   chr5:4427844-4429136 FORWARD   Aliases: MSH12.19, MSH12_19	6.1	5.1	1.0	3.8	45.6%	-0.6
492	AT5G58900.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:23800349-23802560 REVERSE   Aliases: K19M22.10, K19M22_10	7.4	6.4	1.1	3.8	45.6%	-0.6
493	AT3G46620.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:17189709-17191052 REVERSE   Aliases: F12A12.140	8.0	7.0	1.0	3.8	45.6%	-0.7
494	AT5G06760.1   late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein, low similarity to SP:P46515 11 kDa late embryogenesis abundant protein (DS11) {Helianthus annuus}; contains Pfam profile PF03760: Late embryogenesis abundant (LEA) group 1   chr5:2089493-2090431 REVERSE   Aliases: MPH15.12, MPH15_12	6.4	4.6	1.8	3.8	45.6%	-0.6
495	AT3G12500.1   Symbol: ATHCHIB   basic endochitinase, identical to basic endochitinase precursor SP:P19171 from (Arabidopsis thaliana)	4.2	7.2	-3.0	-3.8	45.6%	-0.6
496	AT4G16660.1   heat shock protein 70, putative / HSP70, putative   chr4:9376773-9381529 FORWARD   Aliases: DL4355W, FCAALL.64	4.4	6.6	-2.1	-3.8	45.6%	-0.6
497	AT2G28450.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:12169128-12172971 REVERSE   Aliases: T1B3.3, T1B3_3	5.3	6.9	-1.6	-3.7	45.6%	-0.6
498	AT5G62500.1   Symbol: ATEB1B	4.0	5.7	-1.7	-3.7	45.6%	-0.6
499	AT2G01180.2   Symbol: ATPAP1	5.4	4.2	1.2	3.7	45.6%	-0.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
500	AT5G65300.1   expressed protein   chr5:26112373-26112997 REVERSE   Aliases: MNA5.2, MNA5_2	6.1	4.9	1.2	3.7	45.6%	-0.6
501	AT5G37550.1   expressed protein   chr5:14936131-14937022 REVERSE   Aliases: MPA22.10, MPA22_10	6.5	5.0	1.5	3.7	45.6%	-0.6
502	AT4G01270.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:532351-534891 FORWARD   Aliases: F2N1.19, F2N1_19	3.1	3.8	-0.7	-3.7	45.8%	-0.7
503	AT3G21250.1   Symbol: ATMRP6	6.1	7.4	-1.3	-3.7	45.8%	-0.6
504	AT1G28410.1   similar to myosin heavy chain-related [Arabidopsis thaliana] (TAIR:At4g31340.1); similar to putative stress related-like protein interactor [Oryza sativa (japonica cultivar-group)] (GB:XP_483357.1); similar to unknown [Oryza sativa (japonica cultivar-group)] (GB:AAO72581.1)   chr1:9976168-9979253 REVERSE   Aliases: F3M18.15, F3M18_15	5.5	4.1	1.4	3.7	45.8%	-0.7
505	AT1G32460.1   expressed protein   chr1:11738190-11739306 FORWARD   Aliases: F5D14.24, F5D14_24	11.5	10.2	1.3	3.7	46.1%	-0.8
506	AT3G12630.1   zinc finger (AN1-like) family protein, contains Pfam domain, PF01428: AN1-like Zinc finger   chr3:4012615-4013590 FORWARD   Aliases: T2E22.6	9.9	8.3	1.6	3.7	46.1%	-0.6
507	AT3G16470.2   Symbol: JR1   similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:At1g52040.1); similar to myrosinase binding protein [Brassica napus] (GB:CAA70587.1); contains InterPro domain Jacalin-related lectin (InterPro:IPR001229)   chr3:5595902-5598033 REVERSE   Aliases: T2O4.6	5.3	7.0	-1.6	-3.7	46.3%	-0.6
508	AT3G25780.1   Symbol: AOC2   allene oxide cyclase, putative / early-responsive to dehydration protein, putative / ERD protein, putative, similar to allene oxide cyclase GI:8977961 from (Lycopersicon esculentum); similar to early-responsive to dehydration (ERD12) protein (GI:15320414); contains Pfam profile PF06351: Allene oxide cyclase   chr3:9410527-9411803 FORWARD   Aliases: ALLENE OXIDE CYCLASE 2, K13N2.12	7.6	6.1	1.4	3.7	46.3%	-0.7
509	AT5G26731.1   expressed protein   chr5:9295577-9296383 FORWARD   Aliases: None	7.6	6.4	1.2	3.7	46.8%	-0.7
510	AT3G13930.1   dihydrolipoamide S-acetyltransferase, putative, similar to dihydrolipoamide S-acetyltransferase (Zea mays) GI:5669871; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain   chr3:4595883-4600476 FORWARD   Aliases: MDC16.18	11.1	11.8	-0.8	-3.7	46.8%	-1.1
511	AT2G37040.1   Symbol: PAL1   phenylalanine ammonia-lyase 1 (PAL1), nearly identical to SP:P35510   chr2:15564455-15567442 REVERSE   Aliases: CI0004, T1J8.22, T1J8_22	7.4	9.5	-2.0	-3.7	46.8%	-0.8
512	AT1G63090.1   Symbol: ATPP2 A11   F-box family protein / SKP1 interacting partner 3-related, contains Pfam profile PF00646: F-box domain   chr1:23394728-23396502 REVERSE   Aliases: ATPP2 A11, F16M19.16, F16M19_16	6.2	4.5	1.8	3.7	46.8%	-0.6
513	AT1G10180.1   expressed protein   chr1:3338305-3341573 REVERSE   Aliases: F14N23.6, F14N23_6	7.0	8.3	-1.3	-3.7	46.9%	-0.7
514	AT5G45020.1   expressed protein   chr5:18185909-18187843 FORWARD   Aliases: K21C13.21, K21C13_21	5.2	6.0	-0.8	-3.7	47.2%	-0.8
515	AT1G03070.1   expressed protein, low similarity to N-methyl-D-aspartate receptor-associated protein (Drosophila melanogaster) GI:567104; contains Pfam profile PF01027: Uncharacterized protein family UPF0005	6.6	5.1	1.5	3.7	47.2%	-0.7
516	AT3G59580.2   similar to RWP-RK domain-containing protein [Arabidopsis thaliana] (TAIR:At2g43500.1); similar to OSJNBa0067K08.5 [Oryza sativa (japonica cultivar-group)] (GB:XP_473028.1); contains InterPro domain Plant regulator RWP-RK (InterPro:IPR003035); contains InterPro domain Octicosapeptide/Phox/Bem1p (InterPro:IPR000270)   chr3:22020190-22023743 FORWARD   Aliases: T16L24.130	4.2	3.2	1.0	3.7	48.1%	-0.7
517	AT3G23800.1   selenium-binding family protein, contains Pfam profile: PF05694 56kDa selenium binding protein (SBP56)   chr3:8581661-8583842 FORWARD   Aliases: MYM9.16	5.9	8.1	-2.1	-3.7	48.1%	-0.7
518	AT5G05200.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr5:1543606-1547138 REVERSE   Aliases: K2A11.7, K2A11_7	9.9	9.0	0.9	3.7	48.1%	-0.8
519	AT1G33410.1   expressed protein   chr1:12109600-12118808 REVERSE   Aliases: F10C21.8, F10C21_8	5.6	6.4	-0.8	-3.7	48.1%	-0.8
520	AT1G16220.1   protein phosphatase 2C family protein / PP2C family protein, similar to protein phosphatase-2C; PP2C (GI:3643088) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain;   chr1:5548647-5550547 FORWARD   Aliases: F3O9.3, F3O9_3	4.5	5.2	-0.7	-3.7	48.1%	-0.9
521	AT1G24170.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr1:8557205-8558821 REVERSE   Aliases: F3I6.10, F3I6_10	7.6	6.9	0.6	3.7	48.1%	-1.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
522	AT2G19460.1   expressed protein   chr2:8438564-8439187 FORWARD   Aliases: F27F23.23	4.8	3.2	1.6	3.7	48.1%	-0.7
523	AT2G39570.1   ACT domain-containing protein, contains Pfam ACT domain PF01842   chr2:16514974-16517276 FORWARD   Aliases: F12L6.23, F12L6_23	7.1	5.4	1.7	3.7	48.3%	-0.7
524	AT4G34360.1   protease-related, similar to PIR:I46078 endothelin converting enzyme, Bos primigenius taurus   chr4:16431945-16433962 FORWARD   Aliases: F10M10.130, F10M10_130	3.4	4.4	-1.0	-3.7	48.3%	-0.8
525	AT1G73010.1   expressed protein, similar to phosphatase, orphan 1 (GI:20196841) (Mus musculus), (GI:20196839) (Homo sapiens); contains TIGRFAM TIGR01489: 2,3-diketo-5-methylthio-1-phosphopentane phosphatase profile; contains TIGRFAM TIGR01488: HAD-superfamily hydrolase, subfamily IB (PSPase-like)   chr1:27468233-27469917 REVERSE   Aliases: F3N23.21, F3N23_21	6.6	5.1	1.4	3.7	48.3%	-0.7
526	AT1G66040.1   zinc finger (C3HC4-type RING finger) family protein, contains zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr1:24587483-24590344 REVERSE   Aliases: F15E12.8, F15E12_8	3.4	4.5	-1.0	-3.7	48.6%	-0.7
527	AT1G66050.1   zinc finger (C3HC4-type RING finger) family protein, contains zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr1:24593197-24596279 FORWARD   Aliases: F15E12.5, F15E12_5	3.4	4.5	-1.0	-3.7	48.6%	-0.7
528	AT5G39550.1   zinc finger (C3HC4-type RING finger) family protein, contains zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr5:15854636-15857731 REVERSE   Aliases: MIJ24.3, MIJ24_3	3.4	4.5	-1.0	-3.7	48.6%	-0.7
529	AT4G38340.1   RWP-RK domain-containing protein, similar to nodule inception protein GI:6448579 from (Lotus japonicus); contains Pfam profile: PF02042 RWP-RK domain   chr4:17954704-17957822 FORWARD   Aliases: F22I13.110, F22I13_110	4.4	3.5	0.9	3.7	48.6%	-0.8
530	AT4G29670.2   thioredoxin family protein, contains Pfam profile PF00085: Thioredoxin   chr4:14535613-14537244 REVERSE   Aliases: T16L4.180, T16L4_180	7.9	6.8	1.1	3.7	48.6%	-0.7
531	AT1G44575.2   Symbol: NPQ4   photosystem II 22kDa protein, chloroplast / CP22 (PSBS), identical to photosystem II 22 kDa protein, chloroplast (precursor) SP:Q9XF91 from (Arabidopsis thaliana); contains Pfam profile PF00504: Chlorophyll A-B binding protein   chr1:16874170-16875818 FORWARD   Aliases: NONPHOTOCHEMICAL QUENCHING, PSBS, T18F15.3, T18F15_3	7.2	5.5	1.7	3.7	48.6%	-0.7
532	AT2G27130.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:11602370-11603620 FORWARD   Aliases: T20P8.18, T20P8_18	5.3	6.8	-1.5	-3.7	48.6%	-0.7
533	AT2G29670.1   expressed protein   chr2:12689221-12692164 REVERSE   Aliases: T27A16.23, T27A16_23	9.5	7.9	1.6	3.7	48.7%	-0.8
534	AT3G25470.1   bacterial hemolysin-related, similar to hemolysine GB:AAD36643 from (Thermotoga maritima), contains Pfam profile: PF01479 S4 domain   chr3:9234178-9236450 FORWARD   Aliases: MWL2.14	9.0	9.5	-0.5	-3.7	48.9%	-1.1
535	AT2G29440.1   Symbol: ATGSTU6   glutathione S-transferase, putative   chr2:12627161-12628224 REVERSE   Aliases: F16P2.18, F16P2_18, GLUTATHIONE S TRANSFERASE 24, GST24	5.3	6.5	-1.2	-3.7	48.9%	-0.8
536	AT1G71380.1   glycosyl hydrolase family 9 protein, similar to beta-glucanase GB:AAB72171   chr1:26903446-26905451 REVERSE   Aliases: F3I17.16, F3I17_16	2.5	3.0	-0.5	-3.6	49.0%	-1.2
537	AT5G01670.2   aldose reductase, putative, similar to aldose reductase (Hordeum vulgare)(GI:728592), aldose reductase ALDRXV4 (Xerophyta viscosa)(GI:4539944)   chr5:251975-253957 FORWARD   Aliases: F7A7.190, F7A7_190	7.6	6.3	1.2	3.6	49.0%	-0.7
538	AT3G62420.1   bZIP transcription factor family protein, similar to common plant regulatory factor 6 GI:9650826 from (Petroselinum crispum)   chr3:23102820-23103260 REVERSE   Aliases: T12C14.120	9.5	8.6	0.9	3.6	49.0%	-0.9
539	AT5G47640.1   CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3 ) (AHAP3) family (Hap3b), similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP:P25209) (GI:22380) (Zea mays); contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; identical to cDNA transcription factor Hap3b (Hap3b) mRNA, partial cds GI:9965734   chr5:19326453-19327494 FORWARD   Aliases: MNJ7.23, MNJ7_23	6.7	5.7	1.0	3.6	49.1%	-0.8
540	AT1G65900.1   expressed protein   chr1:24519509-24522111 REVERSE   Aliases: F12P19.7, F12P19_7	3.5	4.2	-0.8	-3.6	49.2%	-0.9
541	AT1G15010.1   expressed protein   chr1:5171202-5171737 FORWARD   Aliases: T15D22.5, T15D22_5	3.2	2.4	0.8	3.6	49.2%	-0.9
542	AT2G34140.1   Dof-type zinc finger domain-containing protein   chr2:14421120-14421805 REVERSE   Aliases: T14G11.26, T14G11_26	7.0	6.1	0.9	3.6	49.4%	-0.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
543	AT1G07440.2   similar to short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] (TAIR:At2g29340.2); similar to short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] (TAIR:At2g29340.1); similar to putative pfam00106, adh_short, short chain dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:NP_912375.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)   chr1:2286146-2287727 REVERSE   Aliases: F22G5.39, F22G5_39	6.4	4.9	1.5	3.6	49.9%	-0.8
544	AT3G02660.1   tRNA synthetase class I (W and Y) family protein, similar to SP:P00952 Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosine--tRNA ligase) (TyrRS) {Bacillus stearothermophilus}; contains Pfam profiles PF00579: tRNA synthetases class I (W and Y), PF01479: S4 domain   chr3:570153-572341 REVERSE   Aliases: F16B3.29, F16B3_29	4.2	5.2	-0.9	-3.6	50.6%	-0.9
545	AT1G444800.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575; contains Pfam profile PF00892: Integral membrane protein   chr1:16916449-16919436 REVERSE   Aliases: T12C22.7, T12C22_7	6.6	4.7	1.9	3.6	50.6%	-0.8
546	AT1G09070.1   C2 domain-containing protein / src2-like protein, putative, similar to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain; identical to cDNA src2-like protein GI:3426059   chr1:2927706-2928971 FORWARD   Aliases: F7G19.6, F7G19_6	7.3	4.5	2.8	3.6	50.7%	-0.8
547	AT1G63470.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr1:23540212-23542885 REVERSE   Aliases: F2K11.28, F2K11_28	6.5	8.0	-1.4	-3.6	51.2%	-0.8
548	AT2G07170.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g27060.1); similar to potyviral helper component protease-interacting protein 2 [Solanum tuberosum subsp. andigena] (GB:CAD45375.1); contains InterPro domain Arabidopsis thaliana protein of unknown function DUF813 (InterPro:IPR008531)   chr2:2975562-2978817 FORWARD   Aliases: T25N22.13, T25N22_13	3.4	4.1	-0.7	-3.6	51.2%	-1.0
549	AT5G01230.2   FtsJ-like methyltransferase family protein, contains Pfam profile: PF01728 FtsJ-like methyltransferase   chr5:92600-95685 REVERSE   Aliases: F7J8.210, F7J8_210	5.6	6.5	-0.9	-3.6	51.3%	-0.9
550	AT3G59710.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short chain dehydrogenase/reductase SDR family   chr3:22065914-22068133 REVERSE   Aliases: T16L24.260	2.7	3.3	-0.6	-3.6	51.3%	-1.0
551	AT3G12740.1   LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein, Similar to GI:4585976; GI:4966357; GI:4835763; GI:9757735 from (Arabidopsis thaliana)   chr3:4049522-4052050 FORWARD   Aliases: MBK21.12	9.9	9.1	0.7	3.6	51.3%	-1.1
552	AT1G17180.1   Symbol: ATGSTU25   glutathione S-transferase, putative, Second of three repeated putative glutathione transferases. 72% identical to glutathione transferase (Arabidopsis thaliana) (gi:4006934). Location of ests 191A10T7 (gb:R90188) and 171N13T7 (gb:R65532)   chr1:5872142-5873079 FORWARD   Aliases: F20D23.12, F20D23_12	4.3	6.0	-1.6	-3.6	51.3%	-0.9
553	AT4G09800.1   Symbol: RPS18C	10.8	11.5	-0.6	-3.6	51.3%	-1.4
554	AT2G16200.1   expressed protein   chr2:7031806-7032186 FORWARD   Aliases: F7H1.22, F7H1_22	3.7	2.9	0.8	3.6	51.3%	-1.0
555	AT5G10580.2   expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599   chr5:3347438-3350072 FORWARD   Aliases: F12B17.70, F12B17_70	5.8	4.2	1.6	3.6	51.3%	-0.9
556	AT2G47910.2   expressed protein   chr2:19621768-19622839 FORWARD   Aliases: F17A22.30, F17A22.40, F17A22_30, F17A22_40	4.4	3.7	0.7	3.6	51.3%	-1.0
557	AT5G60780.1   Symbol: ATNRT2.3   high-affinity nitrate transporter, putative, similar to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362   chr5:24468065-24469982 FORWARD   Aliases: MAE1.4, MAE1_4	5.4	3.4	2.0	3.6	51.3%	-0.9
558	AT5G25880.1   malate oxidoreductase, putative, similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP:P12628) {Phaseolus vulgaris}	3.4	4.4	-1.0	-3.6	51.3%	-0.9
559	AT3G26460.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr3:9685110-9685894 REVERSE   Aliases: F20C19.18	3.7	5.5	-1.8	-3.6	51.6%	-0.8
560	AT3G18280.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to TED4 (Zinnia elegans) GI:493721; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	8.4	10.1	-1.7	-3.6	51.6%	-1.2
561	AT5G43780.1   Symbol: APS4   sulfate adenylyltransferase 4 / ATP-sulfurylase 4 (APS4), identical to ATP sulfurylase precursor (APS4) (Arabidopsis thaliana) GI:4633131   chr5:17606418-17608762 REVERSE   Aliases: MQD19.13, MQD19_13	6.3	8.2	-2.0	-3.6	51.6%	-0.8
562	AT3G01330.1   Symbol: DEL3   transcription factor, putative / E2F-like repressor E2L2 (E2L2), identical to E2F-like repressor E2L2 (Arabidopsis thaliana) GI:20502506	3.6	4.2	-0.6	-3.6	51.6%	-1.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
563	AT5G22840.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:7630720-7633226 REVERSE   Aliases: MRN17.7, MRN17_7	4.1	5.3	-1.2	-3.6	51.7%	-0.8
564	AT3G20670.1   histone H2A, putative, strong similarity to histone H2A GB:AAF64418 GI:7595337 from Arabidopsis thaliana, Triticum aestivum GI:536892; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr3:7229417-7230508 FORWARD   Aliases: F3H11.6	7.8	9.9	-2.2	-3.6	51.7%	-0.8
565	AT3G52800.1   zinc finger (AN1-like) family protein, contains Pfam domain, PF01428: AN1-like Zinc finger   chr3:19580289-19581660 FORWARD   Aliases: F3C22.200	6.9	5.4	1.5	3.6	51.7%	-0.8
566	AT5G54280.1   Symbol: ATM2   myosin heavy chain, putative, similar to myosin (Arabidopsis thaliana) gi:499045:emb:CAA84065   chr5:22055583-22062468 REVERSE   Aliases: ARABIDOPSIS THALIANA MYOSIN 4, ATATM2, ATM4, ATMYOS1, MDK4.10, MDK4_10, MYOSIN 4	4.4	5.8	-1.4	-3.6	51.7%	-0.9
567	AT5G63030.1   glutaredoxin, putative, similar to glutaredoxin (Ricinus communis) gi:1732424:emb:CAA89699   chr5:25303511-25304906 FORWARD   Aliases: MJH22.9, MJH22_9	10.2	9.3	0.8	3.6	51.7%	-1.0
568	AT1G10070.3   similar to branched-chain amino acid aminotransferase 5 / branched-chain amino acid transaminase 5 (BCAT5) [Arabidopsis thaliana] (TAIR:At5g65780.1); similar to branched-chain amino acid aminotransferase [Solanum tuberosum] (GB:AAF07192.1); contains InterPro domain Aminotransferase, class IV (InterPro:IPR001544); contains InterPro domain Branched-chain amino acid aminotransferase II (InterPro:IPR005786)   chr1:3288089-3290841 FORWARD   Aliases: T2711.9, T2711_9	5.5	3.8	1.8	3.6	51.7%	-0.8
569	AT2G21560.1   expressed protein, contains weak similarity to reticulocyte-binding protein 2 homolog A (Plasmodium falciparum) gi:9754767:gb:AAF98066   chr2:9237348-9238588 REVERSE   Aliases: F2G1.17, F2G1_17	11.2	9.3	1.9	3.6	51.7%	-0.9
570	AT5G06050.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr5:1820135-1823771 FORWARD   Aliases: K18J17.25, K18J17_25	6.0	7.2	-1.2	-3.6	51.9%	-0.8
571	AT1G56110.1   Symbol: NOP56   nucleolar protein Nop56, putative, similar to XNop56 protein (Xenopus laevis) GI:14799394; contains Pfam profile PF01798: Putative snoRNA binding domain   chr1:20988055-20990614 REVERSE   Aliases: NOP56 LIKE PROTEIN, T6H22.10, T6H22_10	7.5	9.0	-1.5	-3.6	51.9%	-0.8
572	AT5G04490.1   phosphatidate cytidyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidyltransferase   chr5:1279761-1281670 FORWARD   Aliases: T32M21.90, T32M21_90	5.6	4.4	1.2	3.6	51.9%	-0.8
573	AT1G70710.1   Symbol: CEL1   endo-1,4-beta-glucanase (EGASE) / cellulase, identical to endo-1,4-beta-glucanase GB:CAA67157 GI:2440035 from (Arabidopsis thaliana)   chr1:26662794-26666662 REVERSE   Aliases: F5A18.11, F5A18_11	3.5	5.6	-2.1	-3.6	51.9%	-0.9
574	AT5G19875.1   expressed protein   chr5:6718343-6718997 FORWARD   Aliases: None	7.4	6.2	1.2	3.6	51.9%	-0.9
575	AT4G20430.1   subtilase family protein, contains Pfam profile: PF00082 subtilase family   chr4:11017667-11021116 REVERSE   Aliases: F9F13.80, F9F13_80	4.2	5.2	-0.9	-3.6	52.1%	-0.9
576	AT2G33830.2   dormancy/auxin associated family protein, contains Pfam profile: PF05564 dormancy/auxin associated protein   chr2:14316600-14317417 REVERSE   Aliases: T1B8.13, T1B8_13	8.6	6.8	1.8	3.6	52.1%	-0.9
577	AT4G19540.1   expressed protein   chr4:10657393-10659243 FORWARD   Aliases: F24J7.100, F24J7_100	5.5	6.5	-0.9	-3.6	52.1%	-0.9
578	AT3G06035.1   expressed protein   chr3:1823105-1824188 REVERSE   Aliases: None	8.3	9.4	-1.1	-3.6	52.1%	-0.9
579	AT5G06980.2   expressed protein   chr5:2167624-2169392 FORWARD   Aliases: MOJ9.15, MOJ9_15	6.8	5.2	1.6	3.6	52.2%	-0.9
580	AT2G41820.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:17453822-17457149 FORWARD   Aliases: T11A7.8, T11A7_8	5.1	5.8	-0.7	-3.6	52.4%	-1.0
581	AT5G64710.2   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr5:25887071-25889455 FORWARD   Aliases: MVP7.3, MVP7_3	3.0	3.6	-0.6	-3.5	52.8%	-1.1
582	AT4G17670.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);   chr4:9833681-9834740 REVERSE   Aliases: DL4870C, FCAALL.414	7.2	5.7	1.6	3.5	52.8%	-0.9
583	AT4G27990.1   YGGT family protein, contains Pfam profile PF02325: YGGT family (unknown function)   chr4:13923779-13924698 REVERSE   Aliases: T13J8.100, T13J8_100	6.2	4.5	1.7	3.5	53.1%	-0.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
584	AT3G19580.1   Symbol: AZF2   zinc finger (C2H2 type) protein 2 (AZF2), identical to Cys2/His2-type zinc finger protein 2 (Arabidopsis thaliana) gi:6009885:dbj:BAA85107   chr3:6803172-6804239 REVERSE   Aliases: ARABIDOPSIS ZINC FINGER PROTEIN 2, MMB12.27	5.6	4.4	1.2	3.5	53.2%	-0.9
585	AT3G15450.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g27450.1); similar to unknown [Asparagus officinalis] (GB:CAA54526.1)   chr3:5213004-5214126 FORWARD   Aliases: MJK13.11	7.5	6.3	1.1	3.5	53.2%	-0.9
586	AT2G33850.1   expressed protein, contains 1 transmembrane domain; similar to Protein E6 (Swiss-Prot:Q01197) (Gossypium hirsutum)   chr2:14328138-14329125 REVERSE   Aliases: T1B8.15, T1B8_15	2.8	4.0	-1.2	-3.5	53.2%	-0.9
587	AT2G19770.1   profilin 4 (PRO4) (PFN4), identical to profilin 4 SP:Q38905 GI:1353768 from (Arabidopsis thaliana)   chr2:8526720-8528274 REVERSE   Aliases: F6F22.20, F6F22_20	4.5	3.2	1.3	3.5	53.2%	-0.9
588	AT4G36040.1   DNAJ heat shock N-terminal domain-containing protein (J11), identical to dnaJ heat shock protein J11 (Arabidopsis thaliana) GI:9843641; contains Pfam profile PF00226 DnaJ domain   chr4:17049174-17050277 REVERSE   Aliases: T19K4.170, T19K4_170	6.3	4.5	1.9	3.5	53.2%	-0.9
589	AT5G64670.1   ribosomal protein L15 family protein   chr5:25869493-25871215 REVERSE   Aliases: MUB3.19, MUB3_19	7.7	8.6	-0.9	-3.5	53.2%	-0.9
590	AT4G01700.1   chitinase, putative, similar to peanut type II chitinase GI:1237025 from (Arachis hypogaea)   chr4:732010-733510 REVERSE   Aliases: T15B16.5, T15B16_5	6.0	9.2	-3.1	-3.5	53.2%	-0.9
591	AT5G28150.1   expressed protein   chr5:10135475-10136981 FORWARD   Aliases: T24G3.80, T24G3_80	6.5	7.3	-0.8	-3.5	53.2%	-1.1
592	AT1G80110.1   Symbol: ATPP2 B11   expressed protein, contains similarity to SKP1 interacting partner 3 (Arabidopsis thaliana) GI:10716951   chr1:30140274-30141848 FORWARD   Aliases: ATPP2 B11, F18B13.19, F18B13_19	4.9	4.1	0.8	3.5	53.2%	-1.0
593	AT2G38480.1   integral membrane protein, putative, contains 4 transmembrane domains; contains plant integral membrane protein domain, TIGR01569 and PF04535; Domain of unknown function (DUF588); At3g16300, At1g45222 both share this domain structure; distantly related to GP:14030504 salicylic acid-induced fragment 1 protein {Gossypium hirsutum}; similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)   chr2:16117342-16118875 REVERSE   Aliases: T19C21.23	4.6	3.8	0.8	3.5	53.2%	-1.0
594	AT3G13520.1   Symbol: AGP12   arabinogalactan-protein (AGP12), identical to gi:10880501:gb:AAG24280   chr3:4408932-4409447 FORWARD   Aliases: ARABINO GALACTAN PROTEIN 12, MRP15.18	12.4	11.6	0.8	3.5	53.3%	-1.5
595	AT4G24110.1   expressed protein   chr4:12519942-12520823 REVERSE   Aliases: T19F6.100, T19F6_100	8.9	5.2	3.7	3.5	53.3%	-1.0
596	AT2G30040.1   Symbol: MAPKKK14   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:12828787-12830246 FORWARD   Aliases: F23F1.4, F23F1_4	5.6	4.2	1.3	3.5	53.3%	-0.9
597	AT3G62550.1   universal stress protein (USP) family protein, similar to ER6 protein (Lycopersicon esculentum) GI:5669654; contains Pfam profile PF00582: universal stress protein family   chr3:23146960-23148146 FORWARD   Aliases: T12C14.250	5.0	3.6	1.4	3.5	53.3%	-0.9
598	AT1G48470.1   Symbol: GLN1;5	6.5	4.8	1.7	3.5	53.3%	-0.9
599	AT1G74790.1   expressed protein, contains similarity to hedgehog-interacting protein GI:4868122 from (Mus musculus)   chr1:28102471-28105557 FORWARD   Aliases: F25A4.24, F25A4_24	4.8	5.8	-1.0	-3.5	53.3%	-0.9
600	AT3G47500.1   Dof-type zinc finger domain-containing protein, identical to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana)	7.2	6.5	0.7	3.5	53.7%	-1.0
601	AT2G20920.1   expressed protein   chr2:9005767-9007013 FORWARD   Aliases: F5H14.11, F5H14_11	9.5	8.6	0.9	3.5	53.7%	-1.1
602	AT1G20950.1   pyrophosphate--fructose-6-phosphate 1-phosphotransferase-related / pyrophosphate-dependent 6-phosphofructose-1-kinase-related, similar to pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit SP:Q41140 from (Ricinus communis)   chr1:7297228-7301404 REVERSE   Aliases: F9H16.6, F9H16_6	6.0	8.5	-2.6	-3.5	53.7%	-0.9
603	AT4G12070.1   expressed protein   chr4:7231816-7234495 FORWARD   Aliases: F16J13.140, F16J13_140	5.1	4.2	0.9	3.5	53.9%	-1.0
604	AT5G65070.1   Symbol: MAF4   MADS-box protein (MAF4), contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain); contains Pfam profile PF01486: K-box region	3.3	2.7	0.6	3.5	53.9%	-1.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
605	AT1G28370.1   Symbol: ATERF11/ERF11   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.   chr1:9955955-9956926 REVERSE   Aliases: ATERF11, ERF11, F3M18.20, F3M18_20	5.7	4.1	1.6	3.5	54.0%	-1.0
606	AT3G60490.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr3:22360502-22361346 FORWARD   Aliases: T8B10.150	4.4	3.4	1.0	3.5	54.0%	-1.0
607	AT1G26830.1   Symbol: ATCUL3/ATCUL3A/CUL3/CUL3A   Cullin, putative, similar to Cullin homolog 3 (CUL-3) SP:Q13618, GI:3639052 from (Homo sapiens); contains Pfam profile PF00888: Cullin family. Interacts with other components of E3 ligase complex suggesting it functions in RUB-modification. Forms complexes with BTB domain proteins forming a novel class of E3-based ubiquitin protein-ligase complexes. Mutant is early flowering and has a reduced sensitivity to far-red light. cul3a/cul3b homozygous/heterozygous plants are embryo lethal.   chr1:9295766-9298525 FORWARD   Aliases: ATCUL3, ATCUL3A, CUL3, CUL3A, T24P13.25	7.1	8.4	-1.3	-3.5	54.0%	-0.9
608	AT5G13170.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula); identical to cDNA senescence-associated protein (SAG29) mRNA, partial cds GI:4426938   chr5:4181045-4183309 REVERSE   Aliases: T19L5.130, T19L5_130	6.0	4.3	1.7	3.5	54.0%	-0.9
609	AT3G29170.1   expressed protein, contains Pfam PF05915: Eukaryotic protein of unknown function (DUF872)   chr3:11137243-11139086 REVERSE   Aliases: MXE2.17	7.6	6.8	0.9	3.5	54.0%	-1.0
610	AT3G02980.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile: PF00583 acetyltransferase (GNAT) family   chr3:670904-672222 REVERSE   Aliases: F13E7.7, F13E7_7	5.0	4.3	0.8	3.5	54.0%	-1.0
611	AT1G26770.1   Symbol: ATEXPA10   expansin, putative (EXP10), similar to expansin At-EXP1 GI:1041702 from (Arabidopsis thaliana); alpha-expansin gene family, PMID:11641069   chr1:9259592-9261300 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A10, AT EXP10, ATEXP10, ATHEXP ALPHA 1.1, EXP10, EXPANSIN 10, T24P13.15, T24P13_15	6.4	4.5	1.9	3.5	54.0%	-0.9
612	AT5G08330.1   TCP family transcription factor, putative, similar to PCF1 (GI:2580438) and PCF2 ((GI:2580440) Oryza sativa) ; auxin-induced basic helix-loop-helix transcription factor, Gossypium hirsutum, EMBL:AF165924   chr5:2680745-2681814 FORWARD   Aliases: F8L15.60, F8L15_60	5.1	4.2	0.9	3.5	54.1%	-1.0
613	AT4G16980.1   arabinogalactan-protein family, similar to arabinogalactan protein (Arabidopsis thaliana) gi:10880495:gb:AAG24277; contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:9556997-9557831 FORWARD   Aliases: DL4520C, FCAALL.321	2.9	3.9	-1.0	-3.5	54.3%	-1.0
614	AT1G11790.2   similar to prephenate dehydratase family protein [Arabidopsis thaliana] (TAIR:At3g07630.2); similar to prephenate dehydratase family protein [Arabidopsis thaliana] (TAIR:At3g07630.1); similar to putative prephenate dehydratase [Oryza sativa (japonica cultivar-group)] (GB:XP_479626.1); contains InterPro domain Prephenate dehydratase (InterPro:IPR001086)   chr1:3981247-3985214 FORWARD   Aliases: F25C20.4, F25C20_4	6.0	7.1	-1.1	-3.5	54.3%	-1.0
615	AT5G23750.2   remorin family protein, contains Pfam domain, PF03766: Remorin, N-terminal region; contains Pfam domain, PF03763: Remorin, C-terminal region   chr5:8009812-8011614 REVERSE   Aliases: MRO11.21, MRO11_21	6.4	5.1	1.4	3.5	54.3%	-0.9
616	AT1G69380.1   expressed protein, predicated by genscan+   chr1:26085004-26087269 REVERSE   Aliases: F23O10.4, F23O10_4	5.5	6.8	-1.3	-3.5	54.3%	-0.9
617	AT4G20380.6   Symbol: LSD1   similar to zinc finger protein, putative [Arabidopsis thaliana] (TAIR:At1g32540.1); similar to zinc finger protein, putative [Arabidopsis thaliana] (TAIR:At1g32540.2); similar to zinc finger protein LSD2 [Brassica oleracea] (GB:AAL50982.1); contains InterPro domain Zn-finger, LSD1 type (InterPro:IPR005735)   chr4:11004558-11006799 FORWARD   Aliases: F9F13.30, F9F13_30, LESION SIMULATING DISEASE	8.4	7.3	1.1	3.5	54.3%	-1.0
618	AT5G18850.1   expressed protein   chr5:6286862-6287592 FORWARD   Aliases: F17K4.100, F17K4_100	7.0	6.1	0.9	3.5	54.3%	-1.0
619	AT2G17340.1   pantothenate kinase-related, contains Pfam domain, PF01937: Protein of unknown function; supported by tandem duplication of pantothenate kinase-related protein (TIGR_Ath1:At2g17320) (Arabidopsis thaliana)   chr2:7548494-7551196 REVERSE   Aliases: F5J6.10, F5J6_10	7.8	8.7	-0.9	-3.5	54.4%	-1.1
620	AT1G61890.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:22871438-22874945 REVERSE   Aliases: F8K4.9, F8K4_9	7.1	5.5	1.6	3.5	54.6%	-1.0
621	AT1G35140.1   Symbol: PHI 1   phosphate-responsive protein, putative, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr1:12851975-12853103 FORWARD   Aliases: PHOSPHATE INDUCED 1, T32G9.32, T32G9_32	7.0	5.4	1.6	3.5	54.7%	-1.1
622	AT1G43910.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr1:16658044-16660096 REVERSE   Aliases: F9C16.7, F9C16_7	8.6	6.6	2.0	3.5	54.7%	-1.0
623	AT2G05120.1   expressed protein   chr2:1841906-1846855 REVERSE   Aliases: F5G3.2, F5G3_2	3.2	3.9	-0.7	-3.5	54.7%	-1.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
624	AT3G57770.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr3:21408519-21409830 FORWARD   Aliases: F15B8.40	4.5	3.1	1.4	3.5	54.8%	-1.0
625	AT3G62050.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr3:22989221-22989994 FORWARD   Aliases: T17J13.10	4.8	5.9	-1.1	-3.5	54.8%	-1.0
626	AT2G04795.1   expressed protein   chr2:1682950-1683472 FORWARD   Aliases: None	8.5	7.4	1.1	3.5	54.9%	-1.0
627	AT2G26400.1   acireductone dioxygenase (ARD/ARD') family protein, similar to iron-deficiency induced gene (Hordeum vulgare) GI:14522834, SIPL (Homo sapiens) GI:16551383; contains Pfam profile PF03079: ARD/ARD' family   chr2:11238925-11240352 REVERSE   Aliases: T9J22.7, T9J22_7	7.4	5.9	1.5	3.5	54.9%	-1.0
628	AT4G17340.1   Symbol: DELTA TIP2/TIP2;2   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr4:9699265-9700421 FORWARD   Aliases: DELTA TIP2, DL4705W, FCAALL.412, TIP2;2	6.1	4.5	1.5	3.5	54.9%	-1.0
629	AT1G68600.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.6	3.0	0.6	3.5	54.9%	-1.3
630	AT3G47620.1   TCP family transcription factor, putative, auxin-induced basic helix-loop-helix transcription factor - Gossypium hirsutum, EMBL:AF165924	8.0	7.1	1.0	3.5	55.1%	-1.0
631	AT1G05340.1   expressed protein   chr1:1558849-1559757 REVERSE   Aliases: YUP8H12.4, YUP8H12_4	5.8	3.4	2.5	3.5	55.2%	-1.0
632	AT1G23880.1   NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	3.6	4.1	-0.6	-3.5	55.4%	-1.3
633	AT3G27540.1   glycosyl transferase family 17 protein, low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus (SP:Q10470), Rattus norvegicus (SP:Q02527), Homo sapiens (SP:Q09327) ; contains Pfam profile PF04724 :Glycosyltransferase family 17   chr3:10206545-10208543 FORWARD   Aliases: MMJ24.9	4.1	3.3	0.8	3.5	55.5%	-1.1
634	AT4G21870.1   26.5 kDa class P-related heat shock protein (HSP26.5-P), contains Pfam profile: PF00011 Hsp20/alpha crystallin family: identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.   chr4:11603582-11604343 REVERSE   Aliases: T8O5.80, T8O5_80	8.0	6.7	1.3	3.5	55.5%	-1.0
635	AT3G14650.1   Symbol: CYP72A11   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4922138-4924695 FORWARD   Aliases: MIE1.15	5.4	4.1	1.2	3.5	55.5%	-1.0
636	AT3G06480.1   DEAD box RNA helicase, putative, similar to RNA helicase DRH1 (Arabidopsis thaliana) GI:3149952; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF00397: WW domain   chr3:1985461-1990159 REVERSE   Aliases: F24P17.2, F24P17_2	5.6	4.2	1.4	3.5	55.5%	-1.0
637	AT1G59540.1   Symbol: ZCF125	2.7	3.2	-0.6	-3.4	55.5%	-1.3
638	AT3G19900.1   expressed protein   chr3:6922574-6925029 REVERSE   Aliases: MPN9.15	6.0	4.9	1.2	3.4	55.5%	-1.0
639	AT3G54560.1   histone H2A.F/Z, identical to GI:2407800	6.9	9.1	-2.2	-3.4	55.6%	-1.0
640	AT4G36710.1   scarecrow transcription factor family protein   chr4:17305762-17307647 FORWARD   Aliases: AP22.56, AP22_56	8.2	6.6	1.6	3.4	55.6%	-1.0
641	AT5G48850.1   male sterility MS5 family protein, similar to male sterility MS5 (Arabidopsis thaliana) GI:3859112; contains Pfam profile PF00515 TPR Domain   chr5:19822663-19824985 REVERSE   Aliases: K24G6.19, K24G6_19	4.2	6.3	-2.1	-3.4	55.6%	-1.0
642	AT4G39650.1   similar to gamma-glutamyltranspeptidase family protein [Arabidopsis thaliana] (TAIR:At4g39640.2); similar to gamma-glutamyltranspeptidase family protein [Arabidopsis thaliana] (TAIR:At4g39640.1); similar to gamma-glutamyl transferase [Raphanus sativus] (GB:BAC45233.1); similar to OSJNBa0036B21.10 [Oryza sativa (japonica cultivar-group)] (GB:XP_472730.1); similar to gamma-glutamyltransferase [Allium cepa] (GB:AAL61611.2); contains InterPro domain Gamma-glutamyltranspeptidase (InterPro:IPR000101)   chr4:18403554-18406019 FORWARD   Aliases: T19P19.40, T19P19_40	4.1	3.4	0.7	3.4	55.6%	-1.1
643	AT1G32920.1   expressed protein   chr1:11928787-11929281 FORWARD   Aliases: F9L11.25, F9L11_25	9.0	6.9	2.1	3.4	56.1%	-1.0
644	AT2G27290.1   expressed protein   chr2:11685478-11686870 REVERSE   Aliases: F12K2.13, F12K2_13	5.5	4.6	0.9	3.4	56.1%	-1.0
645	AT3G57880.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr3:21441993-21445363 REVERSE   Aliases: T10K17.90	6.0	5.1	1.0	3.4	56.1%	-1.0
646	AT1G01780.1   LIM domain-containing protein, similar to PGPS/D1 (Petunia x hybrida) GI:4105772, LIM domain protein PLIM1 (Nicotiana tabacum) GI:5932418; contains Pfam profile PF00412: LIM domain   chr1:282772-284082 FORWARD   Aliases: T1N6.19, T1N6_19	5.8	5.0	0.8	3.4	56.1%	-1.2
647	AT5G01350.1   expressed protein   chr5:145635-147199 REVERSE   Aliases: T10O8.60, T10O8_60	11.5	10.6	0.9	3.4	56.1%	-1.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
648	AT3G03320.1   expressed protein, similar to hypothetical protein GB:BAA29429 (Pyrococcus horikoshii)   chr3:781722-783471 FORWARD   Aliases: T21P5.26, T21P5_26	4.9	6.2	-1.4	-3.4	56.1%	-1.0
649	AT5G25360.1   expressed protein   chr5:8799713-8802649 REVERSE   Aliases: F18G18.100, F18G18_100	7.7	5.9	1.8	3.4	56.1%	-1.0
650	AT2G16500.1   Symbol: ADC1   arginine decarboxylase 1 (SPE1) (ARGDC), identical to SP:Q95I64 Arginine decarboxylase 1 (EC 4.1.1.19) (ARGDC 1) (ADC 1) (ADC-O) {Arabidopsis thaliana}   chr2:7157704-7160421 REVERSE   Aliases: ARGDC, ARGDC1, ARGININE DECARBOXYLASE, ARGININE DECARBOXYLASE 1, F1P15.12, F1P15_12	7.7	9.1	-1.4	-3.4	56.1%	-1.0
651	AT1G80050.1   Symbol: APT2   adenine phosphoribosyltransferase 2 (APT2), identical to SP:Q42563 Adenine phosphoribosyltransferase 2 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}   chr1:30116407-30118217 REVERSE   Aliases: ADENINE PHOSPHORIBOSYL TRANSFERASE 2, ATAPT2, F18B13.14, F18B13_14	4.4	5.5	-1.1	-3.4	56.1%	-1.1
652	AT3G04640.1   glycine-rich protein, predicted proteins, Arabidopsis thaliana   chr3:1260912-1261689 REVERSE   Aliases: F7O18.12, F7O18_12	6.3	4.7	1.5	3.4	56.5%	-1.0
653	AT3G60070.1   lactose permease-related, contains weak similarity to Lactose permease (Lactose-proton symport) (Lactose transport protein). (Swiss-Prot:O33814) (Staphylococcus xylosus)   chr3:22194220-22197305 REVERSE   Aliases: T2O9.50	7.9	7.3	0.6	3.4	56.5%	-1.2
654	AT3G19740.1   similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At1g50140.1); similar to spastin-like [Oryza sativa (japonica cultivar-group)] (GB:BAD37292.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr3:6855843-6859040 REVERSE   Aliases: MMB12.22	9.2	9.9	-0.7	-3.4	56.6%	-1.2
655	AT1G65060.2   Symbol: 4CL3   4-coumarate--CoA ligase 3 / 4-coumaroyl-CoA synthase 3 (4CL3), identical to SP:Q9S777 4-coumarate--CoA ligase 3 (EC 6.2.1.12) (4CL3) (4-coumaroyl-CoA synthase 3) {Arabidopsis thaliana}   chr1:24170890-24175165 REVERSE   Aliases: 4 COUMARATE:COA LIGASE, F16G16.6, F16G16_6	4.5	6.0	-1.4	-3.4	56.6%	-1.0
656	AT5G61330.1   rRNA processing protein-related, contains weak similarity to rRNA processing protein EBP2 (EBNA1-binding protein homolog) (Swiss-Prot:P36049) (Saccharomyces cerevisiae)	8.1	7.3	0.8	3.4	56.6%	-1.2
657	AT5G10180.1   Symbol: AST68   sulfate transporter, identical to sulfate transporter (Arabidopsis thaliana) GI:2114104	6.0	8.1	-2.1	-3.4	56.7%	-1.0
658	AT3G47510.1   expressed protein   chr3:17522084-17522600 FORWARD   Aliases: F1P2.60	8.8	8.0	0.8	3.4	56.7%	-1.3
659	AT1G02300.1   cathepsin B-like cysteine protease, putative, similar to cathepsin B-like cysteine proteinase GI:609175 from (Nicotiana rustica)	6.9	5.5	1.4	3.4	56.7%	-1.1
660	AT2G30990.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g29240.1); similar to B1131G08.12 [Oryza sativa (japonica cultivar-group)] (GB:NP_916200.1); contains InterPro domain Protein of unknown function DUF688 (InterPro:IPR007789)   chr2:13194660-13197496 REVERSE   Aliases: F7F1.20, F7F1_20	5.8	4.8	1.0	3.4	56.7%	-1.2
661	AT1G14685.3   expressed protein   chr1:5042583-5044289 FORWARD   Aliases: F10B6.5, F10B6_5	7.0	6.2	0.8	3.4	56.7%	-1.2
662	AT5G05730.1   Symbol: ASA1   anthranilate synthase, alpha subunit, component I-1 (ASA1), identical to SP:P32068   chr5:1719574-1722904 REVERSE   Aliases: A METHYL TRYPTOPHAN RESISTANT 1, AMT1, ANTHRANILATE SYNTHASE ALPHA SUBUNIT, ANTHRANILATE SYNTHASE ALPHA SUBUNIT 1, MJJ3.14, MJJ3_14, TRP5, TRYPTOPHAN BIOSYNTHESIS 5, WEI2	10.4	11.1	-0.7	-3.4	56.7%	-1.5
663	AT4G30190.1   Symbol: AHA2   ATPase 2, plasma membrane-type, putative / proton pump 2, putative / proton-exporting ATPase, putative, strong similarity to SP:P19456 ATPase 2, plasma membrane-type (EC 3.6.3.6) (Proton pump 2) {Arabidopsis thaliana}; contains InterPro accession IPR001757: ATPase, E1-E2 type; contains Pfam profile PF00690: Cation transporter/ATPase, N-terminus   chr4:14770505-14776059 REVERSE   Aliases: F9N11.40, F9N11_40, P TYPE H(+) ATPASE ISOFORM 2, PMA2	10.4	11.5	-1.1	-3.4	57.0%	-1.4
664	AT3G60420.1   expressed protein   chr3:22345406-22346760 FORWARD   Aliases: T8B10.80	3.8	2.4	1.3	3.4	57.1%	-1.2
665	AT1G10780.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:3592747-3595078 REVERSE   Aliases: T16B5.8	3.3	3.9	-0.6	-3.4	57.1%	-1.4
666	AT4G30850.2   expressed protein, contains Pfam domain, PF03006: Uncharacterised protein family (Hly-III / UPF0073)   chr4:15020188-15022451 REVERSE   Aliases: F6I18.240, F6I18_240	6.9	8.0	-1.1	-3.4	57.1%	-1.1
667	AT1G43700.1   Symbol: VIP1   VirE2-interacting protein (VIP1), identical to VirE2-interacting protein VIP1 GB:AAF37279 GI:7258340 from (Arabidopsis thaliana)	8.2	6.8	1.4	3.4	57.1%	-1.1
668	AT4G09010.1   L-ascorbate peroxidase, chloroplast, putative, identical to SP:P82281:TL29_ARATH (EC 1.11.1.11) {Arabidopsis thaliana}; ascorbate peroxidase - Spinacia oleracea, (gi:1669585); contains Pfam domain PF00141: Peroxidase; contains TIGRfam domain TIGR01409: Tat (twin-arginine translocation) pathway signal sequence; identical to ascorbate peroxidase APX4 (AT4g09010) mRNA, partial cds GI:31980499   chr4:5777080-5779418 REVERSE   Aliases: F23J3.40, F23J3_40	8.4	9.7	-1.4	-3.4	57.4%	-1.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
669	AT1G11360.2   universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family domain; similar to ethylene-responsive ER6 protein (GI:5669654) (Lycopersicon esculentum)   chr1:3821529-3823053 REVERSE   Aliases: T23J18.35, T23J18_35	10.1	9.0	1.0	3.4	57.4%	-1.5
670	AT5G54970.1   expressed protein   chr5:22330436-22330990 FORWARD   Aliases: MBG8.24, MBG8_24	5.1	8.0	-2.9	-3.4	57.5%	-1.1
671	AT3G10420.2   sporulation protein-related, similar to hypothetical proteins: GB:P51281 (Chloroplast Porphyra purpurea), GB:BAA16982 (Synechocystis sp), GB:P49540 (Odontella sinensis), GB:AAB82669 (Chloroplast Cyanidium caldarium); similar to stage III sporulation protein AA (GI:18145497) (Clostridium perfringens str. 13); similar to stage III sporulation protein AA (mutants block sporulation after engulfment) (GI:22777578) (Oceanobacillus iheyensis)   chr3:3239185-3242542 FORWARD   Aliases: F13M14.30	5.3	4.2	1.1	3.4	57.6%	-1.1
672	AT4G17350.1   expressed protein   chr4:9701144-9703838 FORWARD   Aliases: DL4710W, FCAALL.415	8.0	7.1	0.8	3.4	57.8%	-1.2
673	AT3G05020.1   Symbol: ACP1   acyl carrier protein 1, chloroplast (ACP-1), identical to SP:P11829 Acyl carrier protein 1, chloroplast precursor (ACP) {Arabidopsis thaliana}   chr3:1391658-1392960 REVERSE   Aliases: ACP, ACYL CARRIER PROTEIN, T9J14.3, T9J14_3	6.8	8.6	-1.8	-3.4	57.8%	-1.1
674	AT3G21770.1   peroxidase 30 (PER30) (P30) (PRXR9), identical to SP:Q9LSY7 Peroxidase 30 precursor (EC 1.11.1.7) (Atperox P30) (PRXR9) (ATP7a) {Arabidopsis thaliana}   chr3:7673283-7674846 FORWARD   Aliases: MSD21.10	7.7	8.8	-1.1	-3.4	57.8%	-1.1
675	AT5G24260.1   prolyl oligopeptidase family protein, similar to dipeptidyl peptidase IV (Stenotrophomonas maltophilia) GI:1753197; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF00930: Dipeptidyl peptidase IV (DPP IV) N-terminal region   chr5:8234726-8238246 REVERSE   Aliases: MOP9.8, MOP9_8	6.0	6.9	-0.8	-3.4	58.0%	-1.2
676	ATMG01370.1   Symbol: ORF111D   hypothetical protein   chrM:360717-361052 REVERSE   Aliases: ORF111D	5.2	8.3	-3.1	-3.4	58.3%	-1.1
677	AT2G02020.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr2:479100-481184 FORWARD   Aliases: F14H20.9, F14H20_9	5.5	4.5	1.1	3.4	58.3%	-1.1
678	AT3G55480.2   adaptin family protein, similar to AP-3 complex beta3A subunit, Homo sapiens, SP:O00203; contains Pfam profile: PF01602 Adaptin N terminal region   chr3:20577226-20582227 REVERSE   Aliases: T22E16.140	4.9	6.2	-1.3	-3.4	58.3%	-1.1
679	AT2G21180.1   expressed protein   chr2:9081741-9082461 REVERSE   Aliases: F26H11.6, F26H11_6	6.5	5.7	0.8	3.4	58.3%	-1.2
680	AT5G03760.1   Symbol: ATCSLA09   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	3.8	4.7	-0.9	-3.4	58.3%	-1.1
681	AT4G21560.3   vacuolar protein sorting-associated protein 28 family protein / VPS28 family protein, contains similarity to Swiss-Prot:Q02767 vacuolar protein sorting-associated protein VPS28 (Saccharomyces cerevisiae)   chr4:11468773-11470490 REVERSE   Aliases: F17L22.20	6.5	5.7	0.8	3.4	58.3%	-1.4
682	AT1G45130.1   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase (Lycopersicon esculentum) GI:7939619, beta-galactosidase BG1 GI:15081596 from (Vitis vinifera); contains Pfam profile PF01301: Glycosyl hydrolases family 35   chr1:17067692-17071702 FORWARD   Aliases: F27F5.20, F27F5_20	8.8	9.8	-1.0	-3.4	58.3%	-1.3
683	AT1G73540.1   MutT/nudix family protein, low similarity to SP:Q09790 Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain   chr1:27649322-27650359 REVERSE   Aliases: T9L24.30, T9L24_30	6.0	5.1	1.0	3.4	58.4%	-1.2
684	AT2G46550.1   expressed protein   chr2:19119061-19121224 REVERSE   Aliases: F13A10.8	7.4	6.3	1.1	3.4	58.7%	-1.2
685	AT3G07180.2   GPI transamidase component PIG-S-related, similar to GPI transamidase component PIG-S (Phosphatidylinositol-glycan biosynthesis, class S protein) (Swiss-Prot:Q96S52) (Homo sapiens)   chr3:2282094-2285519 REVERSE   Aliases: T1B9.16	7.3	8.0	-0.7	-3.4	58.9%	-1.3
686	AT4G22730.1   leucine-rich repeat transmembrane protein kinase, putative, leucine rich repeat receptor-like kinase, Oryza sativa, PATCHX:E267533   chr4:11941395-11943750 FORWARD   Aliases: T12H17.120, T12H17_120	3.2	4.0	-0.7	-3.4	58.9%	-1.3
687	AT5G08410.1   ferredoxin-thioredoxin reductase, putative, similar to ferredoxin-thioredoxin reductase, variable chain (FTR-V, Ferredoxin-thioredoxin reductase subunit A, FTR-A) (Zea mays) SWISS-PROT:P80680	5.8	4.9	0.8	3.4	58.9%	-1.3
688	AT5G10540.1   peptidase M3 family protein / thimet oligopeptidase family protein, similar to SP:P27237 Oligopeptidase A (EC 3.4.24.70) {Salmonella typhimurium}; contains Pfam profile PF01432: Peptidase family M3   chr5:3328093-3334972 FORWARD   Aliases: F12B17.110, F12B17_110	7.8	9.6	-1.8	-3.4	58.9%	-1.1
689	AT4G30900.1   expressed protein   chr4:15039514-15042352 FORWARD   Aliases: F6I18.190, F6I18_190	8.1	6.9	1.2	3.4	58.9%	-1.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
690	AT3G20720.1   expressed protein   chr3:7239914-7247011 FORWARD   Aliases: MOE17.2	5.0	6.5	-1.5	-3.4	58.9%	-1.2
691	AT1G19380.1   expressed protein   chr1:6698051-6698788 FORWARD   Aliases: F18O14.10, F18O14_10	7.1	5.9	1.2	3.4	59.1%	-1.2
692	AT2G45490.1   Encodes a member of a family of Ser/Thr kinases whose activities peak during cell division. Transcripts are abundant in tissues rich in dividing cells like roots and flowers but are low or absent in fully expanded leaves and stems.	2.4	3.0	-0.6	-3.4	59.3%	-1.5
693	AT5G61230.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:24644413-24646174 FORWARD   Aliases: MAF19.22, MAF19_22	8.5	7.6	0.9	3.3	59.3%	-1.2
694	AT5G65360.1   histone H3, identical to histone H3 from Zea mays SP:P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP:P08903, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:26137085-26137807 REVERSE   Aliases: MNA5.9	8.5	9.8	-1.3	-3.3	59.5%	-1.2
695	AT5G13310.1   expressed protein   chr5:4263496-4265340 FORWARD   Aliases: T22N19.1	5.6	4.8	0.7	3.3	59.5%	-1.3
696	AT4G05070.1   expressed protein   chr4:2593596-2594117 REVERSE   Aliases: C17L7.2	8.9	7.8	1.0	3.3	59.7%	-1.2
697	AT1G72280.1   Symbol: AERO1   endoplasmic reticulum oxidoreductin 1 (ERO1) family protein, contains Pfam domain, PF04137: Endoplasmic Reticulum Oxidoreductin 1 (ERO1)   chr1:27215513-27218168 REVERSE   Aliases: T9N14.18, T9N14_18	3.3	4.0	-0.8	-3.3	59.7%	-1.4
698	AT5G27980.1   seed maturation family protein, similar to SP:P09444 Late embryogenesis abundant protein D-34 (LEA D-34) {Gossypium hirsutum}; contains Pfam profile PF04927: Seed maturation protein   chr5:10015803-10016704 REVERSE   Aliases: F15F15.50, F15F15_50	3.2	2.6	0.6	3.3	59.7%	-1.4
699	AT1G70700.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g48500.1)   chr1:26658445-26660726 FORWARD   Aliases: F5A18.12, F5A18_12	2.7	2.3	0.4	3.3	59.7%	-1.9
700	AT3G02040.1   Symbol: SRG3   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family   chr3:348174-350006 REVERSE   Aliases: F1C9.18, F1C9_18, SENESCENCE RELATED GENE 3	5.8	4.9	0.9	3.3	59.8%	-1.2
701	AT3G15590.1   DNA-binding protein, putative, similar to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat   chr3:5275408-5277994 REVERSE   Aliases: MQD17.5	10.1	10.7	-0.7	-3.3	59.8%	-1.5
702	AT2G38280.2   Symbol: FAC1   AMP deaminase, putative / myoadenylate deaminase, putative, similar to SP:P15274 AMP deaminase (EC 3.5.4.6) (Myoadenylate deaminase) {Saccharomyces cerevisiae}; contains Pfam profile PF00962: Adenosine/AMP deaminase   chr2:16040579-16045954 REVERSE   Aliases: EMBRYONIC FACTOR1, F16M14.21, F16M14_21	7.0	8.1	-1.1	-3.3	59.9%	-1.1
703	AT3G12280.1   Symbol: RBR1   retinoblastoma-related protein (RBR1), nearly identical to retinoblastoma-related protein (Arabidopsis thaliana) GI:8777927; contains Pfam profiles: PF01858 retinoblastoma-associated protein A domain, PF01857 retinoblastoma-associated protein B domain   chr3:3913419-3919087 REVERSE   Aliases: F28J15.11, RB, RBL1, RETINOBLASTOMA PROTEIN, RETINOBLASTOMA RELATED 1	5.2	6.4	-1.2	-3.3	59.9%	-1.2
704	AT1G10840.2   Symbol: TIF3H1	8.1	9.4	-1.3	-3.3	59.9%	-1.2
705	AT4G35985.1   senescence/dehydration-associated protein-related, similar to senescence-associated protein 12 (Hemerocallis hybrid cultivar) gi:3551958:gb:AAC34857; similar to early-responsive to dehydration stress ERD7 protein (Arabidopsis thaliana) gi:15320412:dbj:BAB63916   chr4:17032271-17033865 REVERSE   Aliases: None	10.2	9.1	1.1	3.3	59.9%	-1.4
706	AT3G15353.1   Symbol: MT3   metallothionein protein, putative	13.0	11.1	1.9	3.3	60.0%	-1.2
707	AT1G78670.1   gamma-glutamyl hydrolase, putative / gamma-Glu-X carboxypeptidase, putative / conjugase, putative, similar to gamma glutamyl hydrolase GI:1679658 SP:P93164 from (Glycine max)   chr1:29595848-29598392 FORWARD   Aliases: F9K20.29, F9K20_29	9.2	7.8	1.4	3.3	60.0%	-1.2
708	AT3G24360.1   enoyl-CoA hydratase/isomerase family protein, similar to CHY1 (gi:8572760); contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein   chr3:8839735-8842838 REVERSE   Aliases: K7M2.21	4.2	5.2	-1.0	-3.3	60.0%	-1.2
709	AT1G70740.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:26677294-26679543 REVERSE   Aliases: F5A18.8, F5A18_8	4.8	3.9	0.9	3.3	60.0%	-1.4
710	AT5G49910.1   Symbol: cpHSC70 2   heat shock protein 70 / HSP70 (HSC70-7), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746592   chr5:20320640-20324039 FORWARD   Aliases: HEAT SHOCK PROTEIN 70, HEAT SHOCK PROTEIN 70 7, HSC70 7, K9P8.5, K9P8_5	8.7	9.8	-1.1	-3.3	60.0%	-1.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
711	AT2G19610.2   zinc finger (C3HC4-type RING finger) family protein, contains a zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr2:8491067-8493110 FORWARD   Aliases: F3P11.21, F3P11_21	4.7	3.8	0.9	3.3	60.0%	-1.3
712	AT4G31810.1   enoyl-CoA hydratase/isomerase family protein, similar to CHY1 (gi:8572760); contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein   chr4:15387131-15390340 REVERSE   Aliases: F11C18.10, F11C18_10	7.1	8.8	-1.8	-3.3	60.3%	-1.2
713	AT4G28470.1   similar to 26S proteasome regulatory subunit S2 (RPN1) [Arabidopsis thaliana] (TAIR:At2g20580.1); similar to Unknown (protein for MGC:83116) [Xenopus laevis] (GB:AAH68911.1); similar to MGC97650 protein [Xenopus tropicalis] (GB:NP_001015819.1); similar to putative 26S proteasome regulatory subunit S2 [Oryza sativa (japonica cultivar-group)] (GB:BAD54002.1); similar to putative proteasome 26S non-ATPase subunit 2 [Oryza sativa (japonica cultivar-group)] (GB:XP_450542.1); similar to MGC83233 protein [Xenopus laevis] (GB:AAH68957.1); contains InterPro domain Proteasome/cyclosome, regulatory subunit (InterPro:IPR002015)   chr4:14066882-14072549 REVERSE   Aliases: F2009.150, F2009_150	8.3	9.3	-1.0	-3.3	60.3%	-1.2
714	AT5G05440.1   expressed protein, low similarity to cytokinin-specific binding protein (Vigna radiata) GI:4190976   chr5:1609251-1610447 FORWARD   Aliases: K18I23.25, K18I23_25	7.8	6.4	1.4	3.3	60.3%	-1.1
715	AT5G64450.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr5:25789175-25789987 FORWARD   Aliases: T12B11.4, T12B11_4	4.8	3.6	1.2	3.3	60.3%	-1.2
716	AT1G05950.1   expressed protein   chr1:1804572-1807470 REVERSE   Aliases: T21E18.2, T21E18_2	3.7	4.9	-1.2	-3.3	60.3%	-1.2
717	AT4G30820.2   cyclin-dependent kinase-activating kinase assembly factor-related / CDK-activating kinase assembly factor-related, contains similarity to CDK-activating kinase assembly factor MAT1 (RING finger protein MAT1) (Menage a trois) (CDK7/cyclin H assembly factor) (Swiss-Prot:P51950) (Marthasterias glacialis)   chr4:15006500-15008542 FORWARD   Aliases: F6I18.270, F6I18_270	5.5	4.6	0.9	3.3	60.3%	-1.3
718	AT2G21970.1   Symbol: SEP2   stress enhanced protein 2 (SEP2), nearly identical to stress enhanced protein 2; SEP2 (GI:7384980) (Arabidopsis thaliana)   chr2:9364063-9364996 REVERSE   Aliases: F7D8.29, F7D8_29, SEP2, STRESS ENHANCED PROTEIN 2	9.1	8.1	1.0	3.3	60.4%	-1.2
719	AT4G27970.1   C4-dicarboxylate transporter/malic acid transport family protein, contains Pfam profile PF03595: C4-dicarboxylate transporter/malic acid transport protein   chr4:13918296-13920138 REVERSE   Aliases: T13J8.80, T13J8_80	7.6	8.6	-0.9	-3.3	60.5%	-1.3
720	AT4G35770.1   Symbol: SEN1   senescence-associated protein (SEN1), identical to senescence-associated protein GI:1046270 from (Arabidopsis thaliana)   chr4:16944946-16946096 FORWARD   Aliases: ATSEN1, DARK INDUCIBLE 1, DIN1, F4B14.3	3.1	2.5	0.6	3.3	60.5%	-1.5
721	AT1G49170.1   expressed protein   chr1:18186934-18188102 REVERSE   Aliases: F27J15.6, F27J15_6	4.3	3.1	1.1	3.3	60.5%	-1.4
722	AT3G19130.1   Symbol: ATRBP47B   RNA-binding protein, putative, similar to RNA Binding Protein 47 (Nicotiana plumbaginifolia) GI:9663769, DNA binding protein ACBF GB:AAC49850 from (Nicotiana tabacum); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:6611219-6614050 REVERSE   Aliases: ATRBP47B, MVI11.3	9.5	8.6	0.9	3.3	60.5%	-1.4
723	AT1G66260.1   RNA and export factor-binding protein, putative, similar to GI:7159943 from (Mus musculus) (RNA 6 (4), 638-650 (2000))   chr1:24699303-24702093 REVERSE   Aliases: T6J19.1, T6J19_1	10.2	9.3	0.8	3.3	60.5%	-1.4
724	AT3G61980.1   serine protease inhibitor, Kazal-type family protein, contains Pfam domain PF00050: Kazal-type serine protease inhibitor domain   chr3:22967114-22967858 REVERSE   Aliases: F21F14.150	7.8	6.7	1.1	3.3	60.5%	-1.3
725	AT2G42330.1   D111/G-patch domain-containing protein, similar to SP:Q9ERA6 Tuftelin-interacting protein 11 {Mus musculus}; contains Pfam profile PF01585: G-patch domain   chr2:17638909-17641167 REVERSE   Aliases: MHK10.5, MHK10_5	5.1	4.3	0.8	3.3	60.5%	-1.3
726	AT1G74930.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr1:28147793-28148710 FORWARD   Aliases: F25A4.10, F25A4_10	4.0	3.3	0.7	3.3	60.5%	-1.4
727	AT5G24330.1   PHD finger family protein / SET domain-containing protein, contains Pfam domain, PF00628: PHD-finger and PF00856: SET domain   chr5:8295248-8297000 REVERSE   Aliases: MOP9.7, MOP9_7	2.9	3.6	-0.7	-3.3	60.5%	-1.4
728	AT1G13220.2   nuclear matrix constituent protein-related, similar to nuclear matrix constituent protein 1 (NMCP1) (Daucus carota) GI:2190187   chr1:4515696-4520281 FORWARD   Aliases: F3F19.25, F3F19_25	5.2	6.4	-1.2	-3.3	60.5%	-1.2
729	AT1G10470.1   Symbol: ARR4   two-component responsive regulator / response regulator 4 (ARR4), identical to response regulator1 GI:3273195 from (Arabidopsis thaliana); identical to cDNA ARR4 mRNA for response regulator 4 GI:3953596   chr1:3442328-3443958 REVERSE   Aliases: ATRR1, IBC7, INDUCED BY CYTOKININ 7, RESPONSE REGULATOR 4, T10O24.8, T10O24_8	5.8	7.1	-1.3	-3.3	60.5%	-1.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
730	AT1G74690.1   calmodulin-binding family protein, low similarity to SF16 protein ( <i>Helianthus annuus</i> ) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr1:28064275-28068286 REVERSE   Aliases: F25A4.33, F25A4_33	5.9	7.3	-1.4	-3.3	60.6%	-1.2
731	AT5G46350.1   Symbol: WRKY8   WRKY family transcription factor, contains similarity to WRKY-type DNA-binding protein   chr5:18818445-18821267 REVERSE   Aliases: ATWRKY8, MPL12.15, MPL12_15, WRKY8	2.6	3.1	-0.4	-3.3	60.6%	-1.7
732	AT1G70550.2   expressed protein, similar to hypothetical protein GB:AAD31338 ( <i>Arabidopsis thaliana</i> ) and to putative putative carboxyl-terminal peptidase GB:AAC16072 ( <i>Arabidopsis thaliana</i> ) contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr1:26600815-26603882 FORWARD   Aliases: F24J13.12, F24J13_12	4.0	5.1	-1.0	-3.3	60.6%	-1.2
733	AT4G23260.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:12167433-12169904 REVERSE   Aliases: F21P8.150, F21P8_150	2.6	3.5	-0.9	-3.3	60.6%	-1.5
734	AT5G67180.1   AP2 domain-containing transcription factor, putative, similar to (SP:P47927) Floral homeotic protein APETALA2. ( <i>Mouse-ear cress</i> ) { <i>Arabidopsis thaliana</i> }   chr5:26819233-26821245 REVERSE   Aliases: K21H1.22, K21H1_22	4.2	3.4	0.8	3.3	60.6%	-1.4
735	AT1G11260.1   glucose transporter (STP1), nearly identical to glucose transporter GB:P23586 SP:P23586 from ( <i>Arabidopsis thaliana</i> )   chr1:3777329-3780337 FORWARD   Aliases: T28P6.9, T28P6_9	7.2	5.5	1.7	3.3	60.6%	-1.2
736	AT3G07540.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr3:2404515-2407547 REVERSE   Aliases: F21O3.25	5.5	6.8	-1.3	-3.3	60.6%	-1.2
737	AT2G28790.1   osmotin-like protein, putative, similar to SP:Q41350 Osmotin-like protein precursor { <i>Lycopersicon esculentum</i> }; contains Pfam profile PF00314: Thaumatin family   chr2:12361507-12362508 REVERSE   Aliases: F8N16.8, F8N16_8	3.9	5.2	-1.3	-3.3	60.6%	-1.2
738	AT2G41430.4   Symbol: ERD15   dehydration-induced protein (ERD15), identical to dehydration-induced protein ERD15 GI:710626 from ( <i>Arabidopsis thaliana</i> )   chr2:17276388-17277620 FORWARD   Aliases: CID1, DEHYDRATION INDUCED PROTEIN, EARLY RESPONSIVE TO DEHYDRATION 15, LIGHT STRESS REGULATED 1, LSR1, T26J13.2	11.8	10.8	1.0	3.3	60.6%	-1.3
739	AT1G33030.1   O-methyltransferase family 2 protein, similar to caffeic acid 3-O-methyltransferase (SP:Q00763) ( <i>Populus tremuloides</i> ), catechol O-methyltransferase (GI:4808524)( <i>Thalictrum tuberosum</i> )   chr1:11964756-11966256 REVERSE   Aliases: F9L11.18, F9L11_18	4.9	6.5	-1.7	-3.3	60.6%	-1.2
740	AT5G55300.1   DNA topoisomerase I, identical to Swiss-Prot:P30181 DNA topoisomerase I ( <i>Arabidopsis thaliana</i> )   chr5:22441812-22446664 REVERSE   Aliases: MTE17.1, MTE17_1	6.0	6.8	-0.8	-3.3	60.7%	-1.4
741	AT1G72030.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr1:27114527-27115868 FORWARD   Aliases: F28P5.8, F28P5_8	8.8	7.0	1.8	3.3	60.9%	-1.4
742	AT3G04720.1   Symbol: PR4   hevein-like protein (HEL), identical to SP:P43082 Hevein-like protein precursor { <i>Arabidopsis thaliana</i> }; similar to SP:P09762 Wound-induced protein WIN2 precursor { <i>Solanum tuberosum</i> }; contains Pfam profile PF00187: Chitin recognition protein   chr3:1285573-1286568 REVERSE   Aliases: F7O18.21, F7O18_21, HEL, HEVEIN LIKE, PATHOGENESIS RELATED 4, PR 4	6.1	7.4	-1.4	-3.3	61.0%	-1.2
743	AT5G22650.2   Symbol: HD2B   expressed protein, non-consensus AT donor splice site at exon 3, AC acceptor splice site at exon 4;   chr5:7534067-7536276 FORWARD   Aliases: ATHD2B, HD2, HDA4, HDT02, HDT2, HISTONE DEACETYLASE, HISTONE DEACETYLASE 2, HISTONE DEACETYLASE 2B, MDJ22.7, MDJ22_7	9.0	10.0	-1.0	-3.3	61.1%	-1.3
744	AT1G12320.1   expressed protein   chr1:4189353-4190340 FORWARD   Aliases: F5O11.5, F5O11_5	7.3	6.1	1.1	3.3	61.1%	-1.3
745	AT5G35360.2   Symbol: CAC2   similar to methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g03090.2); similar to biotin carboxylase precursor [ <i>Glycine max</i> ] (GB:AAC23573.1); similar to biotin carboxylase precursor [ <i>Glycine max</i> ] (GB:AAC02267.1); similar to acetyl-CoA carboxylase [ <i>Glycine max</i> ] (GB:AAF80469.1); similar to biotin carboxylase subunit (GB:AAC41659.1); contains InterPro domain Carbamoyl-phosphate synthetase large chain, N-terminal (InterPro:IPR005481); contains InterPro domain Acetyl-CoA carboxylase, biotin carboxylase (InterPro:IPR004549); contains InterPro domain Biotin carboxylase, C-terminal (InterPro:IPR005482); contains InterPro domain Carbamoyl-phosphate synthase L chain, ATP-binding (InterPro:IPR005479)   chr5:13601388-13606337 FORWARD   Aliases: ACETYL COA CARBOXYLASE, T26D22.8, T26D22_8	10.3	11.2	-0.9	-3.3	61.1%	-1.7
746	AT5G04750.1   F1F0-ATPase inhibitor protein, putative, similar to F1F0-ATPase inhibitor protein ( <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)) gi:5106371:dbj:BAA81661   chr5:1372148-1374006 FORWARD   Aliases: MUK11.3	11.5	11.0	0.5	3.3	61.2%	-1.7
747	AT4G31210.1   DNA topoisomerase family protein, similar to DNA Topoisomerase I (SP:Q9X3X7) { <i>Zymomonas mobilis</i> }	4.1	5.2	-1.1	-3.3	61.3%	-1.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
748	AT4G30470.1   cinnamoyl-CoA reductase-related, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Saccharum officinarum (GI:3341511)   chr4:14894111-14896819 FORWARD   Aliases: F17I23.190, F17I23_190	8.1	7.2	0.9	3.3	61.3%	-1.4
749	AT1G02700.1   expressed protein, similar to hypothetical protein GB:CAB80707 GI:7268598 from (Arabidopsis thaliana)   chr1:588329-589480 FORWARD   Aliases: T14P4.2, T14P4_2	5.0	3.9	1.1	3.3	61.3%	-1.2
750	AT4G01850.1   S-adenosylmethionine synthetase 2 (SAM2), identical to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) (Arabidopsis thaliana) SWISS-PROT:P17562   chr4:796097-798285 REVERSE   Aliases: T7B11.11, T7B11_11	9.7	10.6	-0.9	-3.3	61.3%	-1.4
751	AT3G46940.1   deoxyuridine 5'-triphosphate nucleotidohydrolase family, contains Pfam profile: PF00692 deoxyuridine 5'-triphosphate nucleotidohydrolase	5.9	7.3	-1.4	-3.3	61.3%	-1.2
752	AT1G67740.1   Symbol: PSBY   photosystem II core complex proteins psbY, chloroplast (PSBY) / L-arginine metabolising enzyme, identical to SP:O49347 Photosystem II core complex proteins psbY, chloroplast precursor (L-arginine metabolising enzyme) (L-AME) (Contains: Photosystem II protein psbY-1 (psbY-A1); Photosystem II protein psbY-2 (psbY-A2)) (Arabidopsis thaliana)   chr1:25397731-25398817 REVERSE   Aliases: F12A21.13, F12A21_13, YCF32	7.6	5.9	1.7	3.3	61.5%	-1.3
753	AT5G19880.1   peroxidase, putative, similar to peroxidase (Lycopersicon esculentum) gi:296910:emb:CAA50597   chr5:6720386-6722477 REVERSE   Aliases: F28I16.30, F28I16_30	2.7	4.1	-1.4	-3.3	61.5%	-1.3
754	AT4G25810.1   Symbol: XTR6   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR6), identical to xyloglucan endotransglycosylase-related protein GI:1244758 from (Arabidopsis thaliana)   chr4:13128655-13129893 FORWARD   Aliases: F14M19.90, F14M19_90, XYLOGLUCAN ENDOTRANSGLYCOSYLASE 6	10.6	8.6	2.0	3.3	61.5%	-1.3
755	AT4G30870.1   similar to repair endonuclease family protein [Arabidopsis thaliana] (TAIR:At5g39770.1); similar to unnamed protein product [Debaryomyces hansenii CBS767] (GB:CAG90230.1); contains InterPro domain ERCC4 domain (InterPro:IPR006166)   chr4:15028592-15032467 FORWARD   Aliases: F6I18.220, F6I18_220	3.1	4.5	-1.4	-3.3	61.5%	-1.2
756	AT2G13360.2   Symbol: AGT   serine-glyoxylate aminotransferase-related, similar to serine-glyoxylate aminotransferase	3.8	3.1	0.7	3.3	61.5%	-1.4
757	AT1G53400.1   expressed protein   chr1:19928439-19930268 FORWARD   Aliases: F12M16.29, F12M16_29	9.7	8.9	0.9	3.3	61.5%	-1.3
758	AT4G16670.1   expressed protein   chr4:9385241-9387776 FORWARD   Aliases: DL4360W, FCAALL.2	4.5	3.8	0.7	3.3	61.5%	-1.5
759	AT5G23460.1   expressed protein   chr5:7912772-7913498 FORWARD   Aliases: K19M13.9, K19M13_9	9.5	8.5	1.0	3.3	61.6%	-1.2
760	AT3G59670.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g37440.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAV32239.1)   chr3:22050454-22053637 FORWARD   Aliases: T16L24.220	4.8	5.9	-1.2	-3.3	61.7%	-1.2
761	AT5G61420.2   Symbol: MYB28   myb family transcription factor (MYB28), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:24706377-24708021 REVERSE   Aliases: MFB13.22, MFB13_22	7.5	6.0	1.4	3.3	61.9%	-1.3
762	AT3G62110.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to polygalacturonase (Lycopersicon esculentum) GI:4325090; contains PF00295: Glycosyl hydrolases family 28	4.5	5.1	-0.7	-3.3	62.1%	-1.4
763	AT2G19350.1   expressed protein   chr2:8383284-8384425 FORWARD   Aliases: F27F23.15, F27F23_15	7.2	6.2	1.1	3.3	62.1%	-1.4
764	AT5G24590.2   Symbol: TIP   turnip crinkle virus-interacting protein / TCV-interacting protein (TIP), contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC2 (GI:6456751) {Arabidopsis thaliana}; identical to cDNA TIP mRNA, GI:9408600   chr5:8416665-8418936 REVERSE   Aliases: ANAC091, K18P6.12, K18P6_12, TCV INTERACTING PROTEIN	5.3	4.7	0.6	3.3	62.1%	-1.5
765	AT3G07150.1   hypothetical protein   chr3:2263812-2264582 REVERSE   Aliases: T1B9.19	3.9	3.1	0.8	3.3	62.1%	-1.4
766	AT3G25100.1   Symbol: CDC45   cell division control protein-related, contains weak similarity to cell division control protein 45 homolog (Suppressor of nda4 protein) (Swiss-Prot:O74113) (Schizosaccharomyces pombe)   chr3:9144006-9146216 FORWARD   Aliases: CELL DIVISION CYCLE 45, MJL12.4	5.0	6.8	-1.8	-3.3	62.2%	-1.3
767	AT1G21460.1   nodulin MtN3 family protein, contains similarity to MTN3 (nodule development protein) GB:Y08726 GI:1619601 from (Medicago truncatula)   chr1:7511850-7513347 REVERSE   Aliases: F24J8.9, F24J8_9	5.0	3.8	1.1	3.3	62.3%	-1.3
768	AT4G34050.2   caffeoyl-CoA 3-O-methyltransferase, putative, nearly identical to GI:2960356 (Populus balsamifera subsp. trichocarpa), GI:684942 (Medicago sativa subsp. sativa) isoform contains a GT-TG intron which removes an internal segment of the protein.   chr4:16310820-16311978 FORWARD   Aliases: F28A23.190, F28A23_190	9.2	11.0	-1.8	-3.2	62.3%	-1.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
769	AT2G37470.1   histone H2B, putative, strong similarity to histone H2B from <i>Lycopersicon esculentum</i> GI:3021483, GI:3021485, <i>Capsicum annuum</i> SP:O49118; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	8.0	9.8	-1.8	-3.2	62.3%	-1.3
770	AT3G07470.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr3:2386903-2388477 REVERSE   Aliases: F21O3.18	6.2	5.5	0.8	3.2	62.3%	-1.4
771	AT1G08560.1   Symbol: SYP111	7.8	6.7	1.1	3.2	62.3%	-1.4
772	AT4G28330.1   expressed protein, similar to hypothetical protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g28340.1)   chr4:14022393-14022993 REVERSE   Aliases: F20O9.10, F20O9_10	7.4	5.8	1.6	3.2	62.3%	-1.2
773	AT1G25550.1   myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain   chr1:8976525-8978080 FORWARD   Aliases: F2J7.21, F2J7_21	6.5	7.4	-0.9	-3.2	62.7%	-1.6
774	AT3G23330.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:8347207-8349354 FORWARD   Aliases: MLM24.6	4.3	5.5	-1.2	-3.2	62.7%	-1.3
775	AT1G31750.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr1:11370640-11372058 REVERSE   Aliases: F5M6.24	5.2	3.7	1.6	3.2	62.7%	-1.3
776	AT2G37540.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr2:15758653-15761045 REVERSE   Aliases: F13M22.4, F13M22_4	3.7	2.8	0.9	3.2	62.7%	-1.6
777	AT1G31170.1   parB-like nuclease domain-containing protein, contains Pfam profile PF02195: ParB-like nuclease domain   chr1:11133470-11134386 FORWARD   Aliases: F28K20.12, F28K20_12	8.4	7.4	1.1	3.2	62.7%	-1.3
778	AT5G67130.1   expressed protein   chr5:26808592-26811253 FORWARD   Aliases: K21H1.9, K21H1_9	6.1	7.0	-0.9	-3.2	62.7%	-1.4
779	AT2G21100.1   disease resistance-responsive protein-related / dirigent protein-related, similar to dirigent protein ( <i>Thuja plicata</i> ) gi:6694699:gb:AAF25360; similar to disease resistance response protein 206-d ( <i>Pisum sativum</i> ) gi:508844:gb:AAB18669	3.0	4.3	-1.4	-3.2	62.7%	-1.3
780	AT2G03280.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g14020.1); similar to putative auxin-independent growth promoter [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:BAD69015.1); contains InterPro domain Hypothetical plant protein (InterPro:IPR004348)	5.4	6.2	-0.8	-3.2	62.7%	-1.5
781	AT4G34590.1   Symbol: GBF6   bZIP transcription factor family protein, similar to common plant regulatory factor 7 GI:9650828 from ( <i>Petroselinum crispum</i> )   chr4:16521866-16523235 FORWARD   Aliases: T4L20.170, T4L20_170	7.9	6.0	2.0	3.2	62.7%	-1.3
782	AT4G13195.1   expressed protein   chr4:7662367-7663173 REVERSE   Aliases: None	2.7	3.4	-0.7	-3.2	62.7%	-1.6
783	AT3G58790.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8; general stress protein gspA, <i>Bacillus subtilis</i> , PIR:S16423   chr3:21753048-21757301 REVERSE   Aliases: T20N10.140	5.2	4.3	0.9	3.2	62.7%	-1.4
784	AT1G64690.1   expressed protein   chr1:24041732-24042742 FORWARD   Aliases: F13O11.1, F13O11_1	5.5	4.5	1.1	3.2	62.7%	-1.3
785	AT2G48120.1   Symbol: PAC   pale cress protein (PAC), identical to PAC ( <i>Arabidopsis thaliana</i> ) gi:1483213:emb:CAA65334	3.0	3.6	-0.6	-3.2	63.2%	-1.6
786	AT4G32800.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr4:15819528-15820875 FORWARD   Aliases: T16I18.10, T16I18_10	4.0	3.4	0.5	3.2	63.2%	-1.6
787	AT3G28340.1   galactinol synthase, putative   chr3:10590184-10591776 REVERSE   Aliases: MZF16.17	5.7	4.8	1.0	3.2	63.2%	-1.3
788	AT1G26930.1   kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain   chr1:9336044-9337574 REVERSE   Aliases: T2P11.12, T2P11_12	7.1	8.3	-1.2	-3.2	63.2%	-1.5
789	AT1G12240.1   Symbol: ATBETAFRUCT4   beta-fructosidase (BFRUCT4) / beta-fructofuranosidase / invertase, vacuolar, identical to beta-fructosidase GI:1871503 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF00251:Glycosyl hydrolases family 32; identical to cDNA beta-fructosidase (vacuolar form) GI:1321683; similar to SP:Q43857   chr1:4153650-4157642 FORWARD   Aliases: ATBETAFRUCT4, T28K15.3, T28K15_3	4.3	5.6	-1.3	-3.2	63.2%	-1.3
790	AT1G53520.1   chalcone-flavanone isomerase-related, low similarity to GI:499036 ( <i>Vitis vinifera</i> )   chr1:19980083-19981623 REVERSE   Aliases: F22G10.11	5.4	6.8	-1.4	-3.2	63.2%	-1.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
791	AT4G28310.1   expressed protein   chr4:14017414-14018554 FORWARD   Aliases: F26K10.190, F26K10_190	4.3	6.1	-1.8	-3.2	63.2%	-1.3
792	AT2G44790.1   Symbol: UCC2   uclacyanin II, strong similarity to uclacyanin II GI:3399769 from (Arabidopsis thaliana); contains Pfam profile PF02298: Plastocyanin-like domain; identical to cDNA uclacyanin II GI:3399768   chr2:18468981-18470384 REVERSE   Aliases: F16B22.32, UCLACYANIN 2	4.0	7.2	-3.2	-3.2	63.2%	-1.3
793	AT1G17460.1   Symbol: TRFL3   myb family transcription factor, contains Pfam PF00249: Myb-like DNA-binding domain   chr1:5998813-6002709 FORWARD   Aliases: F28G4.5, TRF LIKE 3	4.3	3.5	0.7	3.2	63.2%	-1.5
794	AT3G45730.1   expressed protein   chr3:16800965-16801567 FORWARD   Aliases: T6D9.60	2.9	2.5	0.5	3.2	63.2%	-1.8
795	AT2G42760.1   expressed protein   chr2:17803061-17804308 REVERSE   Aliases: F7D19.24, F7D19_24	8.8	7.5	1.3	3.2	63.2%	-1.4
796	AT1G28140.1   expressed protein, contains similarity to cytochrome oxidase I GI:1289267 from (Xantholinus sp.)	6.9	5.8	1.1	3.2	63.2%	-1.3
797	AT2G35410.1   33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative, similar to SP:P19684 33 kDa ribonucleoprotein, chloroplast precursor {Nicotiana sylvestris}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:14905407-14906829 FORWARD   Aliases: T32F12.21, T32F12_21	6.8	8.2	-1.4	-3.2	63.4%	-1.3
798	AT1G31710.1   copper amine oxidase, putative, similar to copper amine oxidase (Lens culinaris) gi:15451834:gb:AAB34918	3.5	4.2	-0.7	-3.2	63.9%	-1.5
799	AT4G25920.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr4:13165484-13166881 FORWARD   Aliases: F20B18.30, F20B18_30	2.6	2.1	0.4	3.2	63.9%	-1.8
800	AT5G07800.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase 2 (FMO2) from Homo sapiens (GI:1834493); contains Pfam profile: PF00743 Flavin-binding monooxygenase-like   chr5:2486607-2489297 REVERSE   Aliases: MXM12.4, MXM12_4	9.1	10.4	-1.3	-3.2	63.9%	-1.3
801	AT5G39890.1   expressed protein   chr5:15991621-15993498 FORWARD   Aliases: MYH19.8, MYH19_8	7.7	5.9	1.8	3.2	63.9%	-1.3
802	AT2G15780.1   glycine-rich protein, similar to Blue copper protein precursor (SP:Q41001) {Pisum sativum}; contains a Pfam PF02298: Plastocyanin-like domain related to blue copper-binding protein; contains a domain related to blue copper-binding protein   chr2:6880658-6881823 REVERSE   Aliases: F19G14.22, F19G14_22	3.2	4.1	-0.9	-3.2	63.9%	-1.4
803	AT4G21680.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr4:11517043-11519777 REVERSE   Aliases: F17L22.140, F17L22_140	7.4	5.8	1.6	3.2	63.9%	-1.3
804	AT1G66620.1   seven in absentia (SINA) protein, putative, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr1:24856469-24857707 REVERSE   Aliases: T12I7.7, T12I7_7	5.8	7.8	-2.1	-3.2	63.9%	-1.3
805	AT3G52870.1   calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:19604151-19606797 REVERSE   Aliases: F8J2.40	6.2	7.2	-1.0	-3.2	63.9%	-1.4
806	AT5G02260.1   Symbol: ATEXPA9   expansin, putative (EXP9), similar to expansin precursor GI:4138914 from (Lycopersicon esculentum); alpha-expansin gene family, PMID:11641069	3.0	2.4	0.6	3.2	63.9%	-1.7
807	AT1G19630.1   Symbol: CYP722A1   cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana)   chr1:6785638-6787958 REVERSE   Aliases: F14P1.4, F14P1_4	4.5	3.6	0.9	3.2	63.9%	-1.7
808	AT4G12840.1   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr4:7533618-7535830 REVERSE   Aliases: T20K18.190, T20K18_190	4.5	5.3	-0.8	-3.2	63.9%	-1.5
809	AT2G17790.1   similar to vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein [Arabidopsis thaliana] (TAIR:At3g51310.1); similar to vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein [Arabidopsis thaliana] (TAIR:At1g75850.1); similar to similar to vacuolar protein sorting 35; maternal-embryonic 3; vacuolar protein sorting 35 (yeast homolog) [Gallus gallus] (GB:NP_001005842.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAF93242.1); similar to novel protein similar to human and mouse vacuolar protein sorting 35 (yeast) (VPS35) [Danio rerio] (GB:CAE49237.1); contains InterPro domain Vacuolar protein sorting-associated protein 35 (InterPro:IPR005378)   chr2:7740717-7746712 FORWARD   Aliases: T17A5.7, T17A5_7	6.1	7.3	-1.2	-3.2	63.9%	-1.4
810	AT5G53190.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr5:21589643-21591510 REVERSE   Aliases: MFH8.13, MFH8_13	6.6	5.1	1.5	3.2	63.9%	-1.3
811	AT3G09730.1   expressed protein   chr3:2984023-2986265 FORWARD   Aliases: F11F8.32	2.7	3.4	-0.7	-3.2	64.1%	-1.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
812	AT3G43230.1   zinc finger (FYVE type) family protein, contains Pfam domain PF01363: FYVE zinc finger   chr3:15218355-15220813 FORWARD   Aliases: F7K15.80	8.6	7.7	0.8	3.2	64.1%	-1.6
813	AT5G51260.1   acid phosphatase, putative, similar to acid phosphatase-1(1); Apase-1(1) (Lycopersicon esculentum) GI:7705154, acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr5:20849409-20850918 REVERSE   Aliases: MWD22.21, MWD22_21	6.4	5.1	1.4	3.2	64.2%	-1.3
814	AT1G26240.1   proline-rich extensin-like family protein, similar to hydroxyproline-rich glycoprotein precursor gi:727264:gb:AAA87902; contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:9078127-9079563 REVERSE   Aliases: F28B23.10, F28B23_10	2.0	2.4	-0.4	-3.2	64.2%	-1.9
815	AT5G11650.1   hydrolase, alpha/beta fold family protein, contains Pfam profile PF00561: hydrolase, alpha/beta fold family; low similarity to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162   chr5:3744981-3747126 FORWARD   Aliases: T22P22.40, T22P22_40	5.2	3.6	1.6	3.2	64.3%	-1.3
816	AT4G30800.1   40S ribosomal protein S11 (RPS11B), ribosomal protein S11, Arabidopsis thaliana, PIR2:C35542   chr4:15001173-15002677 FORWARD   Aliases: T10C21.1	7.5	8.7	-1.2	-3.2	64.5%	-1.3
817	AT3G16140.1   photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH1), identical to SP:Q9SUI7; similar to PSI-H precursor (Nicotiana sylvestris) GI:407353; contains Pfam profile PF03244: Photosystem I reaction centre subunit VI   chr3:5468515-5469482 REVERSE   Aliases: MSL1.18	9.6	8.3	1.3	3.2	64.5%	-1.3
818	AT1G13980.1   Symbol: GN   pattern formation protein (EMB30) (GNOM), identical to SP:Q42510; contains Pfam profile PF01369: Sec7 domain   chr1:4788556-4794651 FORWARD   Aliases: EMB30, EMBRYO DEFECTIVE 30, F16A14.20, GNOM, VAN7	7.1	8.1	-1.0	-3.2	64.6%	-1.4
819	AT5G38510.1   rhomboid family protein, contains Pfam profile PF01694: Rhomboid family   chr5:15435069-15437232 REVERSE   Aliases: MBB18.4, MBB18_4	5.8	4.8	1.0	3.2	64.6%	-1.3
820	AT5G07350.1   tudor domain-containing protein / nuclease family protein, contains Pfam domains PF00567: Tudor domain and PF00565: Staphylococcal nuclease homologue   chr5:2320082-2325420 REVERSE   Aliases: T2I1.60, T2I1_60	8.4	9.3	-0.9	-3.2	64.7%	-1.5
821	AT3G28007.1   nodulin MtN3 family protein, contains Pfam PF03083 MtN3/saliva family; similar to LIM7 GI:431154 (induced in meiotic prophase in lily microsporocytes) from (Lilium longiflorum)	3.1	2.5	0.6	3.2	64.7%	-1.7
822	AT3G05740.1   DNA helicase (RECQ11), identical to DNA Helicase (Arabidopsis thaliana) GI:10944747   chr3:1698118-1701405 FORWARD   Aliases: F18C1.21	3.5	5.0	-1.5	-3.2	64.7%	-1.3
823	AT3G50810.1   integral membrane protein, putative, contains 4 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)   chr3:18898595-18900849 REVERSE   Aliases: F18B3.90	6.4	5.5	1.0	3.2	64.7%	-1.4
824	AT2G36220.1   expressed protein   chr2:15199559-15200777 FORWARD   Aliases: F2H17.17, F2H17_17	3.8	2.6	1.2	3.2	64.8%	-1.3
825	AT2G43040.1   Symbol: NPG1   calmodulin-binding protein, similar to pollen-specific calmodulin-binding protein MPCBP GI:10086260 from (Zea mays); contains Pfam profile PF00515: TPR Domain   chr2:17902960-17906451 REVERSE   Aliases: MFL8.10, MFL8_10, NO POLLEN GERMINATION 1	4.7	5.5	-0.8	-3.2	64.8%	-1.6
826	AT1G49160.2   Symbol: WNK7   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:18182972-18185535 REVERSE   Aliases: F27J15.7, F27J15_7	4.2	5.8	-1.6	-3.2	64.8%	-1.4
827	AT1G32170.1   Symbol: XTR4   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR4), identical to N-terminal partial sequence of xyloglucan endotransglycosylase-related protein XTR4 GI:1244754 from (Arabidopsis thaliana); similar to endoxyloglucan transferase (Arabidopsis thaliana) GI:5533311   chr1:11575301-11577907 FORWARD   Aliases: F3C3.5, F3C3_5, XYLOGLUCAN ENDOTRANSGLYCOSYLASE 4, XYLOGLUCAN ENDOTRANSGLYCOSYLASE RELATED PROTEIN	7.0	5.3	1.7	3.2	64.8%	-1.4
828	AT3G58630.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189   chr3:21694545-21696918 REVERSE   Aliases: F14P22.220	3.3	2.9	0.4	3.2	64.9%	-1.9
829	AT3G09690.2   similar to hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] (TAIR:At5g02970.1); similar to putative alpha/beta hydrolase [Oryza sativa (japonica cultivar-group)] (GB:AAP54670.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAM92284.1); contains InterPro domain Alpha/beta hydrolase fold (InterPro:IPR000073)   chr3:2972228-2974848 FORWARD   Aliases: F11F8.28	5.1	5.8	-0.7	-3.2	64.9%	-1.5
830	AT5G22550.2   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr5:7483876-7485461 REVERSE   Aliases: MQJ16.9, MQJ16_9	2.6	2.2	0.4	3.2	65.3%	-2.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
831	AT5G26770.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g05830.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD86886.1)   chr5:9407855-9410008 REVERSE   Aliases: F2P16.30, F2P16_30	5.2	4.5	0.7	3.2	65.4%	-1.6
832	AT1G30440.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr1:10759457-10762376 FORWARD   Aliases: F26G16.2, F26G16_2	6.2	6.9	-0.7	-3.2	65.6%	-1.6
833	AT1G01510.1   Symbol: AN   C-terminal binding protein (ANGUSTIFOLIA), nearly identical to C-terminal binding protein ANGUSTIFOLIA (Arabidopsis thaliana) GI:15408535; contains Pfam profile PF02826: D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain   chr1:187211-190056 FORWARD   Aliases: ANGUSTIFOLIA, F22L4.6, F22L4_6	5.9	6.7	-0.8	-3.2	65.7%	-1.4
834	AT1G21000.1   zinc-binding family protein, similar to zinc-binding protein (Pisum sativum) GI:16117799; contains Pfam profile PF04640 : Protein of unknown function, DUF597   chr1:7337740-7339441 FORWARD   Aliases: F9H16.1, F9H16_1	6.8	5.9	0.9	3.2	65.7%	-1.5
835	AT1G64790.1   translational activator family protein, similar to HsGCN1 (Homo sapiens) GI:2282576   chr1:24068600-24085571 REVERSE   Aliases: F13O11.35, F13O11_35	5.3	6.2	-0.9	-3.2	65.7%	-1.5
836	AT1G64850.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:24100098-24101271 REVERSE   Aliases: F13O11.15, F13O11_15	10.2	9.6	0.5	3.2	65.7%	-1.9
837	AT3G47850.1   expressed protein   chr3:17665064-17666984 REVERSE   Aliases: T23J7.180	6.2	5.2	1.0	3.2	65.7%	-1.4
838	AT5G64130.2   expressed protein   chr5:25681625-25683425 REVERSE   Aliases: MHJ24.11, MHJ24_11	12.1	11.6	0.5	3.2	65.7%	-1.7
839	AT1G63800.1   ubiquitin-conjugating enzyme 5 (UBC5), E2; identical to gi:431269, SP:P42749   chr1:23671279-23672743 REVERSE   Aliases: T12P18.18, T12P18_18	10.0	8.6	1.4	3.2	65.7%	-1.5
840	AT4G14020.1   rapid alkalinization factor (RALF) family protein   chr4:8095210-8095731 REVERSE   Aliases: DL3050C, FCAALL.138	4.7	3.4	1.3	3.2	65.7%	-1.4
841	AT3G60630.1   scarecrow transcription factor family protein, scarecrow-like 6, Arabidopsis thaliana, EMBL:AF036303   chr3:22421340-22423583 REVERSE   Aliases: T4C21.40	4.6	5.6	-0.9	-3.2	65.8%	-1.4
842	AT5G15120.1   expressed protein   chr5:4898740-4900575 FORWARD   Aliases: F2G14.1	8.1	7.0	1.1	3.2	65.9%	-1.5
843	AT2G28900.1   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr2:12421191-12422655 REVERSE   Aliases: F8N16.19, F8N16_19	11.4	10.4	1.1	3.1	66.1%	-1.4
844	AT3G05060.1   SAR DNA-binding protein, putative, strong similarity to SAR DNA-binding protein-1 (Pisum sativum) GI:3132696; contains Pfam profile PF01798: Putative snoRNA binding domain; encodes NOP58-like protein   chr3:1412873-1415958 REVERSE   Aliases: T12H1.2, T12H1_2	9.4	10.5	-1.1	-3.1	66.1%	-1.4
845	AT1G29395.1   Symbol: COR414 TM1   stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi:18449100:gb:AAL69988; similar to stress-regulated protein SAP1 (Xerophyta viscosa) gi:21360378:gb:AAM47505   chr1:10288236-10289579 REVERSE   Aliases: None	4.7	3.6	1.1	3.1	66.2%	-1.4
846	AT3G15900.1   expressed protein   chr3:5376257-5377089 REVERSE   Aliases: MVC8.2	7.6	6.6	1.1	3.1	66.2%	-1.4
847	AT2G39890.1   Symbol: ProT1   proline transporter 1 (ProT1), identical to proline transporter 1 GI:1769901 from (Arabidopsis thaliana)   chr2:16662757-16665409 FORWARD   Aliases: ATPROT1, PROLINE TRANSPORTER 1, T28M21.5, T28M21_5	8.0	6.7	1.3	3.1	66.2%	-1.5
848	AT5G40780.2   Symbol: LHT1   lysine and histidine specific transporter, putative, strong similarity to lysine and histidine specific transporter GI:2576361 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr5:16340910-16344502 FORWARD   Aliases: K1B16.3, K1B16_3, LYSINE AND HISTIDINE SPECIFIC TRANSPORTER	8.7	10.0	-1.3	-3.1	66.2%	-1.5
849	AT5G52950.1   expressed protein, ; expression supported by MPSS   chr5:21491113-21494165 REVERSE   Aliases: MXC20.3, MXC20_3	3.7	6.1	-2.4	-3.1	66.2%	-1.4
850	AT5G39570.1   expressed protein   chr5:15861187-15863406 FORWARD   Aliases: MIJ24.6, MIJ24_6	13.1	13.6	-0.5	-3.1	66.2%	-1.8
851	AT3G48490.1   expressed protein   chr3:17972274-17972890 FORWARD   Aliases: T29H11.260	3.8	4.8	-1.0	-3.1	66.5%	-1.4
852	AT1G32640.1   Symbol: ATMYC2	6.7	5.6	1.2	3.1	66.6%	-1.4
853	AT5G54500.1   Symbol: FQR1   quinone reductase, putative, similar to 1,4-benzoquinone reductase (Phanerochaete chrysosporium)(GI:4454993); contains flavodoxin domain PF00258	8.5	9.4	-1.0	-3.1	66.8%	-1.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
854	AT3G24500.1   ethylene-responsive transcriptional coactivator, putative, similar to ethylene-responsive transcriptional coactivator ( <i>Lycopersicon esculentum</i> ) gi:5669634:gb:AAD46402   chr3:8918686-8919315 FORWARD   Aliases: MOB24.13	7.3	6.5	0.9	3.1	66.8%	-1.5
855	AT4G01120.1   Symbol: GBF2   G-box binding factor 2 (GBF2), identical to G-box binding factor 2 (GBF2) SP:P42775 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile: PF00170 bZIP transcription factor	8.0	6.5	1.5	3.1	66.8%	-1.5
856	AT3G27060.1   ribonucleoside-diphosphate reductase small chain, putative / ribonucleotide reductase, putative, similar to ribonucleotide reductase R2 ( <i>Nicotiana tabacum</i> ) GI:1044912; contains Pfam profile PF00268: Ribonucleotide reductase, small chain   chr3:9981103-9982532 REVERSE   Aliases: MOJ10.15	6.5	8.3	-1.8	-3.1	66.8%	-1.4
857	AT5G43580.1   protease inhibitor, putative, similar to SP:P19873 Inhibitor of trypsin and hageman factor (CMTI-V) { <i>Cucurbita maxima</i> }; contains Pfam profile PF00280: Potato inhibitor I family	2.9	4.1	-1.3	-3.1	66.9%	-1.4
858	AT4G00670.1   similar to DNA-binding protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g45820.1); similar to OSJNBb0039L24.13 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_473296.1); contains InterPro domain Remorin, C-terminal region (InterPro:IPR005516)   chr4:278335-279184 REVERSE   Aliases: F6N23.13, F6N23_13	5.0	3.4	1.6	3.1	66.9%	-1.4
859	AT1G26330.1   expressed protein   chr1:9107612-9113507 FORWARD   Aliases: F28B23.2, F28B23_2	3.5	4.8	-1.3	-3.1	66.9%	-1.4
860	AT1G52710.1   cytochrome c oxidase-related, similar to SP:P00428 Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (VI) ( <i>Bos taurus</i> )   chr1:19641999-19643891 REVERSE   Aliases: F6D8.4, F6D8_4	7.4	6.4	1.0	3.1	66.9%	-1.4
861	AT5G04320.1   expressed protein   chr5:1209236-1212547 FORWARD   Aliases: T19N18.50, T19N18_50	4.5	5.5	-1.0	-3.1	67.3%	-1.5
862	AT3G11410.1   protein phosphatase 2C, putative / PP2C, putative, identical to protein phosphatase 2C (PP2C) GB:P49598 ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF00481: Protein phosphatase 2C; identical to cDNA protein phosphatase 2C GI:633027   chr3:3583889-3585796 REVERSE   Aliases: F24K9.8	6.4	5.4	1.0	3.1	67.4%	-1.5
863	AT3G50440.1   similar to esterase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g23620.1); similar to methyl jasmonate esterase [ <i>Solanum tuberosum</i> ] (GB:AAV87151.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379); contains InterPro domain Alpha/beta hydrolase fold (InterPro:IPR000073)   chr3:18728292-18729475 REVERSE   Aliases: T20E23.40	8.4	6.5	1.8	3.1	67.5%	-1.5
864	AT5G16980.1   NADP-dependent oxidoreductase, putative, strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), <i>Arabidopsis thaliana</i>   chr5:5579146-5580783 REVERSE   Aliases: F2K13.130, F2K13_130	6.6	5.4	1.3	3.1	67.5%	-1.4
865	AT5G11980.1   conserved oligomeric Golgi complex component-related / COG complex component-related, similar to SP:Q96MW5 Conserved oligomeric Golgi complex component 8 { <i>Homo sapiens</i> }; contains Pfam profile PF04124: Dor1-like family   chr5:3868653-3872270 REVERSE   Aliases: F14F18.150, F14F18_150	5.7	6.8	-1.1	-3.1	67.5%	-1.5
866	AT1G11380.1   expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614   chr1:3832623-3834189 FORWARD   Aliases: T23J18.4, T23J18_4	5.9	4.4	1.5	3.1	67.5%	-1.5
867	AT5G04440.1   expressed protein   chr5:1254949-1256954 FORWARD   Aliases: T19N18.1	7.2	6.2	1.0	3.1	67.6%	-1.5
868	AT5G08750.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:2851980-2854496 FORWARD   Aliases: None	7.9	7.2	0.7	3.1	67.7%	-1.6
869	AT5G44520.1   ribose 5-phosphate isomerase-related, low similarity to SP:P47968 Ribose 5-phosphate isomerase (EC 5.3.1.6) (Phosphoriboisomerase) { <i>Mus musculus</i> }   chr5:17951514-17953751 REVERSE   Aliases: MFC16.20, MFC16_20	6.3	5.4	0.9	3.1	67.7%	-1.5
870	AT1G24020.1   Bet v I allergen family protein, similar to major pollen allergen Bet v 1 GB:CAA96544 GI:1321726 from ( <i>Betula pendula</i> ); contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:8500466-8501504 REVERSE   Aliases: T23E23.28, T23E23_28	3.6	4.3	-0.7	-3.1	67.7%	-1.6
871	AT5G20990.1   Symbol: CHL6/CNX/CNX1/SIR4   Involved in molybdenum cofactor (Moco) biosynthesis, inserting Mo into Molybdopterin. sir loss-of-function mutants are resistant to sirtinol, a modulator of auxin signaling.   chr5:7128477-7133459 REVERSE   Aliases: CHL6, CHLORATE RESISTANT 6, CNX, CNX1, COFACTOR OF NR/CHL6, MOLYBDENUM COFACTOR BIOSYNTHESIS ENZYME CNX1, SIR4, T10F18.20, T10F18_20	7.8	8.5	-0.7	-3.1	67.7%	-1.7
872	AT5G17980.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr5:5953598-5956747 FORWARD   Aliases: MCM23.5, MCM23_5	4.4	3.7	0.7	3.1	67.7%	-1.6
873	AT5G43080.1   Symbol: CYCA3;1   cyclin, putative, similar to A-type cyclins from ( <i>Nicotiana tabacum</i> ) GI:1064931, ( <i>Catharanthus roseus</i> ) GI:2190259; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr5:17310455-17312017 FORWARD   Aliases: CYCA3;1, Cyclin A3;1, MMG4.10, MMG4_10	3.8	4.7	-0.9	-3.1	68.2%	-1.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
874	AT4G38430.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr4:17986461-17988801 FORWARD   Aliases: F22I13.200, F22I13_200, KINASE PARTNER PROTEIN LIKE, KPP LIKE	3.0	4.1	-1.1	-3.1	68.2%	-1.4
875	AT5G60690.1   Symbol: REV   homeodomain-leucine zipper protein Revoluta (REV) / fascicular fiberless 1 (IFL1), identical to HD-zip transcription factor Revoluta (GI:9759333) {Arabidopsis thaliana}; contains Pfam profiles PF01852: START domain and PF00046: Homeobox domain   chr5:24414249-24419779 FORWARD   Aliases: HOMEODOMAIN LEUCINE ZIPPER PROTEIN, HOMEODOMAIN LEUCINE ZIPPER PROTEIN IFL1, IFL, IFL1, INTERFASCICULAR FIBERLESS 1, MUP24.16, MUP24_16, REVOLUTA	6.9	7.9	-1.0	-3.1	68.2%	-1.7
876	AT1G44900.1   DNA replication licensing factor, putative, similar to DNA replication licensing factor MCM2 from {Xenopus laevis} SP:P55861, SP:P49736 {Homo sapiens}; contains Pfam profile PF00493: MCM2/3/5 family   chr1:16972701-16977030 FORWARD   Aliases: T12C22.19, T12C22_19	3.3	4.9	-1.6	-3.1	68.2%	-1.4
877	AT1G77640.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr1:29183631-29184563 FORWARD   Aliases: T5M16.23, T5M16_23	4.9	3.9	1.0	3.1	68.2%	-1.4
878	AT1G29980.2   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr1:10503264-10504827 REVERSE   Aliases: T1P2.9, T1P2_9	5.0	6.9	-1.9	-3.1	68.2%	-1.4
879	AT5G59950.3   RNA and export factor-binding protein, putative   chr5:24157421-24159084 FORWARD   Aliases: MMN10.26, MMN10_26	7.2	6.3	1.0	3.1	68.3%	-1.6
880	AT2G24590.1   splicing factor, putative, similar to to RSZp22 protein (Arabidopsis thaliana) gi:2582645:emb:CAA05352   chr2:10456710-10458240 FORWARD   Aliases: F25P17.11, F25P17_11	5.8	4.9	0.9	3.1	68.3%	-1.5
881	AT3G26830.1   Symbol: PAD3   cytochrome P450 71B15, putative (CYP71B15), Identical to Cytochrome P450 (SP:Q9LW27) (Arabidopsis thaliana); similar to cytochrome P450 71B2 GB:O65788 (Arabidopsis thaliana)   chr3:9889190-9890942 FORWARD   Aliases: CYP71B15, MDJ14.12, PHYTOALEXIN DEFICIENT 3	4.7	6.0	-1.3	-3.1	68.3%	-1.5
882	AT5G02520.1   expressed protein   chr5:562392-564004 FORWARD   Aliases: T22P11.110, T22P11_110	3.9	5.2	-1.2	-3.1	68.3%	-1.6
883	AT5G54680.1   basic helix-loop-helix (bHLH) family protein, similar to unknown protein (pir :B71406)   chr5:22234286-22236830 FORWARD   Aliases: K5F14.2, K5F14_2	9.7	9.0	0.8	3.1	68.3%	-1.7
884	AT1G16170.1   expressed protein   chr1:5538731-5539790 REVERSE   Aliases: T24D18.25, T24D18_25	9.4	8.9	0.6	3.1	68.3%	-1.9
885	AT3G06030.1   Symbol: ANP3   NPK1-related protein kinase, putative (ANP3), similar to protein kinase (Nicotiana tabacum) gi:456309:dbj:BAA05648; identical to cDNA NPK1-related protein kinase 3 GI:2342426   chr3:1818749-1822846 REVERSE   Aliases: F24F17.1, F24F17_1, MAPKKK12	4.5	5.5	-1.0	-3.1	68.3%	-1.5
886	AT5G40480.1   Symbol: EMB3012   expressed protein, ; expression supported by MPSS   chr5:16230589-16241210 FORWARD   Aliases: EMB3012, EMBRYO DEFECTIVE 3012, K21I16.30, K21I16_30	5.8	6.9	-1.1	-3.1	68.4%	-1.5
887	AT1G74410.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:27969215-27971563 FORWARD   Aliases: F1M20.9, F1M20_9	6.3	5.5	0.8	3.1	68.6%	-1.5
888	AT1G70990.1   proline-rich family protein   chr1:26770959-26771738 REVERSE   Aliases: F15H11.18, F15H11_18	4.4	3.7	0.7	3.1	68.6%	-1.7
889	AT1G58170.1   disease resistance-responsive protein-related / dirigent protein-related, similar to dirigent protein (Thuja plicata) gi:6694699:gb:AAF25360; similar to pathogenesis-related protein (Pisum sativum) gi:4585273:gb:AAD25355   chr1:21539793-21540501 FORWARD   Aliases: T15M6.17	4.8	5.4	-0.6	-3.1	68.6%	-1.7
890	AT5G05560.1   Symbol: APC1   E3 ubiquitin ligase, putative, E3, ubiquitin ligase; contains similarity to Apc1/Tsg24 protein, the largest subunit of human anaphase-promoting complex (APC/C) GI:11967711 from (Homo sapiens)   chr5:1641453-1654757 FORWARD   Aliases: MOP10.10, MOP10_10	3.8	4.8	-0.9	-3.1	68.6%	-1.5
891	AT3G06210.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g18980.1); similar to BLE2 protein-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910813.1); contains InterPro domain Armadillo repeat (InterPro:IPR000225)   chr3:1880753-1883497 FORWARD   Aliases: F28L1.15, F28L1_15	6.8	5.8	0.9	3.1	68.6%	-1.7
892	AT1G35230.1   Symbol: AGP5   arabinogalactan-protein (AGP5), identical to gi_3883128_gb_AAC77827   chr1:12917127-12917741 FORWARD   Aliases: ARABINO GALACTAN PROTEIN 5, T9I1.2, T9I1_2	2.9	3.5	-0.6	-3.1	68.6%	-1.8
893	AT3G18500.1   similar to endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana] (TAIR:At1g73875.1); similar to endonuclease/exonuclease/phosphatase family protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD52532.1); contains InterPro domain Endonuclease/exonuclease/phosphatase family (InterPro:IPR005135)   chr3:6352544-6355446 FORWARD   Aliases: MYF24.23	5.1	4.1	1.0	3.1	68.6%	-1.5
894	AT2G37280.1   ABC transporter family protein, similar to PDR5-like ABC transporter GI:1514643 from (Spirodela polyrhiza)   chr2:15657479-15663496 FORWARD   Aliases: F3G5.7, F3G5_7	6.1	7.1	-1.1	-3.1	68.6%	-1.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
895	AT3G54250.1   mevalonate diphosphate decarboxylase, putative, similar to mevalonate diphosphate decarboxylase (Arabidopsis thaliana) gi:2288887:emb:CAA74700   chr3:20093286-20095710 REVERSE   Aliases: F24B22.210	3.8	4.5	-0.7	-3.1	68.6%	-1.6
896	AT2G28200.1   similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At5g04390.1); similar to putative zinc finger protein [Pisum sativum] (GB:CAA60828.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087)	6.2	5.2	1.0	3.1	68.6%	-1.6
897	AT3G05260.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily   chr3:1497495-1498979 REVERSE   Aliases: T12H1.23, T12H1_23	3.3	2.8	0.6	3.1	68.8%	-1.9
898	AT2G41180.1   sigA-binding protein-related, low similarity to SigA binding protein (Arabidopsis thaliana) GI:6980074; contains Pfam domain PF05678: VQ motif   chr2:17172269-17173103 FORWARD   Aliases: T3K9.5, T3K9_5	4.3	3.5	0.8	3.1	68.9%	-1.6
899	AT5G54290.1   cytochrome c biogenesis protein family, low similarity to cytochrome c biogenesis protein CcdA (Paracoccus pantotrophus) GI:11095328; contains Pfam profile PF02683: Cytochrome C biogenesis protein transmembrane region   chr5:22068263-22071604 FORWARD   Aliases: MDK4.11, MDK4_11	9.7	8.4	1.3	3.1	69.2%	-1.5
900	AT2G27970.1   Symbol: CKS2   cyclin-dependent kinase, putative / CDK, putative, similar to Cks1 protein (Arabidopsis thaliana) gi:2274859:emb:CAA03859   chr2:11919295-11920348 REVERSE   Aliases: CDK subunit 2, CKS2, T1E2.11, T1E2_11	8.2	9.9	-1.7	-3.1	69.2%	-1.6
901	AT2G33710.1   encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	3.0	2.7	0.3	3.1	69.2%	-2.3
902	AT1G18540.1   60S ribosomal protein L6 (RPL6A), similar to 60S ribosomal protein L6 GI:7208784 from (Cicer arietinum)   chr1:6377314-6378571 REVERSE   Aliases: F25I16.12, F25I16_12	11.9	12.5	-0.6	-3.1	69.4%	-1.8
903	AT1G73600.2   phosphoethanolamine N-methyltransferase 3, putative (NMT3), strong similarity to SP:Q9FR44 Phosphoethanolamine N-methyltransferase 1 (EC 2.1.1.103) (PEAMT 1) (AtNMT1) {Arabidopsis thaliana}; identical to SP:Q9C6B9 Putative phosphoethanolamine N-methyltransferase 3 {Arabidopsis thaliana}   chr1:27672813-27677230 FORWARD   Aliases: F6D5.1, F6D5_1	6.5	8.4	-1.9	-3.1	69.7%	-1.5
904	AT3G15620.2   Symbol: UVR3   similar to cryptochrome dash (CRYD) [Arabidopsis thaliana] (TAIR:At5g24850.1); similar to 6-4 photolyase [Dunaliella salina] (GB:AAX56342.1); contains InterPro domain FAD binding domain of DNA photolyase (InterPro:IPR005101); contains InterPro domain FAD binding domain of DNA photolyase, N-terminal (InterPro:IPR006051); contains InterPro domain DNA photolyase, N-terminal (InterPro:IPR006050)   chr3:5293313-5296599 REVERSE   Aliases: 6 4 PHOTOLYASE, MSJ11.2, UV REPAIR DEFECTIVE 4	3.1	3.7	-0.6	-3.1	69.7%	-1.8
905	AT5G06460.1   Symbol: ATUBA2	7.7	8.6	-0.9	-3.1	69.7%	-1.6
906	AT5G18670.1   Symbol: BMY3   beta-amylase, putative (BMY3) / 1,4-alpha-D-glucan maltohydrolase, putative, almost identical to beta-amylase BMY3 GI:15149457 from (Arabidopsis thaliana); identical to cDNA putative beta-amylase BMY3 (BMY3) GI:15149456   chr5:6225958-6228134 FORWARD   Aliases: T1A4.50, T1A4_50	7.2	6.6	0.7	3.1	69.7%	-1.7
907	AT3G15580.1   Symbol: APG8H   autophagy 8i (APG8i), identical to autophagy 8i (Arabidopsis thaliana) GI:19912167; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3; supporting cDNA gi:21636957:gb:AF492760.1:   chr3:5273902-5275102 REVERSE   Aliases: MQD17.3	11.9	11.3	0.6	3.1	69.7%	-2.1
908	AT1G04250.1   Symbol: AXR3   auxin-responsive protein / indoleacetic acid-induced protein 17 (IAA17), Identical to SP:P93830 Auxin-responsive protein IAA17 (Indoleacetic acid-induced protein 17) {Arabidopsis thaliana}; ESTs gb:H36782 and gb:F14074 come from this gene   chr1:1136257-1138582 FORWARD   Aliases: AUXIN RESISTANT 3, F19P19.31, F19P19_31, IAA17	4.0	5.7	-1.7	-3.1	69.8%	-1.5
909	AT1G33055.1   expressed protein   chr1:11972220-11972570 REVERSE   Aliases: None	6.9	3.9	3.0	3.1	69.8%	-1.5
910	AT2G15820.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profiles PF01535: PPR repeat, PF03161 LAGLIDADG DNA endonuclease family	3.7	4.3	-0.6	-3.1	69.8%	-1.9
911	AT3G13160.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:4229978-4231293 REVERSE   Aliases: MJG19.11	5.6	7.1	-1.4	-3.1	69.8%	-1.5
912	AT3G50060.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA MYB-related protein (1107 bp) GI:1263096   chr3:18568955-18570089 REVERSE   Aliases: F3A4.140	5.1	4.2	0.8	3.1	69.9%	-1.6
913	AT1G54990.1   expressed protein   chr1:20515186-20517348 FORWARD   Aliases: F14C21.51, F14C21_51	7.1	7.9	-0.8	-3.1	70.0%	-1.6
914	AT5G12970.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr5:4102138-4105330 FORWARD   Aliases: T24H18.140, T24H18_140	3.1	4.8	-1.7	-3.1	70.1%	-1.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
915	AT3G05190.1   aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV   chr3:1471403-1475790 FORWARD   Aliases: T12H1.16, T12H1_16	6.5	5.2	1.3	3.1	70.4%	-1.5
916	AT1G60710.1   Symbol: ATB2   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:22358418-22360407 REVERSE   Aliases: F8A5.23, F8A5_23	10.4	11.7	-1.3	-3.1	70.4%	-1.9
917	AT1G15260.1   expressed protein, EST gb:N65467 comes from this gene   chr1:5249755-5250568 FORWARD   Aliases: F9L1.20, F9L1_20	3.5	4.7	-1.2	-3.1	70.4%	-1.5
918	AT4G32340.1   expressed protein   chr4:15612597-15614259 REVERSE   Aliases: F8B4.40	7.4	6.1	1.3	3.1	70.4%	-1.5
919	AT1G78780.2   pathogenesis-related family protein, contains similarity to pathogen-related protein (GI:499073) (Swiss-Prot:P16273) (Hordeum vulgare)   chr1:29626237-29627338 REVERSE   Aliases: F9K20.18, F9K20_18	7.1	5.5	1.5	3.1	70.4%	-1.5
920	AT1G60970.1   clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	7.8	6.2	1.7	3.1	70.4%	-1.5
921	AT1G53170.1   Symbol: ATERF 8/ATERF8	3.7	4.7	-1.0	-3.1	70.4%	-1.6
922	AT4G26830.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr4:13495047-13496493 REVERSE   Aliases: F10M23.170, F10M23_170	4.2	3.4	0.8	3.0	70.4%	-1.7
923	AT1G66180.1   aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease profile; similar to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) (Nicotiana tabacum)   chr1:24650851-24652476 FORWARD   Aliases: F15E12.7, F15E12_7	7.4	6.5	0.9	3.0	70.4%	-2.0
924	AT5G02550.1   expressed protein   chr5:573052-573556 REVERSE   Aliases: T22P11.140, T22P11_140	3.5	4.7	-1.2	-3.0	70.4%	-1.7
925	AT1G33590.1   disease resistance protein-related / LRR protein-related, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596   chr1:12177757-12179393 FORWARD   Aliases: T1E4.3, T1E4_3	5.7	6.5	-0.8	-3.0	70.6%	-1.6
926	AT5G15230.1   Symbol: GASA4   gibberellin-regulated protein 4 (GASA4) / gibberellin-responsive protein 4, identical to SP:P46690 Gibberellin-regulated protein 4 precursor {Arabidopsis thaliana}   chr5:4944906-4946219 FORWARD   Aliases: F8M21.120, F8M21_120	5.6	7.6	-2.0	-3.0	70.6%	-1.5
927	AT2G46920.2   Symbol: POL   protein phosphatase 2C family protein / PP2C family protein, similar to protein phosphatase-2c (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain   chr2:19285056-19288283 REVERSE   Aliases: F14M4.25, POLTERGEIST	6.1	7.3	-1.2	-3.0	70.8%	-1.6
928	AT5G14340.1   myb family transcription factor (MYB40), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:4623370-4624850 FORWARD   Aliases: F18O22.130, F18O22_130	5.1	4.2	1.0	3.0	70.8%	-1.5
929	AT5G51200.1   expressed protein   chr5:20822152-20836818 FORWARD   Aliases: MWD22.15, MWD22_15	5.7	6.9	-1.2	-3.0	70.8%	-1.6
930	AT2G01990.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g14630.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD38245.1)   chr2:465018-466723 REVERSE   Aliases: F14H20.6, F14H20_6	3.3	4.0	-0.7	-3.0	70.9%	-1.7
931	AT4G29140.1   MATE efflux protein-related, several hypothetical proteins - Arabidopsis thaliana; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr4:14368925-14370898 FORWARD   Aliases: F19B15.170, F19B15_170	9.2	7.9	1.3	3.0	71.0%	-1.5
932	AT3G07130.1   serine/threonine protein phosphatase family protein, contains similarity to purple acid phosphatase (Arabidopsis thaliana) gi:20257489:gb:AAM15914   chr3:2255716-2258011 REVERSE   Aliases: T1B9.21	6.8	7.7	-0.9	-3.0	71.1%	-1.6
933	AT1G31760.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr1:11372407-11373463 REVERSE   Aliases: F5M6.23	6.3	5.4	1.0	3.0	71.1%	-1.6
934	AT1G13990.1   expressed protein   chr1:4794761-4796594 FORWARD   Aliases: F7A19.8, F7A19_8	7.1	6.1	1.0	3.0	71.3%	-1.6
935	AT5G55820.1   expressed protein   chr5:22603513-22611261 FORWARD   Aliases: MDF20.26, MDF20_26	2.8	3.3	-0.5	-3.0	71.4%	-1.9
936	AT1G70370.1   BURP domain-containing protein / polygalacturonase, putative, similar to polygalacturonase isoenzyme 1 beta subunit (Lycopersicon esculentum) GI:170480; contains Pfam profile PF03181: BURP domain   chr1:26516385-26518851 REVERSE   Aliases: F17O7.9, F17O7_9	8.3	9.1	-0.8	-3.0	71.4%	-1.9
937	AT1G23850.1   expressed protein   chr1:8425728-8427062 REVERSE   Aliases: T23E23.1, T23E23_1	6.2	5.2	1.0	3.0	71.8%	-1.6
938	AT2G32150.1   haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	5.8	4.7	1.1	3.0	71.9%	-1.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
939	AT2G06050.2   Symbol: OPR3   12-oxophytodienoate reductase (OPR3) / delayed dehiscence1 (DDE1), nearly identical to DELAYED DEHISCENCE1 (GI:7688991) and to OPR3 (GI:10242314); contains Pfam profile PF00724:oxidoreductase, FAD/FMN-binding; identical to cDNA OPDA-reductase homolog GI:5059114   chr2:2359112-2362124 REVERSE   Aliases: 12 OXO PHYTODIENOATE REDUCTASE, 12 OXOPHYTODIENOATE 10,11 REDUCTASE, F5K7.19, F5K7_19	11.0	9.3	1.7	3.0	72.1%	-1.6
940	AT1G74450.1   expressed protein   chr1:27986170-27987941 FORWARD   Aliases: F1M20.13, F1M20_13	5.7	4.6	1.1	3.0	73.1%	-1.7
941	AT4G31790.2   diphthine synthase, putative (DPH5), similar to	3.6	4.8	-1.2	-3.0	73.2%	-1.6
942	AT1G24010.1   expressed protein   chr1:8498792-8499488 REVERSE   Aliases: T23E23.27, T23E23_27	2.7	3.1	-0.5	-3.0	73.3%	-2.0
943	AT2G46560.1   transducin family protein / WD-40 repeat family protein, similar to CPY (GI:3096961) {Chironomus thummi}; contains Pfam PF00400: WD domain, G-beta repeat (8 copies, 3 weak):9780477:gb:BE522499.1:BE522499   chr2:19122443-19132928 REVERSE   Aliases: F13A10.9	5.9	7.1	-1.2	-3.0	73.6%	-1.6
944	AT3G07560.1   glycine-rich protein   chr3:2411327-2413420 REVERSE   Aliases: F21O3.27	8.8	7.7	1.1	3.0	73.6%	-1.8
945	AT1G28530.2   expressed protein   chr1:10031983-10035485 REVERSE   Aliases: F3M18.3	3.9	4.6	-0.7	-3.0	73.6%	-1.7
946	AT2G46610.2   arginine/serine-rich splicing factor, putative, similar to SP:P92964 Arginine/serine-rich splicing factor RSP31 {Arabidopsis thaliana}   chr2:19143672-19145751 REVERSE   Aliases: F13A10.14	7.2	5.7	1.5	3.0	73.6%	-1.6
947	AT2G44130.1   kelch repeat-containing F-box family protein, very low similarity to SP:Q9ER30 Kelch-related protein 1 (Sarcosin) {Rattus norvegicus}; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:18260686-18262130 FORWARD   Aliases: F6E13.26	5.8	4.6	1.2	3.0	73.7%	-1.6
948	AT5G18040.1   expressed protein   chr5:5972421-5974158 FORWARD   Aliases: MCM23.14, MCM23_14	10.1	9.3	0.8	3.0	73.7%	-1.7
949	AT5G14660.2   Symbol: PDF1B   peptide deformylase, chloroplast / polypeptide deformylase 1B (PDF1B), identical to SP:Q9FUZ2 Peptide deformylase, chloroplast precursor (EC 3.5.1.88) (PDF) (Polypeptide deformylase) {Arabidopsis thaliana}; supporting cDNA gi:11320965:gb:AF269165.1:AF269165   chr5:4726736-4728749 REVERSE   Aliases: DEF2, PEPTIDE DEFORMYLASE, PEPTIDE DEFORMYLASE 1B	4.1	5.1	-1.0	-3.0	73.8%	-1.7
950	AT1G14040.1   similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03250.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03260.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03240.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g35350.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g26730.1); similar to putative PHO1-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_549873.1); contains InterPro domain SPX, N-terminal (InterPro:IPR004331); contains InterPro domain EXS, C-terminal (InterPro:IPR004342)   chr1:4810485-4814540 FORWARD   Aliases: F7A19.13, F7A19_13	5.9	6.8	-0.9	-3.0	74.0%	-1.7
951	AT1G14340.1   RNA recognition motif (RRM)-containing protein   chr1:4897341-4898956 FORWARD   Aliases: F14L17.11, F14L17_11	7.8	6.6	1.2	3.0	74.0%	-1.7
952	AT3G29240.2   expressed protein, similar to At1g33780 (Arabidopsis thaliana); contains Pfam profile PF02622: Uncharacterized ACR, COG1678   chr3:11192843-11194223 FORWARD   Aliases: MXO21.9	7.7	6.9	0.7	3.0	74.0%	-1.7
953	AT3G45980.1   histone H2B, identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr3:16907801-16908998 REVERSE   Aliases: F16L2.190	10.3	11.4	-1.1	-3.0	74.0%	-1.8
954	AT1G06520.1   Symbol: ATGPAT1/GPAT1   Encodes a membrane associated mitochondrial localized protein with glycerol-3-phosphate acyltransferase activity. Expressed in flower buds and siliques. Homozygous mutant plants are male sterile and have abnormal glycerolipid levels.   chr1:1993977-1996111 REVERSE   Aliases: ATGPAT1, F12K11.15, F12K11_15, GPAT1	3.3	3.9	-0.5	-3.0	74.0%	-1.9
955	AT4G36600.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to SP:P20075 Embryonic protein DC-8 {Daucus carota}; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr4:17263656-17265155 FORWARD   Aliases: AP22.17, AP22_17	5.1	4.1	1.1	3.0	74.1%	-1.6
956	AT3G11710.1   lysyl-tRNA synthetase, putative / lysine--tRNA ligase, putative, similar to SP:Q43776 Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) {Lycopersicon esculentum}; contains Pfam profile PF00152: tRNA synthetases class II (D, K and N)   chr3:3702179-3705707 REVERSE   Aliases: T19F11.11, T19F11_11	9.6	10.5	-0.9	-3.0	74.1%	-1.7
957	AT5G42990.1   ubiquitin-conjugating enzyme 18 (UBC18), E2; identical to gi:2801448   chr5:17261219-17263182 REVERSE   Aliases: MBD2.19, MBD2_19	6.5	7.4	-1.0	-3.0	74.2%	-1.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
958	AT1G59760.1   ATP-dependent RNA helicase, putative, similar to SP:P47047 ATP-dependent RNA helicase DOB1 {Saccharomyces cerevisiae}, HUA enhancer 2 (Arabidopsis thaliana) GI:16024936; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr1:21988136-21993838 REVERSE   Aliases: F23H11.8, F23H11_8	6.8	7.8	-0.9	-3.0	74.2%	-1.7
959	AT3G61090.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr3:22620069-22620797 REVERSE   Aliases: T27I15.180	4.2	3.5	0.6	3.0	74.2%	-1.8
960	AT1G67120.1   midasin-related, similar to Midasin (MIDAS-containing protein) (Swiss-Prot:Q12019) (Saccharomyces cerevisiae); similar to Midasin (MIDAS-containing protein) (Swiss-Prot:Q9NU22) (Homo sapiens); contains Prosite PS00017: ATP/GTP-binding site motif A (P-loop)	4.2	4.9	-0.7	-3.0	74.3%	-1.8
961	AT4G36540.2   basic helix-loop-helix (bHLH) family protein, contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	4.8	5.5	-0.7	-3.0	74.4%	-1.7
962	AT3G62300.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr3:23065079-23068163 FORWARD   Aliases: T17J13.260	6.1	7.1	-1.0	-3.0	74.4%	-1.6
963	AT2G17220.2   protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548   chr2:7494757-7497258 REVERSE   Aliases: T23A1.8, T23A1_8	7.9	6.4	1.5	3.0	74.4%	-1.6
964	AT3G12700.1   aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease; similar to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) (Nicotiana tabacum)   chr3:4037077-4039141 FORWARD   Aliases: MBK21.7	4.8	5.8	-1.0	-3.0	74.4%	-1.6
965	AT5G42830.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:17193612-17195246 FORWARD   Aliases: MBD2.2, MBD2_2	4.9	5.8	-1.0	-3.0	74.4%	-1.6
966	AT4G25590.1   similar to actin-depolymerizing factor, putative [Arabidopsis thaliana] (TAIR:At5g52360.1); similar to pollen specific actin-depolymerizing factor 1 [Nicotiana tabacum] (GB:AAL91666.1); contains InterPro domain Actin-binding, cofilin/tropomyosin type (InterPro:IPR002108)   chr4:13058945-13060116 REVERSE   Aliases: M7J2.40, M7J2_40	3.6	3.0	0.6	3.0	74.4%	-1.9
967	AT3G13560.3   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis)	5.8	6.9	-1.1	-3.0	74.4%	-1.6
968	AT2G20680.1   glycosyl hydrolase family 5 protein / cellulase family protein, similar to (1-4)-beta-mannan endohydrolase (Coffea arabica) GI:10178872; contains Pfam profile PF00150: Cellulase (glycosyl hydrolase family 5)   chr2:8927548-8930254 FORWARD   Aliases: F5H14.35, F5H14_35	5.3	5.9	-0.7	-3.0	74.4%	-1.9
969	AT3G03870.2   expressed protein, predicted using genefinder   chr3:995224-997417 FORWARD   Aliases: F20H23.8, F20H23_8	5.3	4.5	0.8	3.0	74.4%	-1.7
970	AT1G30960.1   GTP-binding protein (ERG), identical to GTP-binding protein ERG SP:O82653 from (Arabidopsis thaliana)   chr1:11037635-11039982 REVERSE   Aliases: F17F8.15	4.3	5.5	-1.2	-3.0	74.4%	-1.6
971	AT4G29170.1   Mnd1 family protein, contains Pfam PF03962: Mnd1 family   chr4:14382845-14385381 FORWARD   Aliases: F19B15.200, F19B15_200	3.3	4.3	-1.1	-3.0	74.4%	-1.7
972	AT3G56870.1   expressed protein   chr3:21063452-21066569 FORWARD   Aliases: T8M16.200	3.2	4.1	-0.9	-3.0	74.4%	-1.6
973	AT2G01760.1   Symbol: ARR14   two-component responsive regulator family protein / response regulator family protein, similar to response regulator 9 (GI:14189890) (Zea mays); similar to ARR1 protein (GI:4210449) (Arabidopsis thaliana); contains Pfam profile: PF00072 response regulator receiver domain	3.0	3.5	-0.6	-3.0	74.4%	-1.9
974	AT2G31650.1   trithorax 1 (ATX-1) (TRX1), identical to trithorax-like protein 1 GI:12659210 from (Arabidopsis thaliana); characterized in Alvarez-Venegas R, et al, ATX-1, an Arabidopsis Homolog of Trithorax, Activates Flower Homeotic Genes. (Curr Biol. 2003 Apr 15;13(8):627-37 PMID: 12699618); contains Pfam profiles PF00856: SET domain, PF00855: PWWP domain, PF00628, PHD-finger; identical to cDNA	4.4	5.1	-0.7	-3.0	74.4%	-1.8
975	AT3G02840.1   immediate-early fungal elicitor family protein, similar to immediate-early fungal elicitor protein CMPG1 (GI:14582200) (Petroselinum crispum)   chr3:618416-619693 FORWARD   Aliases: F13E7.22, F13E7_22	5.0	4.2	0.9	3.0	74.4%	-1.7
976	AT5G10750.1   expressed protein   chr5:3398952-3400157 FORWARD   Aliases: MAJ23.2	6.2	5.2	1.0	3.0	74.4%	-1.7
977	AT3G61360.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:22715279-22717113 REVERSE   Aliases: T20K12.260	3.5	4.3	-0.8	-3.0	74.4%	-1.7
978	AT1G78210.1   hydrolase, alpha/beta fold family protein, low similarity to hydrolases from Rhodococcus sp. EtbD2 GI:3273241, EtbD1 GI:3273239; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:29427611-29429268 REVERSE   Aliases: T11I11.15, T11I11_15	6.5	7.3	-0.8	-3.0	74.5%	-1.8
979	AT1G72790.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:27398409-27400461 FORWARD   Aliases: F28P22.2, F28P22_2	3.6	2.8	0.8	3.0	74.5%	-1.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
980	AT2G24170.1   endomembrane protein 70, putative, similar to MURA transposase of maize Mutator transposon   chr2:10281224-10284066 REVERSE   Aliases: F27D4.8, F27D4_8	4.7	5.6	-0.9	-3.0	74.6%	-1.7
981	AT5G59780.3   Symbol: MYB59   myb family transcription factor (MYB59), contains PFAM profile: myb DNA binding domain PF00249   chr5:24099423-24100612 REVERSE   Aliases: MTH12.19, MTH12_19	7.0	5.4	1.6	3.0	74.6%	-1.6
982	AT5G23090.4   similar to TATA-binding protein-associated phosphoprotein Dr1 protein, putative [Arabidopsis thaliana] (TAIR:At5g08190.1); similar to repressor protein [Oryza sativa] (GB:AAL73485.1); contains InterPro domain Transcription factor CBF/NF-Y/archaeal histone (InterPro:IPR003958); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124)   chr5:7749073-7750541 FORWARD   Aliases: MYJ24.8, MYJ24_8	6.9	6.3	0.5	3.0	74.6%	-1.9
983	AT3G46010.1   Symbol: ADF1   actin-depolymerizing factor 1 (ADF1), identical to SP:Q39250 Actin-depolymerizing factor 1 (ADF-1) (AtADF1) {Arabidopsis thaliana}   chr3:16920391-16921805 REVERSE   Aliases: ACTIN DEPOLYMERIZING FACTOR 1, ATADF, ATADF1, F16L2.220	12.9	11.9	1.0	3.0	74.6%	-1.8
984	AT3G50240.1   Symbol: KICP 02   kinesin motor protein-related, KINESIN-LIKE PROTEIN KIF4, Homo sapiens, EMBL:AF179308	4.1	4.9	-0.9	-3.0	74.6%	-1.7
985	AT3G17900.1   expressed protein   chr3:6128539-6133389 FORWARD   Aliases: MEB5.12	4.3	4.9	-0.6	-3.0	74.9%	-1.8
986	AT5G52220.1   expressed protein, ; expression supported by MPSS   chr5:21224456-21224904 REVERSE   Aliases: F17P19.12, F17P19_12	5.3	6.9	-1.7	-3.0	74.9%	-1.6
987	AT4G33090.1   Symbol: APM1   aminopeptidase M, similar to SP:Q11011 Puromycin-sensitive aminopeptidase (EC 3.4.11.-) (PSA) {Mus musculus}; contains Pfam profile PF01433: Peptidase family M1	8.4	9.5	-1.2	-3.0	75.3%	-1.8
988	AT1G25275.3   expressed protein   chr1:8860659-8861349 FORWARD   Aliases: None	11.5	11.0	0.6	3.0	75.3%	-2.3
989	AT4G25900.1   aldose 1-epimerase family protein, similar to apospory-associated protein C; APOC (Chlamydomonas reinhardtii) GI:6970044 Pfam profile PF01263: Aldose 1-epimerase   chr4:13161388-13163607 FORWARD   Aliases: F14M19.180, F14M19_180	6.2	7.5	-1.3	-3.0	75.3%	-1.6
990	AT4G37560.1   formamidase, putative / formamide amidohydrolase, putative, similar to SP:Q50228 Formamidase (EC 3.5.1.49) (Formamide amidohydrolase) {Methylophilus methylotrophus}; contains Pfam profile PF03069: Acetamidase/Formamidase family   chr4:17646402-17648616 FORWARD   Aliases: F19F18.50, F19F18_50	2.6	2.3	0.3	3.0	75.3%	-2.6
991	AT4G18130.1   Symbol: PHYE   phytochrome E (PHYE), identical to SP:P42498 Phytochrome E {Arabidopsis thaliana}   chr4:10041878-10045960 REVERSE   Aliases: F15J5.100, F15J5_100, PHYTOCHROME DEFECTIVE E, PHYTOCHROME E	5.2	5.9	-0.7	-3.0	75.5%	-2.0
992	AT5G48910.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:19850098-19852160 REVERSE   Aliases: K19E20.2, K19E20_2	5.2	5.9	-0.7	-3.0	75.5%	-1.7
993	AT2G43430.2   Symbol: GLX2 1	8.1	7.0	1.1	3.0	75.5%	-1.9
994	AT2G16740.1   ubiquitin-conjugating enzyme, putative, strong similarity to SP:P35133 Ubiquitin-conjugating enzyme E2-17 kDa 10 (EC 6.3.2.19) (Ubiquitin- protein ligase 10) (Ubiquitin carrier protein 10) {Arabidopsis thaliana}; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	6.3	5.0	1.2	3.0	75.5%	-1.6
995	AT1G03510.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:876259-877548 REVERSE   Aliases: F21B7.13	3.3	3.7	-0.4	-3.0	75.9%	-2.4
996	AT4G28706.3   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr4:14167761-14170748 FORWARD   Aliases: None	5.5	6.3	-0.8	-3.0	75.9%	-2.0
997	AT4G17840.1   expressed protein   chr4:9918067-9920488 REVERSE   Aliases: T6K21.20, T6K21_20	7.2	6.2	1.1	2.9	76.1%	-1.7
998	AT4G31910.1   transferase family protein, low similarity to anthranilate N-hydroxycinnamoyl/benzoyltransferase Dianthus caryophyllus GI:3288180, 10-deacetylbaecatin III-10-O-acetyl transferase Taxus cuspidata GI:6746554; contains Pfam profile PF02458 transferase family   chr4:15441088-15443906 FORWARD   Aliases: F11C18.110, F11C18_110	5.8	7.4	-1.6	-2.9	76.1%	-1.6
999	AT3G11660.1   Symbol: NHL1   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)   chr3:3678841-3679949 REVERSE   Aliases: T19F11.6	5.7	4.4	1.3	2.9	76.1%	-1.7
1000	AT5G11320.2   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenases YUCCA (gi:16555352), YUCCA2 (gi:16555354), and YUCCA3 (gi:16555356) from Arabidopsis thaliana   chr5:3611991-3613362 REVERSE   Aliases: F2I11.210, F2I11_210	2.7	3.5	-0.7	-2.9	76.2%	-1.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1001	AT2G18300.2   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain ;supported by cDNA gi:20127067:gb:AF488597.1:   chr2:7959751-7961649 REVERSE   Aliases: T30D6.19, T30D6_19	2.6	3.0	-0.4	-2.9	76.3%	-2.3
1002	AT2G23810.1   similar to senescence-associated family protein [Arabidopsis thaliana] (TAIR:At4g30430.1); similar to senescence-associated protein DH [Zea mays] (GB:AAV31120.1); contains InterPro domain CD9/CD37/CD63 antigen (InterPro:IPR000301)   chr2:10142685-10144531 REVERSE   Aliases: F27L4.1, F27L4_1	8.1	7.3	0.8	2.9	76.3%	-1.7
1003	AT3G47460.1   Symbol: ATSMC2	3.4	4.2	-0.8	-2.9	76.6%	-2.0
1004	AT3G12320.1   expressed protein   chr3:3923742-3925442 FORWARD   Aliases: T2E22.34	7.6	6.3	1.3	2.9	76.7%	-1.6
1005	AT2G34600.1   expressed protein   chr2:14580251-14580899 FORWARD   Aliases: T31E10.6, T31E10_6	3.5	2.3	1.2	2.9	76.7%	-2.1
1006	AT3G49670.1   leucine-rich repeat transmembrane protein kinase, putative, CLAVATA1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879   chr3:18428553-18432091 FORWARD   Aliases: T16K5.20	5.1	6.5	-1.4	-2.9	76.8%	-1.7
1007	AT1G54540.1   expressed protein   chr1:20371369-20372088 REVERSE   Aliases: F20D21.35, F20D21_35	2.8	4.1	-1.3	-2.9	77.1%	-1.7
1008	AT2G34357.1   expressed protein   chr2:14506315-14512806 FORWARD   Aliases: None	5.7	7.0	-1.3	-2.9	77.2%	-1.7
1009	AT4G38400.1   Symbol: ATEXLA2   expansin family protein (EXPL2), contains Pfam profile: PF01357 pollen allergen; expansin-like gene, PMID:11641069, www.bio.psu.edu/expansins	7.1	5.7	1.4	2.9	77.2%	-1.7
1010	AT3G47250.3   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr3:17410862-17412705 REVERSE   Aliases: F13I12.300	4.1	3.2	0.9	2.9	77.5%	-1.7
1011	AT5G66420.2   similar to transcriptional regulator [Clostridium tetani E88] (GB:NP_782382.1)   chr5:26538900-26542307 REVERSE   Aliases: K1F13.7, K1F13_7	7.2	8.2	-1.0	-2.9	77.5%	-1.7
1012	AT4G05590.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g22310.1); similar to light induced protein like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477903.1); contains InterPro domain Protein of unknown function UPF0041 (InterPro:IPR005336)   chr4:2907169-2908532 FORWARD   Aliases: F6H8.10, F6H8_10	5.2	4.1	1.1	2.9	77.5%	-1.7
1013	AT2G23030.1   protein kinase, putative, similar to protein kinase 3 (Glycine max) GP:310582:gb:AAB68961   chr2:9810582-9813759 REVERSE   Aliases: F21P24.9, F21P24_9	5.9	4.6	1.3	2.9	77.5%	-1.7
1014	AT2G28620.1   kinesin motor protein-related   chr2:12272244-12277097 REVERSE   Aliases: T8O18.9, T8O18_9	3.7	4.5	-0.9	-2.9	77.5%	-1.8
1015	AT3G49530.1   Symbol: ANAC062   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC2 - Arabidopsis thaliana, EMBL:AF201456   chr3:18373429-18375898 REVERSE   Aliases: ANAC062, T9C5.120	7.3	6.4	0.8	2.9	77.5%	-1.8
1016	AT5G61300.1   expressed protein   chr5:24668131-24670002 REVERSE   Aliases: MFB13.7, MFB13_7	4.7	5.4	-0.8	-2.9	77.5%	-1.9
1017	AT1G48300.1   expressed protein   chr1:17851024-17852466 FORWARD   Aliases: F11A17.15, F11A17_15	10.0	8.2	1.8	2.9	77.5%	-1.7
1018	AT1G80850.1   methyladenine glycosylase family protein, similar to SP:P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) {Escherichia coli}; contains Pfam profile PF03352: Methyladenine glycosylase   chr1:30390499-30392164 REVERSE   Aliases: F23A5.20, F23A5_20	4.7	5.4	-0.7	-2.9	77.5%	-1.9
1019	AT1G72360.1   encodes a member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12.   chr1:27245474-27246489 FORWARD   Aliases: T10D10.17, T10D10_17	9.5	7.9	1.6	2.9	77.5%	-2.1
1020	AT3G06140.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)   chr3:1856688-1858856 REVERSE   Aliases: F28L1.8, F28L1_8	3.7	4.6	-1.0	-2.9	77.5%	-1.7
1021	AT5G66250.3   kinectin-related, contains weak similarity to kinectin (GI:3766232) (Vulpes vulpes)   chr5:26485761-26487170 FORWARD   Aliases: K1L20.3, K1L20_3	7.0	6.1	1.0	2.9	77.5%	-1.8
1022	AT5G50840.2   expressed protein   chr5:20703046-20706144 FORWARD   Aliases: K7B16.6, K7B16_6	6.7	8.2	-1.5	-2.9	77.5%	-1.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1023	AT4G14580.1   Symbol: CIPK4   CBL-interacting protein kinase 4 (CIPK4), identical to CBL-interacting protein kinase 4 (Arabidopsis thaliana) gi:13249503:gb:AAG01367; identical to cDNA calcineurin B-like (CBL) interacting protein kinase 4 (CIPK4) GI:13249502   chr4:8367883-8369163 REVERSE   Aliases: CBL interacting protein kinase 4, DL3330C, FCAALL.259	8.8	7.9	0.9	2.9	77.5%	-1.9
1024	AT3G10340.1   phenylalanine ammonia-lyase, putative, similar to phenylalanine ammonia-lyase GB:S48726 (Petroselinum crispum)   chr3:3204018-3208027 FORWARD   Aliases: F14P13.6	4.1	5.4	-1.3	-2.9	77.5%	-1.7
1025	AT5G67320.1   WD-40 repeat family protein, strong similarity to unknown protein (ref:NP_005638.1)   chr5:26874380-26878337 FORWARD   Aliases: K8K14.4, K8K14_4	6.6	7.4	-0.8	-2.9	77.6%	-1.9
1026	AT1G26670.1   Symbol: VTI12   vesical transport v-SNARE 12 (VTI12) / vesicle soluble NSF attachment protein receptor VTI1b (VTI1B) receptor VTI1b, identical to SP:Q9SEL5 Vesicle transport v-SNARE 12 (AtVTI12) (Vesicle transport v-SNARE protein VTI1b) (Vesicle soluble NSF attachment protein receptor VTI1b) (AtVTI1b) {Arabidopsis thaliana}   chr1:9215951-9217990 FORWARD   Aliases: ATVTI12, T24P13.5, T24P13_5, VTI1B	10.1	9.5	0.6	2.9	77.6%	-2.2
1027	AT4G17240.1   expressed protein   chr4:9666700-9668386 REVERSE   Aliases: DL4655C, FCAALL.387	2.7	3.0	-0.3	-2.9	77.7%	-2.6
1028	AT5G57960.1   GTP-binding family protein, similar to SP:P25519 GTP-binding protein hflX {Escherichia coli}   chr5:23480024-23483726 REVERSE   Aliases: MTI20.22, MTI20_22	5.0	4.3	0.7	2.9	77.8%	-1.9
1029	AT2G43060.1   expressed protein, similar to cDNA bHLH transcription factor (bHLH zeta gene) GI:32563005   chr2:17916262-17917159 FORWARD   Aliases: MFL8.8	6.4	5.4	1.0	2.9	78.1%	-1.8
1030	AT1G11530.1   Encodes a single cysteine active site thioredoxin-related protein, similar to thioredoxin H-type from Arabidopsis thaliana SP:P29448, Nicotiana tabacum SP:Q07090; contains Pfam profile: PF00085 Thioredoxin;   chr1:3874437-3875484 FORWARD   Aliases: T23J18.19, T23J18_19	6.6	5.9	0.7	2.9	78.1%	-2.0
1031	AT1G79380.1   copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens}   chr1:29865384-29868528 FORWARD   Aliases: T8K14.20, T8K14_20	7.4	5.6	1.7	2.9	78.1%	-1.7
1032	AT5G59550.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:24015485-24017019 REVERSE   Aliases: F2O15.22, F2O15_22	6.9	6.0	0.9	2.9	78.1%	-1.8
1033	AT3G16175.1   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein   chr3:5480470-5482048 FORWARD   Aliases: None	3.7	3.0	0.7	2.9	78.1%	-2.0
1034	AT5G60860.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	5.6	4.4	1.2	2.9	78.1%	-1.8
1035	AT5G17160.1   expressed protein   chr5:5639648-5642515 REVERSE   Aliases: F2K13.310, F2K13_310	3.9	4.7	-0.8	-2.9	78.1%	-1.8
1036	AT1G69070.1   expressed protein   chr1:25970975-25975052 REVERSE   Aliases: F4N2.4, F4N2_4	3.9	4.5	-0.6	-2.9	78.1%	-2.0
1037	AT1G21890.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr1:7682573-7685651 REVERSE   Aliases: T26F17.11, T26F17_11	4.9	3.9	1.0	2.9	78.1%	-1.7
1038	ATCG00580.1   Symbol: PSBE   PSII cytochrome b559. There have been many speculations about the function of Cyt b559, but the most favored at present is that it plays a protective role by acting as an electron acceptor or electron donor under conditions when electron flow through PSII is not optimized.   chrC:64071-64322 REVERSE   Aliases: PSBE	3.6	5.1	-1.5	-2.9	78.1%	-1.7
1039	AT3G19970.1   expressed protein   chr3:6958654-6961466 FORWARD   Aliases: MZE19.2	4.8	3.8	0.9	2.9	78.1%	-1.8
1040	AT2G18700.1   Symbol: ATTPS11   glycosyl transferase family 20 protein / trehalose-phosphatase family protein, similar to trehalose-6-phosphate synthase SL-TPS/P (Selaginella lepidophylla) GI:4100325; contains Pfam profiles PF00982: Glycosyltransferase family 20, PF02358: Trehalose-phosphatase   chr2:8116125-8119092 FORWARD   Aliases: ATTPSB, MSF3.8, MSF3_8, TPS11	5.3	6.2	-0.9	-2.9	78.1%	-1.8
1041	AT1G20890.1   expressed protein, Location of ESTs OAO242 5' end, gb:Z30466 and OAO242 3' end, gb:Z30467   chr1:7265812-7267312 REVERSE   Aliases: F9H16.13, F9H16_13	6.1	5.3	0.7	2.9	78.1%	-1.8
1042	AT5G13960.1   Symbol: SUVH4   SET domain-containing protein (SUVH4), identical to SUVH4 (Arabidopsis thaliana) GI:13517749; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH4 (SUVH4) GI:13517748   chr5:4501449-4506190 FORWARD   Aliases: KRYPTONITE, KYP, MAC12.7, MAC12_7, SU(VAR)3 9 HOMOLOG 4	4.2	5.1	-0.9	-2.9	78.2%	-1.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1043	AT4G11830.2   Symbol: PLDGAMMA2   phospholipase D gamma 2 / PLD gamma 2 (PLDGAMMA2), identical to SP:Q9T051 Phospholipase D gamma 2 (EC 3.1.4.4) (AtPLDgamma2) (PLD gamma 2) (Arabidopsis thaliana)   chr4:7115794-7121239 REVERSE   Aliases: AT4G11835, T26M18.40, T26M18_40	6.7	5.9	0.8	2.9	78.2%	-1.9
1044	AT5G37770.1   Symbol: TCH2   touch-responsive protein / calmodulin-related protein 2, touch-induced (TCH2), identical to calmodulin-related protein 2,touch-induced SP:P25070 from (Arabidopsis thaliana)   chr5:15016084-15016849 REVERSE   Aliases: K22F20.10, K22F20_10, TOUCH 2	6.1	4.5	1.6	2.9	78.2%	-1.7
1045	AT2G16440.1   DNA replication licensing factor, putative, similar to SP:P49717 DNA replication licensing factor MCM4 (CDC21 homolog) {Mus musculus}, SP:P29458 Cdc21 protein {Schizosaccharomyces pombe}; contains Pfam profile PF00493: MCM2/3/5 family   chr2:7133446-7137750 REVERSE   Aliases: F16F14.6, F16F14_6	3.6	5.3	-1.7	-2.9	78.4%	-1.7
1046	AT3G57470.1   peptidase M16 family protein / insulinase family protein, contains weak similarity to Pfam domain, PF05193: Peptidase M16 inactive domain   chr3:21280238-21286904 REVERSE   Aliases: T8H10.70	3.0	3.3	-0.4	-2.9	78.4%	-2.5
1047	AT1G23010.1   multi-copper oxidase type I family protein, similar to SP:P07788 Spore coat protein A {Bacillus subtilis}; contains Pfam profile PF00394: Multicopper oxidase   chr1:8147253-8149801 FORWARD   Aliases: F19G10.5, F19G10_5	3.3	4.4	-1.1	-2.9	78.5%	-1.8
1048	AT4G30390.1   expressed protein   chr4:14862015-14863191 REVERSE   Aliases: F17I23.270, F17I23_270	7.2	5.7	1.5	2.9	78.5%	-1.8
1049	AT3G48040.1   Symbol: ROP10   Rac-like GTP-binding protein (ARAC8), identical to rac GTP binding protein Arac8 GI:3702966 from (Arabidopsis thaliana)	4.2	4.9	-0.7	-2.9	78.6%	-1.9
1050	AT3G27170.1   Symbol: CLC B   chloride channel protein (CLC-b), identical to CLC-b chloride channel protein GB:CAA96058 from (Arabidopsis thaliana) (J. Biol. Chem. 271 (52), 33632-33638 (1996))   chr3:10025254-10028435 FORWARD   Aliases: ATCLC B, MYF5.4	7.3	6.2	1.1	2.9	78.6%	-1.8
1051	AT5G36210.1   expressed protein   chr5:14265143-14270460 REVERSE   Aliases: MAB16.20	7.1	8.4	-1.3	-2.9	78.7%	-1.8
1052	AT5G56600.1   Symbol: PRF3   profilin 5 (PRO5) (PRF3), identical to SP:Q9FE63 Profilin 5 {Arabidopsis thaliana}   chr5:22926914-22928047 REVERSE   Aliases: MIK19.4, MIK19_4, PFN3, PROFILIN, PROFILIN 3	11.9	11.0	0.9	2.9	78.7%	-1.8
1053	AT1G08630.4   similar to threonine aldolase family protein [Arabidopsis thaliana] (TAIR:At3g04520.1); similar to OSJNBa0073E02.3 [Oryza sativa (japonica cultivar-group)] (GB:CAE05443.2)   chr1:2743764-2747970 REVERSE   Aliases: F22O13.11, F22O13_11	4.1	3.4	0.8	2.9	78.7%	-1.8
1054	AT1G03820.1   expressed protein, similar to arabinogalactan-protein; AGP (GI:1087015) {Pyrus communis}; similar to Protein E6. (SP:Q01197) {Gossypium hirsutum}   chr1:959927-960708 REVERSE   Aliases: F21M11.27, F21M11_27	5.0	6.9	-2.0	-2.9	78.7%	-1.7
1055	AT1G01230.1   ORMDL family protein, contains Pfam domain PF04061: ORMDL family	9.2	8.0	1.2	2.9	78.7%	-2.0
1056	AT1G70520.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:26588441-26591082 REVERSE   Aliases: F24J13.9, F24J13_9	4.9	5.6	-0.6	-2.9	78.7%	-2.0
1057	AT4G24160.2   hydrolase, alpha/beta fold family protein, contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:12539787-12542499 FORWARD   Aliases: T19F6.150, T19F6_150	8.7	8.0	0.7	2.9	78.7%	-1.9
1058	AT2G35630.1   Symbol: MOR1   microtubule organization 1 protein (MOR1), identical to microtubule organization 1 protein GI:14317953 from (Arabidopsis thaliana)   chr2:14973757-14987661 FORWARD   Aliases: GEM1, MICROTUBULE ORGANIZATION 1, T20F21.17, T20F21_17	6.0	6.6	-0.6	-2.9	78.8%	-2.1
1059	AT1G68830.1   STN7 protein kinase; required for state transitions, phosphorylation of the major antenna complex (LHCII) between PSII and PSI, and light adaptation   chr1:25876119-25879169 REVERSE   Aliases: STN7, T6L1.2, T6L1_2	5.8	5.1	0.7	2.9	79.0%	-1.9
1060	AT4G02440.1   Symbol: EID1   F-box family protein, to circadian clock coupling factor ZGT (GP:14210079) {Nicotiana tabacum}; contains Pfam PF00646: F-box domain   chr4:1072481-1073779 FORWARD   Aliases: EMPFINDLICHER IM DUNKELROTEN LICHT 1, T14P8.22, T14P8_22	5.9	5.2	0.7	2.9	79.0%	-2.0
1061	AT4G05160.1   Encodes a peroxisomal protein involved in the activation of fatty acids through esterification with CoA. At4g05160 preferentially activates fatty acids with medium chain length (C6:0 and C7:0) as well as even-numbered long-chain fatty acids (C14:0,	10.2	10.7	-0.5	-2.9	79.0%	-2.3
1062	AT5G22340.2   expressed protein   chr5:7394476-7396878 FORWARD   Aliases: MWD9.13, MWD9_13	5.2	6.0	-0.8	-2.9	79.0%	-1.9
1063	AT3G27280.2   prohibitin, putative, strong similarity to prohibitin (Arabidopsis thaliana) GI:1946331; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr3:10078077-10079658 FORWARD   Aliases: K17E12.10	6.1	6.9	-0.8	-2.9	79.0%	-1.9
1064	AT5G44190.1   Symbol: GLK2   myb family transcription factor (GLK2), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:17815596-17818050 FORWARD   Aliases: ATGLK2, GOLDEN2 LIKE 2, GPRI2, MLN1.11, MLN1_11	3.8	3.2	0.6	2.9	79.0%	-2.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1065	AT1G20230.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:7009561-7011843 FORWARD   Aliases: T20H2.1, T20H2_1	3.5	4.3	-0.8	-2.9	79.0%	-1.8
1066	AT5G18290.1   major intrinsic protein-related / MIP-related, contains weak similarity to Pfam profile: MIP PF00230; annotated based on segmental duplication   chr5:6055030-6056702 REVERSE   Aliases: F20L16.1	4.5	5.7	-1.2	-2.9	79.0%	-1.7
1067	AT1G76170.1   expressed protein, contains Pfam profile PF01171: PP-loop family   chr1:28589073-28591119 REVERSE   Aliases: T23E18.11, T23E18_11	4.4	3.8	0.6	2.9	79.0%	-2.1
1068	AT3G55430.1   glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative, similar to beta-1,3 glucanase Gl:7414433 from (Pisum sativum); contains Pfam profile PF00332: Glycosyl hydrolases family 17	9.2	8.0	1.2	2.9	79.1%	-1.8
1069	AT5G18590.2   kelch repeat-containing protein, identical to RanGAP1 interacting protein (Gl:21950739) (Arabidopsis thaliana); similar to Tip elongation aberrant protein 1 (Cell polarity protein tea1) (SP:P87061) (Schizosaccharomyces pombe); contains Pfam PF01344: Kelch motif (5 repeats)   chr5:6177967-6182708 REVERSE   Aliases: T28N17.70, T28N17_70	6.7	7.5	-0.8	-2.9	79.3%	-2.1
1070	AT1G36160.1   Symbol: ACC1   similar to acetyl-CoA carboxylase 2 (ACC2) [Arabidopsis thaliana] (TAIR:At1g36180.1); similar to putative acetyl-CoA carboxylase [Oryza sativa (japonica cultivar-group)] (GB:AAP53321.1); similar to acetyl-CoA carboxylase [Medicago sativa] (GB:AAB42144.1); similar to acetyl-CoA carboxylase [Brassica napus] (GB:CAC19875.1); similar to acetyl-CoA carboxylase [Brassica napus] (GB:CAC19876.1); similar to acetyl CoA carboxylase (GB:AAA75528.1); contains InterPro domain Carboxyl transferase (InterPro:IPR000022); contains InterPro domain Carbamoyl-phosphate synthetase large chain, N-terminal (InterPro:IPR005481); contains InterPro domain Biotin carboxylase, C-terminal (InterPro:IPR005482); contains InterPro domain Biotin/lipoyl attachment (InterPro:IPR000089); contains InterPro domain Carbamoyl-phosphate synthase L chain, ATP-binding (InterPro:IPR005479)   chr1:13535377-13545220 FORWARD   Aliases: ACETYL COA CARBOXYLASE, ACETYL COENZYME A CARBOXYLASE 1, AT ACC1, EMB22, EMBRYO DEFECTIVE 22, F15C21.1, GK, GREEN BLIMP, GURKE, PAS3, PASTICCINO 3	6.2	7.4	-1.2	-2.9	79.4%	-1.8
1071	AT5G07340.1   calnexin, putative, identical to calnexin homolog 2 from Arabidopsis thaliana (SP:Q38798), strong similarity to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP:P29402); contains Pfam profile PF00262 calreticulin family   chr5:2317214-2319650 FORWARD   Aliases: T2I1.50, T2I1_50	5.8	6.8	-1.0	-2.9	79.4%	-1.8
1072	AT1G20350.1   Symbol: ATTIM17 1   mitochondrial import inner membrane translocase subunit Tim17, putative, similar to SP:Q9SP35 Mitochondrial import inner membrane translocase subunit TIM17 {Arabidopsis thaliana}; contains Pfam profile PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr1:7043703-7044582 FORWARD   Aliases: F14O10.5, F14O10_5	3.5	3.1	0.5	2.9	79.4%	-2.3
1073	AT1G62710.1   Symbol: BETA VPE   vacuolar processing enzyme beta / beta-VPE, identical to SP:Q39044 Vacuolar processing enzyme, beta-isozyme precursor (EC 3.4.22.-) (Beta-VPE) {Arabidopsis thaliana}   chr1:23227540-23230581 REVERSE   Aliases: BETAVPE, F23N19.7, F23N19_7	7.8	6.7	1.1	2.9	79.4%	-1.7
1074	AT3G63390.1   expressed protein   chr3:23422141-23422943 REVERSE   Aliases: MAA21.20	9.3	8.5	0.9	2.9	79.4%	-1.9
1075	AT3G50340.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:18676076-18677654 REVERSE   Aliases: F11C1.180	7.4	6.8	0.7	2.9	79.4%	-2.0
1076	AT3G15460.1   brix domain-containing protein, contains Pfam domain, PF04427: Brix domain   chr3:5213343-5216268 REVERSE   Aliases: MJK13.12	6.2	7.3	-1.1	-2.9	79.4%	-1.8
1077	AT1G76930.2   Symbol: ATEXT4	7.3	10.1	-2.8	-2.9	79.4%	-2.2
1078	AT1G17580.1   Symbol: MYA1   myosin, putative, similar to myosin Gl:433663 from (Arabidopsis thaliana)   chr1:6039296-6049549 FORWARD   Aliases: ATMYA1, F1L3.28, F1L3_28	5.3	6.2	-0.8	-2.9	79.4%	-1.8
1079	AT5G35700.1   fimbrin-like protein, putative, similar to fimbrin-like protein (ATFIM1) (Arabidopsis thaliana) Gl:2905893, fimbrin (Schizosaccharomyces pombe) Gl:3057144; contains Pfam profile PF00307: Calponin homology (CH) domain	8.4	9.7	-1.3	-2.9	79.4%	-1.9
1080	AT3G54260.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr3:20095988-20097741 REVERSE   Aliases: F24B22.220	9.8	10.6	-0.9	-2.9	79.4%	-1.9
1081	AT3G56080.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) Gl:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr3:20821288-20824015 REVERSE   Aliases: F18O21.40	4.1	3.4	0.7	2.9	79.4%	-1.9
1082	AT2G27760.1   Symbol: ATIPT2	6.4	7.4	-1.0	-2.9	79.4%	-1.8
1083	AT4G30600.1   signal recognition particle receptor alpha subunit family protein, similar to Signal recognition particle receptor alpha subunit (SR-alpha) (Docking protein alpha) (DP-alpha) (SP:P08240) (Homo sapiens); similar to Signal recognition particle receptor alpha subunit	10.4	9.6	0.8	2.9	79.4%	-2.2
1084	AT2G05940.1   protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821	7.4	5.7	1.7	2.9	79.4%	-1.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1085	AT3G06850.2   Symbol: DIN3   branched chain alpha-keto acid dehydrogenase E2 subunit (din3), identical to branched chain alpha-keto acid dehydrogenase E2 subunit (din3) (Arabidopsis thaliana) GI:7021284   chr3:2157989-2160619 REVERSE   Aliases: DARK INDUCIBLE 3, F3E22.1, LTA1	7.0	7.6	-0.6	-2.9	79.5%	-2.1
1086	AT4G04955.1   Symbol: ATALN   Encodes an allantoinase which is involved in allantoin degradation and assimilation. Gene expression was induced when allantoin was added to the medium. The insertion mutant, ataln m2-1, did not grow well on the MS medium where allantoin, instead of ammonium nitrate, was supplied.   chr4:2522032-2525278 REVERSE   Aliases: ATALN	6.5	5.7	0.9	2.9	79.5%	-1.9
1087	AT3G60510.2   similar to enoyl-CoA hydratase/isomerase family protein [Arabidopsis thaliana] (TAIR:At4g31810.1); similar to enoyl-CoA-hydratase [Avicennia marina] (GB:AAF01467.1); contains InterPro domain Enoyl-CoA hydratase/isomerase (InterPro:IPR001753)   chr3:22367927-22371122 REVERSE   Aliases: T8B10.170	3.9	4.4	-0.6	-2.9	79.5%	-2.0
1088	AT1G49300.2   similar to Ras-related GTP-binding protein, putative [Arabidopsis thaliana] (TAIR:At3g18820.1); similar to putative GTP-binding protein [Cucumis sativus] (GB:AAQ72787.1); contains InterPro domain Small GTP-binding protein domain (InterPro:IPR005225); contains InterPro domain Ras small GTPase, Rab type (InterPro:IPR003579); contains InterPro domain Ras small GTPase, Rho type (InterPro:IPR003578); contains InterPro domain Ras small GTPase, Ras type (InterPro:IPR003577); contains InterPro domain Ras GTPase superfamily (InterPro:IPR001806); contains InterPro domain GTP-binding nuclear protein Ran (InterPro:IPR002041)   chr1:18238417-18241195 FORWARD   Aliases: F13F21.26, F13F21_26	10.0	9.3	0.6	2.9	79.5%	-2.0
1089	AT1G17790.1   DNA-binding bromodomain-containing protein, similar to SP:P13709 Female sterile homeotic protein (Fragile-chorion membrane protein) {Drosophila melanogaster}; contains Pfam profile PF00439: Bromodomain   chr1:6125356-6127397 REVERSE   Aliases: F2H15.2, F2H15_2	4.1	4.7	-0.5	-2.9	79.5%	-2.1
1090	AT3G57060.1   non-SMC condensin subunit, XCAP-D2/Cnd1 family protein, similar to 13S condensin XCAP-D2 subunit (Xenopus laevis) GI:3764087; contains Pfam profile PF04594: Non-SMC condensin subunit, XCAP-D2/Cnd1   chr3:21126057-21132030 REVERSE   Aliases: F24I3.140	3.3	3.9	-0.6	-2.9	79.5%	-2.0
1091	AT5G59870.1   histone H2A, putative, similar to histone H2A Petroselinum crispum SP:P19177, Lycopersicon esculentum SP:P25469, Zea mays SP:P40280; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:24132608-24133444 REVERSE   Aliases: MMN10.22, MMN10_22	10.4	12.0	-1.7	-2.9	79.9%	-1.8
1092	AT5G03210.1   expressed protein   chr5:762786-763320 REVERSE   Aliases: F15A17.240, F15A17_240	5.2	3.6	1.6	2.9	79.9%	-2.1
1093	AT5G46590.1   Symbol: ANAC096   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr5:18922906-18924038 FORWARD   Aliases: ANAC096, F10E10.6, F10E10_6	4.4	3.0	1.3	2.9	79.9%	-1.8
1094	AT2G35820.1   expressed protein   chr2:15057991-15059318 FORWARD   Aliases: F11F19.27, F11F19_27	5.4	3.7	1.6	2.9	79.9%	-1.7
1095	AT2G19900.1   malate oxidoreductase, putative, similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP:P51615) {Vitis vinifera}   chr2:8598981-8602535 REVERSE   Aliases: F6F22.7, F6F22_7	6.7	5.3	1.3	2.9	80.0%	-1.7
1096	AT5G27450.2   mevalonate kinase (MK), identical to mevalonate kinase (Arabidopsis thaliana) SWISS-PROT:P46086   chr5:9690745-9693227 FORWARD   Aliases: F21A20.160, F21A20_160	6.3	7.4	-1.1	-2.9	80.0%	-1.8
1097	AT5G62520.2   Symbol: SRO5   expressed protein   chr5:25115253-25117133 FORWARD   Aliases: K19B1.13, K19B1_13, SIMILAR TO RCD ONE 5, SIMILAR TO RCD ONE 5, SRO5	5.4	4.1	1.3	2.9	80.0%	-1.8
1098	AT3G50950.2   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	5.2	4.1	1.1	2.9	80.0%	-1.8
1099	AT3G25900.2   Symbol: ATHMT 1/HMT 1   homocysteine S-methyltransferase 1 (HMT-1), identical to GB:AAF23821 from (Arabidopsis thaliana)   chr3:9482076-9484163 FORWARD   Aliases: ATHMT 1, HMT 1, MPE11.15	5.0	6.9	-1.8	-2.9	80.1%	-1.8
1100	AT3G11620.4   expressed protein, similar to hypothetical protein DDB0187018 [Dictyostelium discoideum] (GB:EAL64046.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr3:3669325-3672040 REVERSE   Aliases: T19F11.2	5.5	4.6	0.9	2.9	80.2%	-2.0
1101	AT3G03750.2   SET domain-containing protein, low similarity to G9a (Homo sapiens) GI:287865; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif   chr3:939959-942101 FORWARD   Aliases: F20H23.22, F20H23_22	5.0	4.4	0.6	2.9	80.2%	-2.2
1102	AT5G60210.1   cytoplasmic linker protein-related, contains weak similarity to cytoplasmic linker protein CLIP-170 (GI:2905649) (Gallus gallus)	3.7	4.9	-1.1	-2.8	80.4%	-1.8
1103	AT3G51800.2   Symbol: ATG2   metalloproteinase M24 family protein, similar to SP:P50580 Proliferation-associated protein 2G4 {Mus musculus}; contains Pfam profile PF00557: metalloproteinase family M24   chr3:19222004-19224646 REVERSE   Aliases: ATEM1.5	10.6	11.5	-0.8	-2.8	80.4%	-2.3
1104	AT1G51500.1   Symbol: CER5   ABC transporter family protein, similar to GB:AAF61569 from (Bombyx mori)   chr1:19101465-19104735 REVERSE   Aliases: D3, ECERIFERUM 5, F5D21.6, F5D21_6	4.6	3.7	0.9	2.8	80.4%	-1.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1105	AT1G04850.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, weak similarity to SP:P45974 Ubiquitin carboxyl-terminal hydrolase 5 (EC 3.1.2.15) {Homo sapiens}; contains Pfam profile PF00627: UBA/TS-N domain   chr1:1365118-1368792 REVERSE   Aliases: F13M7.16, F13M7_16	8.7	9.8	-1.1	-2.8	80.4%	-2.0
1106	AT2G39820.1   eukaryotic translation initiation factor 6, putative / eIF-6, putative, similar to SP:O55135 Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) {Mus musculus}; contains Pfam profile PF01912: eIF-6 family   chr2:16625355-16626767 FORWARD   Aliases: T517.12, T517_12	5.9	4.8	1.1	2.8	80.4%	-1.8
1107	AT5G01200.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain   chr5:77115-78542 FORWARD   Aliases: F7J8.180, F7J8_180	4.0	3.4	0.6	2.8	80.4%	-2.1
1108	AT4G19230.2   Symbol: CYP707A1   cytochrome P450 family protein, cytochrome P450, Arabidopsis thaliana; supported by cDNA: gi_15293092_gb_AY050980.1_	6.1	4.9	1.2	2.8	80.4%	-1.9
1109	AT2G38000.1   chaperone protein dnaJ-related, weak similarity to Chaperone protein dnaJ (Swiss-Prot:Q9ZFC5) (Methylovorus sp.)	6.1	5.0	1.1	2.8	80.4%	-2.0
1110	AT1G69890.1   expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569   chr1:26326774-26328267 REVERSE   Aliases: T17F3.8, T17F3_8	3.7	3.1	0.6	2.8	80.7%	-2.0
1111	AT4G01870.1   tolB protein-related, contains weak similarity to TolB protein precursor (Swiss-Prot:P44677) (Haemophilus influenzae)   chr4:808376-810446 REVERSE   Aliases: T7B11.13, T7B11_13	6.7	8.1	-1.4	-2.8	80.7%	-1.8
1112	AT1G19180.2   expressed protein   chr1:6622105-6623611 FORWARD   Aliases: T29M8.5, T29M8_5	6.5	5.0	1.5	2.8	80.8%	-1.8
1113	AT3G02380.1   Symbol: COL2   zinc finger protein CONSTANS-LIKE 2 (COL2), identical to putative flowering-time gene CONSTANS (COL2) GB:AAB67879 GI:1507699 SP:Q96502 (Arabidopsis thaliana)   chr3:487250-488700 REVERSE   Aliases: CONSTANS LIKE 2, F11A12.7, F11A12_7	3.6	3.2	0.5	2.8	80.8%	-2.2
1114	AT1G49630.3   peptidase M16 family protein / insulinase family protein, contains Pfam domain, PF05193: Peptidase M16 inactive domain   chr1:18371261-18379049 REVERSE   Aliases: F14J22.13, F14J22_13	3.9	4.6	-0.6	-2.8	80.8%	-2.0
1115	AT5G65140.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) (Arabidopsis thaliana) GI:2944180; contains Pfam profile PF02358: Trehalose-phosphatase   chr5:26036814-26039430 REVERSE   Aliases: MQN23.7, MQN23_7	4.5	3.7	0.8	2.8	80.8%	-1.9
1116	AT1G14360.1   UDP-galactose/UDP-glucose transporter, putative, very similar to UDP-galactose/UDP-glucose transporter (GI:22651763) {Arabidopsis thaliana}   chr1:4910624-4913147 REVERSE   Aliases: F14L17.13, F14L17_13	6.2	6.8	-0.6	-2.8	80.8%	-2.0
1117	AT4G08300.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr4:5244888-5248339 FORWARD   Aliases: T12G13.140, T12G13_140	4.3	3.0	1.2	2.8	80.8%	-1.8
1118	AT5G26330.1   plastocyanin-like domain-containing protein / mavicyanin, putative, similar to mavicyanin SP:P80728 from (Cucurbita pepo)   chr5:9241549-9242704 REVERSE   Aliases: F9D12.16, F9D12_16	4.0	3.4	0.7	2.8	80.8%	-2.0
1119	AT5G46150.2   LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein, similar to GI:835763; GI:4966357; GI:4585976; GI:11994416 from (Arabidopsis thaliana)   chr5:18725043-18727820 REVERSE   Aliases: MCL19.21, MCL19_21	5.9	5.0	0.9	2.8	80.8%	-1.9
1120	AT2G35760.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr2:15039002-15040384 FORWARD   Aliases: T20F21.5, T20F21_5	7.6	6.5	1.1	2.8	80.8%	-1.8
1121	AT1G46264.1   Symbol: AT HSF B4   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr1:17227282-17228720 FORWARD   Aliases: F2G19.8, F2G19_8, HSF B4	4.3	5.2	-0.9	-2.8	80.8%	-1.8
1122	AT1G35420.1   diene lactone hydrolase family protein, low similarity to diene lactone hydrolase (Rhodococcus opacus) GI:23094407; contains Pfam profile PF01738: Diene lactone hydrolase family   chr1:13026292-13027645 FORWARD   Aliases: F12A4.4, F12A4_4	8.0	6.7	1.3	2.8	80.8%	-1.8
1123	AT3G61080.1   fructosamine kinase family protein, contains Pfam PF03881: Fructosamine kinase   chr3:22618105-22620074 FORWARD   Aliases: T27I15.170	6.6	5.4	1.3	2.8	80.8%	-1.8
1124	AT4G11820.2   Symbol: BAP1   hydroxymethylglutaryl-CoA synthase / HMG-CoA synthase / 3-hydroxy-3-methylglutaryl coenzyme A synthase, identical to Hydroxymethylglutaryl-CoA synthase (EC 4.1.3.5) (HMG-CoA synthase) (3-hydroxy-3-methylglutaryl coenzyme A synthase) (Swiss-Prot:P54873) (Arabidopsis thaliana)   chr4:7108909-7112024 REVERSE   Aliases: MVA1, T26M18.30, T26M18_30	3.9	4.9	-1.0	-2.8	80.8%	-1.9
1125	AT2G28890.1   protein phosphatase 2C family protein / PP2C family protein, similar to protein phosphatase-2c (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain   chr2:12412673-12415312 REVERSE   Aliases: F8N16.18, F8N16_18	8.1	8.7	-0.6	-2.8	80.8%	-2.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1126	AT1G32100.1   pinorexinol-laricresinol reductase, putative, similar to pinorexinol-laricresinol reductase TH1 (Tsuga heterophylla)(GI:7578915); contains isoflavone reductase domain PF02716	4.8	7.0	-2.2	-2.8	80.8%	-1.8
1127	AT1G34110.1   leucine-rich repeat transmembrane protein kinase, putative, contains similarity to receptor protein kinase-like protein GI:10177178 from (Arabidopsis thaliana)   chr1:12417154-12421167 REVERSE   Aliases: F12G12.7, F12G12_7	5.0	4.2	0.8	2.8	80.8%	-1.9
1128	AT5G27390.1   expressed protein, CG6949 - Drosophila melanogaster, EMBL:AE003739   chr5:9671848-9676121 REVERSE   Aliases: F21A20.100, F21A20_100	6.1	7.0	-0.9	-2.8	80.8%	-1.8
1129	AT1G19310.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:6676225-6677661 REVERSE   Aliases: F18O14.3, F18O14_3	8.0	6.9	1.1	2.8	80.8%	-1.8
1130	AT2G16990.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g16980.2); similar to tetracycline transporter protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD28125.1)   chr2:7390161-7394936 FORWARD   Aliases: F6P23.2, F6P23_2	6.9	6.3	0.7	2.8	80.8%	-2.1
1131	AT3G03330.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr3:783339-786177 REVERSE   Aliases: T21P5.25, T21P5_25	9.4	8.5	0.9	2.8	80.8%	-2.0
1132	AT3G29270.2   expressed protein   chr3:11235551-11237669 FORWARD   Aliases: MMF24.2	5.7	4.7	1.1	2.8	80.9%	-1.9
1133	AT1G52540.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr1:19573727-19575873 REVERSE   Aliases: F6D8.24, F6D8_24	5.3	4.5	0.8	2.8	80.9%	-2.1
1134	AT1G06020.1   pfkB-type carbohydrate kinase family protein, similar to fructokinase GI:2102693 from (Lycopersicon esculentum)   chr1:1824547-1826100 FORWARD   Aliases: T21E18.7, T21E18_7	3.5	4.0	-0.5	-2.8	80.9%	-2.3
1135	AT4G33920.1   protein phosphatase 2C family protein / PP2C family protein, similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain   chr4:16260689-16262984 FORWARD   Aliases: F17I5.110, F17I5_110	4.4	3.1	1.3	2.8	80.9%	-1.8
1136	AT1G17690.1   expressed protein   chr1:6082748-6088333 REVERSE   Aliases: F11A6.3, F11A6_3	5.7	6.3	-0.6	-2.8	80.9%	-2.1
1137	AT5G64880.1   expressed protein   chr5:25949516-25951373 FORWARD   Aliases: MXK3.11, MXK3_11	5.2	4.3	0.9	2.8	80.9%	-1.9
1138	AT1G35720.1   Symbol: ANNAT1	9.8	12.5	-2.6	-2.8	80.9%	-1.8
1139	AT5G10320.3   expressed protein   chr5:3244006-3246721 REVERSE   Aliases: F18D22.90, F18D22_90	4.5	5.1	-0.6	-2.8	80.9%	-2.1
1140	AT3G17390.1   Symbol: MTO3   S-adenosylmethionine synthetase, putative, similar to S-adenosylmethionine synthetase 2 (Methionine adenosyltransferase 2, AdoMet synthetase 2) (Catharanthus roseus) SWISS-PROT:Q96552   chr3:5952193-5954088 REVERSE   Aliases: MGD8.26, S ADENOSYLMETHIONINE SYNTHETASE, SAMS3	11.1	11.8	-0.8	-2.8	80.9%	-2.2
1141	AT1G27880.1   ATP-dependent DNA helicase, putative, similar to SP:O94761 ATP-dependent DNA helicase Q4 (RecQ4) {Homo sapiens}; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr1:9708923-9714065 FORWARD   Aliases: F28L5.4, F28L5_4	2.6	3.1	-0.5	-2.8	80.9%	-2.3
1142	AT5G25580.1   expressed protein   chr5:8903508-8906314 FORWARD   Aliases: T14C9.120, T14C9_120	4.1	5.7	-1.6	-2.8	80.9%	-1.8
1143	AT3G10200.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr3:3157613-3160186 FORWARD   Aliases: F14P13.20	5.6	6.7	-1.1	-2.8	80.9%	-1.8
1144	AT4G00030.1   plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin   chr4:13527-14413 FORWARD   Aliases: F6N15.13, F6N15_13	5.8	4.7	1.2	2.8	81.4%	-1.8
1145	AT5G67300.1   myb family transcription factor, contains PFAM profile: myb DNA binding domain PF00249   chr5:26871248-26872464 FORWARD   Aliases: K8K14.2, K8K14_2	8.7	6.5	2.2	2.8	81.4%	-1.9
1146	AT4G02500.1   galactosyl transferase GMA12/MNN10 family protein, low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)   chr4:1101507-1103610 FORWARD   Aliases: T10P11.20	5.5	6.6	-1.1	-2.8	81.4%	-1.9
1147	AT4G09890.1   expressed protein   chr4:6218393-6218923 FORWARD   Aliases: T5L19.20, T5L19_20	7.1	6.0	1.1	2.8	81.4%	-1.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1148	AT1G59890.1   paired amphipathic helix repeat-containing protein, similar to transcription co-repressor Sin3 (Xenopus laevis) GI:4960210; contains Pfam profile PF02671: Paired amphipathic helix repeat   chr1:22047991-22054726 FORWARD   Aliases: F23H11.20, F23H11_20	4.7	5.7	-1.0	-2.8	81.5%	-1.8
1149	AT3G61260.1   DNA-binding family protein / remorin family protein, similar to DNA-binding protein gi:601843 (Arabidopsis thaliana), remorin (Solanum tuberosum) GI:1881585; contains Pfam profiles PF03763: Remorin C-terminal region, PF03766: Remorin N-terminal region   chr3:22686226-22687763 REVERSE   Aliases: T20K12.160	8.4	7.0	1.4	2.8	81.5%	-1.9
1150	AT3G23890.1   Symbol: TOPII   DNA topoisomerase, ATP-hydrolyzing / DNA topoisomerase II / DNA gyrase (TOP2), identical to SP:P30182 DNA topoisomerase II (EC 5.99.1.3) {Arabidopsis thaliana}	3.9	5.3	-1.3	-2.8	81.5%	-1.8
1151	AT5G26860.1   Symbol: LON_ARA_ARA   similar to Lon protease, putative [Arabidopsis thaliana] (TAIR:At3g05790.1); similar to Lon protease, putative [Arabidopsis thaliana] (TAIR:At3g05780.1); similar to LON2 [Zea mays] (GB:AAC50021.1); similar to Lon protease, putative [Phytophthora infestans] (GB:CAI72282.1); similar to putative Lon2 protease [Oryza sativa (indica cultivar-group)] (GB:AAO34661.1); similar to putative ATP-dependent proteinase LON2 [Oryza sativa (japonica cultivar-group)] (GB:BAD30597.1); similar to Lon protease-like protein [Homo sapiens] (GB:CAA53625.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain Peptidase family S16 (InterPro:IPR001984); contains InterPro domain Lon protease S16, C-terminal proteolytic (InterPro:IPR008269); contains InterPro domain ATP-dependent protease La, LON (InterPro:IPR003111); contains InterPro domain ATP-dependent protease La (InterPro:IPR004815); contains InterPro domain Peptidase family S16, active site (InterPro:IPR008268); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr5:9451051-9457003 FORWARD   Aliases: F2P16.23, F2P16_23	5.0	5.8	-0.9	-2.8	81.5%	-1.8
1152	AT5G19690.1   Symbol: STT3A   oligosaccharyl transferase STT3 subunit family protein, similar to SP:P39007 Oligosaccharyl transferase STT3 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF02516: Oligosaccharyl transferase STT3 subunit	8.4	9.4	-1.0	-2.8	81.5%	-1.9
1153	AT4G22050.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr4:11683877-11685656 FORWARD   Aliases: F1N20.150, F1N20_150	2.6	3.6	-1.0	-2.8	81.5%	-1.9
1154	AT5G01940.1   eukaryotic translation initiation factor 2B family protein / eIF-2B family protein, similar to SP:P41035 Eukaryotic translation initiation factor 2 subunit (eIF-2-beta) {Oryctolagus cuniculus}; contains Pfam profile PF01873: Domain found in IF2B/IF5   chr5:363591-364766 REVERSE   Aliases: T20L15.210, T20L15_210	5.7	5.0	0.8	2.8	81.5%	-1.9
1155	AT3G49580.1   expressed protein   chr3:18386254-18386762 REVERSE   Aliases: T9C5.170	7.0	10.2	-3.3	-2.8	81.5%	-1.8
1156	AT5G08100.2   L-asparaginase / L-asparagine amidohydrolase, identical to Swiss-Prot:P50287 L-asparaginase (EC 3.5.1.1) (L-asparagine amidohydrolase) (Arabidopsis thaliana)   chr5:2593051-2594628 REVERSE   Aliases: T22D6.40, T22D6_40	10.1	9.2	0.9	2.8	81.5%	-2.0
1157	AT1G28380.1   expressed protein   chr1:9963579-9966306 FORWARD   Aliases: F3M18.18, F3M18_18	5.7	4.9	0.9	2.8	81.5%	-2.0
1158	AT5G63400.2   Symbol: ADK1   similar to adenylate kinase, putative [Arabidopsis thaliana] (TAIR:At5g50370.1); similar to adenylate kinase-a [Oryza sativa] (GB:BAA01180.1); similar to adenylate kinase [Oryza sativa] (GB:BAA94761.1); contains InterPro domain Adenylate kinase, active site lid (InterPro:IPR007862); contains InterPro domain Adenylate kinase (InterPro:IPR000850)   chr5:25410227-25412090 REVERSE   Aliases: ADENYLATE KINASE 1, MLE2.3, MLE2_3	9.1	10.4	-1.3	-2.8	81.5%	-1.9
1159	AT5G62530.1   Symbol: ALDH12A1   delta-1-pyrroline-5-carboxylate dehydrogenase (P5CDH), identical to delta-1-pyrroline-5-carboxylate dehydrogenase precursor (Arabidopsis thaliana) gi:15383744:gb:AAK73756; identical to cDNA delta-1-pyrroline-5-carboxylate dehydrogenase precursor (P5CDH) nuclear gene for mitochondrial product GI:15383743; contains Pfam profile PF00171:aldehyde dehydrogenase (NAD) family protein   chr5:25116229-25120476 REVERSE   Aliases: ATP5CDH, K19B1.14, K19B1_14	6.9	8.5	-1.6	-2.8	81.5%	-1.8
1160	AT2G26690.1   nitrate transporter (NTP2), identical to nitrate transporter (ntp2) (Arabidopsis thaliana) GI:4490321   chr2:11354225-11358071 REVERSE   Aliases: F18A8.6, F18A8_6	3.0	3.6	-0.6	-2.8	81.7%	-2.2
1161	AT3G23400.1   plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin   chr3:8376454-8378307 REVERSE   Aliases: MLM24.13	9.8	8.1	1.7	2.8	81.7%	-1.9
1162	AT3G12170.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9QYI7 DnaJ homolog subfamily B member 8 (Mus musculus); contains Pfam profile: PF00226 DnaJ domain   chr3:3881028-3882662 FORWARD   Aliases: F28J15.2	3.8	5.5	-1.7	-2.8	81.7%	-1.8
1163	AT3G13430.2   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At1g55530.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAT77283.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr3:4367514-4368886 FORWARD   Aliases: MRP15.6	3.6	2.9	0.7	2.8	81.7%	-2.0
1164	AT5G07060.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr5:2194395-2195873 REVERSE   Aliases: MOJ9.23, MOJ9_23	3.4	2.8	0.7	2.8	81.7%	-2.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1165	AT1G68670.1   myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain   chr1:25785745-25787737 FORWARD   Aliases: F24J5.9, F24J5_9	6.0	6.7	-0.7	-2.8	81.8%	-2.0
1166	AT4G02880.1   expressed protein   chr4:1274512-1278165 FORWARD   Aliases: T5J8.20, T5J8_20	4.7	4.0	0.7	2.8	81.8%	-2.0
1167	AT5G25900.1   Symbol: GA3   ent-kaurene oxidase, putative (GA3) / cytochrome P450, identical to GA3 (Arabidopsis thaliana) GI:3342249; similar to ent-kaurene oxidase (Cucurbita maxima) GI:11934675; contains Pfam profile PF00067: Cytochrome P450   chr5:9036046-9038399 FORWARD   Aliases: CYP701A3, ENT KAURENE OXIDASE, GA REQUIRING 3, T1N24.23, T1N24_23	6.9	7.6	-0.7	-2.8	81.8%	-2.0
1168	AT2G42950.1   expressed protein   chr2:17870896-17873564 FORWARD   Aliases: F7D19.5, F7D19_5	6.6	7.1	-0.5	-2.8	81.8%	-2.3
1169	AT3G16330.1   expressed protein   chr3:5535202-5536069 FORWARD   Aliases: MYA6.13	4.5	3.5	1.0	2.8	81.8%	-2.0
1170	AT5G39100.1   Symbol: GLP6   germin-like protein (GLP6), nearly identical to SP:P92997 Germin-like protein subfamily 1 member 13 precursor {Arabidopsis thaliana}; exon 2 interrupted by a stop codon, creating non-consensus donor and acceptor splice sites.   chr5:15670318-15671248 REVERSE   Aliases: GERMIN LIKE PROTEIN 6, MXF12.13, MXF12_13	3.6	4.4	-0.8	-2.8	82.0%	-1.9
1171	AT5G39960.1   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function   chr5:16011423-16014048 FORWARD   Aliases: MYH19.120, MYH19_120	4.8	5.5	-0.7	-2.8	82.1%	-2.0
1172	AT3G05200.1   Symbol: ATL6   zinc finger (C3HC4-type RING finger) family protein (ATL6), contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:1476988-1478736 FORWARD   Aliases: T12H1.17, T12H1_17	7.0	6.1	0.8	2.8	82.1%	-1.9
1173	AT2G40270.2   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr2:16829012-16831539 REVERSE   Aliases: T7M7.19	5.9	5.1	0.8	2.8	82.1%	-2.2
1174	AT1G57770.1   amine oxidase family, contains similarity to carotenoid isomerase (Lycopersicon esculentum) GI:19550437, phytoene dehydrogenase (PDH1) GI:433144 from (Cercospora nicotianae); contains Pfam profile PF01593 amine oxidase, flavin-containing   chr1:21398861-21401945 FORWARD   Aliases: F12K22.18	4.8	3.6	1.2	2.8	82.1%	-1.9
1175	AT1G17410.1   nucleoside diphosphate kinase family protein, contains Pfam PF00334 : Nucleoside diphosphate kinase domain; similar to Nucleoside diphosphate kinase homolog 5 (NDK-H 5) (NDP kinase homolog 5) (nm23-H5) (Testis-specific nm23 homolog) (Inhibitor of p53-induced apoptosis-beta) (IPIA-beta) (SP:P56597) {Homo sapiens}   chr1:5968566-5969893 REVERSE   Aliases: F28G4.12, F28G4_12	6.4	5.6	0.7	2.8	82.1%	-2.1
1176	AT5G46740.1   Symbol: UBP21   ubiquitin-specific protease 21 (UBP21), identical to ubiquitin-specific protease 21 GI:11993482 (Arabidopsis thaliana)   chr5:18982498-18985969 REVERSE   Aliases: MZA15.16, MZA15_16, UBIQUITIN SPECIFIC PROTEASE 21	3.8	4.7	-0.9	-2.8	82.1%	-2.2
1177	AT2G18390.1   Symbol: TTN5   ADP-ribosylation factor-like protein 2 (ARL2), identical to ARL2 G-protein (Halimasch; HAL; TITAN5) GI:20514265 from (Arabidopsis thaliana); identical to cDNA ARL2 G-protein mRNA GI:20514264; contains Pfam profile PF00025: ADP-ribosylation factor family; contains TIGRfam profile TIGR00231: small GTP-binding protein domain   chr2:7995247-7996943 FORWARD   Aliases: ARG1 LIKE 2, ARL2, ATARLC1, HAL, HALLIMASCH, T30D6.10, T30D6_10, TITAN 5	9.7	10.3	-0.6	-2.8	82.1%	-2.3
1178	AT1G78280.1   transcription factor jumonji (jnjC) domain-containing protein, contains Pfam PF00646: F-box domain; contains Pfam PF02373: jnjC domain; similar to apoptotic cell clearance receptor PtdSerR (GI:11037740) (Mus musculus)   chr1:29457448-29462548 FORWARD   Aliases: F3F9.18, F3F9_18	5.1	4.3	0.8	2.8	82.3%	-2.1
1179	AT2G22850.1   bZIP transcription factor family protein, contains a bZIP transcription factor basic domain signature (PDOC00036)   chr2:9739555-9740422 REVERSE   Aliases: T20K9.6, T20K9_6	4.2	3.3	0.9	2.8	82.4%	-2.0
1180	AT1G76640.1   calmodulin-related protein, putative, similar to regulator of gene silencing calmodulin-related protein GI:12963415 from (Nicotiana tabacum)   chr1:28770218-28770697 REVERSE   Aliases: F28O16.1, F28O16_1	4.3	3.5	0.9	2.8	82.4%	-2.0
1181	AT4G21070.1   Symbol: ATBRCA1   similar to zinc finger (C3HC4-type RING finger) family protein / BRCT domain-containing protein [Arabidopsis thaliana] (TAIR:At1g04020.2); similar to putative BRCT domain-containing protein [Oryza sativa (japonica cultivar-group)] (GB:AAV59289.1); contains InterPro domain BRCT (InterPro:IPR001357); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr4:11248089-11252735 FORWARD   Aliases: T13K14.230	2.6	3.2	-0.5	-2.8	82.4%	-2.2
1182	AT1G76020.1   expressed protein   chr1:28535786-28537218 REVERSE   Aliases: T4O12.23, T4O12_23	4.7	3.7	1.0	2.8	82.4%	-2.1
1183	AT3G66658.2   Symbol: ALDH22a1   betaine-aldehyde dehydrogenase, putative, similar to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) (Spinacia oleracea) SWISS-PROT:P17202; contains non-consensus splice site (GC) at intron 13   chr3:2095111-2099143 REVERSE   Aliases: T8E24.4, T8E24_4	5.1	6.1	-1.0	-2.8	82.5%	-1.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1184	AT1G20120.1   family II extracellular lipase, putative, similar to family II lipase EXL3 GI:15054386, SP:P40602 Anther-specific proline-rich protein APG precursor {Arabidopsis thaliana}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr1:6975379-6977235 FORWARD   Aliases: T20H2.29, T20H2_29	3.5	2.8	0.7	2.8	82.5%	-2.2
1185	AT1G61350.1   armadillo/beta-catenin repeat family protein, armadillo/beta-catenin-like repeats, Pfam:PF00514   chr1:22637547-22639559 FORWARD   Aliases: T1F9.16, T1F9_16	4.8	5.7	-0.9	-2.8	82.5%	-1.9
1186	AT2G32440.1   Symbol: KAO2   ent-kaurenoic acid hydroxylase, putative / cytochrome P450, putative, identical to ent-kaurenoic acid hydroxylase / cytochrome P450 CYP88A (GI:13021856) (Arabidopsis thaliana); similar to ent-kaurenoic acid hydroxylase (Arabidopsis thaliana) GI:13021853   chr2:13782665-13785079 FORWARD   Aliases: CYP88A4, ENT KAURENOIC ACID HYDROXYLASE 2, T32F6.4, T32F6_4	5.0	4.2	0.8	2.8	82.5%	-2.0
1187	AT3G21650.1   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative, similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)   chr3:7621578-7624083 REVERSE   Aliases: MIL23.8	4.8	5.4	-0.6	-2.8	82.5%	-2.1
1188	AT3G11700.1   beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein, contains Pfam profile PF02469: Fasciclin domain   chr3:3698845-3701499 FORWARD   Aliases: T19F11.10	7.1	6.4	0.6	2.8	82.7%	-2.2
1189	AT2G19970.1   pathogenesis-related protein, putative, similar to pathogenesis-related protein 1 {Arabidopsis thaliana} GI:166805; contains Pfam profile PF00188: SCP-like extracellular protein   chr2:8630818-8631557 REVERSE   Aliases: T2G17.23, T2G17_23	3.4	4.1	-0.7	-2.8	82.7%	-2.1
1190	AT1G14620.1   Symbol: DECOY   expressed protein   chr1:5014749-5016599 REVERSE   Aliases: DECOY, EXGT A2, T5E21.12, T5E21_12, XTR2	7.5	8.9	-1.4	-2.8	82.9%	-1.9
1191	AT3G54200.1   expressed protein, hin1 protein, Nicotiana tabacum, PIR:T03265   chr3:20076643-20077538 FORWARD   Aliases: F24B22.160	5.9	5.1	0.8	2.8	82.9%	-2.2
1192	AT4G27130.1   eukaryotic translation initiation factor SUI1, putative, similar to SP:P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfam profile PF01253: Translation initiation factor SUI1   chr4:13604601-13606454 REVERSE   Aliases: T24A18.80, T24A18_80	11.4	10.7	0.7	2.8	83.1%	-2.5
1193	AT1G72550.2   tRNA synthetase beta subunit family protein, contains Pfam profiles: PF03484 phenylalanine-tRNA synthetase, B5 domain, PF03483 B3/4 domain; an isoform contains a non-consensus TG acceptor splice site at a terminal exon.   chr1:27323413-27327677 REVERSE   Aliases: F28P22.26, F28P22_26	8.2	9.5	-1.3	-2.8	83.1%	-2.0
1194	AT1G18710.1   myb family transcription factor (MYB47), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr1:6450586-6453106 FORWARD   Aliases: F6A14.18, F6A14_18	4.8	3.8	1.0	2.8	83.1%	-1.9
1195	AT4G26940.2   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr4:13529431-13532681 REVERSE   Aliases: F10M23.280, F10M23_280	6.1	5.2	0.9	2.8	83.1%	-2.0
1196	AT3G14940.1   Symbol: ATPPC3	6.6	8.3	-1.7	-2.8	83.2%	-2.0
1197	AT5G20890.1   chaperonin, putative, similar to SWISS-PROT:P78371- T-complex protein 1, beta subunit (TCP-1-beta) (Homo sapiens); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr5:7086655-7090083 REVERSE   Aliases: F22D1.60, F22D1_60	9.2	10.2	-1.0	-2.8	83.2%	-2.3
1198	AT5G52850.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:21432161-21434842 REVERSE   Aliases: MXC20.7, MXC20_7	3.4	4.0	-0.6	-2.8	83.2%	-2.5
1199	AT5G39040.1   Symbol: ATTAP2	5.8	6.4	-0.5	-2.8	83.2%	-2.2
1200	AT1G16510.1   auxin-responsive family protein, similar to indole-3-acetic acid induced protein (SP:D14414) (Vigna radiata.); ESTs gb:AA712892 and gb:Z17613 come from this gene   chr1:5644565-5645436 REVERSE   Aliases: F3O9.31, F3O9_31	5.9	5.3	0.6	2.8	83.2%	-2.2
1201	AT3G17970.1   chloroplast outer membrane translocon subunit, putative, similar to Toc64 (Pisum sativum) GI:7453538; contains Pfam profile PF00515 TPR Domain   chr3:6147968-6151981 FORWARD   Aliases: AT3G17960, MEB5.19	4.8	5.3	-0.5	-2.8	83.2%	-2.2
1202	AT3G52390.2   tatD-related deoxyribonuclease family protein, similar to SP:P27859 Deoxyribonuclease tatD (EC 3.1.21.-) (DNAse tatD) {Escherichia coli}; contains Pfam profile PF01026: TatD related DNase   chr3:19433692-19436161 REVERSE   Aliases: F22O6.230	6.4	7.6	-1.2	-2.8	83.2%	-1.9
1203	AT3G61640.1   Symbol: AGP20   arabinogalactan-protein (AGP20)	6.9	5.7	1.2	2.8	83.2%	-2.0
1204	AT5G40380.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr5:16169375-16172405 FORWARD   Aliases: MPO12.90, MPO12_90	2.5	2.2	0.2	2.8	83.2%	-2.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1205	AT2G24600.3   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:10459238-10461603 REVERSE   Aliases: F25P17.10, F25P17_10	3.0	3.5	-0.6	-2.8	83.2%	-2.2
1206	AT3G48560.1   Symbol: CSR1   acetolactate synthase, chloroplast / acetohydroxy-acid synthase (ALS), nearly identical to SP:P17597 Acetolactate synthase, chloroplast precursor (EC 2.2.1.6, formerly EC 4.1.3.18) (Acetohydroxy-acid synthase) (ALS) {Arabidopsis thaliana}   chr3:18012297-18014566 REVERSE   Aliases: ACETOHYDROXY ACID SYNTHASE, ACETOLACTATE SYNTHASE, ACETOLACTATE SYNTHASE DEFICIENT, AHAS, ALS, CHLORSULFURON/IMIDAZOLINONE RESISTANT 1, IMIDAZOLE RESISTANT 1, IMR1, T8P19.70, TZP5	11.3	10.4	0.9	2.8	83.6%	-2.1
1207	AT1G24340.1   Symbol: EMB2421   similar to phenol 2-monooxygenase like FAD dependent oxidoreductase of plant origin in apicomplexans [Cryptosporidium parvum] (GB:EAK89698.1); contains InterPro domain Flavoprotein monooxygenase (InterPro:IPR000733); contains InterPro domain Monooxygenase, FAD-binding (InterPro:IPR002938); contains InterPro domain NAD-binding site (InterPro:IPR000205); contains InterPro domain Aromatic-ring hydroxylase (InterPro:IPR003042)   chr1:8635198-8639146 FORWARD   Aliases: EMB2421, EMBRYO DEFECTIVE 2421, F3I6.28, F3I6_28	6.9	7.9	-0.9	-2.8	83.6%	-1.9
1208	AT2G20725.1   CAAX amino terminal protease family protein, contains Pfam profile PF02517 CAAX amino terminal protease family protein   chr2:8940657-8942568 REVERSE   Aliases: F5H14.3, F5H14_3	7.3	6.6	0.8	2.8	83.6%	-2.0
1209	AT2G34050.1   expressed protein, contains Pfam PS00030: Eukaryotic putative RNA-binding region RNP-1 signature	5.5	7.0	-1.5	-2.8	83.7%	-1.9
1210	AT1G01380.1   Symbol: ETC1   myb family transcription factor, similar to myb homolog (CPC) GI:2346966 from (Arabidopsis thaliana)   chr1:147267-147935 FORWARD   Aliases: ENHANCER OF TRY AND CPC 1, F6F3.18, F6F3_18	6.3	5.3	1.0	2.8	83.7%	-2.0
1211	AT5G10560.1   glycosyl hydrolase family 3 protein, beta-xylosidase, Aspergillus nidulans, EMBL:ANXLND   chr5:3336256-3339367 REVERSE   Aliases: F12B17.90, F12B17_90	5.7	6.8	-1.2	-2.8	83.7%	-2.0
1212	AT3G04950.1   expressed protein, contains InterPro domain SEC-C motif (InterPro:IPR004027)   chr3:1371711-1373483 FORWARD   Aliases: T9J14.10, T9J14_10	3.0	3.8	-0.8	-2.8	83.7%	-2.0
1213	AT2G24520.1   ATPase, plasma membrane-type, putative / proton pump, putative, strong similarity to P-type H(+)-transporting ATPase from (Phaseolus vulgaris) GI:758250, (Lycopersicon esculentum) GI:1621440, SP:Q03194 {Nicotiana plumbaginifolia}, (Solanum tuberosum) GI:435001; contains InterPro accession IPR001757: ATPase, E1-E2 type   chr2:10422512-10426863 FORWARD   Aliases: F25P17.18, F25P17_18	4.5	3.9	0.7	2.8	83.7%	-2.2
1214	AT4G18820.1   expressed protein   chr4:10330382-10334279 FORWARD   Aliases: F28A21.230, F28A21_230	5.1	6.0	-0.9	-2.8	83.8%	-2.0
1215	AT1G73430.1   sec34-like family protein, contains Pfam PF04136: Sec34-like family profile; similar to Conserved oligomeric Golgi complex component 3 (Vesicle docking protein SEC34 homolog) (p94) (Swiss-Prot:Q96JB2) (Homo sapiens)   chr1:27607316-27614729 FORWARD   Aliases: T9L24.37, T9L24_37	5.1	5.8	-0.7	-2.8	83.8%	-2.1
1216	AT1G08130.1   DNA ligase / polydeoxyribonucleotide synthase (ATP), identical to SP:Q42572 DNA ligase (EC 6.5.1.1) (Polydeoxyribonucleotide synthase (ATP)) {Arabidopsis thaliana}; contains Pfam profiles: PF01068 ATP dependent DNA ligase domain, PF04679 ATP dependent DNA ligase C terminal region, PF04675 DNA ligase N terminus   chr1:2542699-2547940 REVERSE   Aliases: T6D22.23	5.5	7.2	-1.7	-2.8	83.8%	-2.0
1217	AT4G25620.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; Common family member At5g52430 (Arabidopsis thaliana);   chr4:13066779-13069688 REVERSE   Aliases: M7J2.10, M7J2_10	5.3	4.5	0.8	2.8	83.8%	-2.0
1218	AT3G01400.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeats (4 copies)   chr3:151769-153224 FORWARD   Aliases: T13O15.4, T13O15_4	7.3	6.6	0.7	2.8	84.3%	-2.1
1219	AT4G30020.1   subtilase family protein, contains similarity to meiotic serine proteinase TMP GI:6468325 from (Lycopersicon esculentum)	6.3	7.1	-0.8	-2.8	84.3%	-2.0
1220	AT5G64570.1   Symbol: XYL4   glycosyl hydrolase family 3 protein   chr5:25827341-25830561 REVERSE   Aliases: ATBXL4, MUB3.9, MUB3_9	5.4	6.4	-1.0	-2.8	84.3%	-2.0
1221	AT2G46600.1   calcium-binding protein, putative, similar to EF-hand Ca2+-binding protein CCD1 (Triticum aestivum) GI:9255753   chr2:19143090-19143643 FORWARD   Aliases: F13A10.13	7.9	6.8	1.1	2.8	84.3%	-2.1
1222	AT1G78770.1   cell division cycle family protein, similar to cell division cycle protein GI:603230 from (Homo sapiens); contains Pfam profile PF00515 TPR Domain 148977 (apparently not full-length).   chr1:29621812-29626340 FORWARD   Aliases: F9K20.19, F9K20_19	2.5	3.3	-0.7	-2.8	84.3%	-2.3
1223	AT3G12930.1   expressed protein, contains Pfam domain PF02410: Domain of unknown function DUF143   chr3:4128414-4129963 FORWARD   Aliases: MGH6.4	4.0	4.8	-0.8	-2.8	84.3%	-1.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1224	AT2G17230.1   phosphate-responsive 1 family protein, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr2:7501618-7503098 REVERSE   Aliases: T23A1.9, T23A1_9	6.6	4.9	1.7	2.7	84.4%	-1.9
1225	AT4G27270.1   quinone reductase family protein, similar to 1,4-benzoquinone reductase (Phanerochaete chrysosporium)(GI:4454993); similar to Trp repressor binding protein (Escherichia coli)(SP:P30849); contains flavodoxin domain PF00258   chr4:13661360-13663249 REVERSE   Aliases: M4I22.80, M4I22_80	5.1	5.9	-0.8	-2.7	84.4%	-2.2
1226	AT3G23740.1   expressed protein   chr3:8551779-8554737 REVERSE   Aliases: MYM9.8	2.7	3.2	-0.4	-2.7	84.4%	-2.5
1227	AT2G38810.3   histone H2A, putative, strong similarity to histone H2A.F/Z Arabidopsis thaliana GI:2407800; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr2:16226363-16227907 REVERSE   Aliases: F13I13.4, F13I13_4	7.2	8.8	-1.5	-2.7	84.4%	-1.9
1228	AT4G37730.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr4:17723660-17724909 FORWARD   Aliases: T28I19.10, T28I19_10	5.1	4.3	0.7	2.7	84.4%	-2.1
1229	AT4G29350.1   Symbol: PRF2   profilin 2 (PRO2) (PFN2) (PRF2), identical to profilin 2 SP:Q42418 GI:1353772 from (Arabidopsis thaliana); identical to cDNA profilin (PRF2) GI:9965570   chr4:14450035-14451383 FORWARD   Aliases: F17A13.170, F17A13_170, PFN2, PROFILIN 2	14.2	13.6	0.6	2.7	84.4%	-2.5
1230	AT1G50580.1   glycosyltransferase family protein, similar to UDP rhamnose: anthocyanidin-3-glucoside rhamnosyltransferase GB:CAA81057 GI:397567 from (Petunia x hybrida); contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	5.6	6.4	-0.8	-2.7	84.4%	-2.0
1231	AT4G11470.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:6967724-6970156 FORWARD   Aliases: F25E4.90, F25E4_90	2.7	3.0	-0.4	-2.7	84.4%	-2.6
1232	AT1G76990.4   Symbol: ACR3   similar to ACT domain containing protein (ACR4) [Arabidopsis thaliana] (TAIR:At1g69040.2); similar to ACT domain containing protein (ACR4) [Arabidopsis thaliana] (TAIR:At1g69040.1); similar to putative ACT domain containing protein, ACR4, with alternative splicing forms [Oryza sativa (japonica cultivar-group)] (GB:XP_468663.1); contains InterPro domain Amino acid-binding ACT (InterPro:IPR002912)   chr1:28937056-28940444 FORWARD   Aliases: F22K20.9, F22K20_9	5.4	4.3	1.1	2.7	84.6%	-2.0
1233	AT5G01300.1   phosphatidylethanolamine-binding family protein, similar to cold-regulated protein (Hordeum vulgare subsp. vulgare) GI:10799810; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein	9.7	8.5	1.1	2.7	85.1%	-1.9
1234	AT1G44780.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g08310.1); similar to conserved hypothetical protein [Plasmodium chabaudi] (GB:CAH74933.1)   chr1:16912148-16914710 FORWARD   Aliases: T12C22.5, T12C22_5	3.9	5.5	-1.6	-2.7	85.3%	-2.1
1235	AT1G78480.1   prenyltransferase/squalene oxidase repeat-containing protein, similar to beta-Amyrin Synthase GI:3688600 from (Panax ginseng)   chr1:29530394-29531256 REVERSE   Aliases: F3F9.1	5.0	4.3	0.7	2.7	85.5%	-2.2
1236	AT5G19530.1   Symbol: ACL5   spermine/spermidine synthase family protein, similar to SP:P09158 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) {Escherichia coli}; contains Pfam profile PF01564: Spermine/spermidine synthase   chr5:6588960-6591183 REVERSE   Aliases: ACAULIS 5, SPERMINE SYNTHASE, T20D1.50, T20D1_50	2.6	3.6	-0.9	-2.7	85.6%	-1.9
1237	AT3G28180.1   Symbol: ATCSLC04   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	6.8	5.8	0.9	2.7	85.8%	-2.0
1238	AT5G12930.1   expressed protein   chr5:4082893-4085300 REVERSE   Aliases: T24H18.90, T24H18_90	2.6	2.9	-0.3	-2.7	86.0%	-2.6
1239	AT2G44490.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to anther-specific protein ATA27 (GI:2746341) (Arabidopsis thaliana)   chr2:18371859-18374801 FORWARD   Aliases: F4I1.30	4.6	5.9	-1.3	-2.7	86.0%	-1.9
1240	AT1G69935.1   expressed protein   chr1:26345464-26346789 REVERSE   Aliases: None	6.6	5.7	1.0	2.7	86.0%	-1.9
1241	AT1G31320.1   LOB domain protein 4 / lateral organ boundaries domain protein 4 (LBD4), identical to SP:Q9SHE9 LOB domain protein 4 {Arabidopsis thaliana}   chr1:11212998-11214363 FORWARD   Aliases: T19E23.11, T19E23_11	3.6	3.2	0.5	2.7	86.1%	-2.4
1242	AT5G10400.1   histone H3, identical to several histone H3 proteins, including Zea mays SP:P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP:P08903, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:3270290-3270953 REVERSE   Aliases: F12B17.250	6.5	8.8	-2.3	-2.7	86.1%	-2.0
1243	AT4G26320.1   Symbol: AGP13   arabinogalactan-protein (AGP13), identical to gi:10880503:gb:AAG24281   chr4:13317109-13317479 REVERSE   Aliases: ARABINO GALACTAN PROTEIN 13, T25K17.130, T25K17_130	6.9	5.4	1.5	2.7	86.1%	-2.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1244	AT5G04770.1   Symbol: CAT6   amino acid permease family protein, similar to cationic amino acid transporter-1 (Rattus norvegicus) GI:1589917; contains Pfam profile PF00324: Amino acid permease   chr5:1379081-1382420 FORWARD   Aliases: CATIONIC AMINO ACID TRANSPORTER 6, MUK11.10	5.6	6.3	-0.7	-2.7	86.1%	-2.1
1245	AT5G02780.1   In2-1 protein, putative, similar to In2-1 (Zea mays) EMBL:X58573	4.8	6.5	-1.7	-2.7	86.1%	-2.0
1246	AT2G16400.1   homeodomain-containing protein   chr2:7108412-7110973 REVERSE   Aliases: F16F14.10, F16F14_10	7.0	7.7	-0.7	-2.7	86.1%	-2.3
1247	AT4G19390.1   expressed protein   chr4:10574779-10576439 REVERSE   Aliases: T5K18.170, T5K18_170	9.4	8.5	0.9	2.7	86.1%	-2.0
1248	AT1G21140.1   nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313   chr1:7404372-7405270 FORWARD   Aliases: T22I11.3, T22I11_3	8.8	7.7	1.1	2.7	86.1%	-2.1
1249	AT4G16140.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:9129058-9129853 FORWARD   Aliases: DL4110W, FCAALL.289	3.2	3.8	-0.7	-2.7	86.1%	-2.1
1250	AT1G63150.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23423061-23425244 FORWARD   Aliases: F16M19.13, F16M19_13	2.9	3.3	-0.4	-2.7	86.1%	-2.5
1251	AT1G61770.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9UBS4 DnaJ homolog subfamily B member 11 precursor Homo sapiens; contains Pfam profile PF00226 DnaJ domain   chr1:22813830-22816272 FORWARD   Aliases: T13M11.13, T13M11_13	7.7	8.4	-0.7	-2.7	86.1%	-2.1
1252	AT2G15960.1   expressed protein   chr2:6954391-6954770 FORWARD   Aliases: F19G14.4, F19G14_4	4.6	3.2	1.4	2.7	86.1%	-2.0
1253	AT4G27657.1   expressed protein   chr4:13813050-13813522 FORWARD   Aliases: None	4.7	3.2	1.5	2.7	86.2%	-2.4
1254	AT1G18470.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr1:6356126-6360159 REVERSE   Aliases: F15H18.5, F15H18_5	6.8	5.7	1.1	2.7	86.2%	-2.0
1255	AT3G56170.1   Symbol: CAN   Ca(2+)-dependent nuclease, identical to Ca(2+)-dependent nuclease (Arabidopsis thaliana) GI:7684292; supporting cDNA gi:7684291:dbj:D84226.1:   chr3:20853556-20855437 FORWARD   Aliases: CA 2+ DEPENDENT NUCLEASE, F18O21.130, F18O21_130	6.0	4.8	1.3	2.7	86.2%	-2.0
1256	AT3G15280.1   expressed protein, very low similarity to cold regulated gene REP14 (Secale cereale) GI:20067233, late embryogenesis abundant protein (Picea glauca) GI:1161171   chr3:5143975-5144700 REVERSE   Aliases: K7L4.8	4.4	3.2	1.3	2.7	86.2%	-1.9
1257	AT5G51545.1   expressed protein   chr5:20953660-20954626 FORWARD   Aliases: None	6.6	5.5	1.0	2.7	86.2%	-1.9
1258	AT3G55840.1   expressed protein   chr3:20727974-20729845 REVERSE   Aliases: F27K19.20	4.5	3.5	1.0	2.7	86.2%	-2.2
1259	AT3G27650.1   LOB domain protein 25 / lateral organ boundaries domain protein 25 (LBD25), identical to LOB DOMAIN 25 (Arabidopsis thaliana) GI:17227166   chr3:10239783-10241848 FORWARD   Aliases: MGF10.6	4.8	4.0	0.8	2.7	86.7%	-2.1
1260	AT2G34650.1   Symbol: PID   protein kinase PINOID (PID), identical to protein kinase PINOID (Arabidopsis thaliana) gi:7208442:gb:AAF40202; contains protein kinase domain, Pfam:PF00069   chr2:14596851-14598867 REVERSE   Aliases: ABR, ABRUPTUS, PINOID, PROTEIN KINASE PINOID, T31E10.1, T31E10_1	5.1	6.1	-1.0	-2.7	86.8%	-1.9
1261	AT5G41180.1   leucine-rich repeat protein kinase, putative, contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:16501099-16504654 FORWARD   Aliases: MEE6.25, MEE6_25	4.2	5.0	-0.8	-2.7	86.8%	-2.1
1262	AT1G24510.2   T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative, identical to SWISS-PROT:O04450- T-complex protein 1, epsilon subunit (TCP-1-epsilon) (Arabidopsis thaliana); strong similarity to SP:P54411 T-complex protein 1, epsilon subunit (TCP-1-epsilon) (CCT-epsilon) (TCP-K36) {Avena sativa}; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr1:8685298-8688231 REVERSE   Aliases: F21J9.17	9.1	9.9	-0.8	-2.7	86.8%	-2.6
1263	AT2G30360.1   Symbol: CIPK11	7.8	6.5	1.4	2.7	86.8%	-2.1
1264	AT3G14890.2   phosphoesterase, identical to phosphoesterase (Arabidopsis thaliana) GI:21630064; contains Pfam profile PF00645: Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region   chr3:5008828-5013272 FORWARD   Aliases: K15M2.3	4.7	6.1	-1.4	-2.7	86.8%	-2.0
1265	AT3G46600.2   scarecrow transcription factor family protein, scarecrow-like 11 - Arabidopsis thaliana, EMBL:AF036307   chr3:17168929-17170950 FORWARD   Aliases: F12A12.120	5.3	4.8	0.5	2.7	86.8%	-2.3
1266	AT5G41870.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to polygalacturonase PG1 (Glycine max) GI:5669846; contains PF00295: Glycosyl hydrolases family 28	3.9	4.6	-0.6	-2.7	86.8%	-2.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1267	AT5G60100.1   Symbol: APRR3   pseudo-response regulator 3 (APRR3), identical to pseudo-response regulator 3 GI:10281008 from (Arabidopsis thaliana)   chr5:24215441-24217728 REVERSE   Aliases: MGO3.8, MGO3_8, PRR3, PSEUDO RESPONSE REGULATOR 3	5.1	4.6	0.5	2.7	87.1%	-2.3
1268	AT2G28060.1   protein kinase-related, similar to GAL83 protein (Solanum tuberosum) GI:5702015; contains Pfam profile PF04739: 5'-AMP-activated protein kinase, beta subunit, complex-interacting region; supporting cDNA gi:22652763:gb:AF491295.1:   chr2:11957063-11959279 REVERSE   Aliases: F24D13.15, F24D13_15	7.3	6.6	0.7	2.7	87.2%	-2.2
1269	AT5G46295.1   expressed protein   chr5:18797023-18797429 REVERSE   Aliases: None	4.7	3.7	1.0	2.7	87.2%	-2.1
1270	AT4G26370.2   antitermination NusB domain-containing protein, contains Pfam profile: PF01029 NusB family   chr4:13333733-13336184 REVERSE   Aliases: T25K17.4	4.2	3.4	0.7	2.7	87.2%	-2.2
1271	AT4G19120.2   early-responsive to dehydration stress protein (ERD3), identical to ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase; identical to cDNA ERD3 GI:15320409   chr4:10460306-10463113 REVERSE   Aliases: T18B16.90, T18B16_90	10.4	11.2	-0.8	-2.7	87.2%	-2.3
1272	AT5G03390.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr5:834987-836750 FORWARD   Aliases: F12E4.130, F12E4_130	2.8	3.6	-0.8	-2.7	87.2%	-2.1
1273	AT3G60590.3   expressed protein   chr3:22409203-22410728 FORWARD   Aliases: T4C21.1	4.7	4.0	0.8	2.7	87.2%	-2.3
1274	AT3G50350.1   expressed protein   chr3:18683888-18684688 FORWARD   Aliases: F11C1.190	7.2	6.0	1.2	2.7	87.4%	-2.0
1275	AT2G42200.2   squamosa promoter-binding protein-like 9 (SPL9), identical to squamosa promoter binding protein-like 9 (Arabidopsis thaliana) GI:5931673; contains Pfam profile PF03110: SBP domain   chr2:17594485-17596708 FORWARD   Aliases: T24P15.11, T24P15_11	3.3	4.1	-0.8	-2.7	87.4%	-2.2
1276	AT5G04420.3   similar to acyl-CoA binding family protein [Arabidopsis thaliana] (TAIR:At3g05420.1); similar to acyl-CoA binding family protein [Arabidopsis thaliana] (TAIR:At3g05420.2); similar to putative transcription factor [Oryza sativa (japonica cultivar-group)] (GB:XP_470332.1); contains InterPro domain Kelch repeat (InterPro:IPR006652)   chr5:1246036-1249840 REVERSE   Aliases: T19N18.4	6.1	7.7	-1.6	-2.7	87.4%	-2.0
1277	AT5G66070.2   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At2g17730.1); similar to putative zinc finger protein [Oryza sativa] (GB:AAL79729.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr5:26439081-26440458 FORWARD   Aliases: K2A18.15, K2A18_15	5.7	4.5	1.1	2.7	87.4%	-2.0
1278	AT3G62150.1   multidrug resistant (MDR) ABC transporter, putative, similar to multidrug-resistant protein CjMDR1 GI:14715462 from (Coptis japonica); contains Pfam profiles PF00005: ABC transporter, PF00664: ABC transporter transmembrane region   chr3:23019730-23024554 REVERSE   Aliases: T17J13.110	7.4	6.8	0.7	2.7	87.4%	-2.1
1279	AT1G13030.1   sphere organelles protein-related, contains weak similarity to Swiss-Prot:Q09003 sphere organelles protein SPH-1 (Sphere protein 1) (Xenopus laevis)   chr1:4444041-4447404 REVERSE   Aliases: F3F19.5, F3F19_5	5.3	5.9	-0.6	-2.7	87.4%	-2.3
1280	AT4G23180.1   Symbol: CRK10   receptor-like protein kinase 4, putative (RLK4), nearly identical to receptor-like protein kinase 4 (Arabidopsis thaliana) GI:13506745; contains Pfam domain, PF00069: Protein kinase domain; identical to cDNA receptor-like protein kinase 4 (RLK4) GI:13506744   chr4:12138148-12140932 FORWARD   Aliases: CYSTEINE RICH RLK10, F21P8.70, F21P8_70, RECEPTOR LIKE PROTEIN KINASE 4, RLK4	4.8	5.5	-0.7	-2.7	87.4%	-2.2
1281	AT5G46580.1   pentatricopeptide (PPR) repeat-containing protein, contains similarity to 67kD chloroplastic RNA-binding protein, P67.1 (Raphanus sativus) GI:9755886; contains Pfam profile PF01535: PPR repeat	3.9	4.6	-0.7	-2.7	87.6%	-2.1
1282	AT5G43340.1   Symbol: PHT6   inorganic phosphate transporter, identical to inorganic phosphate transporter (Arabidopsis thaliana) GI:3869190   chr5:17410826-17412376 REVERSE   Aliases: MWF20.3, MWF20_3	3.7	3.1	0.6	2.7	87.9%	-2.3
1283	AT4G34750.1   auxin-responsive protein, putative / small auxin up RNA (SAUR_E), contains similarity to indole-3-acetic acid induced protein ARG7 SP:P32295 from (Phaseolus aureus)   chr4:16577571-16578357 FORWARD   Aliases: F11I11.5	6.5	5.8	0.7	2.7	87.9%	-2.3
1284	AT5G64760.2   similar to 26S proteasome regulatory subunit, putative (RPN5) [Arabidopsis thaliana] (TAIR:At5g09900.1); similar to 26S proteasome regulatory subunit, putative (RPN5) [Arabidopsis thaliana] (TAIR:At5g09900.2); similar to 26S proteasome regulatory particle non-ATPase subunit5 [Oryza sativa (japonica cultivar-group)] (GB:BAB78500.1); contains InterPro domain Proteasome component region PCI (InterPro:IPR000717)   chr5:25910702-25913781 REVERSE   Aliases: MVP7.9, MVP7_9	4.9	6.3	-1.4	-2.7	87.9%	-2.0
1285	AT4G28640.1   Symbol: IAA11   auxin-responsive protein / indoleacetic acid-induced protein 11 (IAA11), identical to SP:Q38829 Auxin-responsive protein IAA11 (Indoleacetic acid-induced protein 11) {Arabidopsis thaliana}   chr4:14142141-14143975 FORWARD   Aliases: T5F17.90, T5F17_90	6.6	5.9	0.7	2.7	87.9%	-2.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1286	AT1G74850.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:28122510-28125975 REVERSE   Aliases: F25A4.18, F25A4_18	4.1	4.5	-0.5	-2.7	88.0%	-2.3
1287	AT5G08535.2   D111/G-patch domain-containing protein, contains Pfam profile PF01585: G-patch domain; contains a 2nt micro-exon, as identified using GeneSeqer.	9.2	8.5	0.7	2.7	88.1%	-2.6
1288	AT4G16340.1   Symbol: SPK1   adapter protein SPIKE1 (SPK1), One model reflects the alignment of a full-length cDNA sequence gi:18496702. There are multiple frame shifts in the gene model resulting in a truncated protein.	4.7	5.8	-1.0	-2.7	88.2%	-2.0
1289	AT3G57630.2   exostosin family protein, contains Pfam profile: PF03016	4.7	5.6	-0.9	-2.7	88.5%	-2.1
1290	AT2G21650.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA-binding domain   chr2:9266663-9267736 FORWARD   Aliases: F2G1.8, F2G1_8	2.7	3.1	-0.4	-2.7	88.5%	-2.4
1291	AT1G09575.1   expressed protein, contains Pfam domain, PF04678: Protein of unknown function, DUF607   chr1:3101673-3102927 REVERSE   Aliases: None	4.2	3.4	0.8	2.7	88.6%	-2.1
1292	AT1G28600.2   similar to GDSL-motif lipase, putative [Arabidopsis thaliana] (TAIR:At1g28610.2); similar to lipase-like [Oryza sativa (japonica cultivar-group)] (GB:BAD68794.1); contains InterPro domain Lipolytic enzyme, G-D-S-L family (InterPro:IPR001087)   chr1:10050987-10053103 REVERSE   Aliases: F1K23.28, F1K23_28	4.2	3.7	0.5	2.7	88.9%	-2.4
1293	AT4G33040.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	6.0	5.3	0.7	2.7	88.9%	-2.4
1294	AT1G15790.2   expressed protein   chr1:5438252-5440082 REVERSE   Aliases: F7H2.13, F7H2_13	4.4	3.9	0.5	2.7	88.9%	-2.4
1295	AT2G03220.1   Symbol: FT1   galactoside 2-alpha-L-fucosyltransferase / xyloglucan alpha-(1,2)-fucosyltransferase (FUT1) (FT1), identical to SP:Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}   chr2:970256-972404 REVERSE   Aliases: A (1,2) FUCOSYLTRANSFERASE, ATFT1, ATFUT1, FUCOSYLTRANSFERASE 1, MUR2, MURUS 2, T18E12.11, T18E12_11, XYLOGLUCAN FUCOSYLTRANSFERASE	5.1	6.4	-1.3	-2.7	88.9%	-2.1
1296	AT4G37550.2   similar to formamidase, putative / formamide amidohydrolase, putative [Arabidopsis thaliana] (TAIR:At4g37560.1); similar to formamidase [Methylophilus methylotrophus] (GB:CAA67953.1); contains InterPro domain Acetamidase/Formamidase (InterPro:IPR004304)   chr4:17643575-17645821 FORWARD   Aliases: F19F18.40, F19F18_40	6.4	7.2	-0.8	-2.7	88.9%	-2.0
1297	AT2G29650.3   inorganic phosphate transporter, putative, similar to brain specific Na+-dependent inorganic phosphate cotransporter (Rattus norvegicus) GI:507415; contains Pfam profile PF00083: major facilitator superfamily protein	7.0	5.7	1.2	2.7	88.9%	-2.0
1298	AT3G22300.1   Symbol: RPS10   40S ribosomal protein S10, mitochondrial (RPS10), identical to SP:P42797 40S ribosomal protein S10, mitochondrial precursor {Arabidopsis thaliana}   chr3:7885675-7886827 FORWARD   Aliases: MCB17.5, RIBOSOMAL PROTEIN S10	6.2	7.3	-1.1	-2.7	88.9%	-2.0
1299	AT1G61260.1   expressed protein, contains similarity to cotton fiber expressed protein 1 (Gossypium hirsutum) gi:3264828:gb:AAC33276   chr1:22597130-22598734 REVERSE   Aliases: F11P17.2, F11P17_2	5.1	3.3	1.8	2.7	89.0%	-2.0
1300	AT1G52800.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to GS-AOP loci (GI:16118889, GI:16118887, GI:16118891, GI:16118893); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:19667712-19669030 FORWARD   Aliases: F14G24.7, F14G24_7	2.3	2.1	0.2	2.7	89.0%	-3.3
1301	AT4G35270.1   RWP-RK domain-containing protein, similar to nodule inception protein GI:6448579 from (Lotus japonicus); contains Pfam profile: PF02042 RWP-RK domain   chr4:16777343-16780829 REVERSE   Aliases: F23E12.170, F23E12_170	6.0	4.9	1.0	2.7	89.0%	-2.1
1302	AT4G15850.1   Symbol: ATRH1   DEAD/DEAH box helicase, putative, similar to D-E-A-D box protein (Drosophila melanogaster) GI:499204; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr4:9001344-9004749 FORWARD   Aliases: DL3965W, FCAALL.401	3.5	4.2	-0.7	-2.7	89.0%	-2.1
1303	AT5G27330.1   expressed protein   chr5:9632706-9634886 REVERSE   Aliases: F21A20.40, F21A20_40	5.5	7.7	-2.2	-2.7	89.0%	-2.0
1304	AT2G40480.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g56270.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAU44189.1); contains InterPro domain Plant protein of unknown function DUF827 (InterPro:IPR008545)   chr2:16917442-16919670 FORWARD   Aliases: T2P4.17, T2P4_17	6.6	7.4	-0.8	-2.7	89.0%	-2.2
1305	AT5G27670.1   histone H2A, putative, similar to histone H2A Lycopersicon esculentum SP:P25469, Pisum sativum SP:P25470, Petroselinum crispum SP:P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:9792579-9793458 REVERSE   Aliases: T1G16.3	8.9	9.6	-0.8	-2.7	89.0%	-2.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1306	AT4G02330.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:1032413-1035037 FORWARD   Aliases: ATPMEPCRB, T14P8.14, T14P8_14	4.2	5.5	-1.3	-2.7	89.0%	-2.1
1307	AT3G29810.1   phytochelatin synthetase family protein / COBRA cell expansion protein COBL2, similar to phytochelatin synthetase (Hordeum vulgare subsp. vulgare) GI:29570314; identified in Roudier, et al, Plant Phys. (2002) 130:538-548 (PMID:12376623); contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region   chr3:11730596-11732718 FORWARD   Aliases: K17E7.12	8.8	7.7	1.2	2.7	89.0%	-2.1
1308	AT2G44080.1   expressed protein   chr2:18244261-18245249 FORWARD   Aliases: F6E13.21	9.5	8.7	0.8	2.7	89.0%	-2.5
1309	AT3G19515.1   expressed protein   chr3:6766674-6769032 REVERSE   Aliases: MLD14.38	7.6	9.0	-1.4	-2.7	89.0%	-2.2
1310	AT4G25280.1   adenylate kinase family protein, contains Pfam profile: PF00406 adenylate kinase	6.4	7.3	-1.0	-2.7	89.0%	-2.2
1311	AT5G37580.1   expressed protein   chr5:14944543-14946800 REVERSE   Aliases: K12B20.4, K12B20_4	4.9	5.8	-0.8	-2.7	89.0%	-2.1
1312	AT5G14940.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:4831751-4834315 REVERSE   Aliases: F2G14.60, F2G14_60	5.6	4.8	0.8	2.7	89.0%	-2.2
1313	AT4G28760.2   expressed protein, predicted protein. Arabidopsis thaliana   chr4:14207467-14212050 FORWARD   Aliases: F16A16.130, F16A16_130	3.7	4.3	-0.6	-2.7	89.0%	-2.3
1314	AT1G11720.1   starch synthase, putative, strong similarity to soluble-starch-synthase (Solanum tuberosum) GI:1911166   chr1:3952511-3957044 FORWARD   Aliases: F25C20.13, F25C20_13	4.6	5.5	-0.9	-2.7	89.0%	-2.0
1315	AT1G05760.1   Symbol: RTM1   jacalin lectin family protein (RTM1), identical to gi:6503088 (GB:AAF14583) from (Arabidopsis thaliana) (Proc. Natl. Acad. Sci. U.S.A. 97 (1), 489-494 (2000)); contains Pfam profile PF01419 jacalin-like lectin domain	4.3	3.2	1.1	2.7	89.0%	-2.0
1316	AT3G15510.1   Symbol: ATNAC2	4.3	3.5	0.8	2.7	89.0%	-2.1
1317	AT4G03320.1   chloroplast protein import component-related, similar to P. sativum Tic20 chloroplast protein import component (GI:3769673)   chr4:1464467-1466164 FORWARD   Aliases: F4C21.25, F4C21_25	7.5	6.4	1.1	2.7	89.0%	-2.1
1318	AT1G60390.1   BURP domain-containing protein / polygalacturonase, putative, similar to polygalacturonase isoenzyme 1 beta subunit GI:170480 from (Lycopersicon esculentum); contains Pfam profile PF03181: BURP domain	4.3	5.6	-1.2	-2.7	89.0%	-2.0
1319	AT1G62040.1   autophagy 8c (APG8c), identical to autophagy 8c (Arabidopsis thaliana) GI:19912155; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3   chr1:22936566-22938088 FORWARD   Aliases: F8K4.23, F8K4_23	9.4	8.6	0.8	2.7	89.0%	-2.3
1320	AT4G31530.1   expressed protein   chr4:15282245-15284222 FORWARD   Aliases: F3L17.100, F3L17_100	5.8	5.2	0.6	2.7	89.0%	-2.3
1321	AT1G77420.1   hydrolase, alpha/beta fold family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:29098393-29100610 FORWARD   Aliases: T5M16.2, T5M16_2	7.6	7.0	0.7	2.7	89.0%	-2.3
1322	AT1G09815.1   DNA polymerase delta subunit 4 family, contains similarity to Swiss-Prot:Q9HCU8 DNA polymerase delta subunit 4 (DNA polymerase delta subunit p12) (Homo sapiens)	9.4	8.9	0.5	2.7	89.0%	-2.4
1323	AT3G01470.1   Symbol: ATHB 1	9.2	8.0	1.1	2.7	89.0%	-2.1
1324	AT1G74000.1   Symbol: SS3   similar to strictosidine synthase family protein [Arabidopsis thaliana] (TAIR:At1g74020.1); similar to strictosidine synthase (GB:AAB40594.1); contains InterPro domain Strictosidine synthase (InterPro:IPR004141)   chr1:27832803-27835088 REVERSE   Aliases: ATSS 3 STRICTOSIDINE SYNTHASE, F2P9.13, F2P9_13, STRICTOSIDINE SYNTHASE 3	5.5	6.7	-1.2	-2.7	89.0%	-2.0
1325	AT5G20660.1   24 kDa vacuolar protein, putative, similar to 24 kDa vacuolar protein VP24 (Ipomoea batatas) gi:5821406:dbj:BAA83809   chr5:6986237-6991045 FORWARD   Aliases: T1M15.60, T1M15_60	9.7	10.3	-0.6	-2.7	89.0%	-2.6
1326	AT5G23840.2   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain   chr5:8035770-8036985 FORWARD   Aliases: MRO11.12, MRO11_12	6.6	5.1	1.5	2.7	89.0%	-2.2
1327	AT4G16155.1   dihydrolipoamide dehydrogenase 2, plastidic / lipoamide dehydrogenase 2 (PTLPD2), identical to plastidic lipoamide dehydrogenase from Arabidopsis thaliana (gi:7159284)   chr4:9153386-9157278 REVERSE   Aliases: None	8.2	9.1	-0.9	-2.7	89.0%	-2.0
1328	AT1G80180.1   expressed protein   chr1:30161718-30162476 REVERSE   Aliases: F18B13.26, F18B13_26	7.2	6.2	1.0	2.7	89.2%	-2.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1329	AT1G70810.1   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr1:26707792-26708898 FORWARD   Aliases: F15H11.6, F15H11_6	4.6	3.8	0.8	2.7	89.2%	-2.1
1330	AT2G25620.1   protein phosphatase 2C, putative / PP2C, putative   chr2:10910021-10912323 REVERSE   Aliases: F3N11.7, F3N11_7	4.1	5.0	-0.9	-2.7	89.2%	-2.1
1331	AT1G64200.1   Symbol: VHA E3	5.3	6.3	-1.0	-2.7	89.2%	-2.1
1332	AT1G23550.1   Symbol: SRO2   Encodes a protein with similarity to RCD1 but without the WWE domain. The protein does have a PARP signature upstream of the C-terminal protein interaction domain. The PARP signature may bind NAD+ and attach the ADP-ribose-moiety from NAD+ to the target molecule. Its presence suggests a role for the protein in ADP ribosylation.   chr1:8350901-8352221 FORWARD   Aliases: F28C11.18, SIMILAR TO RCD ONE 2, SIMILAR TO RCD ONE 2, SRO2	6.5	5.6	0.9	2.7	89.2%	-2.2
1333	AT5G10380.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:3267719-3268814 FORWARD   Aliases: F12B17.270, F12B17_270	3.2	2.6	0.6	2.7	89.5%	-2.4
1334	AT5G52840.1   NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-B subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-13Kd-B) (CI-13Kd-B) (Complex I subunit B13) (Swiss-Prot:Q63362) (Rattus norvegicus)   chr5:21430880-21432232 FORWARD   Aliases: MXC20.6, MXC20_6	10.3	11.3	-1.0	-2.7	89.7%	-2.3
1335	AT5G51070.1   Symbol: ERD1   ATP-dependent Clp protease ATP-binding subunit (ClpD), (ERD1), SAG15/ERD1; identical to ERD1 protein GI:497629, SP:P42762 from (Arabidopsis thaliana); contains Pfam profile PF02861: Clp amino terminal domain   chr5:20781541-20785907 FORWARD   Aliases: CLPD, EARLY RESPONSIVE TO DEHYDRATION 1, K3K7.27, K3K7_27	7.4	6.3	1.1	2.7	89.7%	-2.1
1336	AT2G34510.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr2:14551076-14553886 REVERSE   Aliases: T31E10.15, T31E10_15	5.6	4.5	1.1	2.7	89.7%	-2.0
1337	AT5G19330.2   armadillo/beta-catenin repeat family protein / BTB/POZ domain-containing protein, contains armadillo/beta-catenin-like repeats, Pfam:PF00514 and a BTB/POZ domain, Pfam:PF00651   chr5:6508302-6512746 REVERSE   Aliases: F7K24.80, F7K24_80	5.7	6.3	-0.7	-2.7	90.1%	-2.3
1338	AT3G09770.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:2996283-2998195 REVERSE   Aliases: F11F8.36	7.2	6.4	0.7	2.7	90.1%	-2.2
1339	AT4G24840.1   expressed protein   chr4:12796257-12800948 REVERSE   Aliases: F6I7.50, F6I7_50	6.3	7.1	-0.8	-2.7	90.1%	-2.2
1340	AT1G58250.1   Symbol: SAB   SABRE, putative, similar to SABRE (GI:719291) (Arabidopsis thaliana)   chr1:21590707-21605286 REVERSE   Aliases: F16M22.5, F16M22_5, SABRE	6.6	7.8	-1.2	-2.7	90.1%	-2.2
1341	AT5G19730.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:6670460-6673284 FORWARD   Aliases: T29J13.150, T29J13_150	3.3	4.9	-1.6	-2.7	90.1%	-2.0
1342	AT5G52390.1   photoassimilate-responsive protein, putative, similar to PIR:S62698 photoassimilate-responsive protein precursor (clone PAR-1a) - common tobacco	5.3	7.8	-2.5	-2.6	90.2%	-2.1
1343	AT4G24380.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g65400.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_479601.1)   chr4:12612545-12614027 FORWARD   Aliases: T22A6.210, T22A6_210	9.4	8.3	1.2	2.6	90.3%	-2.2
1344	AT1G21010.1   expressed protein   chr1:7346145-7346957 FORWARD   Aliases: F9H16.19, F9H16_19	4.2	3.8	0.4	2.6	90.7%	-2.5
1345	AT3G60660.1   expressed protein   chr3:22432385-22434452 FORWARD   Aliases: T4C21.70	2.8	3.3	-0.6	-2.6	91.0%	-2.4
1346	AT1G65560.1   allyl alcohol dehydrogenase, putative, similar to allyl alcohol dehydrogenase from Nicotiana tabacum (gi:6692816); similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana   chr1:24375050-24377443 REVERSE   Aliases: F5I14.9, F5I14_9	4.4	5.3	-0.9	-2.6	91.0%	-2.2
1347	AT3G22260.2   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr3:7871015-7873572 FORWARD   Aliases: MMP21.4	5.3	4.4	0.8	2.6	91.0%	-2.1
1348	AT1G68660.1   expressed protein   chr1:25781514-25782824 REVERSE   Aliases: F24J5.10, F24J5_10	9.2	8.3	1.0	2.6	91.0%	-2.1
1349	AT1G61590.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069; similar to serine/threonine protein kinase gi:1066501:gb:AAA81538   chr1:22727166-22729739 REVERSE   Aliases: T25B24.6, T25B24_6	2.3	2.9	-0.5	-2.6	91.0%	-2.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1350	AT1G74940.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana)   chr1:28149720-28150839 FORWARD   Aliases: F25A4.9, F25A4_9	8.4	7.5	0.9	2.6	91.0%	-2.2
1351	AT3G54140.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:20056641-20059550 REVERSE   Aliases: F24B22.100	4.4	3.8	0.6	2.6	91.0%	-2.4
1352	AT4G27350.1   expressed protein   chr4:13690827-13692800 REVERSE   Aliases: F27G19.7, M4I22.160, M4I22_160	7.4	6.7	0.7	2.6	91.0%	-2.4
1353	AT5G55790.1   expressed protein, ; expression supported by MPSS   chr5:22597986-22598561 REVERSE   Aliases: MDF20.23, MDF20_23	3.5	2.8	0.7	2.6	91.0%	-2.5
1354	AT1G11130.1   Symbol: SUB   leucine-rich repeat family protein / protein kinase family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to leucine-rich repeat transmembrane protein kinase 2 (Zea mays) gi:3360291:gb:AAC27895   chr1:3722857-3727443 FORWARD   Aliases: AT1G11140, SCM, SCRAMBLED, STRUBBELIG, T19D16.8	3.4	3.8	-0.4	-2.6	91.1%	-2.5
1355	AT5G46770.1   expressed protein   chr5:18994635-18995387 FORWARD   Aliases: MZA15.19, MZA15_19	2.9	3.2	-0.3	-2.6	91.1%	-3.1
1356	AT1G26560.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) (Prunus serotina)	5.1	4.4	0.7	2.6	91.2%	-2.3
1357	AT3G43800.1   Symbol: ATGSTU27   glutathione S-transferase, putative, glutathione transferase, papaya, PIR:T09781   chr3:15671846-15672912 FORWARD   Aliases: T28A8.90	4.6	5.6	-1.0	-2.6	91.3%	-2.2
1358	AT1G09210.1   calreticulin 2 (CRT2), identical to SP:Q38858 Calreticulin 2 precursor {Arabidopsis thaliana}   chr1:2972844-2976731 REVERSE   Aliases: T12M4.8, T12M4_8	8.0	9.1	-1.1	-2.6	91.3%	-2.3
1359	AT5G55400.1   fimbrin-like protein, putative, similar to fimbrin-like protein (ATFIM1) (Arabidopsis thaliana) GI:2905893; contains Pfam profile PF00307: Calponin homology (CH) domain	7.7	9.9	-2.3	-2.6	91.3%	-2.2
1360	AT2G21380.1   kinesin motor protein-related   chr2:9148711-9156389 FORWARD   Aliases: F3K23.14, F3K23_14	4.4	5.5	-1.2	-2.6	91.3%	-2.3
1361	AT3G52960.1   peroxiredoxin type 2, putative, similar to type 2 peroxiredoxin (Brassica rapa subsp. pekinensis) GI:4928472; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family   chr3:19650646-19651597 FORWARD   Aliases: F8J2.130	7.8	8.8	-1.0	-2.6	91.3%	-2.1
1362	AT3G07310.1   expressed protein   chr3:2327824-2329787 REVERSE   Aliases: T1B9.2	5.1	4.2	0.9	2.6	91.4%	-2.1
1363	AT3G53410.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain: PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:19811930-19813298 REVERSE   Aliases: F4P12.110	6.1	5.5	0.6	2.6	91.4%	-2.3
1364	AT5G33290.1   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr5:12575486-12579250 FORWARD   Aliases: F19N2.10, F19N2_10	6.4	5.6	0.8	2.6	91.4%	-2.3
1365	AT4G15630.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:8917428-8918850 FORWARD   Aliases: DL3855W, FCAALL.230	3.4	4.0	-0.7	-2.6	91.4%	-2.3
1366	AT2G39720.1   Symbol: RHC2A   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:16574287-16575900 REVERSE   Aliases: RING H2 FINGER PROTEIN RHC2A, T5I7.2, T5I7_2	6.2	5.7	0.6	2.6	91.4%	-2.4
1367	AT3G14415.1   (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative, similar to (S)-2-hydroxy-acid oxidase, peroxisomal (Glycolate oxidase, GOX) (Short chain alpha-hydroxy acid oxidase) (Spinacia oleracea) SWISS-PROT:P05414   chr3:4818674-4820755 FORWARD   Aliases: MOA2.13	4.4	3.3	1.0	2.6	91.5%	-2.1
1368	AT3G14420.4   similar to (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative [Arabidopsis thaliana] (TAIR:At3g14415.1); similar to glycolate oxidase [Zantedeschia aethiopica] (GB:AAO17067.1); contains InterPro domain FMN-dependent alpha-hydroxy acid dehydrogenase, active site (InterPro:IPR008259); contains InterPro domain FMN-dependent alpha-hydroxy acid dehydrogenase (InterPro:IPR000262)	4.4	3.3	1.0	2.6	91.5%	-2.1
1369	AT3G22900.1   RNA polymerase Rpb7 N-terminal domain-containing protein, weak similarity to SP:P52433 DNA-directed RNA polymerase II 19 kDa polypeptide (EC 2.7.7.6) (RPB7) {Rattus norvegicus}; contains Pfam profile PF03876: RNA polymerase Rpb7, N-terminal domain   chr3:8115184-8116260 FORWARD   Aliases: F5N5.8	5.1	6.2	-1.0	-2.6	91.5%	-2.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1370	AT5G67470.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr5:26944061-26947686 FORWARD   Aliases: K9I9.3, K9I9_3	6.4	7.0	-0.6	-2.6	91.5%	-2.3
1371	AT2G27060.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:11558405-11561853 FORWARD   Aliases: T20P8.11, T20P8_11	5.1	5.7	-0.7	-2.6	91.5%	-2.3
1372	AT5G63920.1   DNA topoisomerase III alpha, putative, similar to Swiss-Prot:Q9NG98 DNA topoisomerase III alpha (Drosophila melanogaster)   chr5:25591759-25598504 FORWARD   Aliases: MGI19.16	4.2	4.9	-0.7	-2.6	91.5%	-2.2
1373	AT1G01220.1   GHMP kinase-related, contains similarity to L-fucose kinase (Homo sapiens) gi:21212956:emb:CAD29647   chr1:91750-95552 FORWARD   Aliases: F6F3.3, F6F3_3	5.4	6.3	-0.9	-2.6	91.5%	-2.2
1374	AT1G72670.1   calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr1:27360357-27362443 REVERSE   Aliases: F28P22.14, F28P22_14	3.0	3.4	-0.3	-2.6	91.5%	-2.8
1375	AT2G01660.2   33 kDa secretory protein-related, contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa secretory proteins   chr2:290602-292569 REVERSE   Aliases: T8O11.17, T8O11_17	5.9	5.1	0.7	2.6	91.6%	-2.3
1376	AT4G37670.2   GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein, similar to SP:P08205 from Escherichia coli ; contains Pfam profile PF00696: Amino acid kinase family   chr4:17696053-17698830 REVERSE   Aliases: F19F18.160, F19F18_160	4.7	5.9	-1.2	-2.6	91.6%	-2.1
1377	AT3G01620.1   glycosyl transferase family 17 protein, low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus (SP:Q10470), Rattus norvegicus (SP:Q02527), Homo sapiens (SP:Q09327) ; contains Pfam profile PF04724 :Glycosyltransferase family 17   chr3:235204-236932 REVERSE   Aliases: F4P13.16, F4P13_16	3.1	2.8	0.3	2.6	91.7%	-2.8
1378	AT1G17620.1   expressed protein   chr1:6062227-6063284 FORWARD   Aliases: F11A6.25, F1L3.32, F1L3_32	6.6	5.4	1.2	2.6	91.9%	-2.1
1379	AT5G61660.1   glycine-rich protein   chr5:24796441-24797156 REVERSE   Aliases: K11J9.19, K11J9_19	6.5	5.7	0.8	2.6	92.2%	-2.2
1380	AT4G34950.1   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr4:16642321-16644823 REVERSE   Aliases: F11I11.190, F11I11_190	7.8	6.3	1.6	2.6	92.3%	-2.2
1381	AT4G29690.1   type I phosphodiesterase/nucleotide pyrophosphatase family protein, similar to SP:P22413 Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1) (Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) {Homo sapiens}); contains Pfam profile PF01663: Type I phosphodiesterase / nucleotide pyrophosphatase   chr4:14540913-14542487 REVERSE   Aliases: T16L4.200, T16L4_200	2.8	3.8	-1.0	-2.6	92.3%	-2.2
1382	AT5G39840.1   ATP-dependent RNA helicase, mitochondrial, putative, similar to mitochondrial RNA helicase (Arabidopsis thaliana) GI:5823579; contains Pfam profile PF00271: Helicase conserved C-terminal domain   chr5:15963997-15966414 FORWARD   Aliases: K13H13.20, K13H13_20	2.6	3.1	-0.5	-2.6	92.3%	-2.5
1383	AT1G75810.1   expressed protein   chr1:28465326-28466007 FORWARD   Aliases: T4O12.4, T4O12_4	6.5	5.6	0.9	2.6	92.3%	-2.2
1384	AT5G41010.1   DNA-directed RNA polymerases I, II, and III 7 kDa subunit, putative, similar to SP:P53803 DNA-directed RNA polymerases I, II, and III 7.0 kDa polypeptide (EC 2.7.7.6) (ABC10-alpha) (RBP7.0) (RBP10alpha) {Homo sapiens}; contains Pfam profile PF03604: DNA directed RNA polymerase, 7 kDa subunit   chr5:16441278-16442180 FORWARD   Aliases: MEE6.8, MEE6_8	10.8	10.4	0.4	2.6	92.3%	-2.6
1385	AT5G53880.1   expressed protein   chr5:21890020-21890529 REVERSE   Aliases: K19P17.4, K19P17_4	10.2	8.8	1.4	2.6	92.3%	-2.3
1386	AT1G13340.1   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	4.9	3.9	1.0	2.6	92.3%	-2.2
1387	AT3G62190.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein Saccharomyces cerevisiae; contains Pfam profile PF00226 DnaJ domain   chr3:23032096-23034307 FORWARD   Aliases: T17J13.150	9.4	8.8	0.6	2.6	92.3%	-2.6
1388	AT4G37750.1   Symbol: ANT   ovule development protein aintegumenta (ANT), identical to ovule development protein aintegumenta (ANT) (GI:1244708) (Arabidopsis thaliana)   chr4:17739508-17742395 FORWARD   Aliases: AINTEGUMENTA, CKC, CKC1, COMPLEMENTING A PROTEIN KINASE C MUTANT 1, DRAGON, DRG, T28I19.30, T28I19_30	3.9	5.1	-1.2	-2.6	92.3%	-2.1
1389	AT3G23200.1   expressed protein   chr3:8281370-8282785 FORWARD   Aliases: K14B15.11	6.7	5.7	1.0	2.6	92.3%	-2.1
1390	AT5G10390.1   histone H3, identical to histone H3 from Zea mays SP:P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP:P08903, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:3268848-3269551 REVERSE   Aliases: F12B17.260	5.3	7.2	-2.0	-2.6	92.3%	-2.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1391	AT5G42150.1   expressed protein   chr5:16863378-16865507 FORWARD   Aliases: MJC20.26, MJC20_26	8.9	10.0	-1.1	-2.6	92.3%	-2.2
1392	AT5G02470.3   Symbol: DPA   DP-2 transcription factor, putative (DPA), similar to Swiss-Prot:Q14188 transcription factor DP-2 (E2F dimerization partner 2) (Homo sapiens)   chr5:542356-544500 REVERSE   Aliases: DPA TRANSCRIPTION FACTOR, T22P11.60, T22P11_60	5.0	6.0	-1.0	-2.6	92.3%	-2.3
1393	AT5G64850.1   expressed protein   chr5:25938670-25940580 FORWARD   Aliases: MXK3.7, MXK3_7	4.4	3.4	1.0	2.6	92.3%	-2.3
1394	AT2G15630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:6821603-6823486 FORWARD   Aliases: F9O13.18	3.8	4.7	-0.9	-2.6	92.3%	-2.1
1395	AT3G53310.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr3:19777642-19779396 REVERSE   Aliases: F4P12.10	2.8	2.4	0.3	2.6	92.3%	-2.9
1396	AT1G05360.1   expressed protein, Similar to Arabidopsis hypothetical protein PID:e326839 (gb:Z97337) contains transmembrane domains   chr1:1564621-1567464 FORWARD   Aliases: YUP8H12.2, YUP8H12_2	5.3	5.9	-0.6	-2.6	92.6%	-2.6
1397	AT1G66890.1   expressed protein   chr1:24961221-24961777 FORWARD   Aliases: T4O24.4, T4O24_4	7.5	6.9	0.7	2.6	92.6%	-2.3
1398	AT3G09260.1   Symbol: PYK10   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; almost identical to beta-glucosidase GI:1732570 from (Arabidopsis thaliana); similar to beta-glucosidase 1 (GI:12043529) (Arabidopsis thaliana)   chr3:2840486-2843784 REVERSE   Aliases: F3L24.13, PSR3.1	5.2	7.8	-2.6	-2.6	92.6%	-2.1
1399	AT4G24690.1   ubiquitin-associated (UBA)/TS-N domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein, contains Pfam profiles PF00627: Ubiquitin-associated (UBA)/TS-N domain, PF00569: Zinc finger ZZ type domain, PF00564: PB1 domain	8.5	7.5	1.0	2.6	92.6%	-2.3
1400	AT2G01850.1   Symbol: EXGT A3   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXGT-A3), identical to endoxyloglucan transferase (Arabidopsis thaliana) GI:5533313   chr2:385222-387343 FORWARD   Aliases: ATXTH27, T23K3.4, T23K3_4, XTH27	7.5	6.2	1.3	2.6	92.6%	-2.2
1401	AT3G15560.1   expressed protein   chr3:5268599-5270125 FORWARD   Aliases: MQD17.1	3.2	2.9	0.3	2.6	92.6%	-3.0
1402	AT1G17230.1   leucine-rich repeat family protein / protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr1:5891317-5894848 FORWARD   Aliases: F20D23.7, F20D23_7	4.3	3.6	0.7	2.6	92.6%	-2.3
1403	AT1G74240.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:27921057-27923800 FORWARD   Aliases: F1O17.9, F1O17_9	8.0	8.9	-0.9	-2.6	92.6%	-2.2
1404	AT1G69580.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr1:26175802-26177275 FORWARD   Aliases: F24J1.30, F24J1_30	4.0	5.5	-1.6	-2.6	92.6%	-2.2
1405	AT1G79140.1   expressed protein   chr1:29777505-29778801 REVERSE   Aliases: YUP8H12R.47, YUP8H12R_47	2.9	3.5	-0.6	-2.6	92.6%	-2.5
1406	AT4G14550.1   Symbol: IAA14   auxin-responsive AUX/IAA family protein, identical to IAA14 (GI:972931) (Arabidopsis thaliana); similar to SP:Q38825 Auxin-responsive protein IAA7 (Indoleacetic acid-induced protein 7) {Arabidopsis thaliana}	5.3	4.7	0.6	2.6	92.6%	-2.4
1407	AT3G44450.1   expressed protein   chr3:16085084-16085607 REVERSE   Aliases: F14L2.1	6.1	5.0	1.1	2.6	92.6%	-2.1
1408	AT4G18810.1   expressed protein, similar to UV-B and ozone similarly regulated protein 1 UOS1 (Pisum sativum) GI:20339364   chr4:10322449-10325781 REVERSE   Aliases: F28A21.220, F28A21_220	6.8	5.5	1.2	2.6	92.6%	-2.1
1409	AT5G45930.1   Symbol: CHLI2   magnesium-chelatase subunit chlI, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative, similar to SP:P161127 from Arabidopsis thaliana, SP:P93162 from Glycine max, SP:O22436 from Nicotiana tabacum; non-consensus AA donor splice site at exon 1, TG acceptor splice site at exon 2   chr5:18645234-18646907 FORWARD   Aliases: CHL I2, K15I22.13, K15I22_13, MAGNESIUM CHELETASE I2	3.9	4.6	-0.7	-2.6	92.6%	-2.2
1410	AT1G75750.1   Symbol: GASA1   gibberellin-regulated protein 1 (GASA1) / gibberellin-responsive protein 1, identical to SP:P46689 Gibberellin-regulated protein 1 precursor {Arabidopsis thaliana}; supporting cDNA gi:887938:gb:U11766.1:ATU11766   chr1:28445202-28446023 REVERSE   Aliases: F10A5.6, F10A5_6, GAST1 PROTEIN HOMOLOG	10.0	8.8	1.2	2.6	92.6%	-2.3
1411	AT2G35500.1   shikimate kinase-related, low similarity to shikimate kinase precursor from Lycopersicon esculentum (SP:Q00497)   chr2:14921106-14923198 FORWARD   Aliases: T32F12.12, T32F12_12	6.6	5.5	1.1	2.6	92.6%	-2.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1412	AT4G21100.1   Symbol: DDB1B   UV-damaged DNA-binding protein, putative, similar to UV-damaged DNA binding protein (GI:12082087) (Oryza sativa) and damage-specific DNA binding protein 1, Homo sapiens, PIR2:I38908; contains Pfam PF03178 : CPSF A subunit region   chr4:11258804-11265320 REVERSE   Aliases: DAMAGED DNA BINDING PROTEIN 1 B, F7J7.40, F7J7_40	4.6	5.3	-0.7	-2.6	92.6%	-2.2
1413	AT5G48600.1   Symbol: ATSMC3	3.6	4.8	-1.2	-2.6	92.6%	-2.2
1414	AT5G24170.1   expressed protein   chr5:8189489-8191394 REVERSE   Aliases: K12G2.6, K12G2_6	4.6	4.0	0.6	2.6	92.6%	-2.3
1415	AT4G38890.1   dihydrouridine synthase family protein, contains Pfam domain, PF01207: Dihydrouridine synthase (Dus)   chr4:18135903-18139094 REVERSE   Aliases: F19H22.4	8.6	9.4	-0.8	-2.6	92.6%	-2.2
1416	AT3G11770.1   expressed protein   chr3:3721334-3722652 REVERSE   Aliases: F26K24.6	7.9	8.6	-0.7	-2.6	92.6%	-2.3
1417	AT3G06420.1   autophagy 8h (APG8h), identical to autophagy 8h (Arabidopsis thaliana) GI:19912165; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3; supporting cDNA gi:19912164:dbj:AB073182.1:   chr3:1954996-1956399 REVERSE   Aliases: F24P17.11, F24P17_11	6.9	5.8	1.1	2.6	92.6%	-2.1
1418	AT5G23420.1   Symbol: HMGB6   high mobility group (HMG1/2) family protein, similar to high mobility group protein 2 HMG2 (Ipomoea nil) GI:1052956; contains Pfam profile PF00505: HMG (high mobility group) box   chr5:7888516-7890176 REVERSE   Aliases: K19M13.4, K19M13_4	2.8	3.7	-0.9	-2.6	92.6%	-2.3
1419	AT1G11480.1   eukaryotic translation initiation factor-related, contains weak similarity to Swiss-Prot:P23588 eukaryotic translation initiation factor 4B (eIF-4B) (Homo sapiens)   chr1:3864153-3866969 REVERSE   Aliases: T23J18.15, T23J18_15	8.3	7.4	0.9	2.6	92.6%	-2.2
1420	AT1G08260.1   Symbol: EMB2284   DNA-directed DNA polymerase epsilon catalytic subunit, putative, similar to SP:Q07864 DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A) {Homo sapiens}; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain   chr1:2590941-2606889 FORWARD   Aliases: EMB2284, EMBRYO DEFECTIVE 2284, T23G18.21, T23G18_21	4.6	5.1	-0.6	-2.6	92.6%	-2.3
1421	AT5G17610.1   expressed protein   chr5:5803964-5805254 FORWARD   Aliases: K10A8.90, K10A8_90	7.9	7.4	0.5	2.6	92.6%	-2.4
1422	AT4G32590.4   similar to ferredoxin-related [Arabidopsis thaliana] (TAIR:At3g16250.1); similar to 2Fe-2S iron-sulfur cluster protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_478158.1)   chr4:15721385-15722875 FORWARD   Aliases: F4D11.210, F4D11_210	5.8	5.2	0.6	2.6	92.6%	-2.3
1423	AT4G02195.1   Symbol: SYP42   syntaxin 42 (SYP42) / TLG2b, identical to SP:Q95WH4 Syntaxin 42 (AtSYP42) (AtTLG2b) {Arabidopsis thaliana}   chr4:970009-972304 REVERSE   Aliases: ATSYP42, ATTLG2B, SYNTAXIN OF PLANTS 41, TLG2B	7.2	6.5	0.7	2.6	92.6%	-2.6
1424	AT4G23810.1   Symbol: WRKY53	3.2	4.7	-1.5	-2.6	92.6%	-2.1
1425	AT3G23300.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr3:8333155-8336153 FORWARD   Aliases: MLM24.3	7.9	8.6	-0.6	-2.6	92.6%	-2.7
1426	AT2G19810.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:8557395-8558940 FORWARD   Aliases: F6F22.16, F6F22_16	6.6	6.0	0.6	2.6	92.6%	-2.3
1427	AT1G04040.1   acid phosphatase class B family protein, similar to SP:P15490 STEM 28 kDa glycoprotein precursor (Vegetative storage protein A) {Glycine max}, acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase; supporting cDNA gi:13926197:gb:AF370572.1:AF370572   chr1:1042361-1043861 REVERSE   Aliases: F21M11.2, F21M11_2	7.9	8.6	-0.7	-2.6	92.7%	-2.3
1428	AT1G09160.2   protein phosphatase 2C-related / PP2C-related, similar to GB:AAC16260   chr1:2952773-2955606 REVERSE   Aliases: T12M4.15, T12M4_15	6.0	6.8	-0.8	-2.6	92.7%	-2.2
1429	AT4G20850.1   Symbol: TPP2   subtilase family protein, contains similarity to Tripeptidyl-peptidase II (EC 3.4.14.10) (TPP-II) (Tripeptidyl aminopeptidase) (Swiss-Prot:P29144) (Homo sapiens)   chr4:11160732-11169900 REVERSE   Aliases: T13K14.10, T13K14_10, TRIPEPTIDYL PEPTIDASE II	10.3	10.9	-0.6	-2.6	92.7%	-2.4
1430	AT2G35980.1   Symbol: YLS9   harpin-induced family protein (YLS9) / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum); identical to cDNA YLS9 mRNA for hin1 homolog GI:13122295   chr2:15117667-15118550 FORWARD   Aliases: F11F19.11, F11F19_11, NHL10, YELLOW LEAF SPECIFIC GENE 9	2.0	2.3	-0.3	-2.6	92.7%	-3.1
1431	AT2G34690.1   Symbol: ACD11   expressed protein   chr2:14637430-14639029 FORWARD   Aliases: ACCELERATED CELL DEATH 11, T29F13.10, T29F13_10	10.3	9.8	0.6	2.6	92.8%	-2.4
1432	AT2G25250.1   expressed protein   chr2:10760927-10761791 FORWARD   Aliases: T22F11.16, T22F11_16	5.5	4.2	1.4	2.6	93.3%	-2.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1433	AT2G07680.1   Symbol: ATMRP11   ABC transporter family protein   chr2:3515959-3522488 FORWARD   Aliases: T5E7.1	4.2	5.5	-1.4	-2.6	93.4%	-2.2
1434	AT5G05790.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:1740573-1742029 REVERSE   Aliases: MJJ3.20, MJJ3_20	9.1	8.2	0.9	2.6	93.4%	-2.4
1435	AT3G01420.1   Symbol: ALPHA DOX1   pathogen-responsive alpha-dioxygenase, putative, similar to pathogen-inducible alpha-dioxygenase (Nicotiana attenuata) Gl:12539609; contains Pfam profile PF03098: Animal haem peroxidase   chr3:159473-162844 REVERSE   Aliases: ALPHA DIOXYGENASE 1, T13O15.6, T13O15_6	3.2	4.6	-1.4	-2.6	93.4%	-2.1
1436	AT2G40420.1   amino acid transporter family protein, similar to neuronal glutamine transporter (Rattus norvegicus) Gl:6978016; contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr2:16884318-16886292 FORWARD   Aliases: T3G21.19, T3G21_19	5.0	4.1	0.9	2.6	93.4%	-2.3
1437	AT4G32440.2   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr4:15656691-15659754 FORWARD   Aliases: F8B4.140, F8B4_140	5.3	4.6	0.7	2.6	93.5%	-2.3
1438	AT3G10180.1   kinesin motor protein-related, similar to centromere protein E GB:4502781 (Homo sapiens)	2.9	3.2	-0.4	-2.6	93.5%	-2.8
1439	AT2G36230.1   Symbol: BBM II II   N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase, identical to N'-5'-phosphoribosyl-formimino-5-aminoimidazole-4-carboxamide ribonucleotide isomerase Gl:3449284 from (Arabidopsis thaliana); contains Pfam profile: PF00977 histidine biosynthesis protein   chr2:15200779-15202617 REVERSE   Aliases: F2H17.16, F2H17_16, PHOSPHORIBOSYLFORMIMINO 5 AMINOIMIDAZOLE CARBOXAMIDE RIBOTIDE ISOMERASE	8.2	9.1	-0.9	-2.6	93.5%	-2.2
1440	AT5G58575.1   expressed protein   chr5:23691244-23692462 FORWARD   Aliases: None	5.5	4.4	1.1	2.6	93.7%	-2.2
1441	AT2G42690.1   lipase, putative, similar to lipase (Dianthus caryophyllus) Gl:4103627; contains Pfam profile PF01764: Lipase   chr2:17783318-17784794 REVERSE   Aliases: F14N22.2	5.8	7.2	-1.4	-2.6	93.8%	-2.1
1442	AT1G54220.2   similar to dihydrolipoamide S-acetyltransferase, putative [Arabidopsis thaliana] (TAIR:At3g13930.1); similar to dihydrolipoamide S-acetyltransferase [Zea mays] (GB:AAD46491.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477668.1); similar to putative dihydrolipoamide S-acetyltransferase [Oryza sativa (japonica cultivar-group)] (GB:XP_463813.1); contains InterPro domain Catalytic domain of components of various dehydrogenase complexes (InterPro:IPR001078); contains InterPro domain E3 binding domain (InterPro:IPR004167); contains InterPro domain Dihydrolipoamide acetyltransferase, long form (InterPro:IPR006257); contains InterPro domain 2-oxo acid dehydrogenase, lipoyl-binding site (InterPro:IPR003016); contains InterPro domain Biotin/lipoyl attachment (InterPro:IPR000089)   chr1:20249704-20253977 REVERSE   Aliases: F20D21.4, F20D21_4	5.6	6.5	-0.9	-2.6	93.8%	-2.2
1443	AT1G30260.1   Symbol: AGL79   expressed protein   chr1:10651035-10651712 FORWARD   Aliases: F12P21.9, F12P21_9	2.8	2.4	0.4	2.6	93.8%	-2.7
1444	AT2G43500.1   RWP-RK domain-containing protein, low similarity to nodule inception protein (Lotus japonicus) Gl:6448579; contains Pfam profile: PF02042 RWP-RK domain   chr2:18069792-18073527 FORWARD   Aliases: T1O24.24	6.1	5.3	0.9	2.6	93.9%	-2.2
1445	AT2G06005.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g20580.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g20580.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468082.1)   chr2:2332575-2336108 FORWARD   Aliases: None	3.9	3.3	0.6	2.6	93.9%	-2.3
1446	AT3G10880.1   hypothetical protein   chr3:3406300-3407136 FORWARD   Aliases: T7M13.4	3.1	3.6	-0.5	-2.6	94.3%	-2.5
1447	AT4G27470.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:13735005-13736524 FORWARD   Aliases: F27G19.70, F27G19_70	4.4	3.5	1.0	2.6	94.4%	-2.1
1448	AT4G14965.1   cytochrome b5 domain-containing protein, similar to SP:O15173 Membrane associated progesterone receptor component 2 (Steroid receptor protein DG6) {Homo sapiens}; contains Pfam profile PF00173: Heme/Steroid binding domain   chr4:8551240-8553549 FORWARD   Aliases: None	7.6	7.0	0.6	2.6	94.4%	-2.4
1449	AT3G22520.1   expressed protein   chr3:7974769-7977597 FORWARD   Aliases: F16J14.8	4.7	5.6	-0.9	-2.6	94.5%	-2.3
1450	AT5G01890.1   leucine-rich repeat transmembrane protein kinase, putative, leucine-rich receptor-like protein (LRPKm1) - Malus domestica, EMBL:AF053127	5.5	6.2	-0.7	-2.6	94.5%	-2.4
1451	AT4G02030.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g21170.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAR07074.1)   chr4:892176-897318 FORWARD   Aliases: T10M13.4, T10M13_4	6.5	7.0	-0.6	-2.6	94.6%	-2.5
1452	AT1G17860.1   trypsin and protease inhibitor family protein / Kunitz family protein, similar to LeMir (miraculin homolog) Gl:2654440 from (Lycopersicon esculentum), tumor-related protein (Nicotiana tabacum) Gl:1762933; contains Pfam profile PF00197: Trypsin and protease inhibitor   chr1:6149294-6150031 FORWARD   Aliases: F2H15.9, F2H15_9	5.9	7.8	-2.0	-2.6	94.6%	-2.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1453	AT1G31050.1   expressed protein   chr1:11075634-11076180 REVERSE   Aliases: F17F8.3	6.5	4.9	1.6	2.6	94.7%	-2.1
1454	AT5G06830.1   expressed protein, contains Pfam profile: PF05600 protein of unknown function (DUF773)   chr5:2116784-2119630 REVERSE   Aliases: MPH15.20, MPH15_20	4.6	5.3	-0.7	-2.6	94.8%	-2.5
1455	AT3G63160.1   expressed protein   chr3:23344488-23345009 REVERSE   Aliases: F16M2.10	5.3	4.6	0.7	2.6	94.8%	-2.4
1456	AT3G10450.2   Symbol: SCPL7   similar to serine carboxypeptidase S10 family protein [Arabidopsis thaliana] (TAIR:At1g73300.1); similar to serine carboxypeptidase S10 family protein [Arabidopsis thaliana] (TAIR:At1g73270.1); similar to serine carboxypeptidase S10 family protein [Arabidopsis thaliana] (TAIR:At1g73290.1); similar to serine carboxypeptidase S10 family protein [Arabidopsis thaliana] (TAIR:At1g73280.1); similar to serine carboxypeptidase S10 family protein [Arabidopsis thaliana] (TAIR:At5g36180.1); similar to OSJNBb0051N19.2 [Oryza sativa (japonica cultivar-group)] (GB:XP_474646.1); contains InterPro domain Serine carboxypeptidase (S10) (InterPro:IPR001563)   chr3:3249536-3252509 FORWARD   Aliases: F13M14.27, SCPL7	5.4	4.7	0.7	2.6	94.8%	-2.4
1457	AT5G47050.1   expressed protein   chr5:19123567-19125575 FORWARD   Aliases: MQD22.19, MQD22_19	8.2	7.5	0.7	2.6	94.8%	-2.6
1458	AT3G55120.1   Symbol: TT5   chalcone-flavanone isomerase / chalcone isomerase (CHI), identical to SP:P41088   chr3:20441091-20442447 REVERSE   Aliases: A11, CFI, CHALCONE FLAVANONE ISOMERASE, CHALCONE ISOMERASE, CHI, T15C9.120, TRANSPARENT TESTA 5	5.4	6.2	-0.7	-2.6	94.8%	-2.3
1459	AT1G67480.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:25279958-25282381 FORWARD   Aliases: T1F15.5, T1F15_5	7.0	7.5	-0.5	-2.6	94.8%	-2.5
1460	AT1G35530.1   DEAD/DEAH box helicase, putative, low similarity to RNA helicase/RNaseIII CAF protein (Arabidopsis thaliana) GI:6102610; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr1:13089972-13097056 FORWARD   Aliases: F15O4.40	2.3	2.8	-0.5	-2.6	94.9%	-2.7
1461	AT3G14570.1   Symbol: ATGSL04   glycosyl transferase family 48 protein, contains similarity to glucan synthases   chr3:4892650-4902635 FORWARD   Aliases: ATGSL4, GLUCAN SYNTHASE LIKE 4, GSL04, MIE1.7	8.0	6.9	1.1	2.6	94.9%	-2.4
1462	AT1G67470.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:25275845-25277239 FORWARD   Aliases: T1F15.6	4.7	4.0	0.7	2.6	95.0%	-2.3
1463	AT4G21210.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g01200.1); similar to hypothetical protein GSU0450 [Geobacter sulfurreducens PCA] (GB:NP_951509.1); contains InterPro domain Protein of unknown function DUF299 (InterPro:IPR005177)   chr4:11306955-11308752 FORWARD   Aliases: F7J7.150, F7J7_150	5.5	4.6	0.9	2.6	95.0%	-2.2
1464	AT5G11560.1   PQQ enzyme repeat-containing protein, contains Pfam profile PF01011: PQQ enzyme repeat   chr5:3709482-3714042 REVERSE   Aliases: F15N18.150, F15N18_150	8.2	9.4	-1.2	-2.6	95.0%	-2.4
1465	AT2G01710.1   DNAJ heat shock N-terminal domain-containing protein, similar to AHM1 (Triticum aestivum) GI:6691467; contains Pfam profile PF00226: DnaJ domain   chr2:315725-316992 FORWARD   Aliases: T8O11.12, T8O11_12	5.3	4.7	0.6	2.6	95.0%	-2.5
1466	AT5G58420.1   40S ribosomal protein S4 (RPS4D), ribosomal protein S4, Arabidopsis thaliana, PIR:T48480	10.0	10.8	-0.8	-2.6	95.0%	-2.3
1467	AT1G07600.1   Symbol: MT1A   metallothionein-like protein 1A (MT-1A) (MT-Q) (MT-2), identical to Metallothionein-like protein 1A (MT-1A) (MT-Q) (MT-2) SP:P43392 from (Arabidopsis thaliana)   chr1:2338901-2339318 REVERSE   Aliases: ATMT 2, ATMT Q, F22G5.2, LIGHT STRESS REGULATED 4, LSR4, METALLOTHIONEIN 1A, MT Q, MT1	12.9	12.2	0.7	2.6	95.0%	-3.2
1468	AT4G09830.1   expressed protein   chr4:6188764-6190850 FORWARD   Aliases: F17A8.180, F17A8_180	9.4	8.5	0.9	2.6	95.0%	-2.5
1469	AT1G01360.1   expressed protein, similar to hypothetical protein GB:CAB45785 GI:5262156 from (Arabidopsis thaliana)   chr1:142024-143177 FORWARD   Aliases: F6F3.16, F6F3_16	8.2	6.6	1.6	2.6	95.0%	-2.3
1470	AT4G12700.1   expressed protein   chr4:7482463-7484402 REVERSE   Aliases: T20K18.50, T20K18_50	4.8	5.4	-0.6	-2.6	95.0%	-2.3
1471	AT5G36880.2   similar to acyl-activating enzyme 17 (AAE17) [Arabidopsis thaliana] (TAIR:At5g23050.1); similar to Acetyl-CoA synthetase 2, isoform a [Homo sapiens] (GB:AAH12172.1); similar to OTTHUMP00000030713 [Homo sapiens] (GB:CAI19312.1); similar to OSJNBb0118P14.12 [Oryza sativa (japonica cultivar-group)] (GB:XP_472384.1); similar to OJ000315_02.12 [Oryza sativa (japonica cultivar-group)] (GB:CAE05367.3); similar to acetyl-CoA synthetase [Solanum tuberosum] (GB:CAA67130.1); contains InterPro domain AMP-dependent synthetase and ligase (InterPro:IPR000873)   chr5:14551843-14557516 REVERSE   Aliases: F5H8.15, F5H8_15	8.7	9.4	-0.7	-2.6	95.1%	-2.6
1472	AT1G66410.1   Symbol: CAM4   calmodulin-1/4 (CAM4), identical to calmodulin (Arabidopsis thaliana) GI:16223; nearly identical to SP:P25854 Calmodulin-1/4 {Arabidopsis thaliana}   chr1:24777880-24779516 REVERSE   Aliases: ACAM 4, CALMODULIN 4, T27F4.1, T27F4_1	13.7	13.1	0.6	2.6	95.1%	-2.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1473	AT4G29160.2   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr4:14380810-14382672 FORWARD   Aliases: F19B15.190, F19B15_190	9.3	8.6	0.7	2.6	95.2%	-2.5
1474	AT1G80190.1   expressed protein   chr1:30164368-30166007 FORWARD   Aliases: F18B13.27, F18B13_27	4.5	5.6	-1.1	-2.6	95.4%	-2.3
1475	AT5G38690.1   expressed protein   chr5:15496407-15500291 REVERSE   Aliases: MBB18.24, MBB18_24	4.0	4.6	-0.7	-2.6	95.4%	-2.5
1476	AT2G21660.2   Symbol: ATGRP7	12.4	10.2	2.1	2.6	95.5%	-2.2
1477	AT1G69250.2   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein, contains Pfam profiles PF02136: Nuclear transport factor 2 (NTF2) domain, PF00076: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)   chr1:26036558-26039167 FORWARD   Aliases: F4N2.20	4.6	5.8	-1.2	-2.6	95.7%	-2.4
1478	AT3G20370.1   mepirin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:7105377-7107231 FORWARD   Aliases: MQC12.15	3.8	5.0	-1.2	-2.5	95.7%	-2.1
1479	AT1G28540.1   expressed protein   chr1:10035650-10036927 FORWARD   Aliases: F3M18.29	8.1	7.2	0.9	2.5	95.7%	-2.5
1480	AT4G38225.3   expressed protein   chr4:17927216-17928888 FORWARD   Aliases: None	7.1	6.1	1.0	2.5	95.7%	-2.1
1481	AT4G35140.1   transducin family protein / WD-40 repeat family protein, contains 6 (3 significant) WD-40 repeats; similar to PC326 protein (GI:200241) (PIR2:S37694) (Mus musculus); Human (H326) mRNA, Homo sapiens, gb:U06631   chr4:16723726-16726597 REVERSE   Aliases: T12J5.10, T12J5_10	6.2	5.4	0.8	2.5	95.7%	-2.3
1482	AT5G23330.1   riboflavin biosynthesis protein-related, contains weak similarity to Riboflavin biosynthesis protein ribF. (Swiss-Prot:P08391) (Escherichia coli O157:H7)   chr5:7854132-7855816 FORWARD   Aliases: MKD15.19, MKD15_19	8.4	7.7	0.7	2.5	95.8%	-2.3
1483	AT3G11020.1   Symbol: DREB2B	5.0	4.4	0.5	2.5	95.8%	-2.7
1484	AT1G68500.1   expressed protein   chr1:25705666-25706174 FORWARD   Aliases: T26J14.7, T26J14_7	9.3	8.0	1.3	2.5	95.8%	-2.4
1485	AT1G77550.1   expressed protein, similar to hypothetical protein LOC223723 [Mus musculus] (GB:NP_898838.1); contains InterPro domain Tubulin-tyrosine ligase (InterPro:IPR004344)   chr1:29143197-29147859 REVERSE   Aliases: T5M16.14, T5M16_14	6.2	6.9	-0.7	-2.5	96.1%	-2.5
1486	AT3G04470.1   similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At1g04780.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477804.1); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr3:1189646-1192644 REVERSE   Aliases: T27C4.12, T27C4_12	6.5	7.3	-0.7	-2.5	96.4%	-2.5
1487	AT4G24180.1   similar to thaumatin, putative [Arabidopsis thaliana] (TAIR:At4g38660.1); similar to putative thaumatin-like protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52107.1); contains InterPro domain Thaumatin, pathogenesis-related (InterPro:IPR001938)   chr4:12550366-12551309 REVERSE   Aliases: T22A6.10, T22A6_10	4.5	3.5	1.0	2.5	96.4%	-2.2
1488	AT5G25610.1   Symbol: RD22   dehydration-responsive protein (RD22), identical to SP:Q08298 Dehydration-responsive protein RD22 precursor {Arabidopsis thaliana}   chr5:8914236-8916724 REVERSE   Aliases: T14C9.150, T14C9_150	3.3	2.8	0.5	2.5	96.4%	-2.5
1489	AT4G30700.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:14962499-14965020 REVERSE   Aliases: T10C21.50, T10C21_50	3.5	4.2	-0.7	-2.5	96.4%	-2.3
1490	AT4G31840.1   plastocyanin-like domain-containing protein   chr4:15401646-15402623 FORWARD   Aliases: F11C18.40, F11C18_40	3.8	4.7	-0.9	-2.5	96.4%	-2.2
1491	AT2G19310.1   expressed protein   chr2:8376876-8377488 REVERSE   Aliases: F27F23.11, F27F23_11	6.5	5.5	1.1	2.5	96.4%	-2.3
1492	AT3G50380.1   expressed protein   chr3:18697424-18711514 REVERSE   Aliases: F11C1.220	4.7	5.8	-1.1	-2.5	96.4%	-2.3
1493	AT5G63640.1   VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (Homo sapiens) GI:9022389; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain   chr5:25494982-25498715 FORWARD   Aliases: MBK5.12, MBK5_12	4.9	4.2	0.8	2.5	96.4%	-2.3
1494	AT5G52650.1   40S ribosomal protein S10 (RPS10C), contains similarity to 40S ribosomal protein S10   chr5:21372841-21374301 REVERSE   Aliases: F6N7.14, F6N7_14	10.9	11.5	-0.6	-2.5	96.5%	-2.5
1495	AT4G37590.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr4:17662836-17666056 REVERSE   Aliases: F19F18.80, F19F18_80	5.2	5.9	-0.8	-2.5	96.5%	-2.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1496	AT2G01300.1   expressed protein   chr2:151062-151728 REVERSE   Aliases: F10A8.18, F10A8_18	2.9	2.5	0.5	2.5	96.5%	-2.8
1497	AT1G65680.1   Symbol: ATEXPB2   similar to beta-expansin, putative (EXPB4) [Arabidopsis thaliana] (TAIR:At2g45110.1); similar to cim1 protein - soybean (GB:S48032); contains InterPro domain Expansin 45, endoglucanase-like domain (InterPro:IPR007112); contains InterPro domain Major pollen allergen Lol pl (InterPro:IPR005795); contains InterPro domain Expansin/Lol pl (InterPro:IPR007118); contains InterPro domain Pollen allergen/expansin, C-terminal (InterPro:IPR007117)   chr1:24430929-24432062 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN B2, ATEXPB2, ATHEXP BETA 1.4, EXPB2, F1E22.6	3.1	3.7	-0.6	-2.5	96.5%	-2.5
1498	AT1G69310.2   Symbol: WRKY57	3.3	2.9	0.4	2.5	96.5%	-2.8
1499	AT4G21800.2   ATP-binding family protein, contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein   chr4:11572877-11575504 FORWARD   Aliases: F17L22.260, F17L22_260	6.2	6.9	-0.7	-2.5	96.5%	-2.4
1500	AT4G22740.2   glycine-rich protein   chr4:11942812-11945967 REVERSE   Aliases: T12H17.1	10.9	9.7	1.1	2.5	96.6%	-2.4
1501	AT3G05630.1   Symbol: PLDP2   phospholipase D, putative (PLDP2), identical to SP:Q9M9W8 Phospholipase D p2 (EC 3.1.4.4) (AtPLDp2) (Phospholipase D2 PHOX and PX containing domain) (Phospholipase D zeta 2) (PLDzeta2) {Arabidopsis thaliana}; similar to phospholipase D GB:BAA24577 from (Rattus norvegicus); contains Pfam profile: PF00614 phospholipase D, PF00169 PH domain, PF00787 PX domain   chr3:1635265-1640349 FORWARD   Aliases: F18C1.10, F18C1_10, PLDZETA2	6.6	5.4	1.2	2.5	96.7%	-2.2
1502	AT4G35880.1   aspartyl protease family protein, contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141   chr4:16993342-16995821 FORWARD   Aliases: F4B14.150, F4B14_150	4.2	4.9	-0.7	-2.5	96.8%	-2.5
1503	AT5G63570.1   Symbol: GSA1   glutamate-1-semialdehyde 2,1-aminomutase 1 (GSA 1) / glutamate-1-semialdehyde aminotransferase 1 (GSA-AT 1), identical to GSA 1 (SP:P42799)   chr5:25469103-25471067 FORWARD   Aliases: GLUTAMATE 1 SEMIALDEHYDE 2,1 AMINOMUTASE, MBK5.3, MBK5_3	7.7	8.8	-1.1	-2.5	96.9%	-2.3
1504	AT1G73220.1   sugar transporter family protein, contains Pfam profile: PF00083 sugar (and other) transporter   chr1:27541937-27544352 FORWARD   Aliases: T18K17.11, T18K17_11	3.5	2.9	0.6	2.5	96.9%	-2.6
1505	AT1G61610.1   S-locus lectin protein kinase family protein, similar to Kl domain interacting kinase 1 (Zea mays) gi:2735017:gb:AAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22737137-22740174 FORWARD   Aliases: T25B24.4, T25B24_4	2.6	2.9	-0.3	-2.5	96.9%	-3.0
1506	AT5G22860.2   serine carboxypeptidase S28 family protein, contains Pfam profile: PF05577 serine carboxypeptidase S28   chr5:7639855-7642987 REVERSE   Aliases: MRN17.9, MRN17_9	4.2	3.5	0.7	2.5	96.9%	-2.5
1507	AT5G05180.2   expressed protein   chr5:1536227-1538493 FORWARD   Aliases: K2A11.5, K2A11_5	5.9	6.9	-1.0	-2.5	96.9%	-2.2
1508	AT1G05140.1   membrane-associated zinc metalloprotease, putative, similar to Hypothetical zinc metalloprotease All3971 (SP:Q8YQ64) (strain PCC 7120) {Anabaena sp.}; Similar to Synechocystis hypothetical protein (gb:D90908);contains Pfam PF00595: PDZ domain (Also known as DHR or GLGF); contains TIGRFAM TIGR00054: membrane-associated zinc metalloprotease, putative   chr1:1482547-1484049 FORWARD   Aliases: YUP8H12.25, YUP8H12_25	8.5	7.8	0.7	2.5	96.9%	-2.6
1509	AT5G57620.1   Symbol: MYB36   myb family transcription factor (MYB36), contains PFAM profile: myb DNA binding domain PF00249   chr5:23352051-23353792 FORWARD   Aliases: MUA2.20, MUA2_20	3.7	4.3	-0.6	-2.5	97.0%	-2.5
1510	AT3G14740.2   PHD finger family protein, similar to zinc-finger protein BR140 (PIR:JC2069)(Homo sapiens); contains PHD-finger domain PF00628   chr3:4952068-4953430 REVERSE   Aliases: MIE1.25	5.0	5.8	-0.9	-2.5	97.0%	-2.3
1511	AT3G01350.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:135031-137467 FORWARD   Aliases: T13O15.11	4.5	3.7	0.8	2.5	97.0%	-2.3
1512	AT2G46400.1   Symbol: WRKY46	4.5	3.8	0.7	2.5	97.0%	-2.4
1513	AT5G27930.2   protein phosphatase 2C, putative / PP2C, putative, protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075581   chr5:9958102-9961170 REVERSE   Aliases: F15F15.3	5.0	4.2	0.8	2.5	97.0%	-2.3
1514	AT5G03840.1   Symbol: TFL1   terminal flower 1 protein (TFL1), identical go SP:P93003 TERMINAL FLOWER 1 protein {Arabidopsis thaliana}; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein   chr5:1024640-1025811 REVERSE   Aliases: MED24.6, TERMINAL FLOWER 1, TFL 1	3.8	4.2	-0.4	-2.5	97.0%	-2.8
1515	AT3G18610.1   nucleolin, putative, contains Pfam profile: PF00076 RNA recognition motif   chr3:6404276-6407828 REVERSE   Aliases: K24M9.10	7.4	6.3	1.0	2.5	97.1%	-2.2
1516	AT5G13190.1   expressed protein   chr5:4204820-4206408 REVERSE   Aliases: T19L5.5	9.5	8.7	0.8	2.5	97.2%	-2.4
1517	AT3G14700.1   expressed protein   chr3:4940325-4941405 FORWARD   Aliases: MIE1.20	6.2	5.1	1.1	2.5	97.3%	-2.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1518	AT2G32830.1   Symbol: PHT5   inorganic phosphate transporter (PHT5), identical to inorganic phosphate transporter (PHT5) (Arabidopsis thaliana) GI:2780345   chr2:13934776-13936790 REVERSE   Aliases: F24L7.2	6.3	5.0	1.3	2.5	97.5%	-2.2
1519	AT1G06160.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr1:1883003-1883933 FORWARD   Aliases: F9P14.2, F9P14_2	4.1	3.0	1.1	2.5	97.5%	-2.2
1520	AT5G02230.2   haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	4.4	3.2	1.1	2.5	97.5%	-2.4
1521	AT3G06760.1   drought-responsive family protein, similar to drought-induced mRNA, Di19 (Arabidopsis thaliana) gi:469110:emb:CAA55321   chr3:2132977-2134562 FORWARD   Aliases: F3E22.10	6.8	5.9	0.8	2.5	97.5%	-2.4
1522	AT4G24450.1   similar to starch excess protein (SEX1) [Arabidopsis thaliana] (TAIR:At1g10760.1); similar to starch associated protein R1 [Solanum tuberosum] (GB:AAK11735.1); similar to R1 [Citrus reticulata] (GB:AAM18228.1); similar to SPR1b [Ostreococcus tauri] (GB:AAS88899.1)	4.3	3.3	1.0	2.5	97.6%	-2.3
1523	AT1G37130.1   Symbol: NIA2   nitrate reductase 2 (NR2), identical to SP:P11035 Nitrate reductase 2 (formerly EC 1.6.6.1) (NR2) {Arabidopsis thaliana}	11.1	9.7	1.4	2.5	97.6%	-2.5
1524	AT1G33170.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr1:12027064-12030519 FORWARD   Aliases: T9L6.6, T9L6_6	5.7	6.2	-0.5	-2.5	97.6%	-2.7
1525	AT5G03455.1   Symbol: CDC25   rhodanese-like domain-containing protein, contains Rhodanese-like domain PF:00581   chr5:862558-864107 FORWARD   Aliases: ARATH;CDC25	10.6	9.9	0.7	2.5	97.6%	-2.9
1526	AT4G12410.1   auxin-responsive family protein, similar to GP:546362 small auxin up RNA {Arabidopsis thaliana}; auxin-induced protein 10A -Glycine max,PID:g255579   chr4:7342953-7343587 REVERSE   Aliases: T1P17.3	8.5	7.3	1.2	2.5	97.6%	-2.2
1527	AT1G50490.1   Symbol: UBC20   ubiquitin-conjugating enzyme 20 (UBC20), nearly identical to ubiquitin-conjugating enzyme UBC20 (Arabidopsis thaliana) GI:22530867; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	7.3	8.4	-1.1	-2.5	97.6%	-2.3
1528	AT5G49760.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:20233598-20238525 FORWARD   Aliases: K2I5.13, K2I5_13	5.1	6.1	-1.0	-2.5	97.6%	-2.3
1529	AT4G15890.1   expressed protein   chr4:9017468-9022997 FORWARD   Aliases: DL3985W, FCAALL.407	4.9	5.9	-1.0	-2.5	97.7%	-2.3
1530	AT5G18410.2   Symbol: KLK/PIR/PIR121/PIRP/SRA1   expressed protein, similar to p53 inducible protein (Homo sapiens) GI:5616320   chr5:6098571-6104982 REVERSE   Aliases: F20L16.130, F20L16_130, KLK, PIR, PIR121, PIROGI, PIRP, SRA1	5.7	6.5	-0.8	-2.5	97.7%	-2.6
1531	AT2G04850.1   auxin-responsive protein-related, related to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana)   chr2:1704280-1705775 FORWARD   Aliases: F28I8.9, F28I8_9	4.5	4.0	0.5	2.5	97.7%	-2.7
1532	AT3G18110.1   Symbol: EMB1270   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr3:6204810-6209697 REVERSE   Aliases: EMB1270, EMBRYO DEFECTIVE 1270, MRC8.9	5.7	6.8	-1.1	-2.5	97.7%	-2.2
1533	AT5G60250.1   zinc finger (C3HC4-type RING finger) family protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam domain PF01485: IBR domain   chr5:24269384-24272066 FORWARD   Aliases: F15L12.13, F15L12_13	4.3	3.7	0.6	2.5	97.7%	-2.6
1534	AT2G31230.1   Symbol: ATERF15   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr2:13313670-13314552 REVERSE   Aliases: ATERF15, F16D14.7, F16D14_7	4.0	3.4	0.6	2.5	97.7%	-2.5
1535	AT3G09030.1   potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain   chr3:2754787-2756511 FORWARD   Aliases: T16O11.1	5.2	4.7	0.5	2.5	97.7%	-2.8
1536	AT3G15770.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g25360.1); similar to hypothetical protein [Picea mariana] (GB:AAC32109.1)   chr3:5340081-5341346 FORWARD   Aliases: MSJ11.17	6.4	5.5	0.9	2.5	97.8%	-2.5
1537	AT3G27880.1   expressed protein   chr3:10339449-10340673 FORWARD   Aliases: K16N12.10	5.7	4.7	1.0	2.5	98.0%	-2.4
1538	AT1G54130.1   Symbol: RSH3   RelA/SpoT protein, putative (RSH3), identical to RSH3 (RelA/SpoT homolog) GI:7141308 from (Arabidopsis thaliana); contains Pfam profiles PF01966: HD domain, PF04607: Region found in RelA / SpoT proteins   chr1:20214540-20217720 FORWARD   Aliases: AT RSH3, F15I1.23, F15I1_23, RELA/SPOT HOMOLOG 3, RSH3	8.4	7.4	1.0	2.5	98.0%	-2.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1539	AT5G26280.1   meprip and TRAF homology domain-containing protein / MATH domain-containing protein, low similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr5:9208715-9210575 FORWARD   Aliases: F9D12.7	4.1	5.0	-0.9	-2.5	98.0%	-2.4
1540	AT3G10985.1   wound-responsive protein-related, similar to SP:P20144 Wound-induced protein 1 {Solanum tuberosum}   chr3:3442534-3443451 FORWARD   Aliases: None	4.8	3.6	1.2	2.5	98.0%	-2.2
1541	AT1G09200.1   histone H3, identical to histone H3 from Zea mays SP:P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP:P08903, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:2971595-2972201 REVERSE   Aliases: T12M4.9	9.2	11.3	-2.1	-2.5	98.0%	-2.3
1542	AT1G80310.1   expressed protein   chr1:30199510-30201446 FORWARD   Aliases: F5I6.6, F5I6_6	7.3	6.5	0.8	2.5	98.0%	-2.4
1543	AT5G50900.1   armadillo/beta-catenin repeat family protein, armadillo/beta-catenin-like repeats, Pfam:PF00514   chr5:20722030-20724004 REVERSE   Aliases: K3K7.4, K3K7_4	8.4	7.7	0.7	2.5	98.0%	-2.6
1544	AT5G03300.1   Symbol: ADK2   adenosine kinase 2 (ADK2), contains Pfam profile: PF00294 pfkB family carbohydrate kinase; identical to cDNA adenosine kinase 2 (ADK2) GI:12017763   chr5:796441-799153 FORWARD   Aliases: ADENOSINE KINASE 2, F12E4.30, F12E4_30	10.5	11.4	-1.0	-2.5	98.0%	-2.5
1545	AT4G03020.1   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to L. erythrorhizon LEC14B, GenBank accession number Q40153	7.1	8.2	-1.2	-2.5	98.1%	-2.3
1546	AT4G22470.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to hydroxyproline-rich glycoprotein DZ-HRGP from Volvox carteri f. nagariensis GP:6523547; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family	2.5	3.2	-0.7	-2.5	98.1%	-2.7
1547	AT5G51660.1   cleavage and polyadenylation specificity factor (CPSF) A subunit C-terminal domain-containing protein, similar to SP:Q9EPU4 Cleavage and polyadenylation specificity factor, 160 kDa subunit (CPSF 160 kDa subunit) {Mus musculus}; contains Pfam profile PF03178: CPSF A subunit region	5.2	5.8	-0.6	-2.5	98.1%	-2.6
1548	AT1G23070.1   expressed protein, contains Pfam profile PF03619: Domain of unknown function   chr1:8174000-8175747 REVERSE   Aliases: T26J12.15, T26J12_15	4.1	3.5	0.6	2.5	98.1%	-2.6
1549	AT2G34840.1   coatomer protein epsilon subunit family protein / COPE family protein, similar to SP:O14579 Coatomer epsilon subunit (Epsilon-coat protein) (Epsilon-COP) from Homo sapiens, SP:Q60445 from Cricetulus griseus   chr2:14709591-14711432 FORWARD   Aliases: F19I3.7, F19I3_7	6.4	7.1	-0.7	-2.5	98.2%	-2.5
1550	AT5G41400.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHA1a (Arabidopsis thaliana) GI:3790554; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:16586605-16587405 REVERSE   Aliases: MYC6.11, MYC6_11	3.7	3.0	0.7	2.5	98.2%	-2.5
1551	AT1G74030.1   enolase, putative, similar to Swiss-Prot:P15007 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) (Drosophila melanogaster)   chr1:27842845-27845592 REVERSE   Aliases: F2P9.10, F2P9_10	10.0	11.4	-1.4	-2.5	98.2%	-2.4
1552	AT4G30400.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHX1a (Arabidopsis thaliana) GI:3790591; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:14866952-14868634 FORWARD   Aliases: F17I23.260, F17I23_260	4.1	4.6	-0.5	-2.5	98.2%	-2.7
1553	AT3G17350.1   expressed protein   chr3:5934100-5935042 FORWARD   Aliases: MGD8.19	4.6	5.5	-1.0	-2.5	98.2%	-2.2
1554	AT1G50140.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family   chr1:18573449-18579492 REVERSE   Aliases: F2J10.1, F2J10_1	5.8	6.7	-0.9	-2.5	98.2%	-2.5
1555	AT5G55230.1   microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr5:22419276-22422718 FORWARD   Aliases: MCO15.18, MCO15_18	7.1	7.9	-0.8	-2.5	98.2%	-2.5
1556	AT4G23240.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:12160512-12161964 REVERSE   Aliases: F21P8.130, F21P8_130	3.6	3.0	0.6	2.5	98.2%	-2.7
1557	AT5G59720.1   Symbol: HSP18.2   18.1 kDa class I heat shock protein (HSP18.1-CI), identical to 18.2 kDa class I heat shock protein (HSP 18.2) (SP:P19037)(Arabidopsis thaliana); contains Pfam profile: PF00011 Hsp20/alpha crystallin family	4.1	4.8	-0.7	-2.5	98.2%	-2.3
1558	AT2G20390.1   expressed protein   chr2:8803364-8805299 REVERSE   Aliases: F11A3.6, F11A3_6	7.5	8.3	-0.8	-2.5	98.2%	-2.3
1559	AT5G50720.1   Symbol: ATHVA22E   ABA-responsive protein (HVA22e), identical to AtHVA22e (Arabidopsis thaliana) GI:11225589   chr5:20650422-20651778 REVERSE   Aliases: ATHVA22E, MFB16.12, MFB16_12	8.2	7.0	1.2	2.5	98.4%	-2.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1560	AT5G10740.1   protein phosphatase 2C-related / PP2C-related, protein phosphatase 2C, alfalfa, PIR:T09640   chr5:3393570-3396177 REVERSE   Aliases: MAJ23.3	7.2	6.6	0.6	2.5	98.4%	-2.7
1561	AT1G76060.1   Symbol: EMB1793   complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)   chr1:28547998-28548744 REVERSE   Aliases: EMBRYO DEFECTIVE 1793, T4O12.26, T4O12_26	7.1	6.0	1.1	2.5	98.4%	-2.4
1562	AT4G40000.1   NOL1/NOP2/sun family protein, contains Pfam profile PF01189: NOL1/NOP2/sun family   chr4:18543348-18547517 REVERSE   Aliases: T5J17.170, T5J17_170	3.4	4.2	-0.8	-2.5	98.4%	-2.5
1563	AT3G24320.1   Symbol: CHM   DNA mismatch repair MutS family (MSH1), low similarity to SP:Q56239 DNA mismatch repair protein mutS {Thermus aquaticus}; contains Pfam profiles PF05190: MutS family domain IV, PF01624: MutS domain I, PF01541: Endo/excinuclease amino terminal domain	3.4	4.1	-0.8	-2.5	98.4%	-2.3
1564	AT4G23540.1   expressed protein, probable membrane protein YPL012w, Saccharomyces cerevisiae, PIR2:S59681   chr4:12279918-12284693 REVERSE   Aliases: F16G20.240, F16G20_240	4.2	5.2	-0.9	-2.5	98.6%	-2.5
1565	AT5G64470.2   expressed protein, similar to unknown protein (gb:AAD15463.1)   chr5:25793251-25795189 FORWARD   Aliases: T12B11.6, T12B11_6	4.3	4.8	-0.5	-2.5	98.6%	-2.6
1566	AT1G07870.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:2429696-2432018 REVERSE   Aliases: F24B9.4, F24B9_4	7.3	6.3	1.0	2.5	98.6%	-2.3
1567	AT5G49880.1   mitotic checkpoint family protein, similar to mitotic checkpoint protein isoform MAD1a (Homo sapiens) GI:4580767; contains Pfam profile PF05557: Mitotic checkpoint protein   chr5:20299391-20305310 FORWARD   Aliases: K9P8.2, K9P8_2	5.8	6.7	-0.9	-2.5	98.6%	-2.3
1568	AT5G55670.1   RNA recognition motif (RRM)-containing protein   chr5:22561166-22564027 REVERSE   Aliases: MDF20.11, MDF20_11	5.9	5.3	0.6	2.5	98.6%	-2.4
1569	AT2G28420.1   lactoylglutathione lyase family protein / glyoxalase I family protein, contains glyoxalase family protein domain, Pfam:PF00903   chr2:12165000-12165868 FORWARD   Aliases: T1B3.6, T1B3_6	2.5	2.1	0.3	2.5	98.6%	-3.2
1570	AT3G23160.1   expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668); expression supported by MPSS   chr3:8260066-8261634 REVERSE   Aliases: K14B15.5	4.1	4.9	-0.8	-2.5	98.6%	-2.3
1571	AT3G53920.1   Symbol: SIGC   RNA polymerase sigma subunit SigC (sigC) / sigma factor 3 (SIG3), identical to sigma factor SigC (Arabidopsis thaliana) GI:5478585, sigma factor 3 (SIG3) (Arabidopsis thaliana) GI:2353175, plastid RNA polymerase sigma-subunit (Arabidopsis thaliana) GI:2398853; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2   chr3:19971847-19974927 REVERSE   Aliases: F5K20.220, RNA POLYMERASE SIGMA SUBUNIT, SIG3	7.2	6.3	0.9	2.5	98.6%	-2.4
1572	AT5G59910.1   histone H2B, nearly identical to histone H2B Arabidopsis thaliana GI:2407802; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:24144354-24145161 FORWARD   Aliases: MMN10.15, MMN10_15	10.3	10.9	-0.6	-2.5	98.6%	-2.6
1573	AT1G49580.1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK3 (Nicotiana tabacum) gi:16904226;gb:AAL30820; contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.0	4.9	-0.9	-2.5	98.6%	-2.3
1574	AT4G10280.1   expressed protein   chr4:6374742-6376107 REVERSE   Aliases: T9A4.15	4.4	5.6	-1.2	-2.5	98.6%	-2.4
1575	AT4G28025.1   expressed protein   chr4:13935641-13937388 REVERSE   Aliases: None	8.8	8.2	0.6	2.5	98.6%	-2.4
1576	AT2G39650.1   expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506)   chr2:16534922-16536352 REVERSE   Aliases: F12L6.31, F12L6_31	4.4	3.9	0.6	2.5	98.6%	-2.6
1577	AT4G37910.1   Symbol: MTHSC70 1   heat shock protein 70, mitochondrial, putative / HSP70, mitochondrial, putative, strong similarity to SP:Q01899 Heat shock 70 kDa protein, mitochondrial precursor {Phaseolus vulgaris}   chr4:17825074-17828171 REVERSE   Aliases: F20D10.30, F20D10_30, MTHSC70 1	9.6	10.7	-1.1	-2.5	98.6%	-2.4
1578	AT4G26460.1   similar to S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g26420.1)   chr4:13369541-13370019 FORWARD   Aliases: M3E9.110, M3E9_110	3.1	2.8	0.4	2.5	98.8%	-2.9
1579	AT1G50030.1   Symbol: TOR   target of rapamycin protein (TOR), identical to pTOR (Arabidopsis thaliana) GI:12002902; contains Pfam profiles PF00454 Phosphatidylinositol 3- and 4-kinase, PF02259 FAT domain, PF02260 FATC domain   chr1:18526109-18543663 REVERSE   Aliases: F2J10.19, F2J10_19, TARGET OF RAPAMYCIN, TOR	5.5	6.3	-0.8	-2.5	98.9%	-2.4
1580	AT4G23680.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr4:12336196-12337486 REVERSE   Aliases: F9D16.150, F9D16_150	3.1	3.5	-0.4	-2.5	99.0%	-2.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1581	ATCG00800.1   Symbol: RPS3   encodes a chloroplast ribosomal protein S3, a constituent of the small subunit of the ribosomal complex   chrC:82826-83482 REVERSE   Aliases: RPS3	11.0	11.6	-0.6	-2.5	99.0%	-2.6
1582	AT5G09650.1   inorganic pyrophosphatase family protein, similar to SP:Q15181 Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate {Homo sapiens}); contains Pfam profile PF00719: inorganic pyrophosphatase   chr5:2991156-2993214 REVERSE   Aliases: F17I14.160, F17I14_160	9.3	10.4	-1.2	-2.5	99.0%	-2.5
1583	AT5G56520.1   expressed protein   chr5:22902397-22903141 FORWARD   Aliases: MKN22.3, MKN22_3	5.1	4.4	0.7	2.5	99.0%	-2.4
1584	AT1G77600.1   expressed protein, weak similarity to Pds5 (GI:16751524) (Schizosaccharomyces pombe); weak similarity to androgen-induced prostate proliferative shutoff associated protein (GI:4559410) (Homo sapiens)   chr1:29157642-29167856 REVERSE   Aliases: T5M16.19, T5M16_19	4.3	4.9	-0.7	-2.5	99.1%	-2.6
1585	AT2G26560.1   patatin, putative, similar to patatin-like latex allergen (Hevea brasiliensis)(PMID:10589016); contains patatin domain PF01734   chr2:11300847-11302881 REVERSE   Aliases: T9J22.23, T9J22_23	3.3	3.7	-0.4	-2.5	99.1%	-2.8
1586	AT2G24260.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	6.9	6.2	0.6	2.5	99.2%	-2.6
1587	AT1G30135.1   expressed protein   chr1:10596476-10597222 FORWARD   Aliases: None	2.7	2.4	0.3	2.5	99.3%	-3.2
1588	AT3G02110.1   Symbol: SCPL25	3.3	3.9	-0.6	-2.5	99.4%	-2.4
1589	AT3G19000.2   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to SP:P24397 Hyoscyamine 6-dioxygenase (EC 1.14.11.11) (Hyoscyamine 6-beta-hydroxylase) {Hyoscyamus niger}, SP:Q05965 Naringenin,2-oxoglutarate 3-dioxygenase (EC 1.14.11.9) (Flavonone- 3-hydroxylase) (F3H) (FHT) {Matthiola incana}; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family	6.6	7.5	-0.9	-2.5	99.5%	-2.5
1590	AT2G41500.1   WD-40 repeat family protein / small nuclear ribonucleoprotein Prp4p-related, similar to U4/U6 small nuclear ribonucleoprotein hPrp4 (GP:2708305) {Homo sapiens}; contains Pfam PF00400: WD domain, G-beta repeat (7 copies):19877698:gb:AU238529.1:AU238529   chr2:17311209-17314504 REVERSE   Aliases: T26J13.9, T26J13_9	6.5	7.1	-0.6	-2.5	99.5%	-2.5
1591	AT1G10350.1   DNAJ heat shock protein, putative, similar to SP:Q9QYJ3 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr1:3393409-3395057 REVERSE   Aliases: F14N23.23, F14N23_23	5.8	6.5	-0.7	-2.5	99.5%	-2.4
1592	AT2G35190.1   Symbol: NPSN11	6.2	7.3	-1.1	-2.5	99.6%	-2.4
1593	AT4G34190.1   Symbol: SEP1   stress enhanced protein 1 (SEP1), identical to stress enhanced protein 1 (SEP1) GI:7384978 from (Arabidopsis thaliana)   chr4:16372394-16373630 REVERSE   Aliases: F10M10.5, SEP1, STRESS ENHANCED PROTEIN 1	7.4	6.6	0.8	2.5	99.6%	-2.5
1594	AT1G76350.1   RWP-RK domain-containing protein, similar to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	5.1	4.4	0.7	2.5	99.6%	-2.6
1595	AT4G21180.1   DNAJ heat shock N-terminal domain-containing protein / sec63 domain-containing protein, similar to SP:Q9UGP8 Translocation protein SEC63 homolog {Homo sapiens}; contains Pfam profiles PF00226 DnaJ domain, PF02889 Sec63 domain   chr4:11288939-11292776 FORWARD   Aliases: F7J7.120, F7J7_120	4.3	4.8	-0.5	-2.5	99.8%	-2.6
1596	AT5G54180.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr5:22005732-22007454 FORWARD   Aliases: K18G13.5, K18G13_5	5.1	5.7	-0.7	-2.5	99.8%	-2.4
1597	AT3G55460.1   Symbol: SCL30   SC35-like splicing factor, 30 kD (SCL30), nearly identical to SC35-like splicing factor SCL30, 30 kD (Arabidopsis thaliana) GI:9843657; Serine/arginine-rich protein/putative splicing factor, Arabidopsis thaliana, EMBL:AF099940; contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:20571801-20574709 FORWARD   Aliases: T22E16.120	7.4	6.6	0.7	2.5	99.9%	-2.5
1598	AT5G11600.1   expressed protein   chr5:3733685-3735016 REVERSE   Aliases: T22P22.2	6.5	5.8	0.7	2.5	100.0%	-2.6
1599	AT2G36910.1   Symbol: ATPGP1	8.2	9.0	-0.7	-2.5	100.0%	-2.5
1600	AT3G43610.1   tubulin family protein   chr3:15528760-15534915 REVERSE   Aliases: F22J12.50	3.2	4.1	-0.8	-2.5	100.0%	-2.6
1601	AT5G14970.1   expressed protein   chr5:4847281-4848868 FORWARD   Aliases: F2G14.90, F2G14_90	8.6	7.9	0.7	2.5	100.0%	-2.5
1602	AT5G12390.1   expressed protein   chr5:4010444-4012040 REVERSE   Aliases: None	9.6	8.7	0.9	2.5	100.0%	-2.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1603	AT5G23940.1   Symbol: EMB3009   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, <i>Dianthus caryophyllus</i> (gi:2239091); contains Pfam transferase family domain PF002458   chr5:8076332-8079796 REVERSE   Aliases: EMB3009, EMBRYO DEFECTIVE 3009, MRO11.2, MRO11_2	2.8	2.5	0.4	2.5	100.0%	-3.1
1604	AT5G65660.1   hydroxyproline-rich glycoprotein family protein   chr5:26262475-26263605 REVERSE   Aliases: K21L13.18, K21L13_18	9.2	10.0	-0.7	-2.5	100.0%	-2.5
1605	AT3G54000.3   expressed protein   chr3:20007585-20009601 FORWARD   Aliases: F5K20.300	3.7	3.1	0.6	2.5	100.0%	-2.6
1606	AT5G20980.1   5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative, strong similarity to SP:O50008 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) { <i>Arabidopsis thaliana</i> }; contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent   chr5:7124116-7128361 REVERSE   Aliases: F22D1.150, F22D1_150	4.3	5.0	-0.8	-2.5	100.0%	-2.6
1607	AT5G55540.1   expressed protein   chr5:22513422-22517769 REVERSE   Aliases: MTE17.26, MTE17_26	5.9	6.6	-0.7	-2.5	100.0%	-2.4
1608	AT4G38480.1   transducin family protein / WD-40 repeat family protein, contains contains Pfam PF00400: WD domain, G-beta repeat (7 copies, 3 weak);similar to gene PC326 protein - mouse, PIR2:S37694   chr4:18003910-18006134 FORWARD   Aliases: F20M13.40, F20M13_40	3.3	3.6	-0.4	-2.5	100.0%	-2.9
1609	AT5G53850.3   haloacid dehalogenase-like hydrolase family protein, low similarity to enolase-phosphatase E-1 enzyme ( <i>Klebsiella oxytoca</i> ) GI:401712; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:21878223-21882133 REVERSE   Aliases: K19P17.1, K19P17_1	8.9	9.5	-0.6	-2.5	100.0%	-2.7
1610	AT5G25240.1   expressed protein   chr5:8746608-8747200 REVERSE   Aliases: F21J6.107, F21J6_107	5.5	4.4	1.1	2.5	100.0%	-2.5
1611	AT4G08330.1   expressed protein   chr4:5254654-5256701 REVERSE   Aliases: T28D5.20, T28D5_20	4.7	4.1	0.6	2.5	100.0%	-2.5
1612	AT1G69600.1   zinc finger homeobox family protein / ZF-HD homeobox family protein   chr1:26186133-26186861 FORWARD   Aliases: F24J1.29, F24J1_29	4.0	4.8	-0.9	-2.5	100.0%	-2.3
1613	AT1G09620.1   similar to leucyl-tRNA synthetase, putative / leucine--tRNA ligase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g04350.1); similar to leucyl tRNA synthetase [ <i>Homo sapiens</i> ] (GB:BAA95667.1); similar to SYLC_HUMAN Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA ligase) (LeuRS) (GB:Q9P2J5); similar to KIAA1352 protein [ <i>Homo sapiens</i> ] (GB:BAA92590.1); similar to MGC82093 protein [ <i>Xenopus laevis</i> ] (GB:AAH79713.1); similar to PREDICTED: similar to Leucyl-tRNA synthetase, cytoplasmic (Leucine--tRNA ligase) (LeuRS) [ <i>Canis familiaris</i> ] (GB:XP_535229.1); contains InterPro domain Aminoacyl-tRNA synthetase, class I (InterPro:IPR001412); contains InterPro domain Leucyl-tRNA synthetase archae/euk cytosolic, class Ia (InterPro:IPR004493); contains InterPro domain Aminoacyl-tRNA synthetase, class Ia (InterPro:IPR002300)   chr1:3112230-3116700 REVERSE   Aliases: F21M12.1, F21M12_1	5.1	6.1	-0.9	-2.5	100.0%	-2.5
1614	AT4G39840.1   expressed protein   chr4:18484895-18486808 FORWARD   Aliases: T5J17.10, T5J17_10	4.4	4.9	-0.4	-2.5	100.0%	-2.9
1615	AT5G40460.1   expressed protein   chr5:16219475-16220160 FORWARD   Aliases: K21I16.3, K21I16_3	3.9	3.0	0.9	2.5	100.0%	-2.5
1616	AT1G56720.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:21267093-21270033 REVERSE   Aliases: F25P12.84, F25P12_84	3.2	4.1	-0.9	-2.5	100.0%	-2.5
1617	AT4G10330.1   glycine-rich protein   chr4:6406537-6407773 FORWARD   Aliases: F24G24.130, F24G24_130	8.3	7.6	0.7	2.5	100.0%	-2.7
1618	AT4G30840.1   WD-40 repeat protein family   chr4:15017625-15019741 REVERSE   Aliases: F6I18.250, F6I18_250	4.7	5.7	-1.1	-2.5	100.0%	-2.2
1619	AT5G15490.1   UDP-glucose 6-dehydrogenase, putative, very strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) { <i>Glycine max</i> }; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain	5.1	7.5	-2.4	-2.5	100.0%	-2.3
1620	AT3G07990.1   Symbol: SCPL27	2.6	3.1	-0.5	-2.5	100.0%	-2.6
1621	AT4G30110.1   Symbol: HMA2   ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein / heavy-metal-associated domain-containing protein, similar to cadmium efflux pump protein from <i>Geobacillus stearothermophilus</i> (GI:16753175), cadmium resistance protein B from <i>Staphylococcus aureus</i> (GI:14020985)   chr4:14720259-14724583 REVERSE   Aliases: F6G3.140, F6G3_140	5.3	4.2	1.1	2.5	100.0%	-2.3
1622	AT2G25530.1   AFG1-like ATPase family protein, contains Pfam profile: PF03969 AFG1-like ATPase	6.7	7.8	-1.1	-2.5	100.0%	-2.4
1623	AT2G42530.1   cold-responsive protein / cold-regulated protein (cor15b), nearly identical to cold-regulated gene cor15b ( <i>Arabidopsis thaliana</i> ) GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr2:17716114-17717023 REVERSE   Aliases: F14N22.20, F14N22_20	6.5	5.1	1.4	2.5	100.0%	-2.3
1624	AT5G11970.1   expressed protein   chr5:3863072-3863756 REVERSE   Aliases: F14F18.140, F14F18_140	7.2	5.8	1.5	2.5	100.0%	-2.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1625	AT1G18850.1   expressed protein   chr1:6504797-6506412 REVERSE   Aliases: F6A14.6, F6A14_6	5.0	6.0	-1.0	-2.5	100.0%	-2.5
1626	AT3G19200.1   expressed protein   chr3:6649484-6650012 REVERSE   Aliases: MVI11.12	2.9	3.3	-0.4	-2.5	100.0%	-2.8
1627	AT5G36940.1   Symbol: CAT3   amino acid permease family protein, similar to SP:Q09143 High-affinity cationic amino acid transporter-1 (CAT-1) {Mus musculus}; contains Pfam profile PF00324: Amino acid permease   chr5:14607424-14611614 FORWARD   Aliases: CATIONIC AMINO ACID TRANSPORTER 3, MLF18.60, MLF18_60	6.4	5.6	0.8	2.5	100.0%	-2.4
1628	AT3G51500.1   expressed protein, predicted protein, Oryza sativa, EMBL:AP000367   chr3:19119113-19119866 FORWARD   Aliases: F26O13.140	4.7	3.9	0.8	2.5	100.0%	-2.5
1629	AT1G12050.1   fumarylacetoacetase, putative, similar to fumarylacetoacetase (Fumarylacetoacetate hydrolase, Beta-diketonase, FAA)(Rattus norvegicus) SWISS-PROT:P25093	6.9	7.9	-1.0	-2.5	100.0%	-2.5
1630	AT5G38030.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family; putative multidrug efflux protein NorM - Vibrio parahaemolyticus, EMBL:AB010463	2.9	3.6	-0.7	-2.5	100.0%	-2.4
1631	AT1G05320.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g32240.1); similar to unnamed protein product [Candida glabrata CBS138] (GB:CAG58365.1)   chr1:1553607-1557769 FORWARD   Aliases: YUP8H12.6, YUP8H12_6	5.0	5.9	-1.0	-2.5	100.0%	-2.3
1632	AT4G36515.1   expressed protein   chr4:17229557-17230299 REVERSE   Aliases: None	9.9	8.7	1.2	2.5	100.0%	-2.3
1633	AT1G31010.1   expressed protein, contains Pfam PF05329: Protein of unknown function (DUF731)   chr1:11054733-11056859 REVERSE   Aliases: F17F8.7	4.6	5.1	-0.5	-2.5	100.0%	-2.9
1634	AT2G27090.1   expressed protein, contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Protein of unknown function (DUF630)   chr2:11573366-11578890 REVERSE   Aliases: T20P8.14, T20P8_14	5.5	4.6	0.9	2.5	100.0%	-2.5
1635	AT4G18170.1   Symbol: WRKY28	5.5	6.4	-0.9	-2.5	100.0%	-2.3
1636	AT3G44340.2   Symbol: CEF   similar to sec23/sec24 transport protein-related [Arabidopsis thaliana] (TAIR:At4g32640.1); similar to PREDICTED: similar to SEC24-related protein C; protein transport protein SEC24C; SEC24 (S. cerevisiae) related gene family, member C [Gallus gallus] (GB:XP_421617.1); contains InterPro domain Sec23/Sec24 trunk domain (InterPro:IPR006896); contains InterPro domain Sec23/Sec24 zinc finger (InterPro:IPR006895); contains InterPro domain Sec23/Sec24 helical domain (InterPro:IPR006900); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Gelsolin region (InterPro:IPR007123)   chr3:16022608-16031241 REVERSE   Aliases: T22K7.20	6.1	6.9	-0.8	-2.4	100.0%	-2.6
1637	AT1G71230.1   Symbol: AJH2   COP9 signalosome subunit 5A / CSN subunit 5A (CSN5A) / c-JUN coactivator protein AJH2, putative (AJH2), COP9 complex subunit CSN5-2; identical to c-Jun coactivator protein AJH2 GI:3641312 from (Arabidopsis thaliana); identical to cDNA CSN complex subunit 5A (CSN5A) GI:18056660; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr1:26856123-26858058 FORWARD   Aliases: AJH2, CSN5, CSN5A, F3I17.12, F3I17_12	4.3	5.1	-0.8	-2.4	100.0%	-2.6
1638	AT2G17820.1   Symbol: ATHK1   histidine kinase 1, 99% identical to GP:4586626	3.8	4.9	-1.1	-2.4	100.0%	-2.4
1639	AT2G39510.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr2:16498221-16500210 REVERSE   Aliases: F12L6.17, F12L6_17	6.5	5.4	1.2	2.4	100.0%	-2.2
1640	AT5G57700.2   BNR/Asp-box repeat family protein, contains Pfam PF02012: BNR/Asp-box repeat   chr5:23392100-23394348 FORWARD   Aliases: MRI1.6, MRI1_6	6.9	7.8	-0.9	-2.4	100.0%	-2.6
1641	AT5G10910.1   mraW methylase family protein, contains Pfam profile PF01795: MraW methylase family   chr5:3439554-3441583 FORWARD   Aliases: T30N20.180, T30N20_180	5.1	6.2	-1.1	-2.4	100.0%	-2.5
1642	AT1G03730.1   expressed protein, similar to ESTs gb:AA605440 and gb:H37232   chr1:930828-931895 REVERSE   Aliases: F21B7.33	6.3	5.7	0.6	2.4	100.0%	-2.6
1643	AT3G61820.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr3:22890779-22892605 REVERSE   Aliases: F21F14.7	4.5	5.6	-1.1	-2.4	100.0%	-2.4
1644	AT4G18240.1   starch synthase-related protein, contains similarity to starch synthase GI:4582783 from (Vigna unguiculata)   chr4:10082163-10087214 FORWARD   Aliases: T9A21.90, T9A21_90	4.4	4.9	-0.5	-2.4	100.0%	-2.6
1645	AT3G16000.1   Symbol: MFP1   matrix-localized MAR DNA-binding protein-related, similar to matrix-localized MAR DNA binding protein MFP1 GI:1771158 from (Lycopersicon esculentum)   chr3:5430895-5433823 REVERSE   Aliases: MAR BINDING FILAMENT LIKE PROTEIN 1, MSL1.8	6.2	7.0	-0.8	-2.4	100.0%	-2.4
1646	AT5G53560.1   Symbol: ATB5 A	12.3	12.8	-0.5	-2.4	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1647	AT5G48650.1   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein   chr5:19743960-19746880 FORWARD   Aliases: K15N18.17, K15N18_17	3.8	4.8	-0.9	-2.4	100.0%	-2.5
1648	AT2G44670.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);   chr2:18432255-18433135 FORWARD   Aliases: F16B22.16	10.0	8.7	1.3	2.4	100.0%	-2.4
1649	AT3G60240.1   Symbol: EIF4G   MIF4G domain-containing protein / MA3 domain-containing protein, similar to eukaryotic protein synthesis initiation factor (Homo sapiens) GI:3941724; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain	8.5	9.2	-0.8	-2.4	100.0%	-2.6
1650	AT4G33100.1   expressed protein, contains Pfam PF05254: Uncharacterised protein family (UPF0203)   chr4:15971177-15972492 FORWARD   Aliases: F4I10.30, F4I10_30	7.5	6.8	0.7	2.4	100.0%	-2.4
1651	AT5G63810.1   Symbol: BGAL10	4.3	4.9	-0.6	-2.4	100.0%	-2.5
1652	AT5G09840.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr5:3058998-3061971 FORWARD   Aliases: MYH9.5, MYH9_5	2.3	2.6	-0.2	-2.4	100.0%	-3.4
1653	AT1G48440.1   expressed protein   chr1:17910669-17912191 FORWARD   Aliases: T1N15.5, T1N15_5	11.3	10.6	0.7	2.4	100.0%	-3.0
1654	AT3G51670.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to polyphosphoinositide binding protein Ssh2p (GI:2739046) {Glycine max};; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus   chr3:19179829-19182129 FORWARD   Aliases: T18N14.50	6.2	7.8	-1.6	-2.4	100.0%	-2.3
1655	AT5G06950.3   Symbol: AHBP 1B   similar to bZIP family transcription factor [Arabidopsis thaliana] (TAIR:At3g12250.1); similar to bZIP family transcription factor [Arabidopsis thaliana] (TAIR:At3g12250.2); similar to TGA-type basic leucine zipper protein TGA2.1 [Phaseolus vulgaris] (GB:AAK84889.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr5:2151038-2154554 FORWARD   Aliases: MOJ9.12, MOJ9_12, TGA2	4.6	4.0	0.6	2.4	100.0%	-2.6
1656	AT1G79975.2   expressed protein   chr1:30089065-30090457 FORWARD   Aliases: None	5.6	4.8	0.7	2.4	100.0%	-2.5
1657	AT3G08650.2   metal transporter family protein, contains ZIP Zinc transporter domain, Pfam:PF02535   chr3:2624467-2627376 REVERSE   Aliases: F17O14.12	8.3	7.6	0.7	2.4	100.0%	-2.7
1658	AT2G26040.1   Bet v I allergen family protein, similar to ribonucleases from {Panax ginseng} SP:P80890, SP:P80889, SP:Q05736 Pathogenesis-related protein 1 (AOPR1) {Asparagus officinalis}; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr2:11101910-11102482 REVERSE   Aliases: T19L18.15, T19L18_15	4.9	4.1	0.8	2.4	100.0%	-2.5
1659	AT2G26440.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:11254461-11256562 FORWARD   Aliases: T9J22.11, T9J22_11	5.2	6.1	-0.9	-2.4	100.0%	-2.3
1660	AT5G02150.2   similar to armadillo/beta-catenin repeat family protein [Arabidopsis thaliana] (TAIR:At3g09350.1); similar to Zgc:55259 protein [Danio rerio] (GB:AAH49402.1)   chr5:424290-426045 REVERSE   Aliases: T7H20.200, T7H20_200	5.7	5.0	0.8	2.4	100.0%	-2.5
1661	AT1G25400.1   expressed protein, similar to unknown protein GI:6714347 from (Arabidopsis thaliana)   chr1:8911117-8912385 REVERSE   Aliases: F2J7.13, F2J7_13	4.9	4.0	0.8	2.4	100.0%	-2.4
1662	AT1G09450.1   haspin-related, similar to haspin (GI:9229937) {Mus musculus} and haploid germ cell-specific nuclear protein kinase (GI:13561418) {Mus musculus}	2.6	3.1	-0.4	-2.4	100.0%	-2.9
1663	AT1G80460.2   Symbol: NHO1   similar to glycerol kinase [Pandanus amaryllifolius] (GB:AAR88660.1); contains InterPro domain Carbohydrate kinase, FGGY (InterPro:IPR000577); contains InterPro domain Glycerol kinase (InterPro:IPR005999)   chr1:30251637-30254197 REVERSE   Aliases: GLI1, T21F11.21, T21F11_21	9.7	10.5	-0.7	-2.4	100.0%	-2.8
1664	AT1G09950.1   transcription factor-related, low similarity to tumor-related protein (Nicotiana glauca x Nicotiana langsdorffii) GI:688423, SP:P23923 Transcription factor HBP-1b {Triticum aestivum}   chr1:3240608-3241576 REVERSE   Aliases: F21M12.34, F21M12_34	4.9	3.9	1.0	2.4	100.0%	-2.4
1665	AT5G56795.1   Symbol: MT1B   one of the five metallothioneins (MTs) genes identified in Arabidopsis. MTs are cysteine-rich proteins required for heavy metal tolerance. The MT1b gene, however, is indicated to be inactive.   chr5:22988283-22990379 REVERSE   Aliases: None	12.8	12.0	0.7	2.4	100.0%	-3.6
1666	AT5G16130.1   40S ribosomal protein S7 (RPS7C), 40S ribosomal protein S7 homolog - Brassica oleracea, EMBL:AF144752   chr5:5268424-5270091 FORWARD   Aliases: T21H19.50, T21H19_50	10.9	11.6	-0.7	-2.4	100.0%	-2.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1667	AT5G52570.1   Symbol: BETA OHASE 2   beta-carotene hydroxylase, putative, similar to GI:1575296, beta-carotene hydroxylase   chr5:21351630-21354206 REVERSE   Aliases: BETA CAROTENE HYDROXYLASE 2, F6N7.5, F6N7_5	7.1	6.2	0.9	2.4	100.0%	-2.3
1668	AT3G54960.1   Symbol: ATPDIL1 3   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	7.8	8.9	-1.1	-2.4	100.0%	-2.3
1669	AT3G18690.1   Symbol: MKS1   VQ motif-containing protein, contains PF05678: VQ motif   chr3:6429540-6430508 REVERSE   Aliases: MVE11.5	5.9	5.3	0.7	2.4	100.0%	-2.6
1670	AT2G16450.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.3	3.0	0.4	2.4	100.0%	-3.1
1671	AT5G07880.1   Symbol: SNAP29	3.7	3.1	0.6	2.4	100.0%	-2.5
1672	AT2G17870.1   cold-shock DNA-binding family protein, contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	10.2	9.3	0.8	2.4	100.0%	-2.8
1673	AT1G76410.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:28673742-28674540 FORWARD   Aliases: F15M4.9	5.3	4.5	0.8	2.4	100.0%	-2.4
1674	AT1G22190.1   AP2 domain-containing transcription factor, putative, similar to AP2 domain containing protein RAP2.4 GI:2281633 from (Arabidopsis thaliana)   chr1:7835771-7837277 FORWARD   Aliases: F16L1.8, F16L1_8	5.2	4.0	1.1	2.4	100.0%	-2.3
1675	AT5G64310.1   Symbol: AGP1   arabinogalactan-protein (AGP1), identical to gi:3883120 gb:AAC77823   chr5:25739159-25739872 FORWARD   Aliases: ARABINO GALACTAN PROTEIN 1, MSJ1.15, MSJ1_15	10.4	9.2	1.2	2.4	100.0%	-2.4
1676	AT4G20350.1   similar to LOC495973 protein [Xenopus laevis] (GB:AAH87349.1)   chr4:10988405-10989851 FORWARD   Aliases: F9F13.6, F9F13_6	3.4	3.9	-0.5	-2.4	100.0%	-2.9
1677	AT5G42860.1   expressed protein   chr5:17200294-17202144 REVERSE   Aliases: MBD2.5, MBD2_5	5.7	6.4	-0.7	-2.4	100.0%	-2.6
1678	AT4G12040.2   zinc finger (AN1-like) family protein, contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger   chr4:7214704-7215979 FORWARD   Aliases: F16J13.110, F16J13_110	9.2	8.2	1.0	2.4	100.0%	-2.8
1679	AT2G38330.1   MATE efflux family protein, low similarity to enhanced disease susceptibility 5 (Arabidopsis thaliana) GI:16589070; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr2:16071602-16075369 FORWARD   Aliases: T19C21.18, T19C21_18	7.2	6.4	0.8	2.4	100.0%	-2.4
1680	AT4G26200.1   Symbol: ACS7   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to ACC synthase from Malus x domestica, GI:1658062 (U73816), Pyrus pyrifolia GI:4586411   chr4:13275316-13277197 FORWARD   Aliases: T25K17.10, T25K17_10	5.0	6.0	-1.1	-2.4	100.0%	-2.3
1681	AT3G57160.1   expressed protein   chr3:21168589-21169795 REVERSE   Aliases: None	7.7	6.8	0.9	2.4	100.0%	-2.4
1682	AT1G77310.1   wound-responsive protein, putative, similar to wound-responsive protein 14.05 (GI:16506638) (Castanea sativa)   chr1:29056416-29061233 FORWARD   Aliases: F2P24.2, F2P24_2	2.6	2.9	-0.3	-2.4	100.0%	-3.2
1683	AT4G23720.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g01140.1); similar to hypothetical protein-like protein [Sorghum bicolor] (GB:AAO16691.1)   chr4:12358685-12359855 FORWARD   Aliases: F9D16.190, F9D16_190	4.0	4.5	-0.5	-2.4	100.0%	-2.8
1684	AT1G48320.1   thioesterase family protein, similar to ComAB (Bacillus licheniformis) GI:1834379; contains Pfam profile PF03061: thioesterase family protein   chr1:17858481-17859316 REVERSE   Aliases: F11A17.13, F11A17_13	6.0	6.7	-0.7	-2.4	100.0%	-2.6
1685	AT4G02840.1   small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative, similar to small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1, Sm-D1, Sm-D autoantigen) (Mouse) SWISS-PROT:P13641   chr4:1264627-1266486 FORWARD   Aliases: T5J8.16, T5J8_16	8.7	9.3	-0.6	-2.4	100.0%	-2.6
1686	AT5G57230.1   expressed protein   chr5:23207798-23208711 FORWARD   Aliases: MJB24.4, MJB24_4	6.2	7.0	-0.8	-2.4	100.0%	-2.5
1687	AT3G10610.1   40S ribosomal protein S17 (RPS17C), similar to 40S ribosomal protein S17 GB:AAD50774 (Lycopersicon esculentum)   chr3:3319041-3320154 FORWARD   Aliases: F13M14.10	8.1	8.9	-0.8	-2.4	100.0%	-2.5
1688	AT3G02360.2   6-phosphogluconate dehydrogenase family protein, contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate ;similar to 6-phosphogluconate dehydrogenase GB:BAA22812 GI:2529229 (Glycine max)   chr3:482035-484154 FORWARD   Aliases: F11A12.5, F11A12_5	12.0	12.7	-0.7	-2.4	100.0%	-3.2
1689	AT5G20550.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to leucoanthocyanidin dioxygenase (Malus domestica)(SP:P51091), flavonol synthase (Petunia x hybrida)(GI:311658); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr5:6952419-6953883 REVERSE   Aliases: F7C8.140, F7C8_140	6.9	8.2	-1.3	-2.4	100.0%	-2.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1690	AT5G46640.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr5:18941712-18943802 FORWARD   Aliases: MZA15.3, MZA15_3	5.4	4.7	0.8	2.4	100.0%	-2.4
1691	AT5G53570.1   RabGAP/TBC domain-containing protein, similar to GTPase activating protein (Yarrowia lipolytica) GI:2370595; contains Pfam profile PF00566: TBC domain   chr5:21777816-21780688 REVERSE   Aliases: MNC6.11, MNC6_11	6.5	5.5	1.0	2.4	100.0%	-2.5
1692	AT1G70330.1   Symbol: ENT1,AT   equilibrative nucleoside transporter family protein, contains similarity to SWISS-PROT:Q14542 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptapurine riboside-insensitive nucleoside transporter, Equilibrative NBMPR-insensitive nucleoside transporter, Nucleoside transporter, e.i-type, 36 kDa nucleolar protein HNP36, Hydrophobic nucleolar protein, 36 kDa, Delayed-early response protein 12) (Homo sapiens)   chr1:26506572-26508282 FORWARD   Aliases: EQUILIBRATIVE NUCLEOTIDE TRANSPORTER 1	7.8	6.3	1.6	2.4	100.0%	-2.4
1693	AT3G04070.1   Symbol: ANAC047   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM GB:CAA63101 (Petunia x hybrida)   chr3:1061533-1063101 REVERSE   Aliases: ANAC047, T11I18.18, T11I18_18	5.2	4.3	0.9	2.4	100.0%	-2.4
1694	AT5G11430.1   transcription elongation factor-related, contains weak similarity to transcription elongation factors   chr5:3648476-3652405 FORWARD   Aliases: F15N18.20, F15N18_20	4.6	5.3	-0.7	-2.4	100.0%	-2.5
1695	AT2G27260.1   expressed protein   chr2:11676733-11677722 FORWARD   Aliases: F12K2.16, F12K2_16	6.8	6.2	0.6	2.4	100.0%	-2.5
1696	AT1G09850.1   Symbol: XBCP3   cysteine protease, papain-like (XBCP3), identical to papain-like cysteine peptidase XBCP3 GI:14600257 from (Arabidopsis thaliana); contains Pfam profiles PF00112: Papain family cysteine protease and PF00396: Granulin   chr1:3201801-3204152 FORWARD   Aliases: F21M12.24, F21M12_24	7.2	8.2	-1.0	-2.4	100.0%	-2.5
1697	AT1G02160.1   expressed protein   chr1:410785-411590 FORWARD   Aliases: T6A9.18	10.8	10.1	0.7	2.4	100.0%	-2.9
1698	AT2G46735.1   expressed protein   chr2:19211255-19212182 FORWARD   Aliases: None	4.5	3.9	0.6	2.4	100.0%	-2.6
1699	AT3G24190.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr3:8743297-8747861 FORWARD   Aliases: MUJ8.9	7.2	6.4	0.8	2.4	100.0%	-2.6
1700	AT4G13720.1   inosine triphosphate pyrophosphatase, putative / HAM1 family protein, contains Pfam profile PF01725: Ham1 family; similar to inosine triphosphate pyrophosphatase (GI:13398328) (Homo sapiens)   chr4:7966976-7968900 REVERSE   Aliases: F18A5.110, F18A5_110	7.8	8.6	-0.8	-2.4	100.0%	-2.4
1701	AT5G60840.1   expressed protein, predicted protein, Drosophila melanogaster   chr5:24490560-24491717 REVERSE   Aliases: MAE1.8, MAE1_8	4.3	5.3	-1.0	-2.4	100.0%	-2.4
1702	AT4G31830.1   expressed protein   chr4:15400610-15401138 REVERSE   Aliases: F11C18.30, F11C18_30	3.1	2.8	0.3	2.4	100.0%	-3.1
1703	AT3G10040.1   expressed protein, est match   chr3:3096420-3098076 REVERSE   Aliases: T22K18.13	7.2	5.8	1.3	2.4	100.0%	-2.4
1704	AT4G23740.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase - Arabidopsis thaliana RKL1, PID:g4008006   chr4:12366472-12369348 FORWARD   Aliases: F9D16.210, F9D16_210	4.6	5.2	-0.6	-2.4	100.0%	-2.8
1705	ATCG00570.1   Symbol: PSBF   PSII cytochrome b559   chrC:63942-64061 REVERSE   Aliases: PSBF	8.2	10.0	-1.7	-2.4	100.0%	-2.4
1706	AT1G80270.2   DNA-binding protein, putative, similar to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat   chr1:30185926-30188399 FORWARD   Aliases: F5I6.2, F5I6_2	7.4	8.1	-0.7	-2.4	100.0%	-2.5
1707	AT3G47930.1   Symbol: ATGLDH	7.9	9.0	-1.1	-2.4	100.0%	-2.4
1708	AT3G13235.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr3:4271343-4274436 REVERSE   Aliases: None	4.4	5.0	-0.6	-2.4	100.0%	-2.7
1709	AT5G50240.1   Symbol: PIMT2   protein-L-isoaspartate O-methyltransferase, putative / PIMT, putative, similar to SP:Q42539 Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77) (Protein- beta-aspartate methyltransferase) (PIMT) (Protein L-isoaspartyl methyltransferase) (L-isoaspartyl protein carboxyl methyltransferase) {Arabidopsis thaliana}; contains Pfam profile PF01135: Protein-L-isoaspartate(D-aspartate) O-methyltransferase (PCMT)   chr5:20468477-20469687 FORWARD   Aliases: K6A12.10, K6A12_10, PROTEIN L ISOASPARTATE METHYLTRANSFERASE 2	6.2	5.5	0.7	2.4	100.0%	-2.5
1710	AT1G36980.1   expressed protein   chr1:14027484-14029382 FORWARD   Aliases: T32E20.29, T32E20_29	10.2	9.7	0.5	2.4	100.0%	-3.1
1711	AT2G37660.1   expressed protein   chr2:15802392-15804137 REVERSE   Aliases: F13M22.16, F13M22_16	9.1	10.0	-1.0	-2.4	100.0%	-2.4
1712	AT2G37520.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr2:15751847-15756866 REVERSE   Aliases: F13M22.2, F13M22_2	3.6	3.2	0.3	2.4	100.0%	-3.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1713	AT3G55800.1   Symbol: SBPASE	8.6	7.5	1.1	2.4	100.0%	-2.3
1714	AT4G16500.1   cysteine protease inhibitor family protein / cystatin family protein, similar to SP:Q06445 Cysteine proteinase inhibitor (Cystatin) {Vigna unguiculata}; contains Pfam profile PF00031: Cystatin domain   chr4:9301413-9302045 REVERSE   Aliases: DL4275C, FCAALL.171	10.9	11.5	-0.6	-2.4	100.0%	-3.0
1715	AT2G04039.2   expressed protein   chr2:1333268-1334563 FORWARD   Aliases: F3L12.11, F3L12_11	3.2	2.8	0.4	2.4	100.0%	-3.0
1716	AT2G38905.1   hydrophobic protein, putative / low temperature and salt responsive protein, putative, strong similarity to SP:Q9ZNQ7 Hydrophobic protein RCI2A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}; contains Pfam profile PF01679: Uncharacterized protein family   chr2:16251177-16251562 REVERSE   Aliases: None	7.4	5.8	1.6	2.4	100.0%	-2.3
1717	AT5G55490.1   Symbol: GEX1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g68790.1); similar to hypothetical protein S250_18C08.13 [Sorghum bicolor] (GB:AAL73526.1)   chr5:22495938-22498374 REVERSE   Aliases: GAMETE EXPRESSED PROTEIN1, MTE17.20, MTE17_20	3.1	2.7	0.4	2.4	100.0%	-3.2
1718	AT4G34260.1   expressed protein   chr4:16398119-16401814 FORWARD   Aliases: F10M10.30, F10M10_30	5.7	6.4	-0.8	-2.4	100.0%	-2.5
1719	AT1G69850.1   Symbol: NTL1   nitrate transporter (NTL1), identical to nitrate transporter (NTL1) GI:3377517 (Arabidopsis thaliana)   chr1:26300339-26304109 REVERSE   Aliases: ATNRT1.2, NITRATE TRANSPORTER, T17F3.12, T17F3_12	8.3	7.2	1.1	2.4	100.0%	-2.5
1720	AT2G43690.1   lectin protein kinase, putative, similar to receptor-like kinase LECRK1 (Arabidopsis thaliana) gi:2150023:gb:AAB58725   chr2:18119666-18121660 FORWARD   Aliases: F18O19.20	3.0	3.4	-0.4	-2.4	100.0%	-2.9
1721	AT5G50390.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:20538015-20540206 REVERSE   Aliases: MXI22.11, MXI22_11	4.2	4.7	-0.5	-2.4	100.0%	-2.8
1722	AT1G28520.1   expressed protein   chr1:10029179-10031969 FORWARD   Aliases: F3M18.4, F3M18_4	4.7	4.2	0.4	2.4	100.0%	-2.9
1723	AT4G01710.1   Symbol: CRK   actin polymerization factor protein-related, similar to human ARP2/3 complex 16 kd subunit, GenBank accession number O15511 likely functions to control the polymerization of actin   chr4:735753-736604 FORWARD   Aliases: ARPC5, CROOKED, T15B16.22, T15B16_22	7.5	6.4	1.1	2.4	100.0%	-2.5
1724	AT5G42030.1   expressed protein, similar to unknown protein (emb:CAB66408.1)   chr5:16828623-16830333 REVERSE   Aliases: MJC20.13, MJC20_13	4.4	5.4	-0.9	-2.4	100.0%	-2.5
1725	AT3G10970.2   haloacid dehalogenase-like hydrolase family protein, low similarity to genetic modifier (Zea mays) GI:10444400; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr3:3433078-3436284 REVERSE   Aliases: F9F8.21	7.9	7.2	0.6	2.4	100.0%	-2.6
1726	AT3G29970.1   germination protein-related, similar to HvB12D (Hordeum vulgare subsp. vulgare) gi:471319:emb:CAA54065   chr3:11747709-11749049 FORWARD   Aliases: K17E7.15	5.9	3.2	2.6	2.4	100.0%	-2.8
1727	AT5G54910.1   DEAD/DEAH box helicase, putative	4.8	6.2	-1.4	-2.4	100.0%	-2.4
1728	AT4G15790.1   expressed protein   chr4:8982253-8984216 FORWARD   Aliases: DL3935W, FCAALL.69	5.3	6.1	-0.9	-2.4	100.0%	-2.6
1729	AT2G01080.1   expressed protein   chr2:77888-79333 FORWARD   Aliases: F23H14.5, F23H14_5	5.8	5.4	0.5	2.4	100.0%	-2.8
1730	AT2G20740.3   expressed protein   chr2:8943759-8944591 FORWARD   Aliases: AT2G20730, F5H14.29, F5H14_29	6.1	5.4	0.7	2.4	100.0%	-2.7
1731	AT1G12250.1   thylakoid luminal protein-related, weak similarity to SP:O22160 Thylakoid luminal 15 kDa protein, chloroplast precursor (p15) {Arabidopsis thaliana}; contains Pfam profile PF00805: Pentapeptide repeats (8 copies)   chr1:4159268-4161453 FORWARD   Aliases: T28K15.2, T28K15_2	5.8	5.4	0.4	2.4	100.0%	-2.8
1732	AT5G50810.1   Symbol: TIM8   mitochondrial import inner membrane translocase (TIM8), identical to mitochondrial import inner membrane translocase subunit Tim8 (Arabidopsis thaliana) Swiss-Prot:Q9XGY4; contains Pfam domain, PF02953: Tim10/DDP family zinc finger   chr5:20692860-20693816 REVERSE   Aliases: K7B16.3, K7B16_3	7.6	8.6	-1.0	-2.4	100.0%	-2.4
1733	AT5G05450.1   DEAD/DEAH box helicase, putative (RH18)   chr5:1612050-1615337 FORWARD   Aliases: K18I23.26, K18I23_26	5.9	7.7	-1.8	-2.4	100.0%	-2.4
1734	AT4G31700.1   Symbol: RPS6   40S ribosomal protein S6 (RPS6A), ribosomal protein S6, Arabidopsis thaliana, PID:g2662469   chr4:15346083-15347731 REVERSE   Aliases: F28M20.110, F28M20_110, RIBOSOMAL PROTEIN S6	11.0	11.9	-0.9	-2.4	100.0%	-2.7
1735	AT4G27090.1   60S ribosomal protein L14 (RPL14B), ribosomal protein L14 - Human, PIR3:JC5954   chr4:13593911-13595257 REVERSE   Aliases: T24A18.40, T24A18_40	12.6	13.1	-0.5	-2.4	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1736	AT4G19130.1   replication protein-related, similar to replication protein A 70kDa (Oryza sativa) GI:13536993; contains Pfam profile PF00098: Zinc knuckle   chr4:10466488-10468071 REVERSE   Aliases: T18B16.100, T18B16_100	4.4	5.1	-0.7	-2.4	100.0%	-2.5
1737	AT3G16800.3   similar to protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana] (TAIR:At3g05640.1); similar to protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana] (TAIR:At3g05640.2); similar to putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] (GB:XP_483187.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr3:5721026-5723187 FORWARD   Aliases: K20I9.2	5.4	4.6	0.8	2.4	100.0%	-2.4
1738	AT5G58730.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr5:23740634-23742691 REVERSE   Aliases: MZN1.17, MZN1_17	7.4	6.6	0.8	2.4	100.0%	-2.6
1739	AT3G44735.1   phytosulfokines-related, contains similarities to phytosulfokines from (Arabidopsis thaliana)   chr3:16302187-16303137 REVERSE   Aliases: None	6.3	5.4	0.9	2.4	100.0%	-2.4
1740	AT4G03560.1   Symbol: ATTPC1	7.4	8.2	-0.8	-2.4	100.0%	-2.6
1741	AT2G18330.1   AAA-type ATPase family protein, contains Pfam profile: PF00004 ATPase family associated with various cellular activities (AAA)   chr2:7972739-7976187 FORWARD   Aliases: T30D6.16, T30D6_16	6.3	7.3	-1.0	-2.4	100.0%	-2.6
1742	AT1G80820.1   Symbol: CCR2   cinnamoyl-CoA reductase, putative, identical to CCR2 (GI:12407990), similar to cinnamoyl CoA reductase from Eucalyptus gunnii (GI:2058311)   chr1:30375465-30377562 FORWARD   Aliases: CINNAMOYL COA REDUCTASE, F23A5.17, F23A5_17	8.3	9.8	-1.5	-2.4	100.0%	-2.5
1743	AT3G58970.1   magnesium transporter CorA-like family protein, contains Pfam profile PF01544: CorA-like Mg2+ transporter protein   chr3:21800491-21802336 REVERSE   Aliases: F17J16.20	7.5	7.0	0.5	2.4	100.0%	-2.9
1744	AT1G68060.1   Symbol: ATMAP70 1   Encodes a microtubule associated protein (MAP70-1). Expressed in all tissues.   chr1:25514659-25518163 REVERSE   Aliases: ATMAP70 1, T23K23.9, T23K23_9	4.2	4.7	-0.5	-2.4	100.0%	-2.8
1745	AT5G40200.1   DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana)   chr5:16087558-16090542 FORWARD   Aliases: MSN9.100, MSN9_100	5.6	6.6	-1.0	-2.4	100.0%	-2.6
1746	AT1G79310.1   latex-abundant protein, putative (AMC4) / caspase family protein, similar to latex-abundant protein (Hevea brasiliensis) gb:AAD13216; contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain   chr1:29838879-29840438 FORWARD   Aliases: YUP8H12R.7, YUP8H12R_7	3.2	2.9	0.3	2.4	100.0%	-3.0
1747	AT3G14220.1   GDSL-motif lipase/hydrolase family protein, similar to myrosinase-associated proteins GI:1769968, GI:1769970 from (Brassica napus); contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family; contains 1 predicted transmembrane domain;   chr3:4732900-4734616 FORWARD   Aliases: MLE3.1	8.0	8.7	-0.7	-2.4	100.0%	-2.5
1748	AT3G27110.2   peptidase M48 family protein, contains Pfam domain, PF01435: Peptidase family M48   chr3:9999133-10001412 FORWARD   Aliases: MOJ10.19	4.7	3.6	1.1	2.4	100.0%	-2.3
1749	AT3G19720.2   Symbol: ARC5   dynamin family protein, identical to cDNA dynamin-like protein (ARC5) GI: 30349145; contains Pfam profile PF00350: Dynamin family   chr3:6850377-6855519 REVERSE   Aliases: ACCUMULATION AND REPLICATION OF CHLOROPLAST 5, MMB12.21	4.2	4.6	-0.4	-2.4	100.0%	-2.9
1750	AT3G02820.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr3:611543-613390 FORWARD   Aliases: F13E7.24, F13E7_24	3.8	4.6	-0.8	-2.4	100.0%	-2.7
1751	AT1G59640.2   Symbol: ZCW32   basic helix-loop-helix (bHLH) family protein   chr1:21913300-21914837 REVERSE   Aliases: T30E16.21, T30E16_21, ZCW32	7.7	6.7	1.0	2.4	100.0%	-2.4
1752	AT2G04660.1   Symbol: APC2   E3 ubiquitin ligase, putative, E3, ubiquitin ligase; contains similarity to anaphase-promoting complex subunit 2 GI:6180009 from (Homo sapiens)   chr2:1624738-1629159 FORWARD   Aliases: F28I8.30, F28I8_30	4.2	4.8	-0.6	-2.4	100.0%	-2.8
1753	AT1G70300.1   Symbol: KUP6   potassium transporter, putative, similar to potassium transporter HAK2p (Mesembryanthemum crystallinum) gi:14091471:gb:AAK53759; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter   chr1:26481543-26485293 REVERSE   Aliases: F17O7.17, F17O7_17	5.3	6.0	-0.7	-2.4	100.0%	-2.5
1754	AT1G22060.1   expressed protein   chr1:7773052-7780575 REVERSE   Aliases: F2E2.13, F2E2_13	3.9	4.6	-0.7	-2.4	100.0%	-2.7
1755	AT1G77010.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:28947604-28949691 FORWARD   Aliases: F22K20.11, F22K20_11	4.0	4.7	-0.6	-2.4	100.0%	-2.8
1756	AT1G63420.1   expressed protein   chr1:23519539-23522575 FORWARD   Aliases: F2K11.20, F2K11_20	8.3	7.7	0.6	2.4	100.0%	-2.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1757	AT1G51170.1   protein kinase family protein   chr1:18957126-18958560 REVERSE   Aliases: F23H24.1	3.8	4.9	-1.0	-2.4	100.0%	-2.4
1758	AT3G46030.1   histone H2B, putative, strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP:O22582, Lycopersicon esculentum GI:3021489; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr3:16924433-16925116 REVERSE   Aliases: F16L2.240	9.3	10.2	-0.9	-2.4	100.0%	-2.6
1759	AT5G48000.4   Symbol: CYP708A2   similar to cytochrome P450 family protein [Arabidopsis thaliana] (TAIR:At1g78490.1); similar to putative cytochrome P450 [Oryza sativa (japonica cultivar-group)] (GB:CAD30852.1); contains InterPro domain Cytochrome P450 (InterPro:IPR001128); contains InterPro domain E-class P450, group IV (InterPro:IPR002403)   chr5:19461364-19464500 REVERSE   Aliases: MDN11.7, MDN11_7	2.6	3.1	-0.5	-2.4	100.0%	-2.7
1760	AT1G01725.1   expressed protein   chr1:269794-270775 REVERSE   Aliases: None	8.6	7.5	1.1	2.4	100.0%	-2.5
1761	AT3G49860.1   Symbol: ATARLA1B   ADP-ribosylation factor, putative, similar to GTP-binding ADP-ribosylation factor homolog 1 protein (SP:P25160) (Drosophila melanogaster) and various ADP-RIBOSYLATION FACTOR (ARF) - like proteins; contains PF00025: ADP-ribosylation factor family domain	8.9	9.4	-0.5	-2.4	100.0%	-3.0
1762	AT3G02260.1   Symbol: BIG   auxin transport protein (BIG), nearly identical to auxin transport protein; BIG (Arabidopsis thaliana) GI:21779966; contains Pfam profiles PF02207: Putative zinc finger in N-recognin, PF00569: Zinc finger ZZ type   chr3:430991-448496 REVERSE   Aliases: ASA1, ATTENUATED SHADE AVOIDANCE 1, DARK OVER EXPRESSION OF CAB 1, DOC1, F14P3.3, F14P3_3, LOW PHOSPHATE RESISTANT ROOT 1, LPR1, TIR3, TRANSPORT INHIBITOR RESPONSE 3, UMB1	6.1	6.8	-0.7	-2.4	100.0%	-2.8
1763	AT1G56280.2   Symbol: ATDI19	10.0	9.0	1.0	2.4	100.0%	-2.9
1764	AT5G61440.1   thioredoxin family protein, low similarity to thioredoxin (Callithrix jacchus) GI:13560979; contains Pfam profile: PF00085 Thioredoxin   chr5:24724726-24726119 FORWARD   Aliases: MFB13.8, MFB13_8	6.1	5.2	0.9	2.4	100.0%	-2.5
1765	AT1G10370.1   Symbol: ATGSTU17   glutathione S-transferase, putative (ERD9), similar to glutathione S-transferase TSI-1 (Aegilops tauschii) gi:2190992 gb:AAD10129; similar to ESTs gb:R29860, emb:Z29757, and emb:Z29758; identical to cDNA ERD9 mRNA for glutathione S-transferase,	3.6	4.5	-0.9	-2.4	100.0%	-2.6
1766	AT5G40890.2   Symbol: ATCLC A   similar to chloride channel protein (CLC-c) [Arabidopsis thaliana] (TAIR:At5g49890.1); similar to chloride channel-like (CLC) protein, putative [Arabidopsis thaliana] (TAIR:At5g33280.1); similar to chloride channel protein (CLC-b) [Arabidopsis thaliana] (TAIR:At3g27170.1); similar to chloride channel [Oryza sativa (japonica cultivar-group)] (GB:XP_466225.1); similar to chloride channel [Oryza sativa (japonica cultivar-group)] (GB:BA97268.1); similar to chloride channel [Oryza sativa (japonica cultivar-group)] (GB:BA97267.1); similar to chloride channel Stclc1 [Solanum tuberosum] (GB:CAA71369.1); similar to ClC-Nt1 [Nicotiana tabacum] (GB:CAA64829.1); contains InterPro domain Cl- channel, voltage gated (InterPro:IPR001807); contains InterPro domain Chloride channel plant CLC (InterPro:IPR002251); contains InterPro domain CBS domain (InterPro:IPR000644)   chr5:16398542-16401547 REVERSE   Aliases: CHLORIDE CHANNEL A, CLC A, CLCA, MHK7.12, MHK7_12	5.9	6.7	-0.8	-2.4	100.0%	-2.5
1767	AT3G21520.1   expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679)   chr3:7581965-7582799 FORWARD   Aliases: MIL23.9	3.8	4.4	-0.6	-2.4	100.0%	-2.6
1768	ATCG00720.1   Symbol: PETB   Encodes the cytochrome b(6) subunit of the cytochrome b6f complex.   chrC:74841-76292 FORWARD   Aliases: PETB	9.2	7.8	1.4	2.4	100.0%	-2.4
1769	AT2G16940.1   RNA recognition motif (RRM)-containing protein   chr2:7349723-7354490 REVERSE   Aliases: F12A24.12, F12A24_12	5.8	6.6	-0.8	-2.4	100.0%	-2.7
1770	AT1G44414.1   expressed protein   chr1:16850221-16850526 FORWARD   Aliases: T18F15.8, T18F15_8	3.7	3.1	0.6	2.4	100.0%	-2.7
1771	AT2G22910.1   GCN5-related N-acetyltransferase (GNAT) family protein / amino acid kinase family protein, similar to SP:P08205 Amino-acid acetyltransferase (EC 2.3.1.1) (N-acetylglutamate synthase) {Escherichia coli}; contains Pfam profiles PF00696: Amino acid kinase family, PF00583: acetyltransferase, GNAT family   chr2:9756949-9759928 FORWARD   Aliases: T20K9.12, T20K9_12	5.6	6.6	-1.0	-2.4	100.0%	-2.7
1772	AT1G75310.1   Symbol: AUL1   DNA heat shock N-terminal domain-containing protein, low similarity to SP:Q27974 Auxilin {Bos taurus}; contains Pfam profile PF00226: DnaJ domain   chr1:28264665-28269785 FORWARD   Aliases: F22H5.15	6.0	5.3	0.6	2.4	100.0%	-2.6
1773	AT2G41950.1   expressed protein   chr2:17520157-17521921 FORWARD   Aliases: T6D20.26, T6D20_26	6.3	7.2	-0.9	-2.4	100.0%	-2.5
1774	AT4G29820.1   expressed protein   chr4:14595686-14597487 REVERSE   Aliases: F27B13.60, F27B13_60	4.6	3.9	0.6	2.4	100.0%	-2.8
1775	AT1G77090.1   thylakoid lumenal 29.8 kDa protein, identical to SP:O49292:TL30_ARATH (Arabidopsis thaliana); contains a PsbP domain AF370571; SIMILAR TO GI:13926195--F22K20.16   chr1:28965291-28966816 REVERSE   Aliases: F22K20.16, F22K20_16	6.3	5.2	1.1	2.4	100.0%	-2.4
1776	AT5G23000.1   myb family transcription factor (MYB37), contains PFAM profile: myb DNA binding domain PF00249;   chr5:7696237-7697930 FORWARD   Aliases: T2007.2, T2007_2	2.6	3.0	-0.4	-2.4	100.0%	-2.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1777	AT2G21090.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:9052597-9054657 REVERSE   Aliases: F26H11.15, F26H11_15	4.2	4.7	-0.5	-2.4	100.0%	-2.7
1778	AT1G27360.2   squamosa promoter-binding protein-like 11 (SPL11), identical to squamosa promoter binding protein-like 11 (Arabidopsis thaliana) GI:5931665; contains Pfam profile PF03110: SBP domain   chr1:9501064-9503856 FORWARD   Aliases: F17L21.14, F17L21_14	4.3	5.0	-0.7	-2.4	100.0%	-2.6
1779	AT5G27850.1   60S ribosomal protein L18 (RPL18C), 60S ribosomal protein L18, Arabidopsis thaliana, SWISSPROT:RL18_ARATH   chr5:9873160-9874602 FORWARD   Aliases: F14I23.10, F14I23_10	10.6	11.3	-0.7	-2.4	100.0%	-2.7
1780	AT5G03460.1   expressed protein   chr5:864280-865672 FORWARD   Aliases: F12E4.230, F12E4_230	8.2	7.4	0.9	2.4	100.0%	-2.6
1781	AT2G36950.1   heavy-metal-associated domain-containing protein, nearly identical to farnesylated protein ATPF2 (GI:4097545) Pfam profile PF00403: Heavy-metal-associated domain   chr2:15522212-15524010 FORWARD   Aliases: T1J8.13, T1J8_13	10.2	9.1	1.1	2.4	100.0%	-2.7
1782	AT3G50940.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr3:18944744-18946592 FORWARD   Aliases: F18B3.220	3.2	2.7	0.4	2.4	100.0%	-3.1
1783	AT1G33420.1   PHD finger family protein, contains Pfam profile: PF00628: PHD-finger   chr1:12120866-12123556 REVERSE   Aliases: F10C21.9, F10C21_9	5.5	6.1	-0.5	-2.4	100.0%	-2.8
1784	AT3G33520.1   Symbol: ATARP6	5.7	7.0	-1.2	-2.4	100.0%	-2.6
1785	AT1G63080.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23392549-23394393 REVERSE   Aliases: F16M19.17, F16M19_17	5.3	5.8	-0.5	-2.4	100.0%	-3.1
1786	AT2G36160.1   40S ribosomal protein S14 (RPS14A)   chr2:15176897-15178428 FORWARD   Aliases: F9C22.9, F9C22_9	10.8	11.3	-0.5	-2.4	100.0%	-3.3
1787	AT5G60930.1   chromosome-associated kinesin, putative, microtubule-associated motor KIF4 , Mus musculus, PIR:A54803   chr5:24532624-24539737 REVERSE   Aliases: MSL3.50, MSL3_50	3.6	4.3	-0.7	-2.4	100.0%	-2.8
1788	AT2G39370.1   expressed protein   chr2:16451208-16452344 REVERSE   Aliases: F12L6.3, F12L6_3	4.7	5.2	-0.5	-2.3	100.0%	-2.9
1789	AT2G24230.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:10308897-10311892 REVERSE   Aliases: F27D4.14, F27D4_14	3.5	4.0	-0.4	-2.3	100.0%	-2.8
1790	AT5G16380.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:5359413-5360713 REVERSE   Aliases: MQK4.11, MQK4_11	3.4	2.7	0.7	2.3	100.0%	-2.8
1791	AT5G43590.1   patatin, putative, similar to patatin-like latex allergen (Hevea brasiliensis)(PMID:10589016); contains patatin domain PF01734   chr5:17526595-17528704 REVERSE   Aliases: K9D7.9, K9D7_9	2.5	2.9	-0.4	-2.3	100.0%	-3.1
1792	AT5G50350.1   expressed protein   chr5:20515702-20518906 REVERSE   Aliases: MXI22.6, MXI22_6	4.8	5.5	-0.6	-2.3	100.0%	-2.7
1793	AT2G19170.1   Symbol: SLP3   subtilase family protein, contains similarity to meiotic serine proteinase TMP GI:6468325 from (Lycopersicon esculentum)	3.4	3.8	-0.4	-2.3	100.0%	-3.0
1794	AT4G30310.3   ribitol kinase, putative, similar to ribitol kinase (Klebsiella pneumoniae) gi:2905643:gb:AAC26495   chr4:14832322-14835098 FORWARD   Aliases: F17I23.350, F17I23_350	6.4	7.0	-0.6	-2.3	100.0%	-2.8
1795	AT5G67260.1   Symbol: CYCD3;2   cyclin family protein, similar to cyclin D3.1 protein (Nicotiana tabacum) GI:4160300; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr5:26853374-26855037 FORWARD   Aliases: CYCD3;2, Cyclin D3;2, K3G17.2, K3G17_2	5.0	5.9	-0.9	-2.3	100.0%	-2.7
1796	AT1G03780.2   targeting protein-related, similar to microtubule-associated protein / targeting protein for Xklp2 ((TPX2) GI:8926138) {Homo sapiens}; similar to Restricted expression proliferation associated protein 100 (p100) (Differentially expressed in lung cells 2) (DIL-2) (Targeting protein for Xklp2) (C20orf1 protein) (C20orf2 protein) (Protein FLS353)(SP:Q9ULW0) {Homo sapiens}   chr1:947643-951729 REVERSE   Aliases: F21M11.31, F21M11_31	4.4	3.7	0.6	2.3	100.0%	-2.7
1797	AT4G04940.1   transducin family protein / WD-40 repeat family protein, contains seven G-protein beta WD-40 repeats   chr4:2511026-2517191 REVERSE   Aliases: T1J1.5, T1J1_5	4.1	4.8	-0.7	-2.3	100.0%	-2.6
1798	ATMG00150.1   Symbol: ORF116	2.6	2.9	-0.3	-2.3	100.0%	-3.4
1799	AT5G37360.1   expressed protein   chr5:14822459-14825454 REVERSE   Aliases: MNJ8.18, MNJ8_18	6.8	6.2	0.7	2.3	100.0%	-2.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1800	AT4G24700.1   expressed protein   chr4:12744632-12745323 REVERSE   Aliases: F22K18.100, F22K18_100	3.6	3.1	0.5	2.3	100.0%	-2.8
1801	AT5G16910.1   Symbol: ATCSLD2   cellulose synthase family protein, similar to gi:2827143 cellulose synthase catalytic subunit, Arabidopsis thaliana, gi:9622886 cellulose synthase-7 from Zea mays   chr5:5561682-5565583 FORWARD   Aliases: CSLD2, F2K13.60, F2K13_60	6.7	6.1	0.6	2.3	100.0%	-2.7
1802	AT1G36950.1   zinc finger protein-related, contains similarity to zinc finger proteins (C3HC4-type RING finger)   chr1:14012114-14013263 REVERSE   Aliases: T32E20.33, T32E20_33	2.1	1.9	0.1	2.3	100.0%	-4.0
1803	AT4G00070.1   zinc finger protein-related, contains similarity to zinc finger proteins (C3HC4-type RING finger)   chr4:29672-31426 REVERSE   Aliases: F6N15.15, F6N15_15	2.1	1.9	0.1	2.3	100.0%	-4.0
1804	AT1G19270.1   ubiquitin interaction motif-containing protein / LIM domain-containing protein, weak similarity to LIM-homeobox protein (Mus musculus) GI:2149584, Hic-5 (Mus musculus) GI:664955; contains Pfam profiles PF02809: Ubiquitin interaction motif, PF00412: LIM domain   chr1:6662492-6666019 FORWARD   Aliases: T29M8.14, T29M8_14	5.0	4.5	0.5	2.3	100.0%	-2.7
1805	AT5G06590.1   expressed protein   chr5:2016646-2018836 FORWARD   Aliases: F15M7.12, F15M7_12	8.5	9.6	-1.1	-2.3	100.0%	-2.4
1806	AT3G53340.1   CCAAT-box binding transcription factor, putative, similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP:P25209) (GI:22380) (Zea mays); contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone	5.6	6.5	-0.9	-2.3	100.0%	-2.5
1807	AT1G22780.1   Symbol: PFL   40S ribosomal protein S18 (RPS18A), Match to ribosomal S18 gene mRNA gb:Z28701, DNA gb:Z23165 from A. thaliana. ESTs gb:T21121, gb:Z17755, gb:R64776 and gb:R30430 come from this gene   chr1:8067853-8069319 FORWARD   Aliases: 40S RIBOSOMAL PROTEIN S18, PFL1, POINTED FIRST LEAVES, RPS18A, T22J18.5, T22J18_5	10.8	11.4	-0.6	-2.3	100.0%	-2.8
1808	AT1G05570.1   Symbol: CALS1   similar to glycosyl transferase family 48 protein [Arabidopsis thaliana] (TAIR:At5g13000.1); similar to glycosyl transferase family 48 protein [Arabidopsis thaliana] (TAIR:At2g31960.1); similar to glycosyl transferase family 48 protein [Arabidopsis thaliana] (TAIR:At1g06490.1); similar to glycosyl transferase family 48 protein [Arabidopsis thaliana] (TAIR:At3g59100.1); similar to putative callose synthase 1 catalytic subunit [Oryza sativa (japonica cultivar-group)] (GB:BAD72533.1); similar to Putative glucan synthase [Oryza sativa (japonica cultivar-group)] (GB:NP_912480.1); similar to OJ1029_F04.4 [Oryza sativa (japonica cultivar-group)] (GB:NP_918100.1); similar to putative beta-1,3-glucan synthase [Nicotiana glauca] (GB:AAK49452.2); similar to putative callose synthase 1 catalytic subunit [Oryza sativa (japonica cultivar-group)] (GB:BAD62105.1); contains InterPro domain Glycosyl transferase, family 48 (InterPro:IPR003440)   chr1:1647719-1658685 REVERSE   Aliases: ATGSL06, ATGSL6, CALLOSE SYNTHASE 1, F3F20.1, F3F20_1, GLUCAN SYNTHASE LIKE 6, GSL06, GSL6	6.6	5.8	0.8	2.3	100.0%	-2.4
1809	AT1G67720.1   leucine-rich repeat family protein / protein kinase family protein, contains similarity to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686;emb:CAA66376; contains Pfam domains PF00069: Protein kinase domain and PF00560: Leucine Rich Repeat   chr1:25390004-25394736 FORWARD   Aliases: F12A21.30	6.9	6.1	0.7	2.3	100.0%	-2.6
1810	AT5G01770.1   Encodes one of two Arabidopsis RAPTOR/KOG1 homologs. RAPTOR proteins are binding partners of the target of rapamycin kinase that is present in all eukaryotes and play a central role in the stimulation of cell growth and metabolism in response to nutrients. Mutations in this gene have no visible effects on embryo or plant development.   chr5:294536-301770 REVERSE   Aliases: ATRAPTOR2, RAPTOR2, T20L15.40, T20L15_40	3.8	4.4	-0.6	-2.3	100.0%	-2.8
1811	AT3G56400.1   Symbol: WRKY70	4.8	4.1	0.7	2.3	100.0%	-2.6
1812	AT5G23880.1   Symbol: CPSF100   cleavage and polyadenylation specificity factor, identical to cleavage and polyadenylation specificity factor (Arabidopsis thaliana) SWISS-PROT:Q9LKF9   chr5:8052507-8058347 FORWARD   Aliases: CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, EMB1265, EMBRYO DEFECTIVE 1265	5.4	6.0	-0.6	-2.3	100.0%	-2.8
1813	AT1G22510.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:7950808-7952659 REVERSE   Aliases: F12K8.14, F12K8_14	6.0	4.7	1.3	2.3	100.0%	-2.5
1814	AT5G60040.1   Symbol: NRPC1   DNA-directed RNA polymerase, putative, similar to SP:P04051 DNA-directed RNA polymerase III largest subunit (EC 2.7.7.6) {Saccharomyces cerevisiae}; contains InterPro accession IPR000722: RNA polymerase, alpha subunit   chr5:24190816-24200495 FORWARD   Aliases: MGO3.13, MGO3_13	4.1	4.9	-0.8	-2.3	100.0%	-2.5
1815	AT3G60830.1   Symbol: ATARP7	6.9	7.6	-0.8	-2.3	100.0%	-2.6
1816	AT1G70000.1   DNA-binding family protein, contains Pfam domains, PF00249: Myb-like DNA-binding domain and PF00098: Zinc knuckle   chr1:26366941-26368362 REVERSE   Aliases: F20P5.26, F20P5_26	4.9	4.1	0.8	2.3	100.0%	-2.6
1817	AT3G56620.1   integral membrane family protein / nodulin MtN21-related, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr3:20983482-20985585 REVERSE   Aliases: T5P19.270	7.1	6.2	0.9	2.3	100.0%	-2.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1818	AT1G03970.1   Symbol: GBF4   G-box binding factor 4 (GBF4), identical to G-box binding factor 4 (GBF4) SP:P42777 from (Arabidopsis thaliana)   chr1:1018099-1019207 FORWARD   Aliases: F21M11.10, F21M11_10	7.7	6.8	0.9	2.3	100.0%	-2.7
1819	AT3G20820.1   leucine-rich repeat family protein, contains similarity to Cf-2.1 (Lycopersicon pimpinellifolium) gi:1184075:gb:AAC15779; contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611   chr3:7280884-7282183 FORWARD   Aliases: MOE17.11	3.3	4.1	-0.8	-2.3	100.0%	-2.5
1820	AT1G24280.1   Symbol: G6PD3   Encodes a plastidic glucose-6-phosphate dehydrogenase that is sensitive to reduction by DTT and whose mRNA is most highly expressed in root.   chr1:8609434-8612569 FORWARD   Aliases: F3I6.22, F3I6_22, G6PD3, GLUCOSE 6 PHOSPHATE DEHYDROGENASE 3	8.4	9.0	-0.6	-2.3	100.0%	-2.8
1821	AT4G38180.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family and PF04434: SWIM zinc finger   chr4:17906508-17909671 REVERSE   Aliases: F20D10.300, F20D10_300	3.8	4.3	-0.5	-2.3	100.0%	-2.9
1822	AT3G57120.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:21149884-21151589 FORWARD   Aliases: F24I3.200	5.0	4.6	0.4	2.3	100.0%	-3.1
1823	AT1G20030.2   pathogenesis-related thaumatin family protein, similar to receptor serine/threonine kinase PR5K (Arabidopsis thaliana) GI:1235680; contains Pfam profile PF00314: Thaumatin family   chr1:6945416-6947335 FORWARD   Aliases: T20H2.19, T20H2_19	3.8	3.0	0.8	2.3	100.0%	-2.6
1824	AT3G54500.2   expressed protein   chr3:20186382-20189958 REVERSE   Aliases: T14E10.70	5.0	4.1	0.9	2.3	100.0%	-2.5
1825	AT5G09220.1   Symbol: AAP2   amino acid permease 2 (AAP2), identical to amine acid permease AAP2 (Arabidopsis thaliana) GI:510236   chr5:2866253-2869055 FORWARD   Aliases: AMINO ACID PERMEASE 2, T2K12.6	12.2	9.9	2.3	2.3	100.0%	-2.5
1826	AT2G22190.1   similar to trehalose-6-phosphate phosphatase, putative [Arabidopsis thaliana] (TAIR:At4g39770.1); similar to putative trehalose-phosphatase [Oryza sativa (japonica cultivar-group)] (GB:XP_482349.1); contains InterPro domain Trehalose-phosphatase (InterPro:IPR003337); contains InterPro domain HAD-superfamily hydrolase, subfamily IIB (InterPro:IPR006379)   chr2:9440845-9443624 REVERSE   Aliases: T26C19.15, T26C19_15	3.4	2.9	0.5	2.3	100.0%	-2.9
1827	AT2G01750.1   Symbol: ATMAP70 3   Encodes a microtubule associated protein (MAP70-3). Expressed in all tissues.   chr2:328350-332112 FORWARD   Aliases: ATMAP70 3, T8O11.8, T8O11_8	3.9	4.5	-0.6	-2.3	100.0%	-2.8
1828	AT1G09780.1   2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative, strong similarity to SP:Q42908 2,3-biphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}; contains Pfam profile PF01676: Metalloenzyme superfamily   chr1:3165372-3167871 REVERSE   Aliases: F21M12.16, F21M12_16	10.7	11.9	-1.2	-2.3	100.0%	-3.1
1829	AT3G19440.1   pseudouridine synthase family protein, low similarity to SP:P23851 Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70) (Pseudouridylate synthase) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF00849: RNA pseudouridylate synthase	3.7	4.6	-0.9	-2.3	100.0%	-2.6
1830	AT1G01120.1   Symbol: KCS1   fatty acid elongase 3-ketoacyl-CoA synthase 1 (KCS1), nearly identical to GB:AAC99312 GI:4091810 from (Arabidopsis thaliana)   chr1:57269-59167 REVERSE   Aliases: T25K16.11, T25K16_11	3.7	4.7	-1.0	-2.3	100.0%	-2.4
1831	AT2G40550.1   expressed protein   chr2:16941914-16945213 FORWARD   Aliases: T2P4.10, T2P4_10	5.4	7.1	-1.7	-2.3	100.0%	-2.4
1832	AT1G69870.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:26319690-26323883 FORWARD   Aliases: T17F3.10, T17F3_10	2.9	2.5	0.3	2.3	100.0%	-3.1
1833	AT4G37180.2   myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain   chr4:17504558-17506361 FORWARD   Aliases: AP22.100, AP22_100	3.0	3.5	-0.6	-2.3	100.0%	-2.8
1834	AT4G17030.1   Symbol: ATEXLB1   expansin-related, identical to SWISS-PROT:O23547 expansin-related protein 1 precursor (At-EXPR1)(Arabidopsis thaliana); related to expansins, <a href="http://www.bio.psu.edu/expansins/">http://www.bio.psu.edu/expansins/</a>   chr4:9581605-9583309 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN LIKE B1, AT EXPR, ATEXPR1, ATHEXP BETA 3.1, DL4545C, EXPR, FCAALL.341	3.6	2.7	1.0	2.3	100.0%	-2.4
1835	AT1G03110.1   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); similar to WD-repeat domain 4 protein (GI:9955698) (Mus musculus)   chr1:749246-751963 FORWARD   Aliases: F10O3.6, F10O3_6	4.5	5.4	-0.8	-2.3	100.0%	-2.7
1836	AT1G55740.1   alkaline alpha galactosidase, putative, similar to alkaline alpha galactosidase I (Cucumis melo) GI:29838629; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1   chr1:20839033-20842442 REVERSE   Aliases: F20N2.14	6.5	6.0	0.5	2.3	100.0%	-3.0
1837	AT1G10650.1   expressed protein   chr1:3524019-3526336 REVERSE   Aliases: F20B24.9, F20B24_9	8.7	8.2	0.5	2.3	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1838	AT1G14020.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator protein -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr1:4802728-4805323 FORWARD   Aliases: F7A19.11, F7A19_11	4.7	5.5	-0.9	-2.3	100.0%	-2.6
1839	AT1G11870.3   seryl-tRNA synthetase, putative / serine--tRNA ligase, putative, similar to PIR:T03949 serine--tRNA ligase (EC 6.1.1.11) serS {Zea mays}; contains Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF02403: Seryl-tRNA synthetase N-terminal domain   chr1:4003845-4006737 FORWARD   Aliases: F12F1.29, F12F1_29	4.5	5.3	-0.8	-2.3	100.0%	-2.6
1840	AT1G28330.3   Symbol: DRM1   dormancy-associated protein, putative (DRM1), identical to dormancy-associated protein (Arabidopsis thaliana) GI:2995990; similar to dormancy-associated protein GI:2605887 from (Pisum sativum); contains Pfam profile PF05564: Dormancy/auxin associated protein   chr1:9933896-9935251 REVERSE   Aliases: DORMANCY ASSOCIATED PROTEIN 1, DRM1, F3H9.1, F3H9_1	6.3	4.8	1.5	2.3	100.0%	-2.6
1841	AT3G06200.1   guanylate kinase, putative, similar to guanylate kinase (GMP kinase) (Bacillus halodurans) Swiss-Prot:Q9K9Y2; contains Pfam profile: PF00625 guanylate kinase   chr3:1877600-1879244 FORWARD   Aliases: F28L1.14, F28L1_14	6.3	5.5	0.8	2.3	100.0%	-2.6
1842	AT2G21740.1   expressed protein   chr2:9289066-9289443 REVERSE   Aliases: F7D8.6, F7D8_6	2.2	2.5	-0.3	-2.3	100.0%	-3.2
1843	AT5G27540.2   Symbol: EMB2473   similar to GTP-binding protein-related [Arabidopsis thaliana] (TAIR:At3g63150.1); similar to GTP-binding protein-related [Arabidopsis thaliana] (TAIR:At3g05310.1); similar to rac-GTP binding protein -like [Oryza sativa (japonica cultivar-group)] (GB:NP_915455.1); similar to putative mitochondrial Rho 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD81741.1); contains InterPro domain Small GTP-binding protein domain (InterPro:IPR005225); contains InterPro domain Ras small GTPase, Rab type (InterPro:IPR003579); contains InterPro domain Ras small GTPase, Rho type (InterPro:IPR003578); contains InterPro domain Ras GTPase superfamily (InterPro:IPR001806); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048); contains InterPro domain ATP/GTP-binding site motif A (P-loop) (InterPro:IPR001687)   chr5:9722577-9727457 FORWARD   Aliases: EMB2473, EMBRYO DEFECTIVE 2473, F21A20.250, F21A20_250	5.8	7.0	-1.2	-2.3	100.0%	-2.6
1844	AT4G20270.1   leucine-rich repeat transmembrane protein kinase, putative, CLAVATA1 receptor kinase, Arabidopsis th., PATX:G2160756   chr4:10949671-10953089 FORWARD   Aliases: F1C12.190, F1C12_190	6.7	7.3	-0.6	-2.3	100.0%	-3.0
1845	AT4G13030.2   expressed protein   chr4:7607264-7609840 FORWARD   Aliases: F25G13.120, F25G13_120	6.2	5.4	0.7	2.3	100.0%	-2.5
1846	AT3G24760.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr3:9040095-9041841 FORWARD   Aliases: K7P8.5	7.2	6.6	0.6	2.3	100.0%	-2.8
1847	AT1G08070.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:2514189-2516602 REVERSE   Aliases: T6D22.15, T6D22_15	3.8	4.4	-0.6	-2.3	100.0%	-2.9
1848	AT2G42450.1   lipase class 3 family protein, similar to calmodulin-binding heat-shock protein CaMBP (Nicotiana tabacum) GI:1087073; contains Pfam profile PF01764: Lipase, PF03893: Lipase 3 N-terminal region	4.5	5.3	-0.8	-2.3	100.0%	-2.5
1849	AT3G16460.2   similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:At1g52040.1); similar to myrosinase-binding protein [Brassica napus] (GB:AAC08048.1); contains InterPro domain Jacalin-related lectin (InterPro:IPR001229)	6.5	7.3	-0.9	-2.3	100.0%	-2.6
1850	AT1G77120.1   Symbol: ADH1   alcohol dehydrogenase (ADH), identical to alcohol dehydrogenase GI:469467 from (Arabidopsis thaliana)   chr1:28980345-28982311 FORWARD   Aliases: ADH, ALCOHOL DEHYDROGENASE, ALCOHOL DEHYDROGENASE 1, F22K20.19, F22K20_19	13.5	12.4	1.1	2.3	100.0%	-2.8
1851	AT1G60220.1   similar to Ulp1 protease family protein [Arabidopsis thaliana] (TAIR:At1g10570.2); similar to Ulp1 protease family protein [Arabidopsis thaliana] (TAIR:At1g10570.1); similar to OSJNBb0021A09.14 [Oryza sativa (japonica cultivar-group)] (GB:NP_916015.1); contains InterPro domain SUMO/Sentrin/Ubl1 specific protease (InterPro:IPR003653)   chr1:22211890-22215816 FORWARD   Aliases: T13D8.11, T13D8_11	8.1	8.6	-0.5	-2.3	100.0%	-3.0
1852	AT1G10290.1   Symbol: ADL6   dynamin-like protein 6 (ADL6), identical to dynamin-like protein 6 (ADL6) (Arabidopsis thaliana) GI:6651399; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain, PF00169: PH domain   chr1:3370563-3377465 FORWARD   Aliases: ADL6, DRP2A, DYNAMIN LIKE PROTEIN 6, F14N23.17, F14N23_17	6.3	6.9	-0.6	-2.3	100.0%	-2.7
1853	AT2G29560.1   enolase, putative, similar to enolase (Spinacia oleracea) gi:8919731:emb:CAB96173   chr2:12653666-12656983 FORWARD   Aliases: F16P2.6, F16P2_6	7.4	8.2	-0.8	-2.3	100.0%	-2.8
1854	AT5G19500.1   tryptophan/tyrosine permease family protein, contains Pfam profile PF03222: Tryptophan/tyrosine permease family   chr5:6578954-6581947 FORWARD   Aliases: T20D1.20, T20D1_20	4.1	3.6	0.5	2.3	100.0%	-2.8
1855	AT1G25380.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:8903522-8905989 FORWARD   Aliases: F4F7.45	7.5	8.3	-0.8	-2.3	100.0%	-2.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1856	AT2G27580.1   zinc finger (AN1-like) family protein, contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger   chr2:11783488-11784539 REVERSE   Aliases: F10A12.25, F10A12_25	6.8	5.9	0.8	2.3	100.0%	-2.7
1857	AT5G15980.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:5213084-5215623 FORWARD   Aliases: F1N13.120, F1N13_120	5.7	6.7	-1.0	-2.3	100.0%	-2.7
1858	AT1G60690.1   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:22353557-22355333 REVERSE   Aliases: F8A5.21, F8A5_21	6.5	7.1	-0.6	-2.3	100.0%	-2.7
1859	AT2G33210.1   chaperonin, putative, similar to SWISS-PROT:Q05046- chaperonin CPN60-2, mitochondrial precursor (HSP60-2) (Cucurbita maxima); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr2:14081986-14085797 REVERSE   Aliases: F25I18.5, F25I18_5	8.7	9.7	-1.0	-2.3	100.0%	-2.6
1860	AT1G80910.1   expressed protein   chr1:30405628-30408934 FORWARD   Aliases: F23A5.27, F23A5_27	5.6	6.3	-0.7	-2.3	100.0%	-2.6
1861	AT3G18215.1   expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599   chr3:6240890-6242577 FORWARD   Aliases: None	8.6	6.9	1.7	2.3	100.0%	-2.7
1862	AT5G14150.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr5:4565174-4566907 REVERSE   Aliases: MUA22.15, MUA22_15	3.0	3.3	-0.3	-2.3	100.0%	-3.2
1863	AT1G74600.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:28028814-28031501 REVERSE   Aliases: F1M20.28, F1M20_28	4.2	4.7	-0.5	-2.3	100.0%	-3.0
1864	AT2G35736.1   expressed protein, ; expression supported by MPSS   chr2:15030163-15030333 REVERSE   Aliases: None	5.8	5.0	0.8	2.3	100.0%	-2.5
1865	AT4G37260.1   Symbol: MYB73   myb family transcription factor (MYB73), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr4:17540484-17541793 FORWARD   Aliases: AP22.97, AP22_97, MYB73	8.9	8.0	1.0	2.3	100.0%	-2.7
1866	AT2G45820.1   DNA-binding protein, putative, identical to DNA-binding protein gi:601843:gb:AAA57124 (Arabidopsis thaliana); contains Pfam domain, PF03766: Remorin, N-terminal region; contains Pfam domain, PF03763: Remorin, C-terminal region   chr2:18870032-18871735 REVERSE   Aliases: F4I18.20	9.8	9.1	0.7	2.3	100.0%	-2.8
1867	AT5G52020.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr5:21141184-21142174 REVERSE   Aliases: MSG15.10, MSG15_10	4.3	3.4	0.9	2.3	100.0%	-2.5
1868	AT1G13260.1   Symbol: RAV1   DNA-binding protein RAV1 (RAV1), identical to SP:Q9ZWM9 DNA-binding protein RAV1 {Arabidopsis thaliana}, RAV1 GI:3868857 from (Arabidopsis thaliana)   chr1:4542165-4543739 FORWARD   Aliases: RAV1, T6J4.2, T6J4_2	7.6	6.8	0.7	2.3	100.0%	-3.0
1869	AT5G50130.2   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr5:20407223-20410410 FORWARD   Aliases: MPF21.15, MPF21_15	3.5	4.2	-0.7	-2.3	100.0%	-2.7
1870	AT3G27400.1   pectate lyase family protein, similar to pectate lyase GP:7547009 from (Vitis vinifera); contains Pfam profile: PF00544 pectate lyase   chr3:10141560-10144462 FORWARD   Aliases: K1G2.22	8.8	10.3	-1.4	-2.3	100.0%	-2.4
1871	AT5G44310.2   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to 51 kDa seed maturation protein (Glycine max) GI:414977; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr5:17865100-17866739 REVERSE   Aliases: K9L2.7, K9L2_7	5.3	4.5	0.8	2.3	100.0%	-2.8
1872	AT3G02140.1   expressed protein   chr3:385324-386545 REVERSE   Aliases: F1C9.7	7.9	6.9	1.0	2.3	100.0%	-2.7
1873	AT1G30610.1   Symbol: EMB2279   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:10846658-10850499 FORWARD   Aliases: EMB2279, EMBRYO DEFECTIVE 2279, T5I8.6, T5I8_6	6.3	7.0	-0.7	-2.3	100.0%	-2.9
1874	AT4G36740.1   homeobox-leucine zipper family protein, similar to CRHB7 (GP:3868841) {Ceratopteris richardii} and to homeotic protein VAHOX1 (PIR:T07734) (Lycopersicon esculentum)   chr4:17314653-17316318 REVERSE   Aliases: AP22.8, AP22_8, HB 5	3.2	2.8	0.4	2.3	100.0%	-2.9
1875	AT5G58070.1   lipocalin, putative, similar to temperature stress-induced lipocalin (Triticum aestivum) GI:18650668   chr5:23517287-23518435 REVERSE   Aliases: K21L19.9, K21L19_9	11.7	9.8	1.9	2.3	100.0%	-2.5
1876	AT2G28560.2   Symbol: ATRAD51B/RAD51B   similar to DNA repair family protein [Arabidopsis thaliana] (TAIR:At2g45280.1); similar to putative DNA repair protein RAD51 [Oryza sativa (japonica cultivar-group)] (GB:XP_475513.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain RecA bacterial DNA recombination protein (InterPro:IPR001553)   chr2:12243692-12246201 REVERSE   Aliases: ATRAD51B, RAD51B, T17D12.12, T17D12_12	3.3	3.0	0.3	2.3	100.0%	-3.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1877	AT5G48480.1   expressed protein   chr5:19661901-19663103 FORWARD   Aliases: MJE7.12, MJE7_12	7.4	8.5	-1.2	-2.3	100.0%	-2.5
1878	AT2G38010.2   ceramidase family protein, contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase   chr2:15913940-15917009 FORWARD   Aliases: T8P21.8, T8P21_8	6.6	7.1	-0.6	-2.3	100.0%	-2.9
1879	AT3G20420.1   ribonuclease III family protein, similar to CAF protein (RNA helicase/RNaseIII) (Arabidopsis thaliana) GI:6102610; contains Pfam profiles: PF00636 RNase3 domain, PF00035 Double-stranded RNA binding motif   chr3:7119288-7120925 REVERSE   Aliases: MQC12.21	3.8	4.5	-0.6	-2.3	100.0%	-2.6
1880	AT5G06190.1   expressed protein   chr5:1876035-1876638 REVERSE   Aliases: MBL20.7, MBL20_7	6.7	5.1	1.6	2.3	100.0%	-2.6
1881	AT3G60260.3   similar to phagocytosis and cell motility protein ELMO1-related [Arabidopsis thaliana] (TAIR:At2g44770.1); similar to OSJNb0038F03.14 [Oryza sativa (japonica cultivar-group)] (GB:XP_473390.1); contains InterPro domain Protein of unknown function DUF609 (InterPro:IPR006816)   chr3:22285480-22288123 FORWARD   Aliases: F27H5.50	6.8	6.0	0.8	2.3	100.0%	-2.8
1882	AT5G58220.3   similar to putative transthyretin, having alternative splicing products [Oryza sativa (japonica cultivar-group)] (GB:AAR06357.1); contains InterPro domain Transthyretin (InterPro:IPR000895)   chr5:23571153-23573092 REVERSE   Aliases: MCK7.9, MCK7_9	8.0	7.3	0.7	2.3	100.0%	-2.6
1883	AT5G06870.1   Symbol: PGIP2   polygalacturonase inhibiting protein 2 (PGIP2), identical to polygalacturonase inhibiting protein 2 (PGIP2) (Arabidopsis thaliana) gi:7800201:gb:AAF69828; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr5:2133919-2135162 FORWARD   Aliases: MOJ9.4, MOJ9_4, POLYGALACTURONASE INHIBITING PROTEIN 2	3.5	2.9	0.5	2.3	100.0%	-2.8
1884	AT3G08700.1   ubiquitin-conjugating enzyme, putative, strong similar to ubiquitin-conjugating enzymes E2-17 from (Arabidopsis thaliana) SP:P35134, SP:P35132, SP:P35133; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr3:2643488-2644551 FORWARD   Aliases: F17O14.17	4.0	3.7	0.4	2.3	100.0%	-3.1
1885	AT2G41100.3   Symbol: TCH3   similar to calmodulin-2/3/5 (CAM2) (CAL1) [Arabidopsis thaliana] (TAIR:At2g41110.1); similar to calmodulin-2/3/5 (CAM3) [Arabidopsis thaliana] (TAIR:At3g56800.1); similar to calmodulin-2/3/5 (CAM5) (TCH1) [Arabidopsis thaliana] (TAIR:At2g27030.1); similar to calmodulin-2/3/5 (CAM5) (TCH1) [Arabidopsis thaliana] (TAIR:At2g27030.3); similar to calmodulin-7 (CAM7) [Arabidopsis thaliana] (TAIR:At3g43810.1); similar to CALM_PATSP Calmodulin (CaM) (GB:P02595); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048); contains InterPro domain Flagellar calcium-binding protein (calflagin) (InterPro:IPR003299)   chr2:17145157-17146690 FORWARD   Aliases: ATCAL5, CALMODULIN LIKE 5, T3K9.13, T3K9_13, TOUCH 3	6.0	5.0	1.0	2.3	100.0%	-2.6
1886	AT1G52160.1   metallo-beta-lactamase family protein   chr1:19424442-19428108 REVERSE   Aliases: F9I5.1, F9I5_1	6.2	6.7	-0.5	-2.3	100.0%	-3.1
1887	AT1G57590.1   similar to pectinacetyltransferase, putative [Arabidopsis thaliana] (TAIR:At5g26670.1); similar to putative pectinacetyltransferase precursor [Oryza sativa (japonica cultivar-group)] (GB:NP_918013.1); contains InterPro domain Pectinacetyltransferase (InterPro:IPR004963)   chr1:21331025-21333427 REVERSE   Aliases: T8L23.6, T8L23_6	4.2	3.6	0.6	2.3	100.0%	-2.8
1888	ATCG00750.1   Symbol: RPS11   30S chloroplast ribosomal protein S11   chrC:78960-79376 REVERSE   Aliases: RPS11	7.4	9.0	-1.6	-2.3	100.0%	-2.6
1889	AT4G24130.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr4:12527785-12528602 FORWARD   Aliases: T19F6.120, T19F6_120	3.0	4.0	-1.0	-2.3	100.0%	-2.6
1890	AT5G22330.1   TATA box-binding protein-interacting protein-related, similar to TATA box-binding protein-interacting protein SP:O35753 from ( Mus musculus)   chr5:7390799-7394197 REVERSE   Aliases: MWD9.12, MWD9_12	5.6	6.4	-0.8	-2.3	100.0%	-2.7
1891	AT1G10120.1   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g68920.1); similar to TA1 protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD34345.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr1:3304044-3306190 REVERSE   Aliases: T27I1.15, T27I1_15	6.2	7.0	-0.8	-2.3	100.0%	-2.6
1892	AT4G02400.1   U3 ribonucleoprotein (Utp) family protein, contains Pfam profile: PF04615 Utp14 protein   chr4:1054243-1058236 FORWARD   Aliases: T14P8.20, T14P8_20	5.9	7.3	-1.4	-2.3	100.0%	-2.5
1893	AT4G01575.1   serine protease inhibitor, Kazal-type family protein, contains Pfam domain PF00050: Kazal-type serine protease inhibitor domain   chr4:681868-682583 REVERSE   Aliases: T15B16.19, T15B16_19	5.7	5.0	0.7	2.3	100.0%	-2.6
1894	AT1G49500.1   expressed protein   chr1:18325476-18325952 REVERSE   Aliases: F13F21.6, F13F21_6	4.0	4.8	-0.8	-2.3	100.0%	-2.6
1895	AT4G27820.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max)   chr4:13857764-13860577 REVERSE   Aliases: T27E11.60, T27E11_60	4.1	3.6	0.5	2.3	100.0%	-2.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1896	AT5G48870.1   Symbol: SAD1   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to U6 snRNA-associated Sm-like protein LSm5 (Homo sapiens) SWISS-PROT:Q9Y4Y9	9.9	10.3	-0.5	-2.3	100.0%	-2.9
1897	AT1G65010.1   expressed protein, similar to endosome-associated protein (GI:1016368) (Homo sapiens); similar to Centromeric protein E (CENP-E protein) (Swiss-Prot:Q02224) (Homo sapiens)   chr1:24153577-24157937 FORWARD   Aliases: F13O11.30, F13O11_30	4.2	5.3	-1.1	-2.3	100.0%	-2.6
1898	AT4G39380.1   expressed protein   chr4:18309148-18312718 REVERSE   Aliases: F23K16.10, F23K16_10	3.0	3.3	-0.3	-2.3	100.0%	-3.2
1899	AT1G24360.1   3-oxoacyl-(acyl-carrier protein) reductase, chloroplast / 3-ketoacyl-acyl carrier protein reductase, identical to 3-oxoacyl-(acyl-carrier protein) reductase SP:P33207 from (Arabidopsis thaliana)   chr1:8640725-8643467 FORWARD   Aliases: F21J9.2, F21J9.34, F21J9_34	10.7	11.3	-0.7	-2.3	100.0%	-2.9
1900	AT3G01660.1   expressed protein, similar to putative protein GB:CAB45319 (Arabidopsis thaliana)   chr3:245485-246439 FORWARD   Aliases: F4P13.20, F4P13_20	4.9	4.1	0.9	2.3	100.0%	-2.5
1901	AT5G24970.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr5:8604339-8608820 REVERSE   Aliases: F6A4.180, F6A4_180	6.4	7.3	-0.9	-2.3	100.0%	-2.6
1902	AT1G27290.1   expressed protein   chr1:9481546-9482899 FORWARD   Aliases: F17L21.8, F17L21_8	7.2	6.6	0.7	2.3	100.0%	-2.8
1903	AT4G16260.1   glycosyl hydrolase family 17 protein, similar to glucan endo-1,3-beta-glucosidase, basic vacuolar isoform precursor SP:P52407 from (Hevea brasiliensis)   chr4:9200025-9201544 REVERSE   Aliases: DL4170C, FCAALL.386	3.3	4.2	-0.8	-2.3	100.0%	-2.6
1904	AT1G56580.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:21201924-21202621 REVERSE   Aliases: F25P12.97, F25P12_97	10.0	10.8	-0.8	-2.3	100.0%	-3.1
1905	AT4G21120.1   Symbol: AAT1   amino acid permease family protein, similar to cationic amino acid transporter-1 (Rattus norvegicus) GI:1589917; contains Pfam profile PF00324: Amino acid permease   chr4:11270056-11273982 FORWARD   Aliases: CAT1, CATIONIC AMINO ACID TRANSPORTER 1, F7J7.60, F7J7_60	4.8	4.3	0.4	2.3	100.0%	-2.9
1906	AT5G08260.1   Symbol: SCPL35	4.2	4.9	-0.6	-2.3	100.0%	-3.0
1907	AT5G10900.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.4	2.6	-0.3	-2.3	100.0%	-3.4
1908	AT5G41000.1   oligopeptide transporter OPT family protein, contains Pfam profile PF03169: OPT oligopeptide transporter protein	3.6	4.4	-0.8	-2.3	100.0%	-2.7
1909	AT1G51060.1   histone H2A, putative, similar to histone H2A GI:7595337 from Arabidopsis thaliana, Triticum aestivum GI:536892, Picea abies SP:P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	8.9	9.9	-1.0	-2.3	100.0%	-2.7
1910	AT5G67160.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:26814839-26816267 REVERSE   Aliases: K21H1.12, K21H1_12	8.1	6.9	1.2	2.3	100.0%	-2.5
1911	AT1G61550.1   S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida) gi:836954:gb:AAC23542; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22708531-22711491 REVERSE   Aliases: T25B24.10, T25B24_10	4.3	5.1	-0.8	-2.3	100.0%	-2.5
1912	AT1G31910.1   GHMP kinase family protein, contains TIGRFAM profile TIGR01219: phosphomevalonate kinase; contains Pfam PF00288: GHMP kinases putative ATP-binding protein domain; similar to Phosphomevalonate kinase (EC 2.7.4.2) (Swiss-Prot:P24521) (Saccharomyces cerevisiae)   chr1:11459030-11461805 FORWARD   Aliases: F5M6.9, F5M6_9	12.0	12.3	-0.3	-2.3	100.0%	-3.5
1913	AT5G58250.1   expressed protein   chr5:23576703-23577739 FORWARD   Aliases: MCK7.12, MCK7_12	6.1	7.1	-1.1	-2.3	100.0%	-2.5
1914	AT4G14010.1   Symbol: RALFL32   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr4:8092832-8093377 REVERSE   Aliases: DL3045C, FCAALL.140, RALF LIKE 32	9.0	8.3	0.8	2.3	100.0%	-3.0
1915	AT3G59820.2   similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At1g65540.1); similar to OSJNBa0067K08.12 [Oryza sativa (japonica cultivar-group)] (GB:XP_473035.1)   chr3:22109005-22112736 REVERSE   Aliases: F24G16.90	6.9	8.1	-1.2	-2.3	100.0%	-2.5
1916	AT2G32240.1   expressed protein, contains Pfam profile: PF04508 viral A-type inclusion protein repeat   chr2:13691376-13695401 REVERSE   Aliases: F22D22.1, F22D22_1	9.7	8.8	0.9	2.3	100.0%	-2.9
1917	AT5G16610.2   expressed protein   chr5:5444967-5448316 REVERSE   Aliases: MTG13.5, MTG13_5	5.2	4.9	0.4	2.3	100.0%	-3.1
1918	AT2G40030.1   Symbol: NRPD1b	3.6	4.0	-0.4	-2.3	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1919	AT5G65685.1   soluble glycogen synthase-related, contains weak similarity to Soluble glycogen synthase, chloroplast precursor (EC 2.4.1.11) (SS III) (Swiss-Prot:Q43846) (Solanum tuberosum)   chr5:26290361-26293145 REVERSE   Aliases: None	6.8	6.2	0.6	2.3	100.0%	-2.7
1920	AT2G46410.1   Symbol: CPC   myb-related protein CAPRICE (CPC), identical to myb-related protein CAPRICE (CPC) GI:2346965 from (Arabidopsis thaliana)   chr2:19056245-19057414 REVERSE   Aliases: CAPRICE, F11C10.10, MYB FAMILY TRANSCRIPTION FACTOR CPC	5.2	4.5	0.7	2.3	100.0%	-2.8
1921	AT5G22270.1   expressed protein, similar to unknown protein (gb AAF02129.1)   chr5:7372236-7373105 REVERSE   Aliases: T6G21.5	3.2	5.2	-2.0	-2.3	100.0%	-2.5
1922	AT3G10020.1   expressed protein   chr3:3091048-3091771 REVERSE   Aliases: T22K18.16	8.8	8.1	0.8	2.3	100.0%	-2.9
1923	AT1G74370.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:27961323-27963018 REVERSE   Aliases: F1M20.5, F1M20_5	6.6	6.0	0.6	2.3	100.0%	-2.7
1924	AT3G16450.3   similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:At3g16440.1); similar to myrosinase binding protein [Brassica napus] (GB:CAA70587.1); contains InterPro domain Jacalin-related lectin (InterPro:IPR001229)	4.5	5.2	-0.8	-2.3	100.0%	-2.6
1925	AT5G11090.1   serine-rich protein-related, contains some similarity to serine-rich proteins   chr5:3524681-3525847 FORWARD   Aliases: T5K6.80, T5K6_80	5.5	4.4	1.1	2.3	100.0%	-2.6
1926	AT3G03110.1   Symbol: XPO1B   exportin 1, putative, strong similarity to Exportin1 (XPO1) protein (Arabidopsis thaliana) GI:7671510; contains Pfam profile PF03810: Importin-beta N-terminal domain   chr3:708943-717100 FORWARD   Aliases: CRM1B, T17B22.20, T17B22_20	3.9	4.7	-0.8	-2.3	100.0%	-2.8
1927	AT3G62390.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr3:23097996-23100166 REVERSE   Aliases: T12C14.90	4.0	4.7	-0.7	-2.3	100.0%	-2.7
1928	AT5G62860.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr5:25249858-25251793 FORWARD   Aliases: MQB2.19, MQB2_19	3.5	3.1	0.4	2.3	100.0%	-3.0
1929	AT5G41700.4   Symbol: UBC8   ubiquitin-conjugating enzyme 8 (UBC8), E2; identical to gi:297882, SP:P35131   chr5:16693070-16694737 FORWARD   Aliases: ATUBC8, MBK23.24, MBK23_24, UBC8, UBIQUITIN CONJUGATING ENZYME, UBIQUITIN CONJUGATING ENZYME 8	12.8	12.2	0.6	2.3	100.0%	-3.2
1930	AT5G41190.1   expressed protein, ; expression supported by MPSS   chr5:16504856-16507240 REVERSE   Aliases: MEE6.26, MEE6_26	6.2	6.9	-0.7	-2.3	100.0%	-2.8
1931	AT5G23020.1   Symbol: MAM L   2-isopropylmalate synthase 2 (IMS2), identical to 2-isopropylmalate synthase (IMS2) (Arabidopsis thaliana) GI:12330689   chr5:7718206-7721842 FORWARD   Aliases: 2 ISOPROPYLMALATE SYNTHASE 2, IMS2, METHYLTHIOALKYLMALATE SYNTHASE LIKE, MYJ24.1, MYJ24_1	10.0	9.7	0.3	2.3	100.0%	-3.3
1932	AT3G26770.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to sex determination protein tasselseed 2 SP:P50160 from (Zea mays)   chr3:9846721-9848385 FORWARD   Aliases: MDJ14.1	10.1	9.3	0.8	2.3	100.0%	-2.6
1933	AT5G53870.1   plastocyanin-like domain-containing protein, contains similarity to SP:Q02917 Early nodulin 55-2 precursor {Glycine max}; PF02298: Plastocyanin-like domain   chr5:21887259-21888454 REVERSE   Aliases: K19P17.3, K19P17_3	2.3	2.1	0.2	2.3	100.0%	-3.9
1934	AT5G40390.1   raffinose synthase family protein, similar to galactinol-raffinose galactosyltransferase (Vigna angularis) GI:6634701, seed imbibition protein GB:AAA32975 GI:167100 from (Hordeum vulgare); contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1   chr5:16178743-16182585 FORWARD   Aliases: MPO12.100, MPO12_100	5.5	6.2	-0.7	-2.3	100.0%	-2.6
1935	AT5G04150.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534	3.3	3.8	-0.5	-2.3	100.0%	-2.8
1936	AT5G02870.1   60S ribosomal protein L4/L1 (RPL4D), 60S roibosomal protein L4, Arabidopsis thaliana, EMBL:CAA79104   chr5:657784-659716 FORWARD   Aliases: F9G14.180, F9G14_180	11.3	11.8	-0.5	-2.3	100.0%	-3.0
1937	AT5G19250.1   expressed protein   chr5:6471951-6472947 FORWARD   Aliases: T24G5.150, T24G5_150	4.7	5.4	-0.6	-2.3	100.0%	-2.9
1938	AT1G27370.3   similar to squamosa promoter-binding protein-like 11 (SPL11) [Arabidopsis thaliana] (TAIR:At1g27360.2); similar to squamosa promoter-binding protein-like 11 (SPL11) [Arabidopsis thaliana] (TAIR:At1g27360.1); similar to squamosa promoter binding protein 2-like [Oryza sativa (japonica cultivar-group)] (GB:BAD54038.1); contains InterPro domain SBP (InterPro:IPR004333)   chr1:9505126-9508267 REVERSE   Aliases: F17L21.15, F17L21_15	3.5	4.0	-0.6	-2.3	100.0%	-2.8
1939	AT5G05000.3   Symbol: OEP34   translocate of chloroplast 34 (TOC34) / GTP-binding protein (OEP34), contains Pfam PF04548: AIG1 family; contains TIGRFAM TIGR00991: GTP-binding protein and TIGR00231: small GTP-binding protein domain; 99.7% identical to atToc34 protein (GI:11557975) (Arabidopsis thaliana); similar to Chain A,	8.6	9.4	-0.8	-2.3	100.0%	-2.6
1940	AT1G22600.1   expressed protein   chr1:7987297-7989176 REVERSE   Aliases: F12K8.5, F12K8_5	3.7	2.7	0.9	2.3	100.0%	-2.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1941	AT4G26300.1   Symbol: EMB1027   arginyl-tRNA synthetase, putative / arginine--tRNA ligase, putative, similar to SP:P37880 Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) {Cricetulus longicaudatus}; contains Pfam profiles PF00750: arginyl-tRNA synthetase, PF03485: arginyl-tRNA synthetase N-terminal domain   chr4:13307986-13313118 REVERSE   Aliases: EMB1027, EMBRYO DEFECTIVE 1027, T25K17.110, T25K17_110	8.4	9.4	-1.0	-2.3	100.0%	-2.7
1942	AT5G07590.1   WD-40 repeat protein family, contains 3 WD-40 repeats (PF00400); similarity to WD-repeat protein 8 (WDR8)(SP:Q9P2S5) (HOMO SAPIENS)   chr5:2401621-2403855 REVERSE   Aliases: MBK20.2, MBK20_2	4.5	5.0	-0.5	-2.3	100.0%	-2.9
1943	AT5G66410.1   expressed protein   chr5:26537032-26538922 FORWARD   Aliases: K1F13.6, K1F13_6	8.7	9.4	-0.7	-2.3	100.0%	-2.7
1944	AT1G18680.1   HNH endonuclease domain-containing protein, contains Pfam domain PF01844: HNH endonuclease   chr1:6431930-6433437 REVERSE   Aliases: F6A14.21, F6A14_21	6.3	5.7	0.6	2.3	100.0%	-2.7
1945	AT3G47210.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr3:17396298-17398229 FORWARD   Aliases: F13I12.260	5.5	4.7	0.8	2.3	100.0%	-2.6
1946	AT3G02920.1   replication protein-related, similar to replication protein A 30kDa (Oryza sativa (japonica cultivar-group)) GI:13516746; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain	5.9	6.8	-1.0	-2.3	100.0%	-2.7
1947	AT3G01640.1   GHMP kinase family protein, contains GHMP kinases putative ATP-binding protein domain, Pfam:PF00288   chr3:239388-241450 FORWARD   Aliases: F4P13.18, F4P13_18	6.1	6.8	-0.7	-2.3	100.0%	-2.6
1948	AT5G47550.1   cysteine protease inhibitor, putative / cystatin, putative, similar to SP:P09229 Cysteine proteinase inhibitor-I (Oryzacystatin-I) {Oryza sativa}; contains Pfam profile PF00031: Cystatin domain   chr5:19303676-19304221 REVERSE   Aliases: MNJ7.14, MNJ7_14	6.2	7.2	-1.0	-2.3	100.0%	-2.5
1949	AT4G36810.1   Symbol: GGPS1   geranylgeranyl pyrophosphate synthase (GGPS1) / GGPP synthetase / farnesyltranstransferase, identical to GI:413730 to geranylgeranyl pyrophosphate synthase, chloroplast precursor GB:P34802 from (Arabidopsis thaliana) synonymous with farnesyltranstransferase   chr4:17343378-17344869 FORWARD   Aliases: GERANYLGERANYL PYROPHOSPHATE SYNTHASE 1	6.1	5.5	0.6	2.3	100.0%	-2.9
1950	AT3G19590.1   WD-40 repeat family protein / mitotic checkpoint protein, putative, contains 5 WD-40 repeats (PF00400) (1 weak); similar to testis mitotic checkpoint protein BUB3 (GB:AAC28439,SP:O43684)(Homo sapiens)	5.8	6.6	-0.8	-2.3	100.0%	-2.7
1951	AT5G44110.2   Symbol: POP1   similar to ABC transporter family protein [Arabidopsis thaliana] (TAIR:At1g03905.1); similar to hypothetical protein UM03153.1 [Ustilago maydis 521] (GB:EAK84383.1); contains InterPro domain ABC transporter (InterPro:IPR003439); contains InterPro domain ATP/GTP-binding site motif A (P-loop) (InterPro:IPR001687)	8.6	9.4	-0.8	-2.3	100.0%	-2.9
1952	AT3G02770.1   dimethylmenaquinone methyltransferase family protein, similar to bacterial S-adenosylmethionine:2-demethylmenaquinone methyltransferases; contains Pfam profile PF03737: Dimethylmenaquinone methyltransferase   chr3:600900-602218 REVERSE   Aliases: F13E7.29, F13E7_29	10.0	9.1	0.9	2.3	100.0%	-2.6
1953	AT2G21045.1   similar to senescence-associated family protein [Arabidopsis thaliana] (TAIR:At5g66170.1); similar to Ntdin [Nicotiana tabacum] (GB:BAA88985.2); contains InterPro domain Rhodanese-like (InterPro:IPR001763)   chr2:9034933-9036101 FORWARD   Aliases: None	4.0	5.0	-1.0	-2.3	100.0%	-2.5
1954	AT3G20440.1   Symbol: EMB2729   similar to 1,4-alpha-glucan branching enzyme / starch branching enzyme class II (SBE2-1) [Arabidopsis thaliana] (TAIR:At2g36390.1); similar to glucan (1,4-alpha-), branching enzyme 1 [Mus musculus] (GB:NP_083079.1)   chr3:7123203-7130442 REVERSE   Aliases: EMB2729, EMBRYO DEFECTIVE 2729, MQC12.20	3.1	3.8	-0.7	-2.3	100.0%	-2.7
1955	AT1G32190.1   expressed protein   chr1:11592935-11595962 REVERSE   Aliases: F3C3.3, F3C3_3	4.2	4.7	-0.5	-2.3	100.0%	-2.9
1956	AT5G52550.1   expressed protein   chr5:21344938-21347362 REVERSE   Aliases: F6N7.3, F6N7_3	6.1	5.5	0.6	2.3	100.0%	-2.8
1957	AT5G23110.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:7758310-7775512 FORWARD   Aliases: MYJ24.15, MYJ24_15	4.7	5.6	-0.9	-2.3	100.0%	-2.8
1958	AT3G49180.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); GTP-binding protein beta chain homolog, Nicotiana tabacum, PIR:T16970   chr3:18240751-18243209 FORWARD   Aliases: F2K15.40	4.4	4.9	-0.5	-2.3	100.0%	-2.9
1959	AT5G17930.1   similar to MIF4G domain-containing protein / MA3 domain-containing protein [Arabidopsis thaliana] (TAIR:At1g80930.1); similar to nucleolar protein with MIF4G domain 1 [Homo sapiens] (GB:NP_612409.1); contains InterPro domain Initiation factor eIF-4 gamma, MA3 (InterPro:IPR003891); contains InterPro domain Initiation factor eIF-4 gamma, middle (InterPro:IPR003890)   chr5:5940000-5944428 REVERSE   Aliases: MCM23.1, MCM23_1	6.1	6.9	-0.9	-2.3	100.0%	-2.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1960	AT2G02170.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr2:556492-558797 REVERSE   Aliases: F5O4.6, F5O4_6	5.1	5.8	-0.7	-2.3	100.0%	-2.7
1961	AT1G11960.1   early-responsive to dehydration protein-related / ERD protein-related, low similarity to ERD4 protein (Arabidopsis thaliana) GI:15375406	5.1	4.4	0.7	2.3	100.0%	-2.9
1962	AT3G60440.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g60450.1); similar to COG0406: Fructose-2,6-bisphosphatase [Trichodesmium erythraeum IMS101] (GB:ZP_00325866.1)   chr3:22348768-22350421 FORWARD   Aliases: T8B10.100	4.3	4.9	-0.7	-2.3	100.0%	-2.6
1963	AT1G51680.2   Symbol: 4CL1   4-coumarate--CoA ligase 1 / 4-coumaroyl-CoA synthase 1 (4CL1), identical to SP:Q42524 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4CL1) (4-coumaroyl-CoA synthase 1) {Arabidopsis thaliana}   chr1:19163097-19165220 REVERSE   Aliases: 4 COUMARATE:COA LIGASE, 4 COUMARATE:COA LIGASE 1, 4CL.1, AT4CL1, F19C24.11, F19C24_11	8.8	11.0	-2.2	-2.3	100.0%	-2.8
1964	AT5G10440.1   Symbol: CYCD4;2   cyclin family protein, similar to cyclin D2.1 protein (Nicotiana tabacum) GI:4160298; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr5:3280517-3282393 REVERSE   Aliases: CYCLIN D4;2, F12B17.210, F12B17_210	3.3	3.8	-0.5	-2.3	100.0%	-2.8
1965	AT2G23680.1   stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi:18449100:gb:AAL69988; similar to stress-regulated protein SAP1 (Xerophyta viscosa) gi:21360378:gb:AAM47505	3.6	3.2	0.3	2.3	100.0%	-3.4
1966	AT5G09830.1   BolA-like family protein, contains Pfam profile: PF01722 BolA-like protein   chr5:3057658-3058822 REVERSE   Aliases: MYH9.4, MYH9_4	9.8	9.2	0.6	2.3	100.0%	-2.8
1967	AT3G52155.1   expressed protein   chr3:19354673-19355827 FORWARD   Aliases: None	3.4	3.0	0.4	2.3	100.0%	-3.0
1968	AT1G02450.1   NPR1/NIM1-interacting protein 1 (NIMIN-1), identical to NIMIN-1 protein (Arabidopsis thaliana) gi:12057154:emb:CAC19844; identical to cDNA NIMIN-1 protein (nimin-1 gene)GI:12057153   chr1:497976-498516 REVERSE   Aliases: T6A9.23	3.8	3.2	0.5	2.3	100.0%	-3.1
1969	AT5G44130.1   fasciclin-like arabinogalactan-protein, putative, similar to gi_13377784_gb_AAK20861   chr5:17778317-17779230 FORWARD   Aliases: MLN1.5, MLN1_5	5.2	4.3	0.9	2.3	100.0%	-2.6
1970	AT5G16310.1   ubiquitin carboxyl-terminal hydrolase family 1 protein, similar to 26S proteasome regulatory complex subunit p37A (Drosophila melanogaster) GI:6434962; contains Pfam profile PF01088: Ubiquitin carboxyl-terminal hydrolase, family 1   chr5:5342062-5344286 REVERSE   Aliases: MQK4.3, MQK4_3	4.8	5.4	-0.6	-2.3	100.0%	-2.7
1971	AT5G09420.1   chloroplast outer membrane translocon subunit, putative, similar to component of chloroplast outer membrane translocon Toc64 (Pisum sativum) GI:7453538; contains Pfam profiles PF01425: Amidase, PF00515: TPR Domain   chr5:2928317-2931950 FORWARD   Aliases: T5E8.220, T5E8_220	3.3	3.8	-0.5	-2.3	100.0%	-3.0
1972	AT3G02540.2   ubiquitin family protein, contains Pfam profiles PF00240: Ubiquitin family, PF00627: UBA/TS-N domain;   chr3:533461-536302 REVERSE   Aliases: F16B3.17, F16B3_17	8.2	7.1	1.1	2.3	100.0%	-2.6
1973	AT2G32120.2   Symbol: HSP70T 2   heat shock protein 70 family protein / HSP70 family protein, similar to SP:P22953 Heat shock cognate 70 kDa protein 1 (Hsc70.1) {Arabidopsis thaliana}; contains InterPro accession IPR001023: Heat shock protein Hsp70   chr2:13658587-13660998 REVERSE   Aliases: F22D22.13, F22D22_13, HSP70T 2	5.4	5.0	0.5	2.3	100.0%	-2.8
1974	AT5G54650.2   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr5:22214855-22219249 REVERSE   Aliases: MRB17.15, MRB17_15	4.8	5.5	-0.7	-2.3	100.0%	-2.8
1975	AT5G37930.1   seven in absentia (SINA) family protein, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr5:15119430-15120899 REVERSE   Aliases: K18L3.13, K18L3_13	6.4	5.7	0.6	2.3	100.0%	-2.7
1976	AT1G14400.2   Symbol: UBC1   ubiquitin-conjugating enzyme 1 (UBC1), E2; identical to gi:431259, SP:P25865   chr1:4927021-4928528 REVERSE   Aliases: ATUBC1, F14L17.17, F14L17_17, UBIQUITIN CARRIER PROTEIN 1	10.8	10.1	0.7	2.3	100.0%	-3.1
1977	AT1G03400.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967); similar to ESTs emb:Z34690, gb:T04168, gb:H37738, gb:T76913, gb:T43801, amd gb:T21964   chr1:842746-844189 REVERSE   Aliases: F21B7.39, F21B7_39	4.6	3.7	1.0	2.3	100.0%	-2.7
1978	AT3G21400.1   expressed protein   chr3:7534639-7536515 REVERSE   Aliases: MHC9.8	5.9	6.6	-0.7	-2.3	100.0%	-2.8
1979	AT2G28350.1   Symbol: ARF10   auxin-responsive factor (ARF10), similar to auxin response factor 10 GI:6165644 from (Arabidopsis thaliana); identical to cDNA auxin response factor 10 (ARF10) mRNA, partial cds GI:6165643   chr2:12121408-12123914 FORWARD   Aliases: ARF10, AUXIN RESPONSE FACTOR 10, T1B3.13, T1B3_13	6.5	5.9	0.6	2.3	100.0%	-3.0
1980	AT5G13880.1   expressed protein   chr5:4477356-4478111 REVERSE   Aliases: MAC12.16, MAC12_16	4.1	3.7	0.4	2.3	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
1981	AT3G53260.1   Symbol: PAL2   phenylalanine ammonia-lyase 2 (PAL2), nearly identical to SP:P45724   chr3:19755029-19757758 REVERSE   Aliases: T4D2.190	7.3	8.8	-1.5	-2.3	100.0%	-2.9
1982	AT2G39400.1   hydrolase, alpha/beta fold family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:16459721-16461879 FORWARD   Aliases: F12L6.6, F12L6_6	2.6	2.8	-0.3	-2.3	100.0%	-3.5
1983	AT5G61400.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:24698776-24700740 FORWARD   Aliases: MFB13.18, MFB13_18	3.3	3.6	-0.3	-2.3	100.0%	-3.2
1984	AT2G31725.1   expressed protein   chr2:13493394-13494522 REVERSE   Aliases: T9H9.25, T9H9_25	5.0	5.5	-0.5	-2.3	100.0%	-2.9
1985	AT5G04850.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr5:1408063-1409893 REVERSE   Aliases: MUK11.17, MUK11_17	11.3	10.5	0.8	2.2	100.0%	-2.8
1986	AT1G67710.1   Symbol: ARR11   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain; contains similarity to response regulator proteins from (Arabidopsis thaliana)   chr1:25380414-25382807 REVERSE   Aliases: F12A21.15, F12A21_15, RESPONSE REGULATOR 11	4.7	4.1	0.6	2.2	100.0%	-2.9
1987	AT2G25420.1   transducin family protein / WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat (3 repeats)   chr2:10824096-10828129 FORWARD   Aliases: F13B15.8, F13B15_8	4.0	4.6	-0.5	-2.2	100.0%	-3.0
1988	AT5G61760.1   Symbol: ATIPK2BETA   inositol polyphosphate 6-/3-/5-kinase 2b (IPK2b), contains Pfam domain, PF03770: inositol polyphosphate kinase   chr5:24830955-24832657 REVERSE   Aliases: IPK2B, MAC9.7, MAC9_7	6.8	7.3	-0.5	-2.2	100.0%	-3.0
1989	AT2G36660.1   Symbol: PAB7   polyadenylate-binding protein, putative / PABP, putative. Member of the class III family of PABP proteins.   chr2:15368400-15371477 REVERSE   Aliases: F13K3.6, F13K3_6, PAB7, POLY(A) BINDING PROTEIN 7	4.2	4.8	-0.6	-2.2	100.0%	-2.7
1990	AT1G06420.1   expressed protein, ; expression supported by MPSS   chr1:1958986-1959651 FORWARD   Aliases: T2D23.12, T2D23_12	3.8	5.2	-1.4	-2.2	100.0%	-2.6
1991	AT2G01170.2   amino acid permease family protein, weak similarity to GABA permease (Emericella nidulans) GI:4972245; contains Pfam profile PF00324: Amino acid permease   chr2:102210-104514 REVERSE   Aliases: F10A8.5, F10A8_5	6.1	5.0	1.0	2.2	100.0%	-2.5
1992	AT2G23420.1   nicotinate phosphoribosyltransferase family protein / NAPRTase family protein, contains Pfam domain PF04095: Nicotinate phosphoribosyltransferase (NAPRTase)   chr2:9978845-9982272 FORWARD   Aliases: F26B6.7, F26B6_7	4.1	4.7	-0.6	-2.2	100.0%	-3.0
1993	AT4G16570.1   protein arginine N-methyltransferase-related, contains weak similarity to protein arginine N-methyltransferase 2 (EC 2.1.1.-) (Swiss-Prot:P55345) (Homo sapiens)	3.5	4.1	-0.6	-2.2	100.0%	-3.0
1994	AT1G67600.1   expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963   chr1:25340090-25341325 REVERSE   Aliases: F12A21.27, F12A21_27	4.1	3.7	0.4	2.2	100.0%	-3.2
1995	AT5G50420.1   expressed protein, strong similarity to unknown protein (gb:AAD50008.1)   chr5:20547433-20550082 REVERSE   Aliases: MXI22.14, MXI22_14	4.5	5.0	-0.6	-2.2	100.0%	-2.9
1996	AT1G22540.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:7964031-7966425 FORWARD   Aliases: F12K8.12, F12K8_12	6.0	5.4	0.6	2.2	100.0%	-2.8
1997	AT1G50380.1   prolyl oligopeptidase family protein, similar to oligopeptidase B (Leishmania major) GI:4581757; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain   chr1:18665977-18670146 FORWARD   Aliases: F14I3.4, F14I3_4	8.3	9.4	-1.1	-2.2	100.0%	-2.8
1998	AT1G79070.1   SNARE-associated protein-related, contains weak similarity to SNARE-associated protein snapin (Mus musculus) gi:4206090:gb:AAD11418   chr1:29749584-29750708 REVERSE   Aliases: YUP8H12R.31, YUP8H12R_31	3.7	3.3	0.4	2.2	100.0%	-3.1
1999	AT1G05630.2   similar to endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana] (TAIR:At1g65580.1); similar to endonuclease/exonuclease/phosphatase family protein [Arabidopsis thaliana] (TAIR:At2g43900.1); similar to PREDICTED: similar to Type II inositol-1,4,5-trisphosphate 5-phosphatase precursor (Phosphoinositide 5-phosphatase) (5PTase) (75 kDa inositol polyphosphate-5-phosphatase) [Rattus norvegicus] (GB:XP_342910.2); contains InterPro domain Endonuclease/exonuclease/phosphatase family (InterPro:IPR005135); contains InterPro domain Inositol polyphosphate related phosphatase family (InterPro:IPR000300); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr1:1682446-1687353 FORWARD   Aliases: F3F20.8, F3F20_8	3.2	3.6	-0.4	-2.2	100.0%	-3.0
2000	AT2G37330.1   Symbol: ALS3   expressed protein, and genefinder   chr2:15676217-15677744 FORWARD   Aliases: ALUMINUM SENSITIVE 3, F3G5.12, F3G5_12	7.2	6.2	1.0	2.2	100.0%	-2.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2001	AT1G77940.1   60S ribosomal protein L30 (RPL30B), similar to ribosomal protein L30 GI:388034 from (Homo sapiens)   chr1:29308791-29310259 REVERSE   Aliases: F28K19.15, F28K19_15	11.8	12.3	-0.5	-2.2	100.0%	-3.2
2002	AT2G37760.3   aldo/keto reductase family protein, similar to chalcone reductase (Sesbania rostrata)(GI:2792155), and aldose reductase ALDRXV4 (Xerophyta viscosa)(GI:4539944), (Hordeum vulgare)(GI:728592)   chr2:15838948-15840909 FORWARD   Aliases: T8P21.6	9.4	10.3	-1.0	-2.2	100.0%	-2.8
2003	AT3G44020.1   thylakoid lumenal P17.1 protein, contains Pfam PF00684 : DnaJ central domain (4 repeats); SP:Q9LXV9; PMID:11719511; supported by EST AI997589.   chr3:15812359-15813678 FORWARD   Aliases: T15B3.160	3.6	3.2	0.4	2.2	100.0%	-3.0
2004	AT4G24990.1   Symbol: ATGP4   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:12849719-12851643 REVERSE   Aliases: F13M23.130, F13M23_130	9.5	8.7	0.8	2.2	100.0%	-2.9
2005	AT1G21065.1   expressed protein   chr1:7374199-7375778 FORWARD   Aliases: None	9.2	8.5	0.8	2.2	100.0%	-3.1
2006	AT1G15210.1   ABC transporter family protein, Similar to gb:Z70524 GI:1514643 PDR5-like ABC transporter from Spirodela polyrrhiza and is a member of the PF:00005 ABC transporter family. ESTs gb:N97039 and gb:T43169 come from this gene   chr1:5231343-5236568 REVERSE   Aliases: F9L1.15, F9L1_15	6.1	7.0	-0.9	-2.2	100.0%	-2.7
2007	AT5G37055.1   zinc finger (HIT type) family protein, contains Pfam profile: PF04438 HIT zinc finger   chr5:14658781-14659670 REVERSE   Aliases: None	5.4	4.9	0.5	2.2	100.0%	-3.0
2008	AT3G57530.1   Symbol: CPK32   calcium-dependent protein kinase, putative / CDPK, putative, similar to calmodulin-domain protein kinase CDPK isoform 7 (Arabidopsis thaliana) gi:1399277:gb:AAB03247   chr3:21307531-21310568 REVERSE   Aliases: T8H10.130	6.7	5.7	1.0	2.2	100.0%	-2.6
2009	AT5G56740.1   histone acetyltransferase family protein, similar to histone acetyltransferase HAT B (Zea mays) GI:5579441; identical to cDNA histone acetyltransferase partial cds GI:21637256	3.7	4.8	-1.1	-2.2	100.0%	-2.8
2010	AT3G03020.1   expressed protein   chr3:680951-682006 FORWARD   Aliases: F13E7.3, F13E7_3	4.2	3.6	0.6	2.2	100.0%	-2.9
2011	AT5G62290.1   nucleotide-sensitive chloride conductance regulator (ICln) family protein, contains PF03517: Nucleotide-sensitive chloride conductance regulator (ICln)   chr5:25036713-25038357 FORWARD   Aliases: MMI9.12, MMI9_12	5.6	6.1	-0.5	-2.2	100.0%	-2.9
2012	AT1G75370.1   SEC14 cytosolic factor, putative / phosphatidylinositol transfer-like protein, putative, similar to phosphatidylinositol transfer-like protein III (GI:14486705) (Lotus japonicus); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminu   chr1:28280105-28283559 REVERSE   Aliases: F1B16.10, F1B16_10	5.3	5.8	-0.5	-2.2	100.0%	-2.9
2013	AT4G26900.1   Symbol: AT HF   imidazole glycerol phosphate synthase hisHF, chloroplast / IGP synthase / ImGPP synthase / IGPS, identical to SP:Q9SZ30 Imidazole glycerol phosphate synthase hisHF, chloroplast precursor (IGP synthase) {Arabidopsis thaliana}   chr4:13515488-13520317 FORWARD   Aliases: HISHF	8.5	9.4	-0.9	-2.2	100.0%	-2.6
2014	AT3G52400.1   Symbol: SYP122	5.7	4.7	1.0	2.2	100.0%	-2.6
2015	AT5G04410.1   Symbol: NAC2   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) protein; supporting cDNA gi:6456750:gb:AF201456.1:AF201456   chr5:1243759-1247015 FORWARD   Aliases: ANAC078, T19N18.11	8.6	8.0	0.6	2.2	100.0%	-3.0
2016	AT1G65000.1   expressed protein   chr1:24150707-24152352 FORWARD   Aliases: F13O11.34, F13O11_34	6.4	5.8	0.6	2.2	100.0%	-2.8
2017	AT1G51200.1   zinc finger (AN1-like) family protein, contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger   chr1:18988102-18990236 FORWARD   Aliases: F11M15.7, F11M15_7	11.0	9.9	1.0	2.2	100.0%	-2.9
2018	AT3G62360.1   expressed protein   chr3:23083761-23091518 REVERSE   Aliases: T12C14.60	7.5	8.5	-1.0	-2.2	100.0%	-2.8
2019	AT2G45320.1   expressed protein   chr2:18691190-18693219 REVERSE   Aliases: F4L23.17	7.0	6.5	0.5	2.2	100.0%	-3.0
2020	AT5G05940.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr5:1785928-1788437 FORWARD   Aliases: K18J17.10, K18J17_10, KINASE PARTNER PROTEIN LIKE, KPP LIKE	2.8	3.4	-0.5	-2.2	100.0%	-3.0
2021	AT3G53420.2   Symbol: PIP2A   similar to plasma membrane intrinsic protein 2B (PIP2B) / aquaporin PIP2.2 (PIP2.2) [Arabidopsis thaliana] (TAIR:At2g37170.1); similar to Plasma membrane aquaporin (PAQ2) [Raphanus sativus] (GB:BAA32778.1); contains InterPro domain MIP family (InterPro:IPR000425)	4.7	3.9	0.8	2.2	100.0%	-2.7
2022	AT5G63060.1   similar to SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] (TAIR:At4g08690.1); similar to sec14 like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_463685.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251)   chr5:25311788-25314075 REVERSE   Aliases: MDC12.2, MDC12_2	4.3	3.8	0.5	2.2	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2023	AT1G60160.1   potassium transporter family protein, similar to potassium transporter HAK2p (Mesembryanthemum crystallinum) gi:14091471:gb:AAK53759; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter   chr1:22191995-22195060 REVERSE   Aliases: T13D8.5, T13D8_5	4.0	3.6	0.4	2.2	100.0%	-3.1
2024	AT4G36000.1   pathogenesis-related thaumatin family protein, similar to thaumatin-like protein precursor (Pyrus pyrifolia) GI:3241854; contains Pfam profile PF00314: Thaumatin family	3.5	3.2	0.3	2.2	100.0%	-3.4
2025	AT2G36310.1   inosine-uridine preferring nucleoside hydrolase family protein, similar to Chain A, Crystal Structure Of Nucleoside Hydrolase From Leishmania MajorGI:8569431; contains Pfam profile PF01156: Inosine-uridine preferring nucleoside hydrolase   chr2:15231576-15233951 REVERSE   Aliases: F2H17.8, F2H17_8	7.0	7.7	-0.7	-2.2	100.0%	-2.9
2026	AT2G03310.1   expressed protein   chr2:1006253-1007180 REVERSE   Aliases: T4M8.26, T4M8_26	5.1	4.6	0.6	2.2	100.0%	-2.9
2027	AT3G03960.1   chaperonin, putative, similar to SWISS-PROT:P42932- T-complex protein 1, theta subunit (TCP-1-theta) (Mus musculus); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family	6.1	7.2	-1.1	-2.2	100.0%	-2.7
2028	AT5G41350.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:16558751-16561141 REVERSE   Aliases: MYC6.6, MYC6_6	6.3	5.8	0.5	2.2	100.0%	-3.0
2029	AT1G17710.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g73010.1); similar to putative phosphatase [Lycopersicon esculentum] (GB:CAD30863.1); contains InterPro domain HAD-superfamily subfamily IB hydrolase, hypothetical 1 (InterPro:IPR006384); contains InterPro domain HAD-superfamily hydrolase, subfamily IB (PSPase-like) (InterPro:IPR006383)   chr1:6090553-6092011 REVERSE   Aliases: F11A6.5, F11A6_5	4.0	3.4	0.6	2.2	100.0%	-2.9
2030	AT3G59010.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:21813782-21816191 REVERSE   Aliases: F17J16.60	4.6	3.9	0.7	2.2	100.0%	-2.9
2031	AT1G58270.1   Symbol: ZW9   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr1:21615781-21617782 REVERSE   Aliases: F19C14.11, F19C14_11	7.9	9.0	-1.1	-2.2	100.0%	-2.9
2032	AT5G06320.1   Symbol: NHL3   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protein 3, similar to harpin-induced protein hin1 (GI:1619321)(Nicotiana tabacum)   chr5:1930625-1931769 REVERSE   Aliases: MHF15.16, MHF15_16	6.8	5.9	0.9	2.2	100.0%	-2.9
2033	AT1G69523.1   UbiE/COQ5 methyltransferase family protein, low similarity to SP:Q05197 Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) (Rhodospseudomonas sphaeroides) {Rhodobacter sphaeroides}; contains Pfam profile PF01209: methyltransferase, UbiE/COQ5 family   chr1:26133214-26134912 FORWARD   Aliases: None	3.6	3.0	0.5	2.2	100.0%	-3.1
2034	AT5G57130.1   similar to heat shock protein-related [Arabidopsis thaliana] (TAIR:At4g29920.1); similar to heat shock protein-related-like [Oryza sativa (japonica cultivar-group)] (GB:XP_465522.1)   chr5:23162206-23166794 FORWARD   Aliases: MUL3.8, MUL3_8	4.8	5.1	-0.3	-2.2	100.0%	-3.5
2035	AT3G51010.1   expressed protein   chr3:18957681-18959137 REVERSE   Aliases: F24M12.50	6.5	7.7	-1.2	-2.2	100.0%	-2.7
2036	AT1G23040.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich domains, INTERPRO:IPR000694   chr1:8164948-8165851 FORWARD   Aliases: F19G10.19	6.6	5.9	0.7	2.2	100.0%	-2.7
2037	AT5G23580.1   Symbol: CDPK9   calcium-dependent protein kinase 9 (CDPK9), identical to calcium-dependent protein kinase (Arabidopsis thaliana) gi:836938:gb:AAA67653; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr5:7949989-7952535 REVERSE   Aliases: ATCDPK9, CALCIUM DEPENDENT PROTEIN KINASE, CALCIUM DEPENDENT PROTEIN KINASE 9, CPK12, MQM1.15, MQM1_15	6.4	7.3	-1.0	-2.2	100.0%	-2.8
2038	AT1G32360.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:11672911-11675319 FORWARD   Aliases: F27G20.10	7.4	6.8	0.5	2.2	100.0%	-2.9
2039	AT3G02690.1   integral membrane family protein, similar to PecM protein (GI:5852331) {Vogesella indigofera} and PecM protein (SP:P42194) (Erwinia chrysanthemi)   chr3:579593-582136 FORWARD   Aliases: F16B3.32, F16B3_32	7.4	6.5	0.9	2.2	100.0%	-2.6
2040	AT5G35735.1   auxin-responsive family protein, similar to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana)   chr5:13917982-13920227 REVERSE   Aliases: None	7.0	5.8	1.1	2.2	100.0%	-2.8
2041	AT2G41370.1   Symbol: BOP2   ankyrin repeat family protein / BTB/POZ domain-containing protein, contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain   chr2:17244823-17247518 REVERSE   Aliases: BLADE ON PETIOLE2, F13H10.8, F13H10_8	4.4	4.9	-0.5	-2.2	100.0%	-2.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2042	AT2G42880.1   Symbol: ATMPK20   mitogen-activated protein kinase, putative / MAPK, putative (MPK20), mitogen-activated protein kinase (MAPK)(AtMPK20), PMID:12119167   chr2:17847465-17851439 REVERSE   Aliases: F7D19.12, F7D19_12	7.5	8.5	-0.9	-2.2	100.0%	-2.8
2043	AT2G36620.1   60S ribosomal protein L24 (RPL24A)   chr2:15357486-15358944 REVERSE   Aliases: F13K3.2, F13K3_2	10.4	10.9	-0.6	-2.2	100.0%	-2.9
2044	AT5G17490.1   Symbol: RGL3   gibberellin response modulator, putative / gibberellin-responsive modulator, putative, putative member of the VHIID domain transcription factor family RGAL - Arabidopsis thaliana, EMBL:AJ224957   chr5:5764065-5766079 REVERSE   Aliases: K3M16.60, K3M16_60, RGA LIKE PROTEIN	3.0	3.7	-0.6	-2.2	100.0%	-2.9
2045	AT1G20490.1   AMP-dependent synthetase and ligase family protein, similar to SP:Q42524 and SP:Q9S725; contains Pfam AMP-binding enzyme domain PF00501   chr1:7097283-7099685 REVERSE   Aliases: F5M15.28, F5M15_28	4.3	5.0	-0.7	-2.2	100.0%	-3.0
2046	AT4G17550.1   transporter-related, similar to cAMP inducible 2 protein (Mus musculus) GI:4580997, glycerol 3-phosphate permease (Homo sapiens) GI:7543982; contains Pfam profile PF00083: major facilitator superfamily protein   chr4:9777661-9779751 REVERSE   Aliases: DL4810C, FCAALL.41	5.0	4.2	0.8	2.2	100.0%	-2.9
2047	AT1G25560.1   AP2 domain-containing transcription factor, putative, similar to DNA-binding protein RAV2 GI:3868859 from (Arabidopsis thaliana)	5.2	4.7	0.5	2.2	100.0%	-2.9
2048	AT2G02760.1   Symbol: ATUBC2	11.6	11.1	0.6	2.2	100.0%	-3.3
2049	AT4G08770.1   peroxidase, putative, identical to class III peroxidase ATP38 (Arabidopsis thaliana) gi:17530568:gb:AAL40851; similar to peroxidase C2 precursor (Armoracia rusticana) SWISS-PROT: P17179; identical to cDNA class III peroxidase ATP38 GI:17530567   chr4:5598112-5600309 REVERSE   Aliases: T32A17.80, T32A17_80	5.2	6.6	-1.4	-2.2	100.0%	-2.7
2050	AT4G38780.1   splicing factor, putative, strong similarity to splicing factor Prp8 (Homo sapiens) GI:3661610; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr4:18101371-18111023 REVERSE   Aliases: T9A14.60, T9A14_60	3.0	2.6	0.4	2.2	100.0%	-3.2
2051	AT3G53980.2   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:19998559-19999237 REVERSE   Aliases: F5K20.280	5.8	6.9	-1.1	-2.2	100.0%	-2.7
2052	AT1G31930.2   extra-large guanine nucleotide binding protein, putative / G-protein, putative, similar to extra-large G-protein (XLG) (Arabidopsis thaliana) GI:3201680; contains Pfam profile PF00503: G-protein alpha subunit	3.9	4.6	-0.7	-2.2	100.0%	-3.0
2053	AT1G69020.1   prolyl oligopeptidase family protein, similar to SP:Q59536 Protease II (EC 3.4.21.83) (Oligopeptidase B) {Moraxella lacunata}; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain; contains non-consensus GA donor splice site at intron 5   chr1:25947549-25950860 REVERSE   Aliases: T6L1.20, T6L1_20	4.6	4.1	0.5	2.2	100.0%	-2.9
2054	AT3G09620.1   DEAD/DEAH box helicase, putative, similar to RNA helicase GB:A57514 GI:897915 from (Rattus norvegicus); contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr3:2949157-2952210 REVERSE   Aliases: F11F8.21	3.9	3.4	0.6	2.2	100.0%	-2.8
2055	AT1G54960.1   Symbol: ANP2   similar to NPK1-related protein kinase, putative (ANP1) [Arabidopsis thaliana] (TAIR:At1g09000.1); similar to protein kinase [Nicotiana tabacum] (GB:BAA05648.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)	4.4	5.0	-0.6	-2.2	100.0%	-2.8
2056	AT5G45430.1   protein kinase, putative, contains similarity to male germ cell-associated kinase (Homo sapiens) gi:23268497:gb:AAN16405	6.1	5.1	1.0	2.2	100.0%	-2.7
2057	AT2G01210.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:119440-121843 REVERSE   Aliases: F10A8.9, F10A8_9	3.5	4.2	-0.6	-2.2	100.0%	-2.8
2058	AT4G39260.4   Symbol: ATGRP8	11.7	9.9	1.8	2.2	100.0%	-2.6
2059	AT1G53050.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:19775713-19779415 FORWARD   Aliases: F8L10.9, F8L10_9	5.8	6.8	-0.9	-2.2	100.0%	-2.8
2060	AT5G07030.1   similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:At3g54400.1); similar to putative nucleoid DNA-binding-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_463752.1); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461)   chr5:2183361-2185973 REVERSE   Aliases: MOJ9.20, MOJ9_20	3.1	4.9	-1.7	-2.2	100.0%	-2.6
2061	AT3G26000.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr3:9508015-9510495 REVERSE   Aliases: MPE11.17	6.7	6.2	0.5	2.2	100.0%	-3.2
2062	AT3G16720.1   Symbol: ATL2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:5692744-5694133 FORWARD   Aliases: MGL6.26	5.3	4.7	0.6	2.2	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2063	AT4G40045.1   expressed protein   chr4:18559778-18560651 REVERSE   Aliases: None	7.1	6.4	0.7	2.2	100.0%	-2.8
2064	AT1G49560.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr1:18346252-18348005 FORWARD   Aliases: F14J22.20, F14J22_20	3.5	4.0	-0.5	-2.2	100.0%	-2.9
2065	AT3G54930.1   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative, similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)   chr3:20362062-20363637 REVERSE   Aliases: T15C9.2	3.6	4.0	-0.4	-2.2	100.0%	-3.2
2066	AT3G56120.1   Met-10+ like family protein, non-consensus TT donor splice site at exon 4 ; contains Pfam profile PF02475: Met-10+ like-protein   chr3:20834129-20837522 FORWARD   Aliases: F18O21.80	6.2	7.3	-1.1	-2.2	100.0%	-2.7
2067	AT2G10950.1   BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	7.4	6.8	0.6	2.2	100.0%	-3.1
2068	AT1G30090.1   kelch repeat-containing F-box family protein, similar to SP:O95198 Kelch-like protein 2 (Actin-binding protein Mayven) {Homo sapiens}; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:10559545-10561407 REVERSE   Aliases: T2H7.11, T2H7_11	7.7	6.7	1.0	2.2	100.0%	-2.8
2069	AT1G02910.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr1:655577-658148 REVERSE   Aliases: F22D16.9, F22D16_9	5.6	5.0	0.6	2.2	100.0%	-2.9
2070	AT3G63420.2   Symbol: AGG1   heterotrimeric G protein gamma-subunit (AGG1)   chr3:23428292-23429673 FORWARD   Aliases: HETEROTRIMERIC G PROTEIN GAMMA SUBUNIT, MAA21.50	8.6	7.9	0.7	2.2	100.0%	-2.9
2071	AT5G04470.1   expressed protein   chr5:1266692-1267417 REVERSE   Aliases: T19N18.8	7.1	6.4	0.7	2.2	100.0%	-2.9
2072	AT1G59740.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:21971736-21976076 FORWARD   Aliases: F23H11.6, F23H11_6	7.4	6.6	0.8	2.2	100.0%	-3.0
2073	AT5G05860.1   Symbol: UGT76C2   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:1765508-1767456 FORWARD   Aliases: MJJ3.28, MJJ3_28	5.0	5.8	-0.9	-2.2	100.0%	-2.8
2074	AT4G23490.1   fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr4:12251442-12254252 REVERSE   Aliases: F16G20.2	3.5	4.0	-0.5	-2.2	100.0%	-3.0
2075	AT5G62850.1   nodulin MtN3 family protein, contains Pfam PF03083 MtN3/saliva family; similar to LIM7 (cDNAs induced in meiotic prophase in lily microsporocytes) GI:431154 from (Lilium longiflorum)   chr5:25247904-25248503 REVERSE   Aliases: MQB2.17, MQB2_17	4.2	3.7	0.5	2.2	100.0%	-3.2
2076	AT4G33070.1   pyruvate decarboxylase, putative, strong similarity to SP:P51846 Pyruvate decarboxylase isozyme 2 (EC 4.1.1.1) (PDC) {Nicotiana tabacum}; contains InterPro entry IPR000399: Pyruvate decarboxylase   chr4:15952292-15954774 REVERSE   Aliases: F4I10.4	12.2	10.7	1.5	2.2	100.0%	-2.8
2077	AT5G10920.1   argininosuccinate lyase, putative / arginosuccinase, putative, similar to argininosuccinate lyase (Nostoc punctiforme) GI:7672743; contains Pfam profile PF00206: Lyase   chr5:3441753-3444143 FORWARD   Aliases: T30N20.190, T30N20_190	7.2	8.6	-1.3	-2.2	100.0%	-2.6
2078	AT1G63480.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr1:23543222-23545802 REVERSE   Aliases: F2K11.15, F2K11_15	4.3	4.7	-0.4	-2.2	100.0%	-3.2
2079	AT1G06720.1   expressed protein, contains Pfam domain, PF04950: Protein of unknown function (DUF663)   chr1:2060443-2067322 REVERSE   Aliases: F4H5.19, F4H5_19	6.2	7.7	-1.5	-2.2	100.0%	-2.8
2080	AT1G33990.1   hydrolase, alpha/beta fold family protein, similar to polyneuridine aldehyde esterase GI:6651393 from (Rauvolfia serpentina), SP:Q40708 PIR7A protein {Oryza sativa}, ethylene-induced esterase (Citrus sinensis) GI:14279437; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:12355548-12358237 FORWARD   Aliases: F12G12.19, F12G12_19	7.6	8.3	-0.7	-2.2	100.0%	-2.8
2081	AT1G79900.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:30056972-30058624 REVERSE   Aliases: F19K16.14, F19K16_14	4.6	3.9	0.7	2.2	100.0%	-2.8
2082	AT1G15920.2   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, (CAF1) (Mus musculus)   chr1:5469397-5471143 FORWARD   Aliases: T24D18.2, T24D18_2	9.2	8.6	0.6	2.2	100.0%	-2.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2083	AT4G30450.1   glycine-rich protein   chr4:14886033-14886681 REVERSE   Aliases: F17I23.210, F17I23_210	8.7	8.1	0.5	2.2	100.0%	-3.0
2084	AT4G00570.1   malate oxidoreductase, putative, similar to NAD-dependent malic enzyme 59 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) (SP:P37225) {Solanum tuberosum}   chr4:242516-246736 REVERSE   Aliases: F6N23.16, F6N23_16	8.2	9.1	-1.0	-2.2	100.0%	-2.8
2085	AT2G41200.1   expressed protein   chr2:17178704-17180208 FORWARD   Aliases: T3K9.3, T3K9_3	4.0	3.5	0.5	2.2	100.0%	-2.9
2086	AT5G60640.2   Symbol: ATPDIL1 4   thioredoxin family protein, similar to protein disulfide isomerase Gl:5902592 from (Volvox carteri f. nagariensis), Gl:2708314 from Chlamydomonas reinhardtii; contains Pfam profile: PF00085 Thioredoxin   chr5:24388186-24391264 REVERSE   Aliases: ATPDIL1 4, MUP24.6, MUP24_6, PDI LIKE 1 4	11.4	11.8	-0.4	-2.2	100.0%	-3.6
2087	AT3G12520.1   Symbol: SULTR4;2   sulfate transporter family protein, similar to sulfate transporter (Arabidopsis thaliana) Gl:3777483; contains Pfam profiles PF00916: Sulfate transporter family, PF01740: STAS domain   chr3:3967823-3971925 REVERSE   Aliases: SULFATE TRANSPORTER, T2E22.36	5.7	6.4	-0.7	-2.2	100.0%	-3.1
2088	AT5G59020.1   expressed protein   chr5:23844262-23846829 REVERSE   Aliases: K19M22.16, K19M22_16	3.9	4.5	-0.7	-2.2	100.0%	-2.8
2089	AT3G62870.1   60S ribosomal protein L7A (RPL7aB), 60S RIBOSOMAL PROTEIN L7A - Oryza sativa, SWISSPROT:RL7A_ORYSA   chr3:23253640-23255328 REVERSE   Aliases: F26K9.300	11.7	12.1	-0.4	-2.2	100.0%	-3.1
2090	AT4G05040.3   similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At4g14400.1); similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At4g14390.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475255.1); contains InterPro domain Ankyrin (InterPro:IPR002110)	4.0	3.5	0.5	2.2	100.0%	-3.1
2091	AT3G55920.1   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to cyclophilin (Arabidopsis thaliana) gi:2443755:gb:AAB71401	6.9	7.5	-0.6	-2.2	100.0%	-3.0
2092	AT1G75680.1   glycosyl hydrolase family 9 protein, similar to endo-beta-1,4-glucanase GB:AAC12685 Gl:3025470 from (Pinus radiata)   chr1:28420713-28423190 REVERSE   Aliases: F10A5.13, F10A5_13	8.8	9.3	-0.5	-2.2	100.0%	-3.2
2093	AT3G46110.2   expressed protein   chr3:16943097-16944627 FORWARD   Aliases: F12M12.80	4.4	5.1	-0.7	-2.2	100.0%	-2.7
2094	AT1G15480.1   DNA-binding protein, putative, similar to DNA-binding protein (Triticum aestivum) Gl:6958202; contains Pfam profile PF01535: PPR repeat   chr1:5318208-5320589 FORWARD   Aliases: F9L1.43, F9L1_43	4.4	5.1	-0.7	-2.2	100.0%	-2.8
2095	AT1G78180.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:29421821-29423868 FORWARD   Aliases: T11I11.12, T11I11_12	3.9	4.4	-0.5	-2.2	100.0%	-3.0
2096	AT5G44080.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr5:17755879-17757098 REVERSE   Aliases: MRH10.19, MRH10_19	6.4	5.5	0.9	2.2	100.0%	-3.0
2097	AT1G01710.1   acyl-CoA thioesterase family protein, contains Pfam profiles: PF02551 acyl-CoA thioesterase, PF00027 cyclic nucleotide-binding domain   chr1:262828-267771 FORWARD   Aliases: T1N6.10, T1N6.9, T1N6_10, T1N6_9	5.7	6.3	-0.5	-2.2	100.0%	-3.1
2098	AT5G13680.1   IKI3 family protein, weak similarity to SP:O95163 IkappaB kinase complex-associated protein (IKK complex-associated protein) (p150) {Homo sapiens}; contains Pfam profile PF04762: IKI3 family   chr5:4410364-4415474 REVERSE   Aliases: MSH12.15, MSH12_15	5.9	6.4	-0.6	-2.2	100.0%	-2.9
2099	AT2G21120.1   expressed protein   chr2:9058829-9061694 REVERSE   Aliases: F26H11.12, F26H11_12	6.0	5.1	0.9	2.2	100.0%	-2.7
2100	AT4G30150.1   expressed protein   chr4:14742458-14749993 FORWARD   Aliases: F6G3.180, F6G3_180	5.4	5.9	-0.5	-2.2	100.0%	-3.0
2101	AT3G48510.1   expressed protein   chr3:17978341-17979523 REVERSE   Aliases: T8P19.20	7.3	6.2	1.1	2.2	100.0%	-2.6
2102	AT3G63480.2   kinesin heavy chain, putative, kinesin heavy chain, Syncephalastrum racemosum, SWISSPROT:KINH_SYNRA   chr3:23450847-23454981 REVERSE   Aliases: MAA21.110	3.5	4.1	-0.5	-2.2	100.0%	-2.9
2103	AT3G54670.2   Symbol: TTN8   similar to structural maintenance of chromosomes (SMC) family protein [Arabidopsis thaliana] (TAIR:At5g48600.1); similar to hypothetical protein UM03243.1 [Ustilago maydis 521] (GB:EAK84348.1); similar to unnamed protein product [Debaryomyces hansenii CBS767] (GB:CAG89604.1); contains InterPro domain Structural maintenance of chromosome protein SMC, C-terminal (InterPro:IPR003405)   chr3:20246656-20254938 FORWARD   Aliases: ATSMC1, SMC1, STRUCTURAL MAINTENANCE OF CHROMOSOMES 1, T5N23.30, TITAN8	4.7	5.4	-0.7	-2.2	100.0%	-3.1
2104	AT5G08110.1   DEAD/DEAH box helicase, putative, several putative ATP-dependent helicases   chr5:2594971-2600115 REVERSE   Aliases: T22D6.50, T22D6_50	4.2	4.7	-0.4	-2.2	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2105	AT3G26720.1   glycosyl hydrolase family 38 protein, similar to lysosomal alpha-mannosidase GI:3522867 from (Homo sapiens)   chr3:9817891-9824423 FORWARD   Aliases: MLJ15.19	7.3	8.3	-0.9	-2.2	100.0%	-2.8
2106	AT2G30160.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr2:12884915-12886726 FORWARD   Aliases: T27E13.10, T27E13_10	5.0	5.9	-0.9	-2.2	100.0%	-2.7
2107	AT1G61360.1   S-locus lectin protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22641393-22644681 REVERSE   Aliases: T1F9.15, T1F9_15	5.9	6.8	-1.0	-2.2	100.0%	-2.9
2108	AT3G29230.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:11190040-11191842 FORWARD   Aliases: MXO21.8	6.4	7.3	-0.9	-2.2	100.0%	-2.6
2109	AT1G12010.1   1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative, Strong similarity to amino-cyclopropane-carboxylic acid oxidase (ACC ox2) (GI:559407) from Brassica napus. ESTs gb:Z48548 and gb:Z48549 come from this gene	8.1	7.0	1.1	2.2	100.0%	-3.0
2110	AT1G68470.1   exostosin family protein, contains Pfam profile: PF03016	9.2	10.0	-0.8	-2.2	100.0%	-2.9
2111	AT5G52200.1   expressed protein   chr5:21219865-21221976 REVERSE   Aliases: F17P19.10, F17P19_10	8.4	7.9	0.6	2.2	100.0%	-3.0
2112	AT2G38700.1   Symbol: MVD1   mevalonate diphosphate decarboxylase (MVD1), identical to mevalonate diphosphate decarboxylase (Arabidopsis thaliana) gi:2288887:emb:CAA74700   chr2:16187774-16191023 REVERSE   Aliases: ATMVD1, MEVALONATE DIPHOSPHATE DECARBOXYLASE, T6A23.10, T6A23_10	6.0	7.5	-1.5	-2.2	100.0%	-2.7
2113	AT3G61060.2   Symbol: ATPP2 A13   F-box family protein / lectin-related, low similarity to PP2 lectin polypeptide (Cucurbita maxima) GI:410437; contains Pfam profile PF00646: F-box domain   chr3:22613885-22615553 FORWARD   Aliases: ATPP2 A13, T27I15.150	5.4	4.2	1.2	2.2	100.0%	-2.7
2114	AT1G53670.1   transcription factor-related, similar to pilin-like transcription factor (Homo sapiens) GI:5059062; contains Pfam profile PF01641: SelR domain   chr1:20040344-20041871 FORWARD   Aliases: F22G10.17, F22G10_17	8.1	7.4	0.7	2.2	100.0%	-2.9
2115	AT1G08710.1   F-box family protein, similar to ESTs gb:T22270 and gb:T76886 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:2771636-2773463 FORWARD   Aliases: F22O13.19, F22O13_19	5.9	4.8	1.1	2.2	100.0%	-2.7
2116	AT1G54500.1   rubredoxin family protein, similar to SP:P00270 Rubredoxin (Rd) {Desulfovibrio gigas}; contains Pfam profile PF00301: Rubredoxin	7.7	7.0	0.7	2.2	100.0%	-2.8
2117	AT5G45380.1   sodium:solute symporter family protein, contains Pfam profile: PF00474 sodium:solute symporter family   chr5:18408351-18413053 FORWARD   Aliases: MFC19.5, MFC19_5	5.2	4.3	0.9	2.2	100.0%	-2.7
2118	AT4G22770.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr4:11963639-11965695 REVERSE   Aliases: T12H17.160, T12H17_160	5.2	4.5	0.8	2.2	100.0%	-2.7
2119	AT2G44090.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g59910.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:AAX96769.1)	5.6	6.2	-0.6	-2.2	100.0%	-2.9
2120	AT1G57540.2   expressed protein, contains similarity to T-box domain GI:5931592 from (Cynops pyrrhogaster)   chr1:21313995-21315077 REVERSE   Aliases: F25P12.4	10.1	9.3	0.8	2.2	100.0%	-2.8
2121	AT5G06690.2   similar to thioredoxin family protein [Arabidopsis thaliana] (TAIR:At5g04260.1); similar to putative hioredoxin 5 [Oryza sativa (japonica cultivar-group)] (GB:XP_468041.1); contains InterPro domain Thioredoxin domain 2 (InterPro:IPR006663)   chr5:2060504-2061957 REVERSE   Aliases: MPH15.4, MPH15_4, THIOREDOXIN LIKE 5	4.6	4.2	0.3	2.2	100.0%	-3.3
2122	AT1G60490.1   Symbol: ATVPS34   phosphatidylinositol 3-kinase (PI3K), identical to SP:P42339 Phosphatidylinositol 3-kinase (EC 2.7.1.137) (PI3-kinase) (PtdIns-3-kinase) (PI3K) {Arabidopsis thaliana}   chr1:22289249-22293966 REVERSE   Aliases: F8A5.4, F8A5_4, PHOSPHATIDYLINOSITOL 3 KINASE	5.9	6.5	-0.6	-2.2	100.0%	-3.0
2123	AT5G23400.1   disease resistance family protein / LRR family protein, similar to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591; contains leucine rich-repeat domain Pfam:PF00560, INTERPRO:IPR001611   chr5:7880338-7882637 FORWARD   Aliases: K19M13.1, K19M13_1	4.2	4.9	-0.7	-2.2	100.0%	-2.8
2124	AT5G45600.1   Symbol: GAS41   YEATS family protein, contains Pfam domain PF03366: YEATS family   chr5:18505129-18507096 FORWARD   Aliases: K2N11.8, K2N11_8	7.4	8.4	-1.0	-2.2	100.0%	-2.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2125	AT3G26370.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;   chr3:9657983-9661164 FORWARD   Aliases: F20C19.9	6.1	6.9	-0.8	-2.2	100.0%	-2.7
2126	AT3G55890.1   yippee family protein, similar to mdgl-1 (Mus musculus) GI:10441648, Yippee protein (Drosophila melanogaster) GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein   chr3:20751796-20752981 FORWARD   Aliases: F27K19.70	4.3	3.7	0.6	2.2	100.0%	-2.9
2127	AT3G05050.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr3:1408619-1411807 REVERSE   Aliases: T12H1.1, T12H1_1	4.8	5.4	-0.6	-2.2	100.0%	-2.8
2128	AT1G60680.1   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:22350775-22352913 REVERSE   Aliases: F8A5.20, F8A5_20	11.2	11.7	-0.4	-2.2	100.0%	-3.5
2129	AT2G40765.1   expressed protein   chr2:17019276-17020403 FORWARD   Aliases: None	10.5	11.1	-0.5	-2.2	100.0%	-3.0
2130	AT1G78140.1   methyltransferase-related, similar to Probable delta(24)-sterol C-methyltransferase (Swiss-Prot:O14321) (Schizosaccharomyces pombe); similar to C5-O-methyltransferase (GI:5921167) (Streptomyces avermitilis); similar to S-adenosyl-methionine-sterol-C- methyltransferase (GI:3560474) (Nicotiana tabacum)   chr1:29406378-29408839 REVERSE   Aliases: T11I11.8, T11I11_8	8.8	7.6	1.3	2.2	100.0%	-3.0
2131	AT3G09660.1   minichromosome maintenance family protein / MCM family protein, similar to SP:P49717 DNA replication licensing factor MCM4 (CDC21 homolog) {Mus musculus}; contains Pfam profile PF00493: MCM2/3/5 family   chr3:2961319-2966171 REVERSE   Aliases: F11F8.25	4.2	5.1	-0.9	-2.2	100.0%	-2.8
2132	AT3G24240.1   leucine-rich repeat transmembrane protein kinase, putative, similar to CLV1 receptor kinase GB:AAB58929 from (Arabidopsis thaliana)   chr3:8780558-8784157 FORWARD   Aliases: K13K6.1	4.5	5.1	-0.6	-2.2	100.0%	-2.9
2133	AT1G68740.1   EXS family protein / ERD1/XPR1/SYG1 family protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family   chr1:25816112-25820320 REVERSE   Aliases: F24J5.2, F24J5_2	5.0	5.6	-0.6	-2.2	100.0%	-2.9
2134	AT2G21780.1   expressed protein   chr2:9298116-9298749 FORWARD   Aliases: F7D8.10, F7D8_10	3.2	2.8	0.4	2.2	100.0%	-3.3
2135	AT5G25640.1   expressed protein, ; expression supported by MPSS   chr5:8949852-8950334 REVERSE   Aliases: T14C9.180, T14C9_180	4.9	5.5	-0.6	-2.2	100.0%	-2.9
2136	AT1G15100.1   Symbol: RHA2A   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:5193421-5194198 REVERSE   Aliases: RING H2 FINGER PROTEIN RHA2A	6.8	5.8	1.0	2.2	100.0%	-2.8
2137	AT4G10030.1   hydrolase, alpha/beta fold family protein, contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:6269787-6273237 REVERSE   Aliases: T5L19.160, T5L19_160	6.9	6.1	0.8	2.2	100.0%	-2.9
2138	AT3G52610.1   expressed protein   chr3:19521459-19523636 FORWARD   Aliases: F3C22.10	5.9	6.4	-0.5	-2.2	100.0%	-3.0
2139	AT3G43920.1   Symbol: DCL3   ribonuclease III family protein, similar to RNA helicase/RNaseIII CAF protein (Arabidopsis thaliana) GI:6102610; contains Pfam profiles PF02170: PAZ domain, PF00636: RNase3 domain   chr3:15764535-15771817 FORWARD   Aliases: DICER LIKE 3, T15B3.60	5.0	5.6	-0.6	-2.2	100.0%	-2.8
2140	AT1G75150.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28770.1); similar to retinitis pigmentosa GTPase regulator-like protein [Takifugu rubripes] (GB:AAG00554.1)   chr1:28208048-28212234 REVERSE   Aliases: F22H5.12, F22H5_12	2.8	3.6	-0.8	-2.2	100.0%	-3.1
2141	AT2G33420.1   expressed protein   chr2:14165781-14169603 FORWARD   Aliases: F4P9.19, F4P9_19	3.3	2.9	0.3	2.2	100.0%	-3.4
2142	AT3G50650.1   scarecrow-like transcription factor 7 (SCL7)   chr3:18817239-18819191 REVERSE   Aliases: T3A5.30	4.6	4.2	0.4	2.2	100.0%	-3.1
2143	AT1G65960.1   Symbol: GAD2   similar to glutamate decarboxylase 1 (GAD 1) [Arabidopsis thaliana] (TAIR:At5g17330.1); similar to glutamate decarboxylase [Nicotiana tabacum] (GB:AAM48129.1); similar to DCE_PETHY Glutamate decarboxylase (GAD) (GB:Q07346); contains InterPro domain Pyridoxal-dependent decarboxylase (InterPro:IPR002129)   chr1:24558084-24561314 FORWARD   Aliases: F12P19.12, F12P19_12, GLUTAMATE DECARBOXYLASE 2	7.0	8.0	-1.0	-2.2	100.0%	-3.0
2144	AT3G20490.1   expressed protein   chr3:7153600-7156542 REVERSE   Aliases: K10D20.3	3.8	4.2	-0.4	-2.2	100.0%	-3.3
2145	AT4G22930.1   Symbol: PYR4   dihydroorotase, mitochondrial / DHOase (PYR4), identical to SP:O04904 Dihydroorotase, mitochondrial precursor (EC 3.5.2.3) (DHOase) {Arabidopsis thaliana}   chr4:12018906-12021602 FORWARD   Aliases: DIHYDROOROTASE, F7H19.110, F7H19_110	7.0	7.9	-0.9	-2.2	100.0%	-2.8
2146	AT2G27490.2   dephospho-CoA kinase family, similar to Dephospho-CoA kinase (EC 2.7.1.24) (Dephosphocoenzyme A kinase). (Swiss-Prot:Q92BF2) (Listeria innocua); contains Pfam profile PF01121: Dephospho-CoA kinase   chr2:11755165-11757259 REVERSE   Aliases: F10A12.17, F10A12_17	8.0	7.5	0.5	2.2	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2147	AT5G16300.3   similar to putative low density lipoprotein [Oryza sativa (japonica cultivar-group)] (GB:NP_916361.1)   chr5:5338122-5342781 FORWARD   Aliases: MQK4.2, MQK4_2	5.7	6.7	-1.0	-2.2	100.0%	-3.0
2148	AT4G07820.1   pathogenesis-related protein, putative, similar to SP:P33154 Pathogenesis-related protein 1 precursor (PR-1) {Arabidopsis thaliana}; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:4636861-4637348 REVERSE   Aliases: F5K24.6, F5K24_6	3.7	4.4	-0.8	-2.2	100.0%	-2.7
2149	AT1G64890.1   integral membrane transporter family protein, contains 11 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS TIGR00788: folate/biopterin transporter   chr1:24113205-24115063 FORWARD   Aliases: F13O11.19, F13O11_19	6.6	5.4	1.2	2.2	100.0%	-2.9
2150	AT3G50530.1   Symbol: CRK   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK3 (Nicotiana tabacum) gi:16904226:gb:AAL30820   chr3:18764522-18767754 FORWARD   Aliases: T20E23.130	6.1	6.7	-0.6	-2.2	100.0%	-3.1
2151	AT3G15480.1   expressed protein   chr3:5226255-5227794 REVERSE   Aliases: MJK13.14	8.4	7.4	1.0	2.2	100.0%	-2.9
2152	AT5G27430.1   signal peptidase subunit family protein, contains Pfam profile: PF04573 signal peptidase subunit   chr5:9687390-9689366 FORWARD   Aliases: F21A20.140, F21A20_140	5.1	6.1	-1.0	-2.2	100.0%	-2.9
2153	AT4G28980.2   Symbol: CAK1AT	5.1	4.8	0.3	2.2	100.0%	-3.4
2154	AT4G26060.1   expressed protein   chr4:13214755-13216470 REVERSE   Aliases: F20B18.170, F20B18_170	8.3	7.6	0.7	2.2	100.0%	-3.0
2155	AT1G55590.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:20772986-20775537 REVERSE   Aliases: F20N2.2	5.7	5.2	0.6	2.2	100.0%	-2.9
2156	AT3G17920.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr3:6137261-6142029 FORWARD   Aliases: MEB5.14	5.7	5.1	0.6	2.2	100.0%	-3.0
2157	AT4G39770.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) (Arabidopsis thaliana) GI:2944180; contains Pfam profile PF02358: Trehalose-phosphatase   chr4:18448974-18451287 REVERSE   Aliases: T19P19.160, T19P19_160	2.8	2.4	0.4	2.2	100.0%	-3.4
2158	AT4G18140.2   similar to NLI interacting factor (NIF) family protein [Arabidopsis thaliana] (TAIR:At5g46410.1)	4.4	3.9	0.6	2.2	100.0%	-2.9
2159	AT2G15890.1   expressed protein   chr2:6927451-6929084 REVERSE   Aliases: F19G14.11, F19G14_11	6.1	5.5	0.5	2.2	100.0%	-2.9
2160	AT5G16200.1   50S ribosomal protein-related, contains weak similarity to Cyanelle 50S ribosomal protein L35. (Swiss-Prot:P14810) (Cyanophora paradoxa)	5.8	5.1	0.7	2.2	100.0%	-2.8
2161	AT5G41670.2   6-phosphogluconate dehydrogenase family protein, contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate   chr5:16682558-16684399 REVERSE   Aliases: MBK23.20, MBK23_20	10.1	10.7	-0.5	-2.2	100.0%	-3.3
2162	AT5G22440.1   60S ribosomal protein L10A (RPL10aC)   chr5:7435128-7436642 REVERSE   Aliases: MWD9.24, MWD9_24	7.1	8.3	-1.2	-2.2	100.0%	-2.8
2163	AT1G14610.1   Symbol: TWN2   valyl-tRNA synthetase / valine--tRNA ligase (VALRS), nearly identical to SP:P93736 Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (ValRS) {Arabidopsis thaliana}   chr1:5008239-5014512 REVERSE   Aliases: T5E21.11, T5E21_11, TWIN 2, VALRS, VALYL TRNA SYNTHETASE	9.7	10.5	-0.8	-2.2	100.0%	-3.4
2164	AT4G38260.1   expressed protein, contains Pfam PF05742: Protein of unknown function (DUF833)   chr4:17936342-17938266 REVERSE   Aliases: F22I13.30, F22I13_30	6.3	4.9	1.4	2.2	100.0%	-2.8
2165	AT2G24190.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily   chr2:10290820-10292014 REVERSE   Aliases: F27D4.10, F27D4_10	9.2	10.0	-0.8	-2.2	100.0%	-2.8
2166	AT2G27050.1   Symbol: EIL1   ethylene-insensitive3-like1 (EIL1), identical to ethylene-insensitive3-like1 GI:2224927 from (Arabidopsis thaliana)   chr2:11552873-11555371 FORWARD   Aliases: ETHYLENE INSENSITIVE3 LIKE 1, T20P8.10, T20P8_10	6.4	5.7	0.7	2.2	100.0%	-2.9
2167	AT5G01380.1   expressed protein   chr5:155638-157521 REVERSE   Aliases: T10O8.90, T10O8_90	5.4	4.2	1.1	2.2	100.0%	-2.7
2168	AT5G44560.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr5:17963206-17965627 FORWARD   Aliases: MFC16.25, MFC16_25	7.7	8.7	-1.0	-2.2	100.0%	-2.6
2169	AT2G16430.2   purple acid phosphatase (PAP10), identical to purple acid phosphatase (PAP10) GI:20257482 from (Arabidopsis thaliana)   chr2:7127501-7129901 REVERSE   Aliases: F16F14.7, F16F14_7	5.4	6.7	-1.4	-2.2	100.0%	-2.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2170	AT3G50110.1   phosphatase-related, similar to PTEN1 GI:5566292 from ( <i>Drosophila melanogaster</i> ); contains prosite evidence: PS00383: Tyrosine specific protein phosphatases active site   chr3:18591592-18595518 REVERSE   Aliases: F3A4.190	5.2	6.0	-0.7	-2.2	100.0%	-2.9
2171	AT1G01160.1   Symbol: GIF2   SSXT protein-related / transcription co-activator-related, similar to SYT/SSX4 fusion protein (GI:11127695) ( <i>Homo sapiens</i> ); supporting cDNA gi:21539891:gb:AY102640.1; contains Pfam profile PF05030: SSXT protein (N-terminal region)   chr1:72357-74096 FORWARD   Aliases: F6F3.29, GRF1 INTERACTING FACTOR 2	4.9	3.8	1.2	2.2	100.0%	-2.9
2172	AT4G31800.2   Symbol: WRKY18	5.6	4.7	0.9	2.1	100.0%	-2.9
2173	AT4G31560.1   expressed protein   chr4:15295207-15296233 FORWARD   Aliases: F3L17.130, F3L17_130	6.0	5.2	0.8	2.1	100.0%	-2.7
2174	AT1G28280.1   VQ motif-containing protein, contains PF05678: VQ motif   chr1:9886064-9887465 REVERSE   Aliases: F3H9.7, F3H9_7	4.5	5.0	-0.6	-2.1	100.0%	-3.0
2175	AT3G03180.1   Got1-like family protein, contains Pfam profile: PF04178 Got1-like family   chr3:733394-734434 FORWARD   Aliases: T17B22.13, T17B22_13	6.0	5.6	0.4	2.1	100.0%	-3.1
2176	AT2G34200.1   zinc finger (C3HC4-type RING finger) family protein   chr2:14447727-14449084 FORWARD   Aliases: F13P17.4, F13P17_4	6.3	5.5	0.8	2.1	100.0%	-2.7
2177	AT5G57060.2   expressed protein   chr5:23107424-23109196 FORWARD   Aliases: MHM17.20, MHM17_20	6.2	5.4	0.8	2.1	100.0%	-2.9
2178	AT4G37190.2   similar to misato [ <i>Mus musculus</i> ] (GB:NP_659147.1)   chr4:17507253-17510102 FORWARD   Aliases: AP22.7, AP22_7	2.8	3.1	-0.3	-2.1	100.0%	-3.3
2179	AT3G04630.3   Symbol: WDL1   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g54460.1); similar to BRI1-KD interacting protein 116 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:BAD11344.1)   chr3:1258804-1260824 FORWARD   Aliases: F7O18.11, F7O18_11	3.7	4.9	-1.2	-2.1	100.0%	-2.9
2180	AT2G21430.1   cysteine proteinase A494, putative / thiol protease, putative, identical to SP:P43295 Probable cysteine proteinase A494 precursor ( <i>Arabidopsis thaliana</i> ); strong similarity to cysteine proteinase RD19A (thiol protease) GI:435618, SP:P43296 from ( <i>Arabidopsis thaliana</i> )   chr2:9178971-9180399 REVERSE   Aliases: F3K23.19, F3K23_19	5.4	4.4	1.0	2.1	100.0%	-2.7
2181	AT3G14595.1   expressed protein   chr3:4908957-4910483 FORWARD   Aliases: None	10.6	10.2	0.5	2.1	100.0%	-3.3
2182	AT3G16570.1   Symbol: RALFL23   rapid alkalization factor (RALF) family protein, similar to RALF precursor ( <i>Nicotiana tabacum</i> ) GI:16566316   chr3:5644704-5645420 FORWARD   Aliases: MGL6.3, RALF LIKE 23	7.0	6.2	0.8	2.1	100.0%	-2.9
2183	AT1G32520.1   expressed protein, similar to hypothetical protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_475242.1)   chr1:11758198-11759260 REVERSE   Aliases: F5D14.31, F5D14_31	4.5	3.9	0.6	2.1	100.0%	-3.3
2184	AT5G16240.1   acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative, similar to Acyl-(acyl-carrier protein) desaturase from <i>Sesamum indicum</i> GI:575942, <i>Cucumis sativus</i> SP:P32061, <i>Ricinus communis</i> SP:P22337; contains Pfam profile PF03405 Fatty acid desaturase   chr5:5306810-5309935 FORWARD   Aliases: T21H19.160, T21H19_160	5.2	4.6	0.6	2.1	100.0%	-2.8
2185	AT3G05250.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:1495603-1497475 FORWARD   Aliases: T12H1.22, T12H1_22	6.5	5.8	0.6	2.1	100.0%	-3.0
2186	AT4G33170.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:15995704-15998676 REVERSE   Aliases: F4I10.100, F4I10_100	3.0	3.3	-0.3	-2.1	100.0%	-3.5
2187	AT4G30860.1   SET domain-containing protein, low similarity to IL-5 promoter REII-region-binding protein ( <i>Homo sapiens</i> ) GI:12642795; contains Pfam profile PF00856: SET domain	3.9	4.8	-0.8	-2.1	100.0%	-2.7
2188	AT1G55620.2   Symbol: CLC F   voltage-gated chloride channel family protein, contains Pfam profiles PF00654: Voltage gated chloride channel, PF00571: CBS domain   chr1:20790872-20794855 REVERSE   Aliases: ATCLC F, CHLORIDE CHANNEL F, F20N2.5	3.6	4.4	-0.8	-2.1	100.0%	-2.9
2189	AT1G04810.1   26S proteasome regulatory subunit, putative, contains similarity to 26S proteasome regulatory subunit S1 SP:O88761, GI:3288594 from ( <i>Rattus norvegicus</i> )   chr1:1350179-1355441 FORWARD   Aliases: F13M7.20, F13M7_20	6.4	7.3	-0.9	-2.1	100.0%	-3.0
2190	AT2G35110.2   Symbol: GRL/NAP1/NAPP   similar to similar to <i>Mus musculus</i> (Mouse). Similar to NCK-associated protein 1 [ <i>Dictyostelium discoideum</i> ] (GB:AAO52562.1)   chr2:14802794-14811009 REVERSE   Aliases: GRL, NAP1, NAPP, T4C15.22, T4C15_22	4.5	5.1	-0.7	-2.1	100.0%	-3.1
2191	AT1G21310.1   Symbol: ATEXT3	3.3	5.4	-2.1	-2.1	100.0%	-2.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2192	AT3G49490.1   expressed protein   chr3:18355729-18359665 REVERSE   Aliases: T9C5.90	8.3	8.7	-0.4	-2.1	100.0%	-3.2
2193	AT5G42400.1   SET domain-containing protein (TXR7), contains Pfam profile PF00856: SET domain   chr5:16971697-16977899 REVERSE   Aliases: MDH9.9, MDH9_9	4.7	5.3	-0.6	-2.1	100.0%	-3.0
2194	AT3G20410.1   Symbol: CPK9   calmodulin-domain protein kinase isoform 9 (CPK9), identical to calmodulin-domain protein kinase CDPK isoform 9 (Arabidopsis thaliana) gi:1399265:gb:AAB03242   chr3:7116207-7119127 FORWARD   Aliases: CALMODULIN DOMAIN PROTEIN KINASE 9, MQC12.23	5.2	5.9	-0.7	-2.1	100.0%	-2.9
2195	AT3G23560.1   Symbol: ALF5   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family   chr3:8454134-8456688 REVERSE   Aliases: ABERRANT LATERAL ROOT FORMATION 5, MDB19.4	5.1	4.4	0.7	2.1	100.0%	-3.0
2196	AT5G64905.1   expressed protein   chr5:25956800-25957285 FORWARD   Aliases: None	2.7	3.3	-0.6	-2.1	100.0%	-3.0
2197	AT1G46768.1   Symbol: RAP2.1	4.1	3.5	0.5	2.1	100.0%	-2.9
2198	AT3G25490.1   wall-associated kinase, putative, similar to wall-associated kinase 4 GB:CAA08793 from (Arabidopsis thaliana)   chr3:9242962-9244722 FORWARD   Aliases: MWL2.11	2.6	2.4	0.2	2.1	100.0%	-3.9
2199	AT3G10640.2   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr3:3323315-3325051 REVERSE   Aliases: F13M14.7	8.6	7.8	0.8	2.1	100.0%	-3.0
2200	AT3G56880.1   VQ motif-containing protein, contains PF05678: VQ motif   chr3:21070894-21071944 FORWARD   Aliases: T8M16.210	9.3	8.5	0.8	2.1	100.0%	-3.1
2201	AT5G25500.1   expressed protein, ; expression supported by MPSS   chr5:8881121-8882383 FORWARD   Aliases: T14C9.40, T14C9_40	4.9	5.6	-0.7	-2.1	100.0%	-2.8
2202	AT3G21670.1   nitrate transporter (NTP3), nearly identical to nitrate transporter (Arabidopsis thaliana) GI:4490323; contains Pfam profile: PF00854 POT family	5.0	4.2	0.8	2.1	100.0%	-2.9
2203	AT2G34680.1   Symbol: AIR9   similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:At1g78230.1); similar to putative leucine rich repeat protein [Oryza sativa (japonica cultivar-group)] (GB:XP_476635.1); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr2:14623701-14636208 REVERSE   Aliases: T29F13.11, T29F13_11	7.4	8.0	-0.7	-2.1	100.0%	-2.9
2204	AT1G06760.1   histone H1, putative, similar to histone H1-1 GB:CAA44312 GI:16314 from (Arabidopsis thaliana); identical to cDNA H1-1C mRNA for histone H1-1 (partial) GI:732560   chr1:2076503-2077697 REVERSE   Aliases: F4H5.15, F4H5_15	9.6	10.3	-0.7	-2.1	100.0%	-3.5
2205	AT5G27920.1   F-box family protein, contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from (Homo sapiens)   chr5:9941909-9944782 REVERSE   Aliases: F15F15.2	6.4	5.9	0.5	2.1	100.0%	-3.1
2206	AT3G13880.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:4572187-4574433 FORWARD   Aliases: MCP4.10	2.8	3.0	-0.3	-2.1	100.0%	-3.5
2207	AT2G02500.1   Symbol: ATMEPCT/ISPD   expressed protein, contains Pfam profile: PF01128 uncharacterized protein family UPF0007; identical to GP:12697583 2-C-methyl-D-erythritol 4-phosphate cytidyltransferase {Arabidopsis thaliana}; identical to cDNA 4-Diphosphocytidyl-2C-methyl-D-erythritol synthase (ISPD) GI:7385140   chr2:670877-673154 REVERSE   Aliases: 2 C METHYL D ERYTHRITOL 4 PHOSPHATE CYTIDYLTRANSFERASE, 4 DIPHOSPHOCYTIDYL 2C METHYL D ERYTHRITOL SYNTHASE, T8K22.20, T8K22_20	5.1	5.8	-0.7	-2.1	100.0%	-2.8
2208	AT4G32950.1   protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase, Arabidopsis thaliana, PIR2:S55457	6.4	5.4	1.0	2.1	100.0%	-2.7
2209	AT2G13790.1   Symbol: ATSERK4   leucine-rich repeat family protein / protein kinase family protein   chr2:5748917-5753875 FORWARD   Aliases: AT2G13780, ATSERK4, F13J11.14, F13J11_14, SOMATIC EMBRYOGENESIS RECEPTOR LIKE KINASE 4	2.9	2.6	0.3	2.1	100.0%	-3.5
2210	AT4G32150.1   Symbol: VAMP7C	7.4	6.8	0.5	2.1	100.0%	-3.0
2211	AT3G16850.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to SP:P05117 Polygalacturonase 2A precursor (EC 3.2.1.15) (Pectinase) {Lycopersicon esculentum}; contains PF00295: Glycosyl hydrolases family 28   chr3:5748580-5751303 FORWARD   Aliases: K20I9.8	5.5	4.8	0.7	2.1	100.0%	-2.8
2212	AT2G38460.1   iron transporter-related, contains transmembrane domains; similar to iron-regulated transporter IREG1 (GI:7264727) (Mus musculus); similar to ferroportin1 (GI:7109247) (Mus musculus)   chr2:16110681-16113255 FORWARD   Aliases: T19C21.5, T19C21_5	7.4	6.7	0.6	2.1	100.0%	-2.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2213	AT4G08690.2   similar to SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] (TAIR:At1g22180.2); similar to putative sec14 like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81256.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_912885.1); contains InterPro domain Cellular retinaldehyde-binding)/triple function, C-terminal (InterPro:IPR001251); contains InterPro domain Cellular retinaldehyde-binding/triple function, N-terminal (InterPro:IPR008273)   chr4:5550937-5552953 REVERSE   Aliases: T32A17.1	5.0	5.4	-0.5	-2.1	100.0%	-3.2
2214	AT5G58260.1   Encodes subunit NDH-N of NAD(P)H:plastoquinone dehydrogenase complex (Ndh complex) present in the thylakoid membrane of chloroplasts. This subunit is thought to be required for Ndh complex assembly.   chr5:23578108-23579167 REVERSE   Aliases: MCK7.13, MCK7_13, NDH N	4.2	3.8	0.4	2.1	100.0%	-3.2
2215	AT2G41410.1   calmodulin, putative, identical to SP:P30188 Calmodulin-like protein {Arabidopsis thaliana}   chr2:17268806-17269962 REVERSE   Aliases: F13H10.4, F13H10_4	7.8	7.1	0.7	2.1	100.0%	-3.0
2216	AT3G45040.1   phosphatidate cytidyltransferase family protein, weak similarity to SP:P20048 Dolichol kinase (EC 2.7.1.108) {Saccharomyces cerevisiae}; contains Pfam profile: PF01148 phosphatidate cytidyltransferase   chr3:16483647-16486738 REVERSE   Aliases: F14D17.110	7.3	6.7	0.5	2.1	100.0%	-2.9
2217	AT2G42040.1   expressed protein   chr2:17550112-17552308 FORWARD   Aliases: T6D20.7, T6D20_7	7.1	5.7	1.3	2.1	100.0%	-2.7
2218	AT5G40040.1   60S acidic ribosomal protein P2 (RPP2E), acidic ribosomal protein P2, Parthenium argentatum, SWISSPROT:RLA2_PARAR	5.0	6.0	-1.0	-2.1	100.0%	-2.7
2219	AT1G27460.1   Symbol: NPGR1   calmodulin-binding protein, similar to calmodulin-binding protein MPCBP (Zea mays) GI:10086260; contains Pfam profile PF00515: TPR Domain   chr1:9534519-9537548 FORWARD   Aliases: F17L21.25, F17L21_25, NO POLLEN GERMINATION RELATED 1	3.9	4.8	-0.9	-2.1	100.0%	-2.7
2220	AT5G20600.1   expressed protein   chr5:6966206-6968035 REVERSE   Aliases: F7C8.190, F7C8_190	5.8	6.6	-0.8	-2.1	100.0%	-2.8
2221	AT2G01270.1   Symbol: ATQSOX2   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily. This protein also belongs to the quiescin-sulphydryl oxidase (QSOX) family, which possess an Erv1-like domain at the COOH terminus in addition to a TRX domain.   chr2:139334-142559 FORWARD   Aliases: ATQSOX2, F10A8.15, F10A8_15	8.0	6.8	1.2	2.1	100.0%	-2.7
2222	AT1G60660.1   Symbol: B5 #5   cytochrome b5 domain-containing protein, contains InterPro accession IPR001199: Cytochrome b5   chr1:22346079-22346679 REVERSE   Aliases: F8A5.18, F8A5_18	7.6	8.4	-0.8	-2.1	100.0%	-2.8
2223	AT5G61790.1   calnexin 1 (CNX1), identical to calnexin homolog 1, Arabidopsis thaliana, EMBL:AT08315 (SP:P29402)   chr5:24844328-24846981 REVERSE   Aliases: MAC9.15, MAC9_15	7.1	8.1	-1.1	-2.1	100.0%	-2.9
2224	AT5G43710.1   glycoside hydrolase family 47 protein, similar to mannosyl-oligosaccharide 1,2-alpha-mannosidase IB (Mus musculus)(SP:P39098)   chr5:17569357-17573856 REVERSE   Aliases: MQD19.4, MQD19_4	4.8	5.6	-0.8	-2.1	100.0%	-2.9
2225	AT4G16410.1   expressed protein, contains Pfam PF05421: Protein of unknown function (DUF751)   chr4:9261708-9262614 REVERSE   Aliases: DL4233C, FCAALL.144	7.0	6.0	0.9	2.1	100.0%	-2.7
2226	AT1G31660.1   bystin family, contains Pfam profile: PF05291 Bystin   chr1:11331157-11333519 REVERSE   Aliases: F27M3.14, F27M3_14	4.3	4.9	-0.6	-2.1	100.0%	-3.1
2227	AT1G55325.1   expressed protein   chr1:20641103-20650885 FORWARD   Aliases: None	2.7	3.0	-0.3	-2.1	100.0%	-3.4
2228	AT1G03190.2   Symbol: UVH6   DNA repair protein / transcription factor protein (UVH6), identical to DNA repair/transcription factor protein (UVH6) gi:22651569 gb:AY090788   chr1:775622-780062 FORWARD   Aliases: ATXPD, ULTRAVIOLET HYPERSENSITIVE 6	4.5	5.2	-0.7	-2.1	100.0%	-3.0
2229	AT1G23860.2   Symbol: SRZ 21	6.5	5.5	1.1	2.1	100.0%	-2.8
2230	AT4G13830.2   Symbol: J20   DNAJ heat shock N-terminal domain-containing protein (J20), identical to DnaJ-like protein (Arabidopsis thaliana) GI:6691127; similar to SP:Q05646 Chaperone protein dnaJ Erysipelothrix rhusiopathiae, J11 protein (Arabidopsis thaliana) GI:9843641; contains Pfam profile PF00226 DnaJ domain   chr4:8011420-8012749 FORWARD   Aliases: DNAJ LIKE 20, F18A5.220, F18A5_220	4.6	4.2	0.5	2.1	100.0%	-3.2
2231	AT1G32690.1   expressed protein, similar to hypothetical protein GB:AAC61817 GI:3668085 from (Arabidopsis thaliana)   chr1:11820888-11821690 REVERSE   Aliases: F6N18.23, F6N18_23	6.1	5.4	0.7	2.1	100.0%	-2.9
2232	AT4G08920.1   Symbol: CRY1   cryptochrome 1 apoprotein (CRY1) / flavin-type blue-light photoreceptor (HY4), contains Pfam PF03441: FAD binding domain of DNA photolyase; member of Pfam PF00875: deoxyribodipyrimidine photolyase superfamily; 99% identical to Cryptochrome 1 apoprotein (Blue light photoreceptor) (flavin-type blue-light photoreceptor) (SP:Q43125) (Arabidopsis thaliana)   chr4:5724131-5727250 FORWARD   Aliases: BLU1, BLUE LIGHT UNINHIBITED 1, CRYPTOCHROME 1, CRYPTOCHROME 1 APOPROTEIN (BLUE LIGHT PHOTORECEPTOR, ELONGATED HYPOCOTYL 4, HY4, T3H13.14, T3H13_14	5.0	4.6	0.4	2.1	100.0%	-3.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2233	AT1G10750.1   expressed protein, similar to gi 3128199 F4I1.5 putative proteinase from Arabidopsis thaliana BAC gb AC004521   chr1:3574808-3578475 REVERSE   Aliases: T16B5.11, T16B5_11	5.9	6.9	-1.1	-2.1	100.0%	-2.6
2234	AT5G48485.1   Symbol: DIR1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:19663458-19664028 REVERSE   Aliases: DEFECTIVE IN INDUCED RESISTANCE 1	3.7	3.3	0.4	2.1	100.0%	-3.5
2235	AT1G79760.1   Symbol: DTA4   expressed protein   chr1:30016947-30018045 FORWARD   Aliases: DOWNSTREAM TARGET OF AGL15 4, F19K16.26, F19K16_26	3.3	4.4	-1.1	-2.1	100.0%	-3.1
2236	AT5G01600.1   Symbol: ATFER1	10.7	11.6	-0.9	-2.1	100.0%	-2.9
2237	AT5G57500.1   expressed protein   chr5:23303463-23304797 REVERSE   Aliases: MUA2.7, MUA2_7	3.0	2.7	0.3	2.1	100.0%	-3.4
2238	AT1G55150.1   DEAD box RNA helicase, putative (RH20), similar to ethylene-responsive RNA helicase GI:5669638 from (Lycopersicon esculentum); contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr1:20578151-20580977 FORWARD   Aliases: T7N22.9, T7N22_9	5.6	6.2	-0.6	-2.1	100.0%	-3.1
2239	AT5G24270.1   Symbol: SOS3   calcineurin B-like protein, putative / calcium sensor homolog (SOS3), identical to calcium sensor homolog (Arabidopsis thaliana) GI:3309575; similar to calcineurin B-like protein 8 (GI:15866276) (Arabidopsis thaliana)   chr5:8238784-8240182 REVERSE   Aliases: CALCINEURIN B LIKE PROTEIN 4, CBL4, MOP9.19, MOP9_19, SALT OVERLY SENSITIVE 3	3.4	4.3	-1.0	-2.1	100.0%	-2.6
2240	AT1G56050.1   GTP-binding protein-related, similar to GTP-binding protein GI:10176676 from (Bacillus halodurans)   chr1:20967384-20970006 FORWARD   Aliases: T6H22.14, T6H22_14	4.3	5.2	-0.9	-2.1	100.0%	-2.7
2241	AT5G61210.1   Symbol: SNAP33	11.1	9.8	1.2	2.1	100.0%	-2.9
2242	AT2G23540.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr2:10031433-10033265 FORWARD   Aliases: F26B6.19, F26B6_19	2.9	4.0	-1.1	-2.1	100.0%	-2.6
2243	AT4G36920.1   Symbol: AP2   floral homeotic protein APETALA2 (AP2), Identical to (SP:P47927) Floral homeotic protein APETALA2. (Mouse-ear cress) {Arabidopsis thaliana}   chr4:17400844-17403329 FORWARD   Aliases: AP22.49, AP22_49, APETALA 2, APETALA2, FL1, FLO2, FLORAL HOMEOTIC PROTEIN APETALA 2, FLOWER1	5.4	4.7	0.7	2.1	100.0%	-2.8
2244	AT2G22610.1   kinesin motor protein-related   chr2:9606630-9611827 FORWARD   Aliases: T9I22.5, T9I22_5	4.2	5.0	-0.8	-2.1	100.0%	-2.9
2245	AT3G06530.1   BAP28-related, similar to Protein BAP28 (Swiss-Prot:Q9H583) (Homo sapiens)   chr3:2022602-2033643 FORWARD   Aliases: F5E6.14, F5E6_14	4.2	4.6	-0.4	-2.1	100.0%	-3.2
2246	AT3G58520.1   expressed protein   chr3:21654333-21656463 REVERSE   Aliases: F14P22.110	3.1	3.4	-0.2	-2.1	100.0%	-3.8
2247	AT3G63050.1   expressed protein   chr3:23308866-23309364 REVERSE   Aliases: T20O10.150	4.2	3.7	0.5	2.1	100.0%	-3.2
2248	AT3G24890.1   Symbol: ATVAMP728   synaptobrevin-related, similar to SYNAPTOBREVIN-RELATED PROTEIN GB:P47192 from (Arabidopsis thaliana) (Proc. Natl. Acad. Sci. U.S.A. (1992) 89(9), 3894-3898); contains Pfam profile PF00957: synaptobrevin	4.7	3.8	0.8	2.1	100.0%	-2.9
2249	AT5G43690.1   sulfotransferase family protein, similar to steroid sulfotransferase 3 (Brassica napus) GI:3420008, steroid sulfotransferase 1 (Brassica napus) GI:3420004; contains Pfam profile PF00685: Sulfotransferase domain   chr5:17563500-17564561 FORWARD   Aliases: MQD19.2, MQD19_2	4.6	5.4	-0.8	-2.1	100.0%	-2.8
2250	AT4G37310.1   Symbol: CYP81H1   cytochrome P450, putative   chr4:17555921-17558887 REVERSE   Aliases: F6G17.6	4.6	5.8	-1.2	-2.1	100.0%	-2.7
2251	AT2G30830.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967)   chr2:13139784-13141361 REVERSE   Aliases: F7F1.4, F7F1_4	3.7	3.2	0.6	2.1	100.0%	-3.5
2252	AT3G55770.5   similar to LIM domain-containing protein [Arabidopsis thaliana] (TAIR:At2g39900.1); similar to LIM domain protein [Gossypium hirsutum] (GB:AAL38006.1); contains InterPro domain Zn-binding protein, LIM (InterPro:IPR001781)   chr3:20714379-20716299 FORWARD   Aliases: F1I16.180	10.6	9.8	0.8	2.1	100.0%	-3.5
2253	AT1G16850.1   expressed protein   chr1:5764800-5765644 REVERSE   Aliases: F17F16.17, F6I1.15, F6I1_15	5.0	4.4	0.6	2.1	100.0%	-3.0
2254	AT4G38010.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:17859576-17861255 REVERSE   Aliases: F20D10.130, F20D10_130	3.8	4.1	-0.3	-2.1	100.0%	-3.3
2255	AT5G01180.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:61016-63847 REVERSE   Aliases: F7J8.160, F7J8_160	2.7	3.0	-0.3	-2.1	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2256	AT3G14180.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189   chr3:4707120-4708855 REVERSE   Aliases: MAG2.16	5.0	4.2	0.8	2.1	100.0%	-3.0
2257	AT5G58787.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g47160.1); similar to zinc finger protein family-like [Oryza sativa (japonica cultivar-group)] (GB:XP_479418.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr5:23759676-23761845 FORWARD   Aliases: None	7.1	6.5	0.6	2.1	100.0%	-3.0
2258	AT3G48550.1   expressed protein, putative zinc-finger protein - Arabidopsis thaliana,PID:g4406777   chr3:18004984-18005677 FORWARD   Aliases: T8P19.60	3.6	3.1	0.5	2.1	100.0%	-3.1
2259	AT5G05750.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9QYI4 Dnaj homolog subfamily B member 12 Mus musculus; contains Pfam profile PF00226 Dnaj domain   chr5:1727430-1728934 FORWARD   Aliases: MJJ3.16, MJJ3_16	5.4	4.3	1.1	2.1	100.0%	-2.9
2260	AT2G14890.2   Symbol: AGP9   arabinogalactan-protein (AGP9), identical to gi:10880495:gb:AAG24277   chr2:6406703-6408064 FORWARD   Aliases: ARABINO GALACTAN PROTEIN 9, T26I20.5, T26I20_5	8.9	9.7	-0.8	-2.1	100.0%	-2.9
2261	AT4G17500.1   Symbol: ATERF 1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ATERF-1). The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr4:9759337-9760353 FORWARD   Aliases: DL4785W, ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 1, FCAALL.123	6.1	5.5	0.6	2.1	100.0%	-3.0
2262	AT4G29900.1   Symbol: ACA10   calcium-transporting ATPase, plasma membrane-type, putative / Ca <sup>2+</sup> -ATPase, putative (ACA10), identical to SP:Q9SZR1 Potential calcium-transporting ATPase 10, plasma membrane-type (EC 3.6.3.8) (Ca <sup>2+</sup> )-ATPase isoform 10) {Arabidopsis thaliana}; similar to SP:Q9LF79 Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca <sup>2+</sup> )-ATPase isoform 8) {Arabidopsis thaliana}   chr4:14610889-14618781 REVERSE   Aliases: ATACA10, AUTOINHIBITED CA(2+) ATPASE, F27B13.140, F27B13_140	7.0	6.3	0.7	2.1	100.0%	-3.0
2263	AT1G07640.3   Symbol: OBP2   similar to Dof-type zinc finger domain-containing protein [Arabidopsis thaliana] (TAIR:At2g28810.1); similar to putative DNA-binding protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470142.1); contains InterPro domain Zn-finger, Dof type (InterPro:IPR003851)   chr1:2354351-2356224 REVERSE   Aliases: F24B9.30, F24B9_30, ZINC FINGER PROTEIN OBP2	6.7	6.0	0.6	2.1	100.0%	-2.8
2264	AT1G50430.1   Symbol: DWF5   7-dehydrocholesterol reductase / 7-DHC reductase / sterol delta-7-reductase (ST7R) / dwarf5 protein (DWF5), identical to SP:Q9LDU6 7-dehydrocholesterol reductase (EC 1.3.1.21) (7-DHC reductase) (Sterol delta-7-reductase) (Dwarf5 protein) {Arabidopsis thaliana}   chr1:18685614-18689307 REVERSE   Aliases: 7RED, DWARF 5, F11F12.21, F11F12_21, LE, LEPIDA, PA, PARVA, ST7R, STEROL DELTA 7 REDUCTASE, STEROL DELTA7 REDUCTASE	8.7	9.3	-0.5	-2.1	100.0%	-3.1
2265	AT5G18070.1   Symbol: DRT101	6.0	6.6	-0.6	-2.1	100.0%	-3.0
2266	AT1G15020.2   Symbol: ATQSOX1   thioredoxin family protein, low similarity to FAD-dependent sulfhydryl oxidase-2 (Rattus norvegicus) GI:12483919; contains Pfam profiles PF00085: Thioredoxin, PF04777: Erv1 / Alr family   chr1:5173120-5176215 REVERSE   Aliases: ATQSOX1, QUIESCIN SULFHYDRYL OXIDASE 1, T15D22.7, T15D22_7	5.5	4.9	0.5	2.1	100.0%	-3.2
2267	AT2G24180.1   Symbol: CYP71B6   cytochrome P450 family protein   chr2:10288927-10290815 FORWARD   Aliases: CYTOCHROME P450 71B6, CYTOCHROME P450 MONOOXYGENASE 71B6, F27D4.9, F27D4_9	7.3	8.0	-0.7	-2.1	100.0%	-3.0
2268	AT3G51890.1   expressed protein, protein At2g40060 - Arabidopsis thaliana, EMBL:AF002109   chr3:19260457-19261942 REVERSE   Aliases: ATEM1.14	7.1	6.2	0.9	2.1	100.0%	-2.8
2269	AT3G05360.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to elicitor-inducible LRR receptor-like protein EILP (Nicotiana tabacum) gi:6635236:dbj:BAA88636; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr3:1530741-1533294 REVERSE   Aliases: F22F7.23	3.0	3.5	-0.4	-2.1	100.0%	-3.2
2270	AT5G57950.1   26S proteasome regulatory subunit, putative, contains similarity to 26S proteasome non-ATPase subunit 9 SP:O00233 from (Homo sapiens)   chr5:23477935-23479614 FORWARD   Aliases: MTI20.21, MTI20_21	4.9	4.4	0.6	2.1	100.0%	-3.1
2271	AT5G18840.1   sugar transporter, putative, similar to ERD6 protein {Arabidopsis thaliana} GI:3123712, sugar-porter family protein 1 (Arabidopsis thaliana) GI:14585699; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:6282883-6286709 FORWARD   Aliases: F17K4.90, F17K4_90	3.7	3.4	0.3	2.1	100.0%	-3.6
2272	AT1G12130.1   flavin-containing monooxygenase family protein / FMO family protein, contains similarity to flavin-containing monooxygenase 2 (FMO2) from Homo sapiens (GI:1834493); contains Pfam profile PF00743 Flavin-binding monooxygenase-like   chr1:4118592-4120869 FORWARD   Aliases: T28K15.13, T28K15_13	2.8	3.0	-0.2	-2.1	100.0%	-3.9
2273	AT5G06140.1   phox (PX) domain-containing protein, similar to SP:O60749 Sorting nexin 2 {Homo sapiens}; contains Pfam profile PF00787: PX domain   chr5:1856009-1858767 REVERSE   Aliases: K16F4.11, K16F4_11	6.5	7.4	-0.8	-2.1	100.0%	-2.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2274	AT3G13340.1   WD-40 repeat family protein, contains Pfam profile: PF00400 WD domain, G-beta repeat (3 copies, 1 significant); similar to Trp-Asp repeat protein (PIR:T40094) (Schizosaccharomyces)   chr3:4331766-4335080 FORWARD   Aliases: MDC11.14	3.7	3.2	0.5	2.1	100.0%	-3.2
2275	AT2G28800.2   Symbol: ALB3   chloroplast membrane protein (ALBINO3), Oxa1p homolog {PMID:11148275}; identical to chloroplast membrane protein ALBINO3 (Arabidopsis thaliana) GI:2209332   chr2:12364233-12366329 REVERSE   Aliases: ABL3, ALBINA 3, ALBINO 3, CHLOROPLAST MEMBRANE PROTEIN ALB3, F8N16.9, F8N16_9	8.7	7.6	1.1	2.1	100.0%	-2.8
2276	AT5G07330.1   expressed protein   chr5:2315981-2316875 FORWARD   Aliases: T2I1.40, T2I1_40	4.7	3.7	1.0	2.1	100.0%	-2.8
2277	AT1G72520.1   lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum), gi:1654140 (Lycopersicon esculentum), GB:CAB56692 (Arabidopsis thaliana)	5.3	4.6	0.8	2.1	100.0%	-2.8
2278	AT2G32060.3   40S ribosomal protein S12 (RPS12C)   chr2:13646122-13647257 REVERSE   Aliases: F22D22.19, F22D22_19	10.8	11.5	-0.7	-2.1	100.0%	-3.1
2279	AT1G76140.1   similar to prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative [Arabidopsis thaliana] (TAIR:At1g20380.1); similar to putative prolyl endopeptidase [Oryza sativa (japonica cultivar-group)] (GB:NP_908392.1); similar to OTTHUMP00000040498 [Homo sapiens] (GB:CAH72545.1); similar to OSJNBa0084K11.14 [Oryza sativa (japonica cultivar-group)] (GB:XP_473492.1); similar to similar to Prolyl endopeptidase (Post-proline cleaving enzyme) (PE) [Gallus gallus] (GB:NP_001006410.1); similar to prolyl endopeptidase [Mus musculus] (GB:NP_035286.1); contains InterPro domain Prolyl oligopeptidase serine protease (S9A) (InterPro:IPR002470); contains InterPro domain Prolyl oligopeptidase (InterPro:IPR001375); contains InterPro domain Prolyl oligopeptidase, N-terminal beta-propeller domain (InterPro:IPR004106)   chr1:28576024-28579930 FORWARD   Aliases: T23E18.8, T23E18_8	8.9	9.7	-0.8	-2.1	100.0%	-3.1
2280	AT5G52300.2   Symbol: RD29B   similar to stress-responsive protein-related [Arabidopsis thaliana] (TAIR:At4g25580.1); similar to cor78 (GB:AAA32776.1)   chr5:21254282-21256755 FORWARD   Aliases: K24M7.3, K24M7_3, LTI65, RESPONSIVE TO DESSICATION 29B	7.2	6.3	0.9	2.1	100.0%	-2.9
2281	AT1G15170.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:5220636-5222968 FORWARD   Aliases: F9L1.11, F9L1_11	5.4	4.8	0.6	2.1	100.0%	-2.9
2282	AT5G61990.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:24916832-24920343 REVERSE   Aliases: MTG10.2, MTG10_2	3.4	3.7	-0.3	-2.1	100.0%	-3.5
2283	AT5G40870.1   uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative, similar to SP:O65583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Arabidopsis thaliana}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family   chr5:16392155-16395876 FORWARD   Aliases: MHK7.10, MHK7_10	6.5	7.5	-1.0	-2.1	100.0%	-3.0
2284	AT1G15430.2   expressed protein   chr1:5304454-5306007 FORWARD   Aliases: F9L1.39, F9L1_39	8.1	6.9	1.2	2.1	100.0%	-2.9
2285	AT3G19520.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr3:6772696-6774449 FORWARD   Aliases: T31J18.2	7.1	6.6	0.5	2.1	100.0%	-3.1
2286	AT4G35830.1   aconitate hydratase, cytoplasmic / citrate hydro-lyase / aconitase (ACO), identical to SP:Q42560 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Arabidopsis thaliana}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain   chr4:16972602-16978061 REVERSE   Aliases: F4B14.100, F4B14_100	9.5	10.0	-0.5	-2.1	100.0%	-3.4
2287	AT2G06000.2   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:2327391-2329662 REVERSE   Aliases: T6P5.20, T6P5_20	4.6	5.0	-0.5	-2.1	100.0%	-3.2
2288	AT5G66750.1   Symbol: DDM1   SNF2 domain-containing protein / helicase domain-containing protein, similar to proliferation-associated SNF2-like protein (Homo sapiens) GI:8980660; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr5:26666177-26670299 FORWARD   Aliases: DECREASED DNA METHYLATION 1, MSN2.14, MSN2_14, SOM1, SOM4, SOMNIFEROUS 1	2.9	3.6	-0.7	-2.1	100.0%	-3.2
2289	AT1G62045.1   expressed protein   chr1:22938353-22939008 REVERSE   Aliases: None	6.3	5.4	0.9	2.1	100.0%	-2.9
2290	AT3G15080.1   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr3:5074272-5076528 FORWARD   Aliases: K15M2.23	6.2	7.0	-0.8	-2.1	100.0%	-3.0
2291	AT5G64990.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:550072 from (Homo sapiens)   chr5:25980788-25982018 REVERSE   Aliases: MXK3.22, MXK3_22	6.0	5.0	1.0	2.1	100.0%	-2.7
2292	AT3G60840.1   microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr3:22488548-22491438 REVERSE   Aliases: T4C21.250	3.6	4.1	-0.5	-2.1	100.0%	-3.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2293	AT5G22920.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles:PF05495 CHY zinc finger, PF00097 zinc finger, C3HC4 type (RING finger)   chr5:7664994-7667268 FORWARD   Aliases: MRN17.15, MRN17_15	8.2	7.4	0.8	2.1	100.0%	-3.2
2294	AT1G58100.1   TCP family transcription factor, putative, similar to auxin-induced basic helix-loop-helix transcription factor Gl:5731257 from (Gossypium hirsutum)   chr1:21516112-21517592 REVERSE   Aliases: T15M6.11	6.4	5.8	0.6	2.1	100.0%	-3.2
2295	AT3G23150.1   Symbol: ETR2   ethylene receptor, putative (ETR2), similar to putative ethylene receptor; ETR2 (Arabidopsis thaliana) gi:3687654:gb:AAC62208.   chr3:8254670-8257742 FORWARD   Aliases: ETHYLENE RESPONSE 2, ETR2, K14B15.9	5.9	5.0	0.9	2.1	100.0%	-2.9
2296	AT4G17360.1   formyltetrahydrofolate deformylase, putative, similar to formyltetrahydrofolate deformylase (strain PCC 6803- Synechocystis sp.) SWISS-PROT:Q55135   chr4:9703187-9705480 REVERSE   Aliases: DL4715C, FCAALL.417	4.4	3.9	0.5	2.1	100.0%	-3.0
2297	AT3G07790.1   DGCR14-related, similar to DGCR14 protein (DiGeorge syndrome critical region 14) (ES2 protein) (Swiss-Prot:Q96DF8) (Homo sapiens)   chr3:2487375-2489226 FORWARD   Aliases: MLP3.24	8.4	7.5	0.9	2.1	100.0%	-2.9
2298	AT2G03670.1   Symbol: CDC48B	3.9	4.7	-0.8	-2.1	100.0%	-3.0
2299	AT1G65295.1   expressed protein   chr1:24255174-24255966 FORWARD   Aliases: None	6.7	5.8	0.8	2.1	100.0%	-2.9
2300	AT1G73930.2   similar to FLJ00229 protein [Homo sapiens] (GB:BAB84982.1)   chr1:27798781-27801642 REVERSE   Aliases: F2P9.20, F2P9_20	5.8	6.3	-0.5	-2.1	100.0%	-3.1
2301	AT2G17660.1   nitrate-responsive NOI protein, putative, similar to nitrate-induced NOI protein (Zea mays) Gl:2642213   chr2:7680364-7680794 FORWARD   Aliases: T17A5.20, T17A5_20	4.4	3.3	1.1	2.1	100.0%	-2.9
2302	AT1G79210.1   20S proteasome alpha subunit B, putative, nearly identical to SP:O23708 Proteasome subunit alpha type 2 (EC 3.4.25.1) (20S proteasome alpha subunit B) {Arabidopsis thaliana} and to At1g16470   chr1:29800987-29803624 REVERSE   Aliases: YUP8H12R.19, YUP8H12R_19	7.2	8.3	-1.1	-2.1	100.0%	-2.9
2303	AT5G57930.2   Symbol: APO2   expressed protein   chr5:23471843-23473719 FORWARD   Aliases: ACCUMULATION OF PHOTOSYSTEM ONE 2, EMB1629, EMBRYO DEFECTIVE 1629, MTI20.19, MTI20_19	7.2	6.7	0.5	2.1	100.0%	-3.0
2304	AT2G32020.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:13638139-13638845 REVERSE   Aliases: F22D22.23, F22D22_23	3.6	3.2	0.4	2.1	100.0%	-3.6
2305	AT2G40820.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr2:17041814-17046552 REVERSE   Aliases: T20B5.2, T20B5_2	4.5	5.0	-0.5	-2.1	100.0%	-3.0
2306	AT4G36010.2   similar to pathogenesis-related thaumatin family protein [Arabidopsis thaliana] (TAIR:At2g17860.1); similar to putative thaumatin-like protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52110.1); contains InterPro domain Thaumatin, pathogenesis-related (InterPro:IPR001938)   chr4:17039066-17041134 REVERSE   Aliases: T19K4.140, T19K4_140	4.7	3.9	0.8	2.1	100.0%	-2.8
2307	AT1G22740.1   Symbol: RAB7   Ras-related protein (RAB7) / AtRab75 / small GTP-binding protein, putative, identical to SP:O04157 Ras-related protein Rab7 (AtRab75) (Arabidopsis thaliana)   chr1:8049089-8050697 FORWARD   Aliases: T22J18.9, T22J18_9	4.6	4.0	0.6	2.1	100.0%	-3.0
2308	AT3G20790.1   oxidoreductase family protein, weak similarity to SP:Q07982 Glucose--fructose oxidoreductase precursor (EC 1.1.99.28) {Zymomonas mobilis}; contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain   chr3:7268768-7271517 FORWARD   Aliases: MOE17.10	8.8	9.5	-0.8	-2.1	100.0%	-2.9
2309	AT1G12000.1   pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative, strong similarity to SP:Q41141 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit (EC 2.7.1.90) (PFP) ((PPI-PFK) {Ricinus communis}); contains Pfam profile PF00365: Phosphofructokinase   chr1:4049894-4053833 REVERSE   Aliases: F12F1.13, F12F1_13	7.5	9.2	-1.7	-2.1	100.0%	-2.9
2310	AT1G68560.1   Symbol: XYL1   alpha-xylosidase (XYL1), identical to alpha-xylosidase precursor GB:AAD05539 Gl:4163997 from (Arabidopsis thaliana); contains Pfam profile PF01055: Glycosyl hydrolases family 31; identical to cDNA alpha-xylosidase precursor (XYL1) partial cds Gl:4163996   chr1:25737845-25741658 REVERSE   Aliases: F24J5.20, F24J5_20	3.5	4.4	-0.9	-2.1	100.0%	-2.9
2311	AT3G28350.1   hypothetical protein   chr3:10609596-10611901 FORWARD   Aliases: MFJ20.3	2.7	2.5	0.2	2.1	100.0%	-3.8
2312	AT2G47630.1   esterase/lipase/thioesterase family protein, similar to monoglyceride lipase from (Homo sapiens) Gl:14594904, (Mus musculus) Gl:2632162; contains Interpro entry IPR000379   chr2:19541573-19544073 FORWARD   Aliases: F17A22.2	6.4	7.4	-1.1	-2.1	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2313	AT4G19880.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g45020.1); similar to putative transferase [Escherichia coli O157:H7 EDL933] (GB:AAG58235.1)   chr4:10784401-10786433 REVERSE   Aliases: T16H5.240, T16H5_240	8.9	9.4	-0.4	-2.1	100.0%	-3.6
2314	AT1G04190.1   tetratricopeptide repeat (TPR)-containing protein, low similarity to protein antigen LmST11 (Leishmania major) GI:1698880; contains Pfam profile PF00515 TPR Domain; EST gb:Z47802 and gb:Z48402 come from this gene   chr1:1106427-1108707 REVERSE   Aliases: F20D22.4, F20D22_4	7.5	8.5	-1.0	-2.1	100.0%	-2.9
2315	AT2G46520.1   cellular apoptosis susceptibility protein, putative / importin-alpha re-exporter, putative, similar to cellular apoptosis susceptibility protein (Homo sapiens) GI:3598795, SP:Q9ERK4 Importin-alpha re-exporter (Chromosome segregation 1-like protein) (Cellular apoptosis susceptibility protein) {Mus musculus}; contains Pfam profiles PF03810: Importin-beta N-terminal domain, PF03378: CAS/CSE protein C-terminus   chr2:19103840-19107344 FORWARD   Aliases: F11C10.33	4.5	5.0	-0.6	-2.1	100.0%	-3.1
2316	AT5G02880.1   Symbol: UPL4   HECT-domain-containing protein / ubiquitin-transferase family protein / armadillo/beta-catenin-like repeat-containing protein, similar to SP:Q14669 Thyroid receptor interacting protein 12 (TRIP12) {Homo sapiens}; contains Pfam profiles PF00632: HECT-domain (ubiquitin-transferase), PF00514: Armadillo/beta-catenin-like repeat   chr5:662641-669105 FORWARD   Aliases: F9G14.190, F9G14_190	5.7	6.4	-0.6	-2.1	100.0%	-2.9
2317	AT4G34880.1   amidase family protein, similar to peptide amidase (Stenotrophomonas maltophilia) GI:19744118; contains Pfam profile PF01425: Amidase   chr4:16615554-16617429 FORWARD   Aliases: F11I11.120, F11I11_120	3.3	4.1	-0.8	-2.1	100.0%	-3.1
2318	AT4G37170.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:17498574-17500649 REVERSE   Aliases: AP22.43, AP22_43	4.3	5.0	-0.7	-2.1	100.0%	-3.2
2319	AT1G16710.1   TAZ zinc finger family protein / zinc finger (ZZ type) family protein, contains Pfam profiles PF02135: TAZ zinc finger, PF00569: Zinc finger, ZZ type   chr1:5714685-5722359 FORWARD   Aliases: F19K19.17	4.2	3.6	0.6	2.1	100.0%	-3.1
2320	AT5G27470.1   seryl-tRNA synthetase / serine--tRNA ligase, identical to SP:Q39230 Seryl-tRNA synthetase (EC 6.1.1.11) (Serine--tRNA ligase) (SerRS) {Arabidopsis thaliana}   chr5:9695011-9697392 FORWARD   Aliases: F21A20.180, F21A20_180	7.8	8.4	-0.7	-2.1	100.0%	-3.2
2321	AT3G01430.1   expressed protein   chr3:165415-166254 REVERSE   Aliases: T13O15.7, T13O15_7	5.7	5.1	0.6	2.1	100.0%	-3.0
2322	AT3G54010.2   Symbol: PAS1   peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative / pasticino 1-D (PAS1-D), nearly identical to pasticino 1-D (Arabidopsis thaliana) GI:3080740   chr3:20011867-20016161 FORWARD   Aliases: F5K20.310, PASTICCINO 1	8.7	9.4	-0.6	-2.1	100.0%	-3.3
2323	AT5G65480.1   expressed protein   chr5:26193247-26195140 FORWARD   Aliases: MNA5.18	9.8	9.1	0.7	2.1	100.0%	-3.2
2324	AT2G36880.1   S-adenosylmethionine synthetase, putative, similar to S-adenosylmethionine synthetase 3 (Methionine adenosyltransferase 3, AdoMet synthetase 3) (Lycopersicon esculentum) SWISS-PROT:P43282   chr2:15486445-15488486 REVERSE   Aliases: T1J8.6, T1J8_6	7.0	8.7	-1.7	-2.1	100.0%	-2.9
2325	AT2G20260.1   photosystem I reaction center subunit IV, chloroplast, putative / PSI-E, putative (PSAE2), identical to SP:Q9S714; similar to SP:P12354 Photosystem I reaction center subunit IV, chloroplast precursor (PSI-E) {Spinacia oleracea}; contains Pfam profile PF02427: Photosystem I reaction centre subunit IV / PsaE   chr2:8743818-8744843 FORWARD   Aliases: F11A3.19, F11A3_19	7.3	6.6	0.8	2.1	100.0%	-3.0
2326	AT2G46230.1   expressed protein, contains Pfam profile: PF04900 protein of unknown function, DUF652   chr2:18991045-18993032 REVERSE   Aliases: T3F17.12	7.7	8.6	-0.9	-2.1	100.0%	-3.0
2327	AT1G32410.2   vacuolar protein sorting 55 family protein / VPS55 family protein, contains Pfam domain PF04133: Vacuolar protein sorting 55   chr1:11693837-11695534 FORWARD   Aliases: F5D14.32	7.9	7.2	0.7	2.1	100.0%	-3.2
2328	AT2G16710.1   hesB-like domain-containing protein, similar to IscA (putative iron-sulfur cluster assembly protein) (Azotobacter vinelandii) GI:2271523; contains Pfam profile PF01521: HesB-like domain   chr2:7255255-7257367 FORWARD   Aliases: T24I21.12, T24I21_12	10.3	9.5	0.8	2.1	100.0%	-3.2
2329	AT4G33280.1   similar to transcriptional factor B3 family protein [Arabidopsis thaliana] (TAIR:At3g18990.1); similar to putative auxin response factor [Oryza sativa (japonica cultivar-group)] (GB:XP_463202.1); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340)   chr4:16047361-16049359 REVERSE   Aliases: F17M5.40, F17M5_40	4.0	3.5	0.6	2.1	100.0%	-3.0
2330	AT2G40400.2   expressed protein, similar to GI:7572912 (At3g56140)(Arabidopsis thaliana)   chr2:16876412-16880336 FORWARD   Aliases: T3G21.17, T3G21_17	4.8	5.7	-0.9	-2.1	100.0%	-3.0
2331	AT2G31690.1   lipase class 3 family protein, similar to DEFECTIVE IN ANther DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase   chr2:13483170-13484624 REVERSE   Aliases: T9H9.21, T9H9_21	2.0	2.2	-0.2	-2.1	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2332	AT4G18070.4   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g29530.1); similar to hypothetical protein DDB0183896 [Dictyostelium discoideum] (GB:EAL61706.1); contains domain SER_RICH (PS50324)   chr4:10030709-10032947 FORWARD   Aliases: F15J5.40, F15J5_40	6.7	5.8	0.9	2.1	100.0%	-3.2
2333	AT5G39320.1   UDP-glucose 6-dehydrogenase, putative, very strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain	3.8	4.8	-1.0	-2.1	100.0%	-2.9
2334	AT3G23805.1   Symbol: RALFL24   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr3:8586389-8587063 FORWARD   Aliases: RALF LIKE 24	5.7	6.5	-0.7	-2.1	100.0%	-3.0
2335	AT2G47250.1   RNA helicase, putative, similar to SP:P53131 Pre-mRNA splicing factor RNA helicase PRP43 (Helicase JA1) {Saccharomyces cerevisiae}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr2:19406765-19410107 REVERSE   Aliases: T8I13.9	7.4	8.1	-0.6	-2.1	100.0%	-3.0
2336	AT5G19510.1   elongation factor 1B alpha-subunit 2 (eEF1Balpha2), identical to elongation factor 1B alpha-subunit (Arabidopsis thaliana) GI:6686821   chr5:6581660-6583213 REVERSE   Aliases: T20D1.30, T20D1_30	11.3	11.7	-0.4	-2.1	100.0%	-3.3
2337	AT2G38140.1   Symbol: PSRP4   chloroplast 30S ribosomal protein S31 (PSRP4)   chr2:15987961-15988676 FORWARD   Aliases: 30S RIBOSOMAL PROTEIN S31, F16M14.7, F16M14_7, PLASTID SPECIFIC RIBOSOMAL PROTEIN 4	8.8	9.7	-0.8	-2.1	100.0%	-2.9
2338	AT1G03520.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile PF02485: Core-2/l-Branching enzyme   chr1:877863-880159 REVERSE   Aliases: F21B7.14	5.7	5.2	0.5	2.1	100.0%	-3.2
2339	AT4G25240.1   Symbol: SKS1   multi-copper oxidase type I family protein, pollen-specific protein precursor -Nicotiana tabacum, PID:g19902; contains Pfam profile: PF00394 Multicopper oxidase	3.0	3.4	-0.3	-2.1	100.0%	-3.4
2340	AT3G29330.1   expressed protein   chr3:11258939-11260290 REVERSE   Aliases: MUO10.3	4.6	4.1	0.4	2.1	100.0%	-3.2
2341	AT2G28600.1   expressed protein   chr2:12258862-12261900 FORWARD   Aliases: T8O18.11, T8O18_11	5.7	6.5	-0.8	-2.1	100.0%	-2.8
2342	AT1G29530.1   expressed protein   chr1:10324731-10326721 REVERSE   Aliases: F15D2.11, F15D2_11	4.7	5.5	-0.7	-2.1	100.0%	-2.8
2343	AT4G23860.2   PHD finger protein-related, similar to Pfam profiles PF02207: Putative zinc finger in N-recognin, weak hit to PF00628: PHD-finger   chr4:12409033-12411575 FORWARD   Aliases: T32A16.30, T32A16_30	3.6	4.0	-0.5	-2.1	100.0%	-3.1
2344	AT1G17100.1   SOUL heme-binding family protein, similar to SOUL protein (Mus musculus) GI:4886906; contains Pfam profile PF04832: SOUL heme-binding protein   chr1:5844729-5846215 FORWARD   Aliases: F20D23.21, F20D23_21	9.0	8.4	0.6	2.1	100.0%	-2.9
2345	AT5G46680.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:18958196-18959789 FORWARD   Aliases: MZA15.9, MZA15_9	5.1	6.3	-1.2	-2.1	100.0%	-2.9
2346	AT2G30200.2   similar to malonyl-CoA:ACP transacylase [Perilla frutescens] (GB:AAG43518.1); contains InterPro domain Acyl transferase domain (InterPro:IPR001227)   chr2:12890074-12892845 REVERSE   Aliases: T27E13.6, T27E13_6	9.7	10.7	-1.0	-2.1	100.0%	-2.9
2347	AT1G26960.1   homeobox-leucine zipper protein, putative / HD-ZIP transcription factor, putative, similar to homeobox-leucine zipper protein HAT7 (HD-ZIP protein 7) (HD-ZIP protein ATHB-3 (SP:Q00466: (Arabidopsis thaliana); similar to Helianthus annuus gi:349379, and carrot, gi:1435022. Contains Homeobox domain motif   chr1:9355907-9357437 FORWARD   Aliases: T2P11.15, T2P11_15	3.1	2.8	0.3	2.1	100.0%	-3.7
2348	AT2G23560.1   hydrolase, alpha/beta fold family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polynuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:10036416-10037362 REVERSE   Aliases: F26B6.21, F26B6_21	7.7	8.5	-0.8	-2.1	100.0%	-3.0
2349	AT5G24490.1   30S ribosomal protein, putative, similar to SP:P19954 Plastid-specific 30S ribosomal protein 1, chloroplast precursor (CS-S5) (CS5) (S22) (Ribosomal protein 1) (PSRP-1) {Spinacia oleracea}; contains Pfam profile PF02482: Sigma 54 modulation protein / S30EA ribosomal protein   chr5:8365624-8367429 FORWARD   Aliases: T31K7.7, T31K7_7	8.3	9.0	-0.7	-2.1	100.0%	-2.9
2350	AT5G56250.2   expressed protein   chr5:22785803-22790118 REVERSE   Aliases: K24C1.6, K24C1_6	3.6	3.3	0.3	2.1	100.0%	-3.7
2351	AT1G76080.1   thioredoxin family protein, low similarity to thioredoxin (TRX) (Fasciola hepatica) GI:6687568; contains Pfam profile PF00085: Thioredoxin   chr1:28552680-28554313 REVERSE   Aliases: T23E18.2, T23E18_2	8.3	7.6	0.7	2.1	100.0%	-2.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2352	AT1G05850.1   Symbol: ELP   chitinase-like protein 1 (CTL1), similar to class I chitinase GI:7798656 from (Halimolobos perplexa var. perplexa); contains Pfam profile PF00182: Chitinase class I; identical to cDNA chitinase-like protein 1 (CTL1) CTL1-ELP1 allele GI:17226328   chr1:1766502-1768662 REVERSE   Aliases: CHITINASE LIKE PROTEIN 1, CTL1, ECTOPIC DEPOSITION OF LIGNIN IN PITH, ELP1, T20M3.12, T20M3_12	10.1	8.7	1.3	2.1	100.0%	-3.3
2353	AT5G37540.1   aspartyl protease family protein, weak similarity to CND41, chloroplast nucleoid DNA binding protein (Nicotiana tabacum) GI:2541876; contains Prosite PS00141: Eukaryotic and viral aspartyl proteases active site; contains 1 predicted transmembrane domain   chr5:14930065-14931661 FORWARD   Aliases: MPA22.8, MPA22_8	4.9	4.2	0.8	2.1	100.0%	-3.0
2354	AT1G17070.1   D111/G-patch domain-containing protein, Similar to SP:Q9ERA6 Tuftelin-interacting protein 11 {Mus musculus}; contains Pfam profile PF01585: G-patch domain   chr1:5837583-5840261 FORWARD   Aliases: F20D23.23, F20D23_23	5.3	6.1	-0.8	-2.1	100.0%	-2.9
2355	AT1G29570.1   zinc finger protein-related, contains similarity to zinc finger proteins (CCCH type)   chr1:10335896-10337840 FORWARD   Aliases: F15D2.36, F15D2_36	2.9	2.7	0.2	2.1	100.0%	-3.8
2356	AT2G47800.1   Symbol: ATMRP4	4.1	4.7	-0.6	-2.1	100.0%	-3.4
2357	AT1G09010.1   glycoside hydrolase family 2 protein, low similarity to mannosidase (gi:5359712) from Cellulomonas fimi   chr1:2895169-2899385 REVERSE   Aliases: F7G19.12, F7G19_12	6.1	6.8	-0.7	-2.1	100.0%	-3.3
2358	AT2G14170.1   Symbol: ALDH6B2   methylmalonate-semialdehyde dehydrogenase, putative, similar to methylmalonate-semialdehyde dehydrogenase (acylating), mitochondrial precursor (MMSDH) (Rattus norvegicus) SWISS-PROT:Q02253   chr2:5984438-5988981 REVERSE   Aliases: T22C12.10, T22C12_10	11.0	10.7	0.3	2.1	100.0%	-3.7
2359	AT4G26860.1   alanine racemase family protein, contains Pfam domain, PF01168: Alanine racemase, N-terminal domain   chr4:13503092-13504756 REVERSE   Aliases: F10M23.200, F10M23_200	6.7	6.2	0.5	2.1	100.0%	-3.1
2360	AT1G19525.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:6761511-6762769 FORWARD   Aliases: None	5.9	6.7	-0.8	-2.1	100.0%	-3.0
2361	AT5G05980.2   Symbol: ATDFB   similar to dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS4) [Arabidopsis thaliana] (TAIR:At3g55630.3); similar to folylpoly-gammaglutamate synthetase precursor [Cricetulus griseus] (GB:AAK69546.1); contains InterPro domain Folylpolyglutamate synthetase (InterPro:IPR001645)   chr5:1799491-1804296 REVERSE   Aliases: A. THALIANA DHFS FPGS HOMOLOG B, K18J17.17, K18J17_17	8.3	8.8	-0.5	-2.1	100.0%	-3.1
2362	AT3G45960.2   Symbol: ATEXLA3   similar to expansin family protein (EXPL2) [Arabidopsis thaliana] (TAIR:At4g38400.1); similar to putative pollen allergen [Oryza sativa (japonica cultivar-group)] (GB:AAP54861.1); contains InterPro domain Expansin 45, endoglucanase-like domain (InterPro:IPR007112); contains InterPro domain Major pollen allergen Lol pl (InterPro:IPR005795); contains InterPro domain Expansin/Lol pl (InterPro:IPR007118); contains InterPro domain Pollen allergen/expansin, C-terminal (InterPro:IPR007117)   chr3:16903741-16904884 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN LIKE A3, ATEXPL3, ATHEXP BETA 2.3, EXPL3, F16L2.170, F16L2_170	7.6	6.6	1.0	2.1	100.0%	-3.2
2363	AT4G05180.1   oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ2), identical to SP:Q41932 Oxygen-evolving enhancer protein 3-2, chloroplast precursor (OEE3) (16 kDa subunit of oxygen evolving system of photosystem II) (OEC 16 kDa subunit) {Arabidopsis thaliana}; similar to SP:P12301 Oxygen-evolving enhancer protein 3, chloroplast precursor (OEE3) (16 kDa subunit of oxygen evolving system of photosystem II) (OEC 16 kDa subunit) {Spinacia oleracea}; contains Pfam profile PF05757: Oxygen evolving enhancer protein 3 (PsbQ)   chr4:2671820-2673241 REVERSE   Aliases: C17L7.100, C17L7_100	9.7	8.4	1.3	2.1	100.0%	-2.8
2364	AT1G12775.1   similar to helicase domain-containing protein / pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g12700.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g12300.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g12620.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At3g22470.1); similar to fertility restorer homologue A [Raphanus sativus] (GB:CAD80166.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr1:4353904-4355927 FORWARD   Aliases: None	4.3	4.8	-0.5	-2.1	100.0%	-3.2
2365	AT5G37790.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:15025402-15028382 REVERSE   Aliases: K22F20.5, K22F20_5	5.7	6.3	-0.6	-2.1	100.0%	-3.3
2366	AT4G29510.1   protein arginine N-methyltransferase, putative, similar to protein arginine N-methyltransferase 1-variant 2 (Homo sapiens) GI:7453575   chr4:14491631-14494007 FORWARD   Aliases: T16L4.20, T16L4_20	7.6	8.8	-1.2	-2.1	100.0%	-3.0
2367	AT1G54290.1   eukaryotic translation initiation factor SUI1, putative, similar to P:P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfam profile PF01253: Translation initiation factor SUI1   chr1:20272152-20273774 REVERSE   Aliases: F20D21.11, F20D21_11	8.4	7.4	0.9	2.1	100.0%	-2.8
2368	AT5G42000.1   ORMDL family protein, contains Pfam domain PF04061: ORMDL family	6.1	5.1	1.0	2.1	100.0%	-3.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2369	AT3G55510.1   expressed protein   chr3:20589963-20593382 FORWARD   Aliases: T22E16.170	4.2	5.2	-0.9	-2.1	100.0%	-2.9
2370	AT4G39190.1   expressed protein, ; expression supported by MPSS   chr4:18252026-18252859 REVERSE   Aliases: T22F8.90, T22F8_90	5.3	4.5	0.8	2.1	100.0%	-3.2
2371	AT3G43960.1   cysteine proteinase, putative, contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from (Arabidopsis thaliana)   chr3:15785042-15786644 REVERSE   Aliases: T15B3.100	3.6	5.0	-1.3	-2.1	100.0%	-2.9
2372	AT4G22530.1   embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531   chr4:11859015-11860159 REVERSE   Aliases: F7K2.110, F7K2_110	6.4	7.2	-0.8	-2.1	100.0%	-2.9
2373	AT2G29680.2   Symbol: CDC6   cell division control protein CDC6, putative, almost identical to DNA replication protein CDC6 GI:18056480 from (Arabidopsis thaliana); identical to cDNA CDC6 protein (2g29680 gene) GI:18056479   chr2:12696626-12700101 FORWARD   Aliases: T27A16.22, T27A16_22, cell division control protein 6	2.9	3.2	-0.3	-2.1	100.0%	-3.5
2374	AT5G65080.1   Symbol: MAF5   MADS-box family protein   chr5:26014730-26019691 FORWARD   Aliases: F15O5.4, F15O5_4, MADS AFFECTING FLOWERING 5 VARIANT I, MADS AFFECTING FLOWERING 5 VARIANT II, MAF5.1	3.0	2.4	0.6	2.1	100.0%	-3.1
2375	AT5G64340.1   expressed protein   chr5:25747561-25750539 REVERSE   Aliases: MSJ1.18, MSJ1_18	3.7	4.3	-0.6	-2.1	100.0%	-3.1
2376	AT1G79660.1   expressed protein   chr1:29980756-29981666 FORWARD   Aliases: F20B17.9, F20B17_9	10.9	10.1	0.9	2.1	100.0%	-3.6
2377	AT5G62910.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr5:25267960-25269430 FORWARD   Aliases: MQB2.23, MQB2_23	5.9	5.2	0.7	2.1	100.0%	-3.2
2378	AT1G52730.2   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to UNR-interacting protein (WD-40 repeat protein PT-WD) (SP:Q9Y3F4) (Homo sapiens)   chr1:19646158-19648802 FORWARD   Aliases: F6D8.2, F6D8_2	8.4	8.9	-0.5	-2.1	100.0%	-3.3
2379	AT4G25380.1   zinc finger (AN1-like) family protein, contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger   chr4:12975946-12976338 REVERSE   Aliases: T30C3.50, T30C3_50	3.7	3.3	0.4	2.1	100.0%	-3.3
2380	AT4G19610.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr4:10677675-10681633 FORWARD   Aliases: F24J7.162, F24J7_162	6.6	7.3	-0.7	-2.1	100.0%	-3.2
2381	AT5G04340.1   Symbol: C2H2   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:1216132-1217107 REVERSE   Aliases: C2H2 ZINC FINGER TRANSCRIPTION FACTOR, T19N18.70, T19N18_70	4.5	3.4	1.1	2.1	100.0%	-2.8
2382	AT5G60730.1   anion-transporting ATPase family protein, low similarity to SP:O43681 Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I) {Homo sapiens}; contains Pfam profile PF02374: Anion-transporting ATPase   chr5:24439961-24442718 FORWARD   Aliases: MUP24.8, MUP24_8	3.5	3.9	-0.4	-2.1	100.0%	-3.3
2383	AT4G25650.2   Rieske (2Fe-2S) domain-containing protein, similar to cell death suppressor protein lls1 from Zea mays (gi:1935909), Rieske iron-sulfur protein Tic55 from Pisum sativum (gi:2764524); contains Pfam PF00355 Rieske (2Fe-2S) domain   chr4:13080914-13083206 REVERSE   Aliases: L73G19.30, L73G19_30	9.5	8.8	0.7	2.0	100.0%	-3.2
2384	AT5G13410.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, SP:Q9LYR5; similar to FK506-binding protein (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (SP:P25138) ({Neisseria meningitidis}); peptidyl-prolyl cis-trans isomerase, Spodoptera frugiperda, EMBL:SF15038; contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr5:4299744-4301770 REVERSE   Aliases: T22N19.60, T22N19_60	7.3	6.3	1.0	2.0	100.0%	-2.9
2385	AT5G28770.3   Symbol: BZO2H3	4.5	3.7	0.9	2.0	100.0%	-3.0
2386	AT2G02370.1   expressed protein   chr2:621154-623343 FORWARD   Aliases: T16F16.16, T16F16_16	6.4	5.6	0.9	2.0	100.0%	-2.9
2387	AT1G18280.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to lipid transfer protein GI:2627141 from (Picea abies); contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family   chr1:6294333-6295356 FORWARD   Aliases: T10O22.25, T10O22_25	3.3	2.9	0.3	2.0	100.0%	-3.5
2388	AT5G55730.1   Symbol: FLA1   fasciclin-like arabinogalactan-protein (FLA1), identical to gi:13377776::AAK20857:13377775:gb:AF333970   chr5:22575374-22577687 REVERSE   Aliases: MDF20.17, MDF20_17, fasciclin like arabinogalactan protein 1	3.8	4.5	-0.7	-2.0	100.0%	-2.9
2389	AT5G48070.1   Symbol: ATXTH20   putative xyloglucan endotransglycosylase/hydrolase, expressed primarily in the stele of mature non-elongating regions of both the main and the lateral root. Is expressed in lateral root primordia but expression ceases after lateral root begins to grow.	2.9	3.5	-0.6	-2.0	100.0%	-3.0
2390	AT1G11310.1   Symbol: MLO2   seven transmembrane MLO family protein / MLO-like protein 2 (MLO2), identical to membrane protein Mlo2 (Arabidopsis thaliana) gi:14091574:gb:AAK53795; similar to Mlo (Hordeum vulgare subsp. vulgare) gi:1877221:emb:CAB06083 SWISS-PROT:P93766   chr1:3800747-3804144 REVERSE   Aliases: T28P6.4, T28P6_4	5.5	6.4	-0.9	-2.0	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2391	AT1G71000.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:O35723 DnaJ homolog subfamily B member 3 Mus musculus, SP:Q9QYI7 DnaJ homolog subfamily B member 8 Mus musculus; contains Pfam profile PF00226 DnaJ domain   chr1:26772998-26773773 REVERSE   Aliases: F15H11.19, F15H11_19	3.0	2.7	0.3	2.0	100.0%	-3.8
2392	AT1G51090.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr1:18936605-18937618 FORWARD   Aliases: F23H24.15, F23H24_15	2.9	2.6	0.3	2.0	100.0%	-3.5
2393	AT4G28220.1   NADH dehydrogenase-related, similar to 64 kDa mitochondrial NADH dehydrogenase (Neurospora crassa) GI:4753821, alternative NADH-dehydrogenase (Yarrowia lipolytica) GI:3718005; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr4:13993003-13998353 FORWARD   Aliases: F26K10.100, F26K10_100	5.3	5.9	-0.6	-2.0	100.0%	-3.0
2394	AT1G31150.1   expressed protein, EST gb:Z33866 comes from this gene   chr1:11120078-11122568 FORWARD   Aliases: F28K20.8, F28K20_8	4.4	5.0	-0.6	-2.0	100.0%	-3.0
2395	AT1G18630.1   glycine-rich RNA-binding protein, putative, similar to glycine-rich RNA-binding protein from {Sorghum bicolor} SP:Q99070, GI:1778373 from (Pisum sativum); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:6414717-6416445 FORWARD   Aliases: F25I16.4, F25I16_4	6.1	5.6	0.5	2.0	100.0%	-3.2
2396	AT4G39670.1   expressed protein   chr4:18410166-18410994 FORWARD   Aliases: T19P19.60, T19P19_60	4.4	3.3	1.0	2.0	100.0%	-2.8
2397	AT5G50740.1   copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID: 9701579); similar to farnesylated protein ATPF3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:20654374-20655086 REVERSE   Aliases: MFB16.14, MFB16_14	3.9	4.5	-0.6	-2.0	100.0%	-3.1
2398	AT3G25640.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr3:9334956-9336041 FORWARD   Aliases: T5M7.9	3.3	4.2	-0.9	-2.0	100.0%	-2.9
2399	AT2G40960.1   expressed protein   chr2:17102600-17104527 FORWARD   Aliases: T20B5.16, T20B5_16	3.5	4.0	-0.5	-2.0	100.0%	-3.1
2400	AT2G37570.2   Symbol: SLT1   expressed protein   chr2:15767955-15770461 REVERSE   Aliases: F13M22.7, F13M22_7, SLT1 PROTEIN, SODIUM AND LITHIUM TOLERANT 1	5.5	6.5	-0.9	-2.0	100.0%	-3.0
2401	AT5G44010.1   expressed protein   chr5:17724192-17726426 REVERSE   Aliases: MRH10.12, MRH10_12	2.3	2.6	-0.2	-2.0	100.0%	-3.9
2402	AT1G31920.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:11461835-11463782 REVERSE   Aliases: F5M6.8, F5M6_8	3.4	3.9	-0.6	-2.0	100.0%	-3.3
2403	AT1G33330.1   peptide chain release factor, putative, similar to peptide chain release factor 2 (Campylobacter jejuni) GI:6469929; contains Pfam profile PF00472: Peptidyl-tRNA hydrolase domain   chr1:12084931-12086508 FORWARD   Aliases: F10C21.2	6.2	5.6	0.6	2.0	100.0%	-2.9
2404	AT1G26450.1   beta-1,3-glucanase-related, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis); C-terminal homology only	3.2	2.6	0.6	2.0	100.0%	-3.0
2405	AT4G24440.2   transcription initiation factor IIA gamma chain / TFIIA-gamma (TFIIA-S), identical to transcription initiation factor IIA gamma chain SP:Q39236 from (Arabidopsis thaliana);   chr4:12633190-12634767 FORWARD   Aliases: T22A6.270, T22A6_270	9.0	8.0	0.9	2.0	100.0%	-3.0
2406	AT5G58300.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:23589105-23592587 FORWARD   Aliases: MCK7.17, MCK7_17	4.0	4.9	-0.9	-2.0	100.0%	-2.9
2407	AT3G18190.1   chaperonin, putative, similar to SWISS-PROT:P50991- T-complex protein 1, delta subunit (TCP-1-delta) (Homo sapiens); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family	6.1	6.8	-0.7	-2.0	100.0%	-3.1
2408	AT4G33470.1   histone deacetylase family protein, similar to histone deacetylase 10 isoform alpha (Homo sapiens) GI:15213865; contains Pfam profile PF00850: Histone deacetylase family   chr4:16102598-16105484 REVERSE   Aliases: F17M5.230, F17M5_230	3.5	3.2	0.4	2.0	100.0%	-3.4
2409	ATCG00810.1   Symbol: RPL22   encodes a chloroplast ribosomal protein L22, a constituent of the large subunit of the ribosomal complex   chrC:83467-83949 REVERSE   Aliases: RPL22	8.4	10.4	-1.9	-2.0	100.0%	-3.2
2410	AT5G22880.1   histone H2B, putative, strong similarity to histone H2B-3 Lycopersicon esculentum GI:3021485, H2B Gossypium hirsutum SP:O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	7.9	9.2	-1.4	-2.0	100.0%	-2.8
2411	AT4G10320.1   isoleucyl-tRNA synthetase, putative / isoleucine--tRNA ligase, putative, similar to SP:P41252 Isoleucyl-tRNA synthetase, cytoplasmic (EC 6.1.1.5) (Isoleucine--tRNA ligase) (IleRS) (IRS) {Homo sapiens}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)   chr4:6397326-6404505 REVERSE   Aliases: F24G24.120, F24G24_120	10.2	10.9	-0.7	-2.0	100.0%	-3.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2412	AT5G66240.2   transducin family protein / WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat (4 copies, 1 weak); similar to Will die slowly protein. {Drosophila melanogaster} (SP:Q9V3J8) {Drosophila melanogaster}	8.6	8.0	0.5	2.0	100.0%	-3.4
2413	AT5G03560.1   expressed protein   chr5:900462-902740 REVERSE   Aliases: F12E4.360, F12E4_360	6.1	5.4	0.7	2.0	100.0%	-3.0
2414	AT1G31940.1   expressed protein   chr1:11470039-11471320 REVERSE   Aliases: F5M6.6	6.7	5.8	0.9	2.0	100.0%	-3.2
2415	AT5G08280.1   hydroxymethylbilane synthase / porphobilinogen deaminase, chloroplast / pre-uroporphyrinogen synthase, identical to SP:Q43316   chr5:2663191-2665793 REVERSE   Aliases: F8L15.10, F8L15_10	5.2	6.4	-1.2	-2.0	100.0%	-2.9
2416	AT3G10620.1   diadenosine 5',5'''-P1,P4-tetrphosphate hydrolase, putative, similar to diadenosine 5',5'''-P1,P4-tetrphosphate hydrolase from (Lupinus angustifolius) GI:1888557, (Hordeum vulgare subsp. vulgare) GI:2564253; contains Pfam profile PF00293: NUDIX domain   chr3:3320268-3322022 FORWARD   Aliases: F13M14.9	7.1	8.1	-0.9	-2.0	100.0%	-2.8
2417	AT3G51720.1   expressed protein, contains Pfam PF05701: Plant protein of unknown function (DUF827)   chr3:19196030-19197613 FORWARD   Aliases: T18N14.100	6.8	8.0	-1.2	-2.0	100.0%	-2.9
2418	AT5G51910.2   TCP family transcription factor, putative, similar to PCF2 ((GI:2580440) Oryza sativa)   chr5:21111811-21113058 REVERSE   Aliases: MJM18.6, MJM18_6	3.7	4.2	-0.5	-2.0	100.0%	-3.3
2419	AT2G25100.1   ribonuclease HII family protein, contains Pfam profile: PF01351 ribonuclease HII	5.0	5.6	-0.6	-2.0	100.0%	-3.1
2420	AT2G32410.2   similar to auxin-resistance protein AXR1 (AXR1) [Arabidopsis thaliana] (TAIR:At1g05180.1); similar to putative ubiquitin-activating enzyme (alternative splicing product) [Oryza sativa (japonica cultivar-group)] (GB:XP_470134.1); similar to putative ubiquitin-activating enzyme (alternative splicing product) [Oryza sativa (japonica cultivar-group)] (GB:XP_470133.1); contains InterPro domain UBA/THIF-type NAD/FAD binding fold (InterPro:IPR000594)   chr2:13764670-13768154 FORWARD   Aliases: T32F6.7, T32F6_7	3.9	4.2	-0.3	-2.0	100.0%	-3.6
2421	AT4G00990.1   transcription factor jumonji (jnjC) domain-containing protein, contains Pfam domain, PF02373: jnjC domain   chr4:426944-431821 FORWARD   Aliases: F3I3.10	5.5	5.9	-0.4	-2.0	100.0%	-3.3
2422	AT4G15930.1   dynein light chain, putative, similar to dynein light chain 2 (Mus musculus) GI:15545995; contains Pfam profile PF01221: Dynein light chain type 1   chr4:9036236-9038077 FORWARD   Aliases: DL4005W, FCAALL.238	10.5	10.0	0.5	2.0	100.0%	-3.4
2423	AT3G47590.1   esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase Cln1 (Butyrivibrio fibrisolvens) GI:1622732; contains Interpro entry IPR000379   chr3:17546605-17548508 REVERSE   Aliases: F1P2.140	7.8	8.5	-0.6	-2.0	100.0%	-3.0
2424	AT4G36180.1   leucine-rich repeat family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr4:17120088-17123844 REVERSE   Aliases: F23E13.70, F23E13_70	4.8	5.8	-1.0	-2.0	100.0%	-3.1
2425	AT3G05400.1   sugar transporter, putative, similar to sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701, integral membrane protein GB:U43629 from (Beta vulgaris); contains Pfam profile PF00083: major facilitator superfamily protein   chr3:1549592-1554154 FORWARD   Aliases: F22F7.16, F22F7_16	4.5	5.5	-1.0	-2.0	100.0%	-2.8
2426	AT5G43360.1   Symbol: PHT3   inorganic phosphate transporter (PHT3), identical to inorganic phosphate transporter (Arabidopsis thaliana) GI:2780347   chr5:17426752-17428442 FORWARD   Aliases: ATPT4, MWF20.5, MWF20_5	6.8	5.0	1.9	2.0	100.0%	-3.0
2427	AT1G14000.1   protein kinase family protein / ankyrin repeat family protein, contains Pfam profiles: PF00069 protein kinase domain, PF00023 ankyrin repeat   chr1:4797355-4800278 FORWARD   Aliases: F7A19.9, F7A19_9	7.9	8.6	-0.8	-2.0	100.0%	-3.1
2428	AT1G51440.1   lipase class 3 family protein, similar to DEFECTIVE IN ANTHOR DEHISCENCE1 (Arabidopsis thaliana) GI:16215706, lipase (Dianthus caryophyllus) GI:4103627; contains Pfam profile PF01764: Lipase   chr1:19074585-19076362 FORWARD   Aliases: F5D21.19, F5D21_19	3.3	3.8	-0.5	-2.0	100.0%	-3.1
2429	AT4G02800.1   expressed protein, similar to A. thaliana hypothetical protein T6B20.12 (1946366)   chr4:1250077-1251681 FORWARD   Aliases: T5J8.12, T5J8_12	3.2	3.5	-0.4	-2.0	100.0%	-3.4
2430	AT5G09620.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, predicted proteins, Arabidopsis thaliana and Drosophila melanogaster contains Pfam profile PF00564: PB1 domain   chr5:2983450-2985436 REVERSE   Aliases: F17I14.190, F17I14_190	7.6	7.1	0.5	2.0	100.0%	-3.4
2431	AT3G57070.1   glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	4.3	4.0	0.3	2.0	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2432	AT3G46790.1   Symbol: CRR2   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:17242758-17244933 REVERSE   Aliases: CHLORORESPIRATORY REDUCTION 2, T6H20.180	6.3	7.0	-0.7	-2.0	100.0%	-3.5
2433	AT5G53060.1   KH domain-containing protein   chr5:21532252-21535663 FORWARD   Aliases: MNB8.12, MNB8_12	4.9	5.6	-0.6	-2.0	100.0%	-3.1
2434	AT5G55830.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:22611881-22614069 FORWARD   Aliases: MDF20.27, MDF20_27	2.8	3.3	-0.4	-2.0	100.0%	-3.4
2435	AT3G53560.1   chloroplast lumen common family protein   chr3:19870605-19872009 REVERSE   Aliases: F4P12.260	6.3	7.1	-0.8	-2.0	100.0%	-3.0
2436	AT5G33300.1   chromosome-associated kinesin-related, contains weak similarity to chromosome-associated kinesin KIF4A (Chromokinesin) (Swiss-Prot:P33174) (Mus musculus)   chr5:12579660-12582970 REVERSE   Aliases: F19N2.20, F19N2_20	4.1	4.6	-0.5	-2.0	100.0%	-3.2
2437	AT5G54660.1   heat shock protein-related, contains weak similarity to 17.6 kDa class I heat shock protein (HSP 17.6) (Swiss-Prot:P13853) (Arabidopsis thaliana)   chr5:22221131-22222378 FORWARD   Aliases: MRB17.16, MRB17_16	7.0	6.3	0.7	2.0	100.0%	-3.2
2438	AT3G44200.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.7	5.3	-0.6	-2.0	100.0%	-3.0
2439	AT4G12080.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr4:7239213-7241488 FORWARD   Aliases: F16J13.150, F16J13_150	7.9	7.0	0.8	2.0	100.0%	-3.1
2440	AT3G24820.1   BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	5.9	5.4	0.5	2.0	100.0%	-3.2
2441	AT5G14750.1   Symbol: WER   myb family transcription factor (MYB66) / werewolf (WER), contains PFAM profile: Myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB66) mRNA, partial cds GI:3941491; identical to GP:9755743 myb transcription factor werewolf (WER)/ MYB66 {Arabidopsis thaliana}   chr5:4763455-4764741 REVERSE   Aliases: T9L3.50, T9L3_50, WER1, WEREWOLF 1	2.5	2.8	-0.3	-2.0	100.0%	-3.8
2442	AT2G26700.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr2:11375691-11378092 FORWARD   Aliases: F18A8.7, F18A8_7	2.4	2.8	-0.4	-2.0	100.0%	-3.4
2443	AT1G51940.1   protein kinase family protein / peptidoglycan-binding LysM domain-containing protein, contains protein kinases ATP-binding region signature, PROSITE:PS00107   chr1:19299598-19302787 REVERSE   Aliases: T14L22.13, T14L22_13	6.2	6.8	-0.6	-2.0	100.0%	-3.0
2444	AT5G05270.2   chalcone-flavanone isomerase family protein, contains very low similarity to chalcone-flavanone isomerase (chalcone isomerase), GI:1705761 from Vitis vinifera; contains Pfam profile PF02431: Chalcone-flavanone isomerase   chr5:1563431-1565007 FORWARD   Aliases: K18I23.7, K18I23_7	4.1	4.7	-0.5	-2.0	100.0%	-3.1
2445	AT2G21510.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein, Saccharomyces cerevisiae; contains Pfam profile PF00226 DnaJ domain   chr2:9217735-9220138 REVERSE   Aliases: F3K23.27, F3K23_27	3.9	3.3	0.6	2.0	100.0%	-3.1
2446	AT2G32770.3   purple acid phosphatase (PAP13), identical to purple acid phosphatase (PAP13) (Arabidopsis thaliana) GI:20257489; contains Pfam profile PF00149: Ser/Thr protein phosphatase   chr2:13902915-13905354 FORWARD   Aliases: F24L7.9, F24L7_9	2.9	3.3	-0.3	-2.0	100.0%	-3.4
2447	AT1G15230.1   expressed protein, ESTs gb:R30529, gb:Z48463, gb:Z48467, gb:AA597369 and gb:AA394772 come from this gene	6.6	5.9	0.7	2.0	100.0%	-3.2
2448	AT4G02170.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g38700.1); similar to disease resistance gene [Pinus sylvestris] (GB:AAR36911.1)   chr4:958049-958641 FORWARD   Aliases: T10M13.17, T10M13_17	2.5	2.3	0.2	2.0	100.0%	-4.0
2449	AT3G05580.1   serine/threonine protein phosphatase, putative, similar to serine/threonine protein phosphatase PP1 isozyme 8 SP:O82734 from (Arabidopsis thaliana)   chr3:1617853-1619995 REVERSE   Aliases: F18C1.15, F18C1_15	5.8	5.0	0.8	2.0	100.0%	-3.0
2450	AT5G42480.1   Symbol: ARC6   DNAJ plastid division protein (ARC6), almost identical to dnaJ plastid division protein ARC6 (GI:33436339) (Arabidopsis thaliana); low similarity to cell division protein Ftn2 (Synechococcus sp. PCC 7942) GI:16226084; contains Pfam profile PF00226: DnaJ domain   chr5:17002410-17005668 FORWARD   Aliases: ACCUMULATION AND REPLICATION OF CHLOROPLASTS 6, MDH9.18, MDH9_18	8.4	8.8	-0.5	-2.0	100.0%	-3.2
2451	AT5G56090.1   cytochrome oxidase assembly family protein, contains PF02628: Cytochrome oxidase assembly protein   chr5:22731744-22734061 FORWARD   Aliases: MDA7.15, MDA7_15	7.3	8.6	-1.3	-2.0	100.0%	-2.9
2452	AT2G26340.1   expressed protein   chr2:11222353-11223701 FORWARD   Aliases: T1D16.2, T1D16_2	7.5	6.9	0.6	2.0	100.0%	-3.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2453	AT1G24625.1   zinc finger (C2H2 type) family protein (ZFP7), identical to zinc finger protein, ZFP7 gi:790685:gb:AAA87303; contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:8725869-8727198 REVERSE   Aliases: F21J9.29	6.6	6.2	0.5	2.0	100.0%	-3.5
2454	AT5G23730.1   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At5g52250.1); similar to COP1 homolog [Lycopersicon esculentum] (GB:AAC98912.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr5:8005237-8006633 FORWARD   Aliases: MRO11.23, MRO11_23	6.9	6.2	0.7	2.0	100.0%	-3.2
2455	AT3G46230.1   Symbol: ATHSP17.4   17.4 kDa class I heat shock protein (HSP17.4-CI), identical to 17.4 kDa class I heat shock protein SP:P19036 from (Arabidopsis thaliana)   chr3:16994886-16995826 REVERSE   Aliases: F12M12.200, SMALL HEAT SHOCK PROTEIN 17.4	6.2	5.5	0.8	2.0	100.0%	-3.0
2456	AT2G31180.1   myb family transcription factor (MYB14), similar to myb-related transcription factor GI:1370140 from (Lycopersicon esculentum)   chr2:13293798-13295252 REVERSE   Aliases: F16D14.2	3.8	4.3	-0.5	-2.0	100.0%	-3.3
2457	AT3G57040.1   Symbol: ARR9   two-component responsive regulator / response reactor 4 (RR4), identical to response reactor4 GI:3273202 from (Arabidopsis thaliana); contains Pfam profile: PF00072 response regulator receiver domain   chr3:21120593-21122411 FORWARD   Aliases: ATRR4, F24I3.120, F24I3_120, RESPONSE REACTOR 4	3.6	4.5	-0.9	-2.0	100.0%	-2.9
2458	AT1G69920.1   Symbol: ATGSTU12   glutathione S-transferase, putative, similar to glutathione transferase GB:CAA09188 (Alopecurus myosuroides); supported by cDNA gi:15451157 gb:AY050343.   chr1:26337913-26339206 REVERSE   Aliases: T17F3.5, T17F3_5	4.9	6.1	-1.1	-2.0	100.0%	-2.7
2459	AT4G34350.1   Symbol: CLB6   Arabidopsis ISPH is involved in the plastid nonmevalonate pathway of isoprenoid biosynthesis. It was shown to complement the lethal phenotype of E.coli ispH mutant and is therefore most likely encodes a protein with 4-hydroxy-3-methylbut-2-en-1-yl diphosphate reductase activity involved in the last step of mevalonate-independent isopentenyl biosynthesis.   chr4:16428484-16431117 REVERSE   Aliases: CHLOROPLAST BIOGENESIS, F10M10.120, F10M10_120, ISPH	10.1	9.4	0.8	2.0	100.0%	-3.1
2460	AT2G46420.1   expressed protein   chr2:19060759-19064163 FORWARD   Aliases: F11C10.11	6.6	5.1	1.5	2.0	100.0%	-2.8
2461	NA	4.7	4.2	0.5	2.0	100.0%	-3.6
2462	AT1G20110.1   zinc finger (FYVE type) family protein, contains Pfam profile: PF01363 FYVE zinc finger   chr1:6971476-6974812 FORWARD   Aliases: T20H2.10, T20H2_10	9.1	8.5	0.5	2.0	100.0%	-3.3
2463	AT1G53540.1   17.6 kDa class I small heat shock protein (HSP17.6C-CI) (AA 1-156), identical to (17.6 kDa class I heat shock protein (HSP 17.6) (AA 1-156)(SP:P13853) (GI:4376161) (Arabidopsis thaliana) (Nucleic Acids Res. 17 (19), 7995 (1989))   chr1:19984130-19984775 FORWARD   Aliases: F22G10.20	5.7	5.0	0.7	2.0	100.0%	-3.1
2464	AT3G06580.1   Symbol: GAL1   galactokinase (GAL1), identical to galactokinase (Galactose kinase) (Arabidopsis thaliana) SWISS-PROT:Q9SEE5   chr3:2048911-2052031 REVERSE   Aliases: F5E6.9, F5E6_9, GALACTOSE KINASE 1	9.1	10.4	-1.3	-2.0	100.0%	-3.0
2465	AT5G63850.1   Symbol: AAP4   amino acid transporter 4, putative (AAP4), identical to amino acid transporter GI:608671 from (Arabidopsis thaliana);   chr5:25568281-25570746 FORWARD   Aliases: MGI19.6, MGI19_6	11.2	8.5	2.7	2.0	100.0%	-2.8
2466	AT1G70510.1   Symbol: KNAT2   homeobox protein knotted-1 like 2 (KNAT2) (K1), identical to homeobox protein knotted-1 like 2 ( KNAT2/ ATK1) SP: from (Arabidopsis thaliana)   chr1:26580168-26586094 FORWARD   Aliases: F24J13.8, F24J13_8, KNOTTED LIKE FROM ARABIDOPSIS THALIANA 2	3.1	2.7	0.3	2.0	100.0%	-3.6
2467	AT5G09530.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:2959735-2961272 REVERSE   Aliases: T5E8.2	2.8	3.5	-0.7	-2.0	100.0%	-3.3
2468	AT5G56270.1   Symbol: WRKY2   WRKY family transcription factor   chr5:22796919-22800494 FORWARD   Aliases: ATWRKY2, MXK23.1, MXK23_1	4.9	4.4	0.5	2.0	100.0%	-3.1
2469	AT5G16440.1   Symbol: IPP1   similar to MutT/nudix family protein [Arabidopsis thaliana] (TAIR:At1g79690.1); similar to isopentenyl pyrophosphate:dimethylallyl pyrophosphate isomerase [Adonis palaestina] (GB:AAF29973.1); similar to isopentenyl pyrophosphate isomerase [Pueraria montana var. lobata] (GB:AAQ84167.1); contains InterPro domain Isopentenyl-diphosphate delta-isomerase (InterPro:IPR002667); contains InterPro domain NUDIX hydrolase (InterPro:IPR000086)   chr5:5371743-5373738 FORWARD   Aliases: IDI1, ISOPENTENYL DIPHOSPHATE ISOMERASE, MQK4.17, MQK4_17	6.2	7.9	-1.7	-2.0	100.0%	-3.0
2470	AT1G55900.1   Symbol: TIM50   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr1:20906733-20909393 FORWARD   Aliases: EMB1860, EMBRYO DEFECTIVE 1860, F14J16.15, F14J16_15	6.4	7.4	-1.0	-2.0	100.0%	-2.9
2471	AT3G47160.1   expressed protein, similar to MTD2 (Medicago truncatula) GI:9294812; supporting cDNA gi:25083983:gb:BT002136.1:   chr3:17370976-17372990 REVERSE   Aliases: F13I12.210	6.8	6.0	0.8	2.0	100.0%	-2.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2472	AT1G54690.1   histone H2A, putative, strong similarity to histone H2A GI:3204129 SP:O65759 from Cicer arietinum, Picea abies SP:P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:20417983-20418954 REVERSE   Aliases: T22H22.12, T22H22_12	9.4	10.7	-1.3	-2.0	100.0%	-2.9
2473	AT4G02200.2   drought-responsive family protein, similar to drought-induced mRNA, Di19 (Arabidopsis thaliana) gi:469110:emb:CAA55321   chr4:972707-974692 FORWARD   Aliases: T2H3.13	8.3	7.5	0.8	2.0	100.0%	-3.1
2474	AT4G11270.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); related to TGF-beta resistance-associated protein TRAG (GI:15624071) {Mus musculus}; similar to beta-transducin repeats containing protein - Homo sapiens,PID:e1284220; 3' EST no_NP:TC8031   chr4:6854457-6859660 FORWARD   Aliases: F8L21.60, F8L21_60	6.9	7.5	-0.7	-2.0	100.0%	-3.2
2475	AT1G68880.1   bZIP transcription factor family protein, similar to common plant regulatory factor 6 GI:9650826 from (Petroselinum crispum); contains Pfam profile: PF00170 bZIP transcription factor   chr1:25898162-25898578 REVERSE   Aliases: T6L1.5	4.6	5.6	-1.0	-2.0	100.0%	-3.0
2476	AT1G31360.1   DNA helicase, putative (RECQ12), nearly identical to DNA Helicase (Arabidopsis thaliana) GI:11121445   chr1:11232314-11237511 FORWARD   Aliases: T19E23.16, T19E23_16	3.2	3.9	-0.7	-2.0	100.0%	-3.5
2477	AT2G42430.1   Symbol: LBD16   LOB domain protein 16 / lateral organ boundaries domain protein 16 (LBD16), identical to LOB DOMAIN 16 (Arabidopsis thaliana) GI:17227162   chr2:17670522-17672370 FORWARD   Aliases: MHK10.15, MHK10_15	4.2	4.8	-0.6	-2.0	100.0%	-3.1
2478	AT1G22920.2   Symbol: AJH1   COP9 signalosome subunit 5B / CSN subunit 5B (CSN5B) / c-JUN coactivator protein AJH1, putative (AJH1), COP9 complex subunit CSN5-1; identical to Arabidopsis homologs of a c-Jun coactivator AJH1 GI:3641314 from (Arabidopsis thaliana); identical to cDNA CSN complex subunit 5B (CSN5B) GI:18056662; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr1:8109703-8112040 REVERSE   Aliases: CSN5, CSN5B, F19G10.12, F19G10_12, JAB1, PUTATIVE JUN KINASE ACTIVATOR	6.8	7.9	-1.1	-2.0	100.0%	-3.0
2479	AT1G26380.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:9126724-9128515 REVERSE   Aliases: T1K7.24, T1K7_24	2.3	2.5	-0.2	-2.0	100.0%	-4.0
2480	AT5G39970.1   expressed protein, low similarity to up-regulated by thyroid hormone in tadpoles; expressed specifically in the tail and only at metamorphosis; membrane bound or extracellular protein; C-terminal basic region (Xenopus laevis) GI:1234787   chr5:16015253-16018850 FORWARD   Aliases: MYH19.17, MYH19_17	4.7	3.9	0.8	2.0	100.0%	-3.0
2481	AT1G62300.1   Symbol: WRKY6   WRKY family transcription factor, similar to putative DNA-binding protein GI:7268215 from (Arabidopsis thaliana)   chr1:23020348-23022944 REVERSE   Aliases: F19K23.22, F19K23_22	4.6	5.6	-1.0	-2.0	100.0%	-2.9
2482	AT2G47450.1   Symbol: CAO   chloroplast signal recognition particle component (CAO), nearly identical to CAO (Arabidopsis thaliana) GI:4102582   chr2:19479751-19481384 FORWARD   Aliases: CHAOS, CHLOROPHYLL A/B BINDING PROTEIN HARVESTING ORGANELLE SPECIFIC, CPSRP43, T30B22.25	9.6	8.7	0.9	2.0	100.0%	-3.1
2483	AT2G29630.2   thiamine biosynthesis family protein / thiC family protein, contains Pfam profile: PF01964 ThiC family   chr2:12674111-12677388 FORWARD   Aliases: T27A16.27, T27A16_27	7.5	6.5	1.0	2.0	100.0%	-2.8
2484	AT1G15370.1   expressed protein   chr1:5287057-5288506 FORWARD   Aliases: F9L1.32, F9L1_32	9.1	8.4	0.7	2.0	100.0%	-3.2
2485	AT5G13760.1   expressed protein, similar to unknown protein (gb AAF63775.1)   chr5:4442017-4444938 FORWARD   Aliases: MXE10.1, MXE10_1	4.7	3.9	0.8	2.0	100.0%	-3.1
2486	AT2G20810.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr2:8964874-8966861 FORWARD   Aliases: F5H14.44	6.3	6.8	-0.5	-2.0	100.0%	-3.1
2487	AT2G41350.2   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At2g21980.1); similar to unnamed protein product [Mus musculus] (GB:BAC36526.1)   chr2:17238428-17240536 FORWARD   Aliases: F13H10.10, F13H10_10	7.4	8.1	-0.7	-2.0	100.0%	-3.1
2488	AT5G64980.1   expressed protein   chr5:25978001-25980461 REVERSE   Aliases: MXK3.21, MXK3_21	3.6	4.1	-0.6	-2.0	100.0%	-3.0
2489	AT4G16450.1   expressed protein   chr4:9280104-9280740 FORWARD   Aliases: DL4250W, FCAALL.388	10.3	10.8	-0.5	-2.0	100.0%	-3.5
2490	AT1G29680.1   expressed protein   chr1:10377503-10378947 REVERSE   Aliases: F15D2.23, F15D2_23	3.3	2.9	0.4	2.0	100.0%	-3.6
2491	AT1G29250.1   expressed protein, contains TIGRFAM TIGR00285: conserved hypothetical protein TIGR00285   chr1:10223252-10224713 REVERSE   Aliases: F28N24.7, F28N24_7	9.3	10.0	-0.7	-2.0	100.0%	-3.0
2492	AT1G64680.1   expressed protein   chr1:24039684-24041064 FORWARD   Aliases: F1N19.25, F1N19_25	5.5	4.9	0.7	2.0	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2493	AT5G62440.1   expressed protein   chr5:25089709-25091215 REVERSE   Aliases: AT5G62450, K19B1.5, K19B1_5	7.2	7.6	-0.5	-2.0	100.0%	-3.4
2494	AT4G37970.1   mannitol dehydrogenase, putative, similar to ELI3-2 (SP:Q02972), sinapyl alcohol dehydrogenase (Populus tremuloides) (gi:14279694); contains Pfam zinc-binding dehydrogenase domain PF00107   chr4:17849666-17852233 FORWARD   Aliases: F20D10.90, F20D10_90	5.8	6.6	-0.9	-2.0	100.0%	-2.9
2495	AT5G06700.1   expressed protein, strong similarity to unknown protein (emb:CAB82953.1)	7.9	8.8	-0.8	-2.0	100.0%	-3.1
2496	AT1G74430.1   Symbol: MYB95   myb family transcription factor (MYB95), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr1:27978842-27981095 FORWARD   Aliases: F1M20.11, F1M20_11, MYB95	3.7	3.1	0.6	2.0	100.0%	-3.3
2497	AT3G22150.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:7812975-7815497 FORWARD   Aliases: MKA23.11	3.1	3.5	-0.5	-2.0	100.0%	-3.3
2498	AT5G27740.1   expressed protein   chr5:9823744-9827068 FORWARD   Aliases: T1G16.70, T1G16_70	4.8	5.5	-0.7	-2.0	100.0%	-3.0
2499	AT3G20560.1   Symbol: ATPDIL5 3   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	6.4	7.1	-0.8	-2.0	100.0%	-3.0
2500	AT5G15810.1   N2,N2-dimethylguanosine tRNA methyltransferase family protein, similar to SP:Q9P804 N(2),N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32) (tRNA(guanine-26,N(2)-N(2)) methyltransferase) {Schizosaccharomyces pombe}; contains Pfam profile PF02005: N2,N2-dimethylguanosine tRNA methyltransferase   chr5:5157801-5161361 FORWARD   Aliases: F14F8.190, F14F8_190	6.7	7.4	-0.6	-2.0	100.0%	-3.1
2501	AT5G38980.1   expressed protein   chr5:15624001-15624579 FORWARD   Aliases: K15E6.160, K15E6_160	3.1	2.8	0.3	2.0	100.0%	-3.6
2502	AT3G56900.1   aladin-related / adracalin-related, weak similarity to SP:Q9NRG9 Aladin (Adracalin) (GL003) {Homo sapiens}; non-consensus AT-AC splice sites at intron 6	5.5	6.4	-0.9	-2.0	100.0%	-2.9
2503	AT3G05230.2   similar to signal peptidase subunit family protein [Arabidopsis thaliana] (TAIR:At5g27430.1); similar to signal peptidase protein-like [Cucumis melo] (GB:AAT52230.1); contains InterPro domain Signal peptidase subunit (InterPro:IPR007653)   chr3:1492161-1493395 FORWARD   Aliases: T12H1.20, T12H1_20	6.4	7.1	-0.7	-2.0	100.0%	-3.0
2504	AT1G25250.1   zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	2.6	2.4	0.2	2.0	100.0%	-4.0
2505	AT1G10270.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat; similar to ESTs gb:R30192 and gb:AA651017   chr1:3363506-3366490 FORWARD   Aliases: F14N23.15, F14N23_15	7.4	7.9	-0.5	-2.0	100.0%	-3.1
2506	AT1G53460.1   expressed protein   chr1:19958158-19960300 REVERSE   Aliases: T3F20.22, T3F20_22	9.8	10.4	-0.6	-2.0	100.0%	-3.1
2507	AT1G35550.1   elongation factor Tu C-terminal domain-containing protein, similar to SP:P13905 Elongation factor 1-alpha (EF-1-alpha) {Arabidopsis thaliana}; contains Pfam profile PF03143: Elongation factor Tu C-terminal domain   chr1:13112484-13113014 FORWARD   Aliases: F15O4.37	5.7	6.4	-0.7	-2.0	100.0%	-2.9
2508	AT5G49280.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:19993820-19994675 REVERSE   Aliases: K21P3.16, K21P3_16	5.8	5.1	0.7	2.0	100.0%	-3.0
2509	AT1G62830.1   amine oxidase family protein / SWIRM domain-containing protein, contains Pfam profile: PF01593 Flavin containing amine oxidase   chr1:23268155-23270867 REVERSE   Aliases: F23N19.21, F23N19_21	4.8	5.2	-0.4	-2.0	100.0%	-3.4
2510	AT2G27810.2   similar to xanthine/uracil permease family protein [Arabidopsis thaliana] (TAIR:At4g38050.1); similar to putative permease [Gossypium hirsutum] (GB:AAT64019.1); contains InterPro domain Xanthine/uracil/vitamin C permease family (InterPro:IPR006043)	4.3	5.0	-0.6	-2.0	100.0%	-3.1
2511	AT3G17770.1   dihydroxyacetone kinase family protein, contains Pfam domains, PF02733: DAK1 domain and PF02734: DAK2 domain   chr3:6081677-6085963 REVERSE   Aliases: MIG5.7	6.0	6.7	-0.7	-2.0	100.0%	-3.1
2512	AT5G18150.1   expressed protein, similar to unknown protein (emb:CAB87627.1)   chr5:6000016-6000333 REVERSE   Aliases: MRG7.11, MRG7_11	8.0	7.5	0.5	2.0	100.0%	-3.2
2513	AT1G64960.1   expressed protein   chr1:24133581-24137712 FORWARD   Aliases: F13O11.26, F13O11_26	5.2	5.6	-0.4	-2.0	100.0%	-3.6
2514	AT5G43180.1   expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599   chr5:17353566-17355080 REVERSE   Aliases: K24F5.2, K24F5_2	5.1	4.0	1.1	2.0	100.0%	-2.9
2515	AT5G06730.1   peroxidase, putative, similar to peroxidase (Arabidopsis thaliana) gi:1491617:emb:CAA68212   chr5:2079956-2081685 REVERSE   Aliases: MPH15.9, MPH15_9	6.2	7.8	-1.6	-2.0	100.0%	-2.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2516	AT2G45790.1   eukaryotic phosphomannomutase family protein, contains Pfam profile: PF03332 eukaryotic phosphomannomutase   chr2:18862853-18865442 FORWARD   Aliases: F4I18.23	9.9	10.7	-0.8	-2.0	100.0%	-3.3
2517	AT1G28395.3   expressed protein   chr1:9969428-9971504 REVERSE   Aliases: None	7.6	8.5	-0.9	-2.0	100.0%	-3.0
2518	AT3G45850.1   kinesin motor protein-related, kinesin-related protein TKRP125, Nicotiana tabacum, PIR:T02017   chr3:16866597-16871935 REVERSE   Aliases: F16L2.60	4.1	4.6	-0.5	-2.0	100.0%	-3.5
2519	AT3G60860.1   guanine nucleotide exchange family protein, similar to guanine nucleotide exchange factor, Homo sapiens, GI:5456754; contains Pfam profile PF01369: Sec7 domain   chr3:22495779-22502555 FORWARD   Aliases: T4C21.270	7.4	8.2	-0.8	-2.0	100.0%	-3.2
2520	AT5G55140.1   ribosomal protein L30 family protein, contains similarity to 50S ribosomal protein L30   chr5:22398262-22399254 FORWARD   Aliases: MCO15.9, MCO15_9	6.7	5.6	1.0	2.0	100.0%	-2.9
2521	AT1G08280.1   glycosyl transferase family 29 protein / sialyltransferase family protein, contains Pfam profile: PF00777 sialyltransferase (Glycosyltransferase family 29)   chr1:2608405-2609850 FORWARD   Aliases: T23G18.14, T23G18_14	5.5	6.4	-0.9	-2.0	100.0%	-2.9
2522	AT3G20300.1   expressed protein   chr3:7079623-7081925 REVERSE   Aliases: MQC12.4	4.2	3.8	0.4	2.0	100.0%	-3.5
2523	AT5G64260.1   Symbol: MSJ1.10   phosphate-responsive protein, putative, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region	7.3	6.2	1.2	2.0	100.0%	-2.8
2524	AT5G13830.1   FtsJ-like methyltransferase family protein, contains Pfam profile: PF01728 FtsJ-like methyltransferase   chr5:4467366-4468490 FORWARD   Aliases: MAC12.22, MAC12_22	4.0	4.4	-0.4	-2.0	100.0%	-3.4
2525	AT4G31900.1   chromatin remodeling factor, putative, strong similarity to chromatin remodeling factor CHD3 (PICKLE) (Arabidopsis thaliana) GI:6478518; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr4:15431534-15438449 FORWARD   Aliases: F11C18.100, F11C18_100	2.3	2.6	-0.3	-2.0	100.0%	-3.8
2526	AT1G48850.3   Symbol: EMB1144   similar to 3-phosphoshikimate 1-carboxyvinyltransferase, putative / 5-enolpyruvylshikimate-3-phosphate, putative / EPSP synthase, putative [Arabidopsis thaliana] (TAIR:At1g48860.1); similar to chorismate synthase 1 [Lycopersicon esculentum] (GB:CAA79859.1); contains InterPro domain Chorismate synthase (InterPro:IPR000453)   chr1:18068245-18071758 REVERSE   Aliases: EMB1144, EMBRYO DEFECTIVE 1144, T24P22.3, T24P22_3	10.9	11.6	-0.7	-2.0	100.0%	-3.5
2527	AT5G09900.2   Symbol: EMB2107   26S proteasome regulatory subunit, putative (RPN5), p55 protein-like   chr5:3089279-3092537 REVERSE   Aliases: EMB2107, EMBRYO DEFECTIVE 2107, MYH9.11, MYH9_11	7.7	8.5	-0.7	-2.0	100.0%	-3.3
2528	AT1G02280.1   Symbol: TOC33   GTP-binding protein (TOC33), identical to atToc33 protein (GI:11557973) (Arabidopsis thaliana); Carboxyl-terminal end highly similar to GTP-binding protein SP:U43377, location of EST gb:AA394770 and gb:R30089; identical to cDNA for chloroplast atToc33 protein GI:11557972	7.0	8.0	-1.0	-2.0	100.0%	-2.9
2529	AT2G15760.1   calmodulin-binding protein, similar to AR781 GI:1669593 from (Arabidopsis thaliana); AR781 complements pheromone receptor deficient mutant of Shizosaccharomyces pombe   chr2:6872692-6873959 REVERSE   Aliases: F9O13.1	5.9	6.3	-0.4	-2.0	100.0%	-3.4
2530	AT5G52470.1   Symbol: FIB1   fibrillarlin 1 (FBR1) (FIB1) (SKIP7), identical to fibrillarlin 1 GI:9965653 from (Arabidopsis thaliana); C-terminus identical to SKP1 interacting partner 7 GI:10716959 from (Arabidopsis thaliana); contains Pfam domain PF01269: Fibrillarlin   chr5:21311454-21313902 FORWARD   Aliases: ATFBR1, ATFIB1, FBR1, FIBRILLARIN 1, K24M7.22, K24M7_22, SKIP7, SKP1 INTERACTING PARTNER 7	11.0	11.4	-0.4	-2.0	100.0%	-3.7
2531	AT3G63180.1   expressed protein   chr3:23347293-23351211 REVERSE   Aliases: F16M2.30	4.4	4.9	-0.5	-2.0	100.0%	-3.5
2532	AT3G18760.1   ribosomal protein S6 family protein, contains TIGRFAM profile TIGR00166: ribosomal protein S6   chr3:6457696-6459633 REVERSE   Aliases: MVE11.12	7.3	8.1	-0.8	-2.0	100.0%	-3.0
2533	AT5G57160.1   Symbol: ATLIG4	5.8	6.5	-0.7	-2.0	100.0%	-3.2
2534	AT5G53120.3   Symbol: SPDS3   spermidine synthase, putative / putrescine aminopropyltransferase, putative, similar to SP:O82147 Spermidine synthase (EC 2.5.1.16) (Putrescine aminopropyltransferase) (SPDSY) {Coffea arabica}; contains Pfam profile PF01564: Spermine/spermidine synthase   chr5:21552058-21555474 FORWARD   Aliases: MFH8.5, MFH8_5, SPERMIDINE SYNTHASE 3, SPMS	10.4	11.1	-0.7	-2.0	100.0%	-3.5
2535	AT5G64410.1   Symbol: ATOPT4	3.8	4.7	-1.0	-2.0	100.0%	-2.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2536	AT3G20520.1   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to glycerophosphodiester phosphodiesterase (GI:1399038) (Borrelia hermsii)   chr3:7162834-7165865 FORWARD   Aliases: K10D20.6	3.7	3.3	0.4	2.0	100.0%	-3.4
2537	AT5G17620.1   expressed protein   chr5:5805762-5808563 REVERSE   Aliases: K10A8.100, K10A8_100	5.4	6.3	-0.9	-2.0	100.0%	-3.2
2538	AT1G09220.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:2977794-2978970 REVERSE   Aliases: T12M4.7, T12M4_7	3.0	3.3	-0.3	-2.0	100.0%	-3.8
2539	AT3G15120.1   AAA-type ATPase family protein, contains PROSITE domains, PS00674: AAA-protein family signature and PS00017: ATP/GTP-binding site motif A (P-loop)   chr3:5088494-5095489 REVERSE   Aliases: F4B12.4	6.2	6.7	-0.5	-2.0	100.0%	-3.3
2540	AT5G01740.1   expressed protein, wound-inducible protein wun1 protein - Solanum tuberosum, PIR:JQ0398   chr5:280719-281442 FORWARD   Aliases: T20L15.10, T20L15_10	4.6	3.8	0.8	2.0	100.0%	-2.9
2541	AT3G24120.2   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:8705643-8708322 REVERSE   Aliases: MUJ8.2	6.7	5.9	0.8	2.0	100.0%	-3.3
2542	AT1G29160.1   Dof-type zinc finger domain-containing protein, similar to ascorbate oxidase promoter-binding protein GB:D45066 GI:853689 from (Cucurbita maxima)   chr1:10183783-10184310 REVERSE   Aliases: F28N24.35	6.5	6.2	0.3	2.0	100.0%	-3.5
2543	AT1G19835.1   expressed protein, contains Pfam PF05911: Plant protein of unknown function (DUF869)   chr1:6855943-6860323 REVERSE   Aliases: F14P1.24, F14P1_24	8.7	9.2	-0.6	-2.0	100.0%	-3.4
2544	AT3G22750.1   protein kinase, putative, similar to protein kinase ATMRK1 (Arabidopsis thaliana) gi:2351097:dbj:BAA22079   chr3:8037223-8039910 REVERSE   Aliases: MWI23.12	4.7	5.3	-0.6	-2.0	100.0%	-3.0
2545	AT1G14150.2   oxygen evolving enhancer 3 (PsbQ) family protein, extrinsic pII protein; contains Pfam profile PF05757: Oxygen evolving enhancer protein 3 (PsbQ)   chr1:4839850-4840449 FORWARD   Aliases: F7A19.23, F7A19_23	3.1	2.6	0.5	2.0	100.0%	-3.4
2546	AT1G70130.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733   chr1:26413406-26415464 REVERSE   Aliases: F20P5.15, F20P5_15	2.8	3.2	-0.3	-2.0	100.0%	-3.5
2547	AT5G39250.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr5:15741758-15742984 FORWARD   Aliases: K3K3.16, K3K3_16	6.0	5.6	0.4	2.0	100.0%	-3.3
2548	AT3G54720.1   Symbol: AMP1   glutamate carboxypeptidase, putative (AMP1), identical to GI:15624092 glutamate carboxypeptidase {Arabidopsis thaliana}; ileal peptidase, Rattus norvegicus, EMBL:AF009921; identical to cDNA glutamate carboxypeptidase (AMP1) GI:15624091; contains Pfam profiles PF04389: Peptidase family M28, PF04253: Transferrin receptor-like dimerisation domain and PF02225 PA domain	4.8	5.3	-0.5	-2.0	100.0%	-3.3
2549	AT1G48240.1   Symbol: ATNPSN12   novel plant SNARE 12 (NPSN12), identical to Novel plant SNARE 12 (AtNPSN12) (Swiss-Prot:Q9LNH6) (Arabidopsis thaliana)   chr1:17812676-17815563 REVERSE   Aliases: F21D18.4, NPSN12	7.3	6.1	1.1	2.0	100.0%	-3.1
2550	AT3G47560.2   esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase CinI (Butyrivibrio fibrisolvens) GI:1622732; contains InterPro entry IPR000379   chr3:17536162-17537963 REVERSE   Aliases: F1P2.110	6.5	7.6	-1.1	-2.0	100.0%	-2.9
2551	AT4G24190.2   Symbol: SHD   shepherd protein (SHD) / clavata formation protein, putative, nearly identical to SHEPHERD (Arabidopsis thaliana) GI:19570872; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein   chr4:12551731-12555915 REVERSE   Aliases: SHEPHERD, T22A6.20, T22A6_20	11.2	12.0	-0.8	-2.0	100.0%	-3.4
2552	AT3G21610.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g67600.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82112.1); contains InterPro domain Protein of unknown function DUF212 (InterPro:IPR003832)	7.2	6.5	0.7	2.0	100.0%	-3.3
2553	AT1G19110.1   inter-alpha-trypsin inhibitor heavy chain-related, similar to SP:Q61704 Inter-alpha-trypsin inhibitor heavy chain H3 precursor {Mus musculus}; contains Pfam profile PF00092: von Willebrand factor type A domain   chr1:6602117-6605899 FORWARD   Aliases: F14D16.26, F14D16_26	8.8	8.4	0.4	2.0	100.0%	-3.3
2554	AT1G01480.2   Symbol: ACS2   1-aminocyclopropane-1-carboxylate synthase 2 / ACC synthase 2 (ACS2) (ACC1), identical to 1-aminocyclopropane-1-carboxylate synthase SP:Q06402 (GI:166578) from (Arabidopsis thaliana)	3.7	4.2	-0.6	-2.0	100.0%	-3.2
2555	AT1G53390.1   ABC transporter family protein, similar to ATP-binding cassette, sub-family G, member 2 (Placenta-specific ATP-binding cassette transporter) (Breast cancer resistance protein) SP:Q9UNQ0 from (Homo sapiens)   chr1:19921715-19927475 FORWARD   Aliases: F12M16.28, F12M16_28	4.9	5.4	-0.5	-2.0	100.0%	-3.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2556	AT1G26100.1   cytochrome B561 family protein, contains Pfam domain, PF03188: Cytochrome b561   chr1:9022588-9024068 REVERSE   Aliases: F14G11.7, F14G11_7	5.5	5.9	-0.4	-2.0	100.0%	-3.4
2557	AT1G12450.1   expressed protein   chr1:4244308-4245990 FORWARD   Aliases: F5O11.19, F5O11_19	4.3	3.8	0.5	2.0	100.0%	-3.4
2558	AT1G68810.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.5	4.8	0.7	2.0	100.0%	-3.0
2559	AT1G19860.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:6891420-6894708 REVERSE   Aliases: F6F9.9, F6F9_9	4.2	4.7	-0.5	-2.0	100.0%	-3.4
2560	AT3G53950.1   glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594   chr3:19986597-19988417 FORWARD   Aliases: F5K20.250	6.2	5.5	0.6	2.0	100.0%	-3.3
2561	AT5G63950.1   SNF2 domain-containing protein / helicase domain-containing protein, low similarity to SP:Q03468 Excision repair protein ERCC-6 (Cockayne syndrome protein CSB) {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr5:25609182-25615731 REVERSE   Aliases: MBM17.5, MBM17_5	3.5	3.9	-0.3	-2.0	100.0%	-3.5
2562	AT2G42540.2   Symbol: COR15A	6.5	5.0	1.5	2.0	100.0%	-2.9
2563	AT2G23950.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr2:10194171-10197365 REVERSE   Aliases: T29E15.15, T29E15_15	5.0	4.2	0.8	2.0	100.0%	-3.0
2564	AT3G53540.1   expressed protein   chr3:19857478-19861946 REVERSE   Aliases: F4P12.240	5.3	5.8	-0.5	-2.0	100.0%	-3.3
2565	AT1G02750.1   drought-responsive family protein, contains similarity to drought-induced mRNA, Di19 (Arabidopsis thaliana) gi:469110:emb:CAA55321   chr1:602673-604286 FORWARD   Aliases: T14P4.27	5.0	4.4	0.6	2.0	100.0%	-3.1
2566	AT3G25980.1   mitotic spindle checkpoint protein, putative (MAD2), identical to Swiss-Prot:Q9LU93 mitotic spindle checkpoint protein MAD2 (Arabidopsis thaliana)   chr3:9504469-9505639 FORWARD   Aliases: MPE11.16	5.0	4.5	0.4	2.0	100.0%	-3.5
2567	AT5G59480.2   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:P53078 SSM1 protein {Saccharomyces cerevisiae}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:23996649-23998793 REVERSE   Aliases: F2O15.10, F2O15_10	8.1	9.6	-1.5	-2.0	100.0%	-2.9
2568	AT3G56130.3   similar to biotin/lipoyl attachment domain-containing protein [Arabidopsis thaliana] (TAIR:At1g52670.1); similar to acetyl-CoA carboxylasesubunit (biotin carboxyl carrier subunit) [Geobacillus kaustophilus HTA426] (GB:YP_148253.1); contains InterPro domain Biotin/lipoyl attachment (InterPro:IPR000089)   chr3:20837637-20840249 FORWARD   Aliases: F18O21.90	4.4	5.4	-1.0	-2.0	100.0%	-3.0
2569	AT3G53320.1   expressed protein   chr3:19780154-19783347 REVERSE   Aliases: F4P12.20	4.8	5.3	-0.5	-2.0	100.0%	-3.5
2570	AT5G66010.1   heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, similar to Heterogeneous nuclear ribonucleoprotein SP:P55795, SP:P31943, SP:P52597 {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain	5.7	5.2	0.5	2.0	100.0%	-3.3
2571	AT2G37310.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:15672181-15674154 REVERSE   Aliases: F3G5.10, F3G5_10	3.1	3.4	-0.3	-2.0	100.0%	-3.5
2572	AT5G03340.1   cell division cycle protein 48, putative / CDC48, putative, very strong similarity to SP:P54609 Cell division cycle protein 48 homolog {Arabidopsis thaliana}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain; supporting cDNA gi:26449351:dbj:AK117125.1   chr5:809947-813227 REVERSE   Aliases: F12E4.70, F12E4_70	6.4	7.0	-0.7	-2.0	100.0%	-3.0
2573	AT1G05940.1   Symbol: CAT9   amino acid permease family protein, low similarity to SP:P30823 High-affinity cationic amino acid transporter-1 (CAT-1) {Rattus norvegicus}; contains Pfam profile PF00324: Amino acid permease   chr1:1801177-1803975 REVERSE   Aliases: CATIONIC AMINO ACID TRANSPORTER 9, T21E18.1, T21E18_1	7.2	6.7	0.5	2.0	100.0%	-3.3
2574	AT1G74310.1   Symbol: ATHSP101   heat shock protein 101 (HSP101), identical to heat shock protein 101 GI:6715468 GB:AAF26423 from (Arabidopsis thaliana)   chr1:27939597-27943851 REVERSE   Aliases: F1O17.2, F1O17_2, HEAT SHOCK PROTEIN 101, HEAT SHOCK PROTEIN ATHSP101, HOT1, HSP101	5.7	5.2	0.5	2.0	100.0%	-3.2
2575	AT1G67360.2   rubber elongation factor (REF) family protein, contains Pfam profile: PF05755 rubber elongation factor protein (REF)   chr1:25240474-25241757 REVERSE   Aliases: F1N21.18	7.8	7.1	0.7	2.0	100.0%	-3.3
2576	AT3G04490.1   exportin-related, weak similarity to Exportin 4 (Exp4) (Swiss-Prot:Q9ESJ0) (Mus musculus) and (Swiss-Prot:Q9C0E2) (Homo sapiens)	5.0	5.9	-1.0	-2.0	100.0%	-2.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2577	AT3G26580.1   expressed protein   chr3:9760124-9761781 FORWARD   Aliases: MFE16.11	9.2	8.4	0.9	2.0	100.0%	-3.1
2578	AT3G05750.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g26910.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g58650.1); similar to serine-threonine rich antigen [Staphylococcus aureus] (GB:AAL58470.1)	2.7	3.0	-0.3	-2.0	100.0%	-3.7
2579	AT1G36380.1   expressed protein, similar to vanilloid receptor-like protein GB:AAD26363 from (Homo sapiens)   chr1:13702026-13702844 FORWARD   Aliases: F7F23.10, F7F23_10	7.3	6.5	0.8	2.0	100.0%	-3.3
2580	AT4G26555.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, similar to FK506-binding protein (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (SP:P25138) ({Neisseria meningitidis); contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases; similar to FK506-binding protein 39 kDa (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8) (SP:O74191) {Schizosaccharomyces pombe}   chr4:13404485-13406210 REVERSE   Aliases: None	6.2	5.6	0.6	2.0	100.0%	-3.3
2581	AT4G23960.1   F-box family protein, similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr4:12444775-12445333 FORWARD   Aliases: T32A16.130, T32A16_130	3.4	3.0	0.4	2.0	100.0%	-3.5
2582	AT5G20230.1   Symbol: ATBCB   plastocyanin-like domain-containing protein   chr5:6826508-6827601 FORWARD   Aliases: ARABIDOPSIS BLUE COPPER BINDING PROTEIN, BCB, F5O24.120, F5O24_120	5.9	4.6	1.3	2.0	100.0%	-3.0
2583	AT1G63880.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:23715939-23719787 REVERSE   Aliases: T12P18.10, T12P18_10	2.9	2.6	0.3	2.0	100.0%	-3.6
2584	AT1G72650.2   Symbol: TRFL6   myb family transcription factor, contains Pfam PF00249: Myb-like DNA-binding domain   chr1:27353129-27357402 FORWARD   Aliases: F28P22.16, F28P22_16, TRF LIKE 6	6.4	5.7	0.6	2.0	100.0%	-3.1
2585	AT2G04530.1   Symbol: CPZ   RNase Z, 97% identical to RNase Z (GI:20975607) (Arabidopsis thaliana); similar to RNase Z (GI:20975609) (Arabidopsis thaliana); identical to cDNA RNase Z (At2g04530) GI:20975606   chr2:1576768-1578738 FORWARD   Aliases: T1O3.6, T1O3_6	5.2	6.1	-0.9	-2.0	100.0%	-2.8
2586	AT4G00080.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Lycopersicon esculentum SP:Q43143, Arabidopsis thaliana SP:Q42534; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr4:32893-33705 FORWARD   Aliases: F6N15.9, F6N15_9	2.3	2.1	0.2	2.0	100.0%	-4.1
2587	AT5G60850.1   Symbol: OBP4   Dof-type zinc finger domain-containing protein, similar to zinc finger protein OBP4 gi:5059396 from (Arabidopsis thaliana); EMBL:AF155817   chr5:24497675-24499094 FORWARD   Aliases: MAE1.2, MAE1_2, ZINC FINGER PROTEIN OBP4	4.8	4.3	0.5	2.0	100.0%	-3.2
2588	AT1G29970.1   expressed protein, similar to GI:3128228 from (Arabidopsis thaliana) (Nature 402 (6763), 761-768 (1999))	6.9	6.5	0.4	2.0	100.0%	-3.4
2589	AT3G25480.1   rhodanese-like domain-containing protein, contains Rhodanese-like domain PF:00581   chr3:9236435-9237844 REVERSE   Aliases: MWL2.9	3.7	4.1	-0.4	-2.0	100.0%	-3.4
2590	AT3G23550.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family   chr3:8448321-8450704 REVERSE   Aliases: MDB19.3	4.8	4.1	0.7	2.0	100.0%	-3.2
2591	AT4G34480.1   glycosyl hydrolase family 17 protein, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum)   chr4:16481884-16483992 REVERSE   Aliases: T4L20.60, T4L20_60	4.2	3.7	0.5	2.0	100.0%	-3.3
2592	AT1G07130.1   OB-fold nucleic acid binding domain-containing protein, contains InterPro entry IPR004365: OB-fold nucleic acid binding domain   chr1:2187775-2188732 FORWARD   Aliases: F10K1.17, F10K1_17	3.5	3.3	0.3	2.0	100.0%	-3.8
2593	AT3G03530.1   Symbol: NPC4   phosphoesterase family protein, low similarity to SP:P95246 Phospholipase C 2 precursor (EC 3.1.4.3) {Mycobacterium tuberculosis}; contains Pfam profile PF04185: Phosphoesterase family	2.6	2.9	-0.3	-2.0	100.0%	-3.9
2594	AT3G03540.1   phosphoesterase family protein, similar to SP:P95246 Phospholipase C 2 precursor (EC 3.1.4.3) {Mycobacterium tuberculosis}; contains Pfam profile PF04185: Phosphoesterase family   chr3:846357-848304 REVERSE   Aliases: T21P5.4	2.6	2.9	-0.3	-2.0	100.0%	-3.9
2595	AT5G60670.1   60S ribosomal protein L12 (RPL12C), 60S RIBOSOMAL PROTEIN L12 (like), Arabidopsis thaliana, PIR:T45883   chr5:24398136-24398819 REVERSE   Aliases: MUP24.13, MUP24_13	9.1	9.7	-0.6	-2.0	100.0%	-3.2
2596	AT4G21820.1   calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612   chr4:11577536-11584065 FORWARD   Aliases: T8O5.30, T8O5_30	2.6	2.8	-0.2	-2.0	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2597	AT4G23800.1   high mobility group (HMG1/2) family protein, similar to HMG2B (Homo sapiens) GI:32335; contains Pfam profile PF00505: HMG (high mobility group) box   chr4:12390177-12393008 FORWARD   Aliases: None	4.0	5.3	-1.3	-2.0	100.0%	-2.9
2598	AT5G23050.1   acyl-activating enzyme 17 (AAE17), nearly identical to acyl-activating enzyme 17 (Arabidopsis thaliana) GI:29893266; similar to acetyl-CoA synthetase (SP:P27095) from Methanotherix soehngenii; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA acyl-activating enzyme 17 (At5g23050) GI:29893265   chr5:7731272-7735442 REVERSE   Aliases: MYJ24.4, MYJ24_4	7.0	7.6	-0.6	-2.0	100.0%	-3.4
2599	AT3G58780.1   Symbol: SHP1   agamous-like MADS box protein AGL1 / shatterproof 1 (AGL1) (SHP1), identical to SP:P29381 Agamous-like MADS box protein AGL1 (Protein Shatterproof 1) {Arabidopsis thaliana}   chr3:21749437-21752884 FORWARD   Aliases: AGL1, SHATTERPROOF 1, T20N10.130	4.1	3.6	0.5	2.0	100.0%	-3.2
2600	AT5G01880.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:338896-340250 FORWARD   Aliases: T20L15.150, T20L15_150	5.3	4.5	0.8	2.0	100.0%	-3.0
2601	AT1G18040.1   Symbol: CDKD1;3   cell division protein kinase, putative, similar to cell division protein kinase 7 (Homo sapiens) SWISS-PROT:P50613   chr1:6206864-6209493 REVERSE   Aliases: CDKD1;3, Cyclin dependent kinase D1;3, T10F20.5, T10F20_5	5.6	6.4	-0.9	-2.0	100.0%	-3.0
2602	AT3G23750.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr3:8558339-8561435 FORWARD   Aliases: MYM9.9	4.9	5.6	-0.7	-2.0	100.0%	-3.2
2603	AT2G05630.1   Symbol: atg8d   autophagy 8d (APG8d), identical to autophagy 8d (Arabidopsis thaliana) GI:19912157; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3   chr2:2082983-2084879 REVERSE   Aliases: T20G20.2, T20G20_2	9.2	8.5	0.7	2.0	100.0%	-3.4
2604	AT5G25590.1   expressed protein, contains Pfam profile PF04783: Protein of unknown function (DUF630)   chr5:8906601-8909923 REVERSE   Aliases: T14C9.130, T14C9_130	3.5	3.8	-0.3	-2.0	100.0%	-3.5
2605	AT1G04200.1   expressed protein, Contains similarity to gb:Z69902 from C. elegans   chr1:1109489-1114049 FORWARD   Aliases: F20D22.3, F20D22_3	4.8	5.5	-0.7	-2.0	100.0%	-3.2
2606	NA	2.8	2.6	0.2	2.0	100.0%	-4.1
2607	AT3G05880.1   Symbol: RCI2A   hydrophobic protein (RCI2A) / low temperature and salt responsive protein (LTI6A), identical to SP:Q9ZLNQ7 Hydrophobic protein RCI2A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}   chr3:1755503-1756546 REVERSE   Aliases: F10A16.18, F10A16_18, RARE COLD INDUCIBLE 2A	11.4	10.8	0.6	2.0	100.0%	-3.6
2608	AT4G18880.1   Symbol: AT HSFA4A   heat shock transcription factor 21 (HSF21), identical to heat shock transcription factor 21 (Arabidopsis thaliana) GI:3399765; contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr4:10347593-10349573 REVERSE   Aliases: F13C5.50, F13C5_50, HSFA4A	4.4	3.8	0.6	2.0	100.0%	-3.2
2609	AT1G66430.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr1:24781959-24784278 FORWARD   Aliases: F28G11.11, F28G11_11	4.8	5.6	-0.8	-2.0	100.0%	-3.1
2610	AT5G59880.2   Symbol: ADF3   actin-depolymerizing factor 3 (ADF3), identical to SP:Q9ZSK4 Actin-depolymerizing factor 3 (ADF 3) (AtADF3) {Arabidopsis thaliana}   chr5:24137457-24139105 FORWARD   Aliases: ACTIN DEPOLYMERIZING FACTOR 3, MMN10.4, MMN10_4	13.2	12.6	0.6	2.0	100.0%	-3.3
2611	AT5G49630.1   Symbol: AAP6   amino acid permease 6 (AAP6), identical to amino acid permease 6 (AAP6) (Arabidopsis thaliana) GI:1769887   chr5:20159696-20163712 REVERSE   Aliases: AMINO ACID PERMEASE 6, MNI5.1, MNI5_1	12.1	10.9	1.2	2.0	100.0%	-3.0
2612	AT1G57630.1   disease resistance protein (TIR class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:21349304-21349822 FORWARD   Aliases: T8L23.10, T8L23_10	2.9	3.3	-0.4	-2.0	100.0%	-3.6
2613	AT1G14730.1   similar to cytochrome B561 family protein [Arabidopsis thaliana] (TAIR:At4g25570.1); similar to putative cytochrome protein [Oryza sativa (japonica cultivar-group)] (GB:XP_469562.1); contains InterPro domain Cytochrome b561 / ferric reductase transmembrane (InterPro:IPR006593); contains InterPro domain Cytochrome b561 (InterPro:IPR004877)   chr1:5073100-5074774 FORWARD   Aliases: F10B6.13, F10B6_13	8.7	8.3	0.4	2.0	100.0%	-3.4
2614	AT1G23710.1   expressed protein   chr1:8385240-8386415 FORWARD   Aliases: F5O8.26, F5O8_26	5.5	4.1	1.3	2.0	100.0%	-3.0
2615	AT4G27900.2   expressed protein   chr4:13890670-13893079 FORWARD   Aliases: T13J8.10, T13J8_10	5.9	5.3	0.6	2.0	100.0%	-3.0
2616	AT3G18080.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase BGQ60 precursor GB:A57512 (Hordeum vulgare); similar to beta-mannosidase enzyme (GI:17226270) (Lycopersicon esculentum)   chr3:6191565-6194458 FORWARD   Aliases: MRC8.20	6.2	7.3	-1.1	-2.0	100.0%	-3.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2617	AT5G67510.1   60S ribosomal protein L26 (RPL26B)   chr5:26955039-26955677 REVERSE   Aliases: K9I9.7, K9I9_7	8.1	8.8	-0.7	-2.0	100.0%	-3.1
2618	AT3G42600.1   hypothetical protein   chr3:14708749-14709408 FORWARD   Aliases: T12K4.50	2.6	2.8	-0.2	-2.0	100.0%	-4.3
2619	AT2G20840.1   secretory carrier membrane protein (SCAMP) family protein, contains Pfam domain, PF04144: SCAMP family   chr2:8978843-8981551 REVERSE   Aliases: F5H14.19, F5H14_19	5.2	4.8	0.4	2.0	100.0%	-3.3
2620	AT4G37280.1   MRG family protein, contains Pfam domain PF05712: MRG   chr4:17546578-17549409 REVERSE   Aliases: AP22.79, AP22_79	7.2	7.9	-0.7	-2.0	100.0%	-3.1
2621	AT5G55760.1   transcriptional regulator Sir2 family protein, contains Pfam domain PF02146: transcriptional regulator, Sir2 family   chr5:22584448-22588189 FORWARD   Aliases: MDF20.20, MDF20_20	5.8	6.3	-0.6	-2.0	100.0%	-3.3
2622	AT5G44380.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr5:17895949-17898666 REVERSE   Aliases: K9L2.18, K9L2_18	3.3	4.0	-0.7	-2.0	100.0%	-3.2
2623	AT3G23050.2   Symbol: IAA7   auxin-responsive protein / indoleacetic acid-induced protein 7 (IAA7), identical to SP:Q38825:AXI7_ARATH Auxin-responsive protein IAA7 (Indoleacetic acid-induced protein 7)   chr3:8194718-8196521 FORWARD   Aliases: AUXIN RESISTANT 2, AXR2, MXC7.8	5.3	6.2	-0.9	-2.0	100.0%	-2.9
2624	AT1G76100.1   plastocyanin, identical to plastocyanin GI:1865683 from (Arabidopsis thaliana)   chr1:28558881-28559651 REVERSE   Aliases: T23E18.3, T23E18_3	5.5	4.6	0.9	2.0	100.0%	-2.8
2625	AT3G55640.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr3:20650818-20653638 FORWARD   Aliases: F1I16.50	3.8	3.5	0.3	2.0	100.0%	-3.7
2626	AT1G28680.1   transferase family protein, similar to elicitor inducible gene product EIG-I24 (Nicotiana tabacum) (gi:10798748); contains Pfam transferase family domain PF00248   chr1:10078175-10080015 FORWARD   Aliases: F1K23.12, F1K23_12	8.7	9.4	-0.8	-2.0	100.0%	-3.5
2627	AT1G26290.1   expressed protein   chr1:9098038-9098542 FORWARD   Aliases: F28B23.5, F28B23_5	3.6	3.1	0.5	2.0	100.0%	-3.5
2628	AT5G67420.1   LOB domain protein 37 / lateral organ boundaries domain protein 37 (LBD37), identical to LOB DOMAIN 37 (Arabidopsis thaliana) GI:17227170   chr5:26921515-26923252 REVERSE   Aliases: K8K14.16, K8K14_16	3.9	5.0	-1.1	-2.0	100.0%	-2.9
2629	AT4G37200.1   Symbol: HCF164	7.5	6.9	0.5	2.0	100.0%	-3.2
2630	AT1G59750.3   Symbol: ARF1   similar to transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related [Arabidopsis thaliana] (TAIR:At2g46530.1); similar to OSJNBa0064D20.11 [Oryza sativa (japonica cultivar-group)] (GB:CAE04227.2); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340); contains InterPro domain AUX/IAA protein (InterPro:IPR003311)   chr1:21983067-21988098 FORWARD   Aliases: ARF1, AUXIN RESPONSE FACTOR 1, F23H11.7, F23H11_7	5.8	6.2	-0.4	-2.0	100.0%	-3.3
2631	AT1G76940.1   RNA recognition motif (RRM)-containing protein, contains Pfam PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); similar to RNA-binding protein with multiple splicing homolog (RBP-MS) (HEart, RRM Expressed Sequence) (Hermes) (Swiss-Prot:Q9YGI5) (Xenopus laevis); similar to RNA-binding protein with multiple splicing (RBP-MS) (Swiss-Prot:Q93062) (Homo sapiens)   chr1:28907322-28909149 REVERSE   Aliases: F22K20.4, F22K20_4	5.3	4.8	0.5	2.0	100.0%	-3.3
2632	AT3G27870.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from {Mus musculus} SP:P98200, Homo sapiens SP:O43520, {Arabidopsis thaliana} SP:P98204; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr3:10332187-10336542 FORWARD   Aliases: K16N12.23	3.5	3.2	0.3	2.0	100.0%	-3.7
2633	AT1G16650.1   expressed protein   chr1:5687936-5691191 FORWARD   Aliases: F19K19.6, F19K19_6	4.4	3.9	0.5	2.0	100.0%	-3.3
2634	AT1G04490.1   expressed protein   chr1:1218004-1219913 REVERSE   Aliases: F19P19.4, F19P19_4	3.9	3.5	0.4	2.0	100.0%	-3.5
2635	AT3G27340.2   similar to B1065G12.33 [Oryza sativa (japonica cultivar-group)] (GB:NP_915228.1)	8.2	7.6	0.6	2.0	100.0%	-3.1
2636	AT3G18860.2   transducin family protein / WD-40 repeat family protein, contains seven G-protein beta WD-40 repeats; similar to phospholipase a-2-activating protein SP:P27612 from (Mus musculus)   chr3:6501688-6508542 FORWARD   Aliases: MCB22.3	7.8	8.6	-0.8	-2.0	100.0%	-3.3
2637	AT1G77760.1   Symbol: NIA1   nitrate reductase 1 (NR1), identical to SP:P11832 Nitrate reductase 1 (formerly EC 1.6.6.1) (NR1){Arabidopsis thaliana}   chr1:29240697-29244339 REVERSE   Aliases: GNR1, NITRATE REDUCTASE, NITRATE REDUCTASE 1, NITRATE REDUCTASE DEFECTIVE 1, NR1, T32E8.9, T32E8_9	9.3	7.5	1.8	2.0	100.0%	-3.1
2638	AT4G04790.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At4g21880.1); similar to B1358B12.18 [Oryza sativa (japonica cultivar-group)] (GB:XP_472769.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr4:2434905-2439401 REVERSE   Aliases: T4B21.17, T4B21_17	4.0	4.6	-0.6	-2.0	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2639	AT1G18840.2   similar to calmodulin-binding family protein [Arabidopsis thaliana] (TAIR:At1g74690.1); similar to calmodulin-binding family protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87380.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048)   chr1:6500839-6504388 REVERSE   Aliases: F6A14.7, F6A14_7	3.9	4.4	-0.5	-2.0	100.0%	-3.2
2640	AT2G01620.1   expressed protein   chr2:278126-279295 FORWARD   Aliases: T8O11.21, T8O11_21	7.9	7.3	0.6	2.0	100.0%	-3.2
2641	AT1G04900.1   expressed protein, contains Pfam PF02636: Uncharacterized ACR, COG1565   chr1:1383840-1388520 FORWARD   Aliases: F13M7.11, F13M7_11	4.1	4.7	-0.6	-2.0	100.0%	-3.2
2642	AT2G38170.3   Symbol: CAX1   calcium exchanger (CAX1), identical to high affinity calcium antiporter CAX1 (Arabidopsis thaliana) gi:9256741:gb:AAB05913, except a possible frameshift at base 58008. Sequence has been confirmed with 5 sequencing reads.; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563   chr2:15997127-16000354 REVERSE   Aliases: ATCAX1, F16M14.10, F16M14_10, HIGH AFFINITY CALCIUM ANTIPORTER CAX1, RARE COLD INDUCIBLE4, RCI4	7.3	8.1	-0.8	-2.0	100.0%	-3.0
2643	AT2G02570.3   expressed protein, similar to hypothetical protein DDB0192063 [Dictyostelium discoideum] (GB:EAL60630.1); contains InterPro domain Tudor domain (InterPro:IPR002999)   chr2:697950-700908 REVERSE   Aliases: T8K22.13, T8K22_13	6.9	6.1	0.8	2.0	100.0%	-3.2
2644	AT1G60080.1   3' exoribonuclease family domain 1-containing protein, similar to SP:Q96B26 Exosome complex exonuclease RRP43 (EC 3.1.13.-) (Ribosomal RNA processing protein 43) {Homo sapiens}; contains Pfam profile PF01138: 3' exoribonuclease family, domain 1   chr1:22155895-22158246 REVERSE   Aliases: T2K10.14, T2K10_14	5.8	6.4	-0.6	-2.0	100.0%	-3.0
2645	AT4G34490.1   Symbol: ATCAP1	8.2	8.8	-0.6	-2.0	100.0%	-3.3
2646	AT3G52730.1   ubiquinol-cytochrome C reductase UQCRX/QCR9-like family protein, contains Pfam profile: PF05365 ubiquinol-cytochrome C reductase, UQCRX/QCR9 like   chr3:19553909-19555242 REVERSE   Aliases: F3C22.130	11.6	12.1	-0.4	-2.0	100.0%	-3.6
2647	AT1G49670.1   ARP protein (REF), identical to ARP protein GB:CAA89858 GI:886434 from (Arabidopsis thaliana); contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family   chr1:18384930-18389775 REVERSE   Aliases: F14J22.10, F14J22_10	10.0	10.8	-0.8	-2.0	100.0%	-3.3
2648	AT1G10900.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr1:3632274-3637141 REVERSE   Aliases: T19D16.18, T19D16_18	4.9	5.5	-0.6	-2.0	100.0%	-3.2
2649	AT1G30330.2   Symbol: ARF6   similar to auxin-responsive factor (ARF8) [Arabidopsis thaliana] (TAIR:At5g37020.1); similar to auxin response factor 6b [Oryza sativa] (GB:BAD85915.1); similar to OSJNBb0004A17.5 [Oryza sativa (japonica cultivar-group)] (GB:XP_474307.1); similar to auxin response factor 4 [Cucumis sativus] (GB:BAD19064.1); similar to putative auxin response factor [Oryza sativa (japonica cultivar-group)] (GB:BAD45924.1); similar to putative auxin response transcription factor(ARF6) [Oryza sativa (japonica cultivar-group)] (GB:XP_464221.1); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340)   chr1:10685804-10690018 REVERSE   Aliases: ARF6, AUXIN RESPONSE FACTOR 6, T4K22.6, T4K22_6	5.2	5.8	-0.6	-2.0	100.0%	-3.1
2650	AT4G00585.1   expressed protein   chr4:250955-252532 REVERSE   Aliases: None	11.0	11.6	-0.6	-2.0	100.0%	-3.5
2651	AT5G54770.1   Symbol: THI1   thiazole biosynthetic enzyme, chloroplast (ARA6) (THI1) (THI4), identical to SP:Q38814 Thiazole biosynthetic enzyme, chloroplast precursor (ARA6) {Arabidopsis thaliana}	12.8	11.4	1.4	2.0	100.0%	-2.9
2652	AT1G52870.2   peroxisomal membrane protein-related, contains weak similarity to Swiss-Prot:Q07066 22 kDa peroxisomal membrane protein (Rattus norvegicus)   chr1:19689415-19691531 FORWARD   Aliases: F14G24.14, F14G24_14	7.1	6.0	1.1	2.0	100.0%	-3.0
2653	AT3G53880.1   aldo/keto reductase family protein, similar to chalcone reductase (Sesbania rostrata)(GI:2792155), and aldose reductase ALDRXV4 (Xerophyta viscosa)(GI:4539944), (Hordeum vulgare)(GI:728592)   chr3:19964151-19966268 FORWARD   Aliases: F5K20.180	6.4	6.9	-0.5	-2.0	100.0%	-3.4
2654	AT5G09460.1   expressed protein   chr5:2944438-2945418 REVERSE   Aliases: T5E8.260, T5E8_260	5.0	5.9	-0.8	-2.0	100.0%	-3.0
2655	AT4G31140.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr4:15141294-15143397 FORWARD   Aliases: F6E21.60, F6E21_60	6.0	5.3	0.7	2.0	100.0%	-3.2
2656	AT2G18450.1   Symbol: SDH1 2	5.6	4.4	1.3	2.0	100.0%	-3.0
2657	AT1G02970.1   Symbol: WEE1   protein kinase, putative, similar to Wee1-like protein GI:5821717 from (Zea mays)   chr1:673306-676378 FORWARD   Aliases: F22D16.3, F22D16_3, WEE1, WEE1 kinase	2.8	3.2	-0.4	-2.0	100.0%	-3.6
2658	AT1G64500.1   glutaredoxin family protein   chr1:23956896-23958155 FORWARD   Aliases: F1N19.7, F1N19_7	5.1	4.6	0.5	2.0	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2659	AT1G44890.1   expressed protein   chr1:16965584-16967406 FORWARD   Aliases: T12C22.18, T12C22_18	7.4	6.6	0.8	2.0	100.0%	-3.1
2660	AT3G27770.1   expressed protein   chr3:10286072-10288979 REVERSE   Aliases: MGF10.17	10.3	9.1	1.2	2.0	100.0%	-3.3
2661	AT2G37860.3   Symbol: LCD1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g22790.1); similar to chloroplast lumen common protein family-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477219.1); contains domain GLY_RICH (PS50315)   chr2:15863710-15865998 FORWARD   Aliases: LOWER CELL DENSITY 1, T8P21.23, T8P21_23	7.5	8.9	-1.4	-2.0	100.0%	-3.0
2662	AT5G44350.1   ethylene-responsive nuclear protein -related, contains weak similarity to ethylene-regulated nuclear protein ERT2 (Arabidopsis thaliana) gi:2765442:emb:CAA75349	5.4	4.8	0.6	2.0	100.0%	-3.3
2663	AT2G45280.1   Symbol: ATRAD51C   DNA repair family protein, contains similarity to Swiss-Prot:O43502 DNA repair protein RAD51 homolog 3 (Homo sapiens)   chr2:18677083-18679351 FORWARD   Aliases: F4L23.21, RAD51C	5.2	4.6	0.6	2.0	100.0%	-3.2
2664	AT1G65270.3   expressed protein   chr1:24245411-24248615 FORWARD   Aliases: T8F5.4, T8F5_4	8.4	7.5	0.8	2.0	100.0%	-3.2
2665	AT2G33530.1   Symbol: SCPL46	6.8	7.4	-0.6	-2.0	100.0%	-3.0
2666	AT4G34220.1   leucine-rich repeat transmembrane protein kinase, putative, protein kinase TMKL1, Arabidopsis thaliana, PID:E353150   chr4:16381510-16384198 REVERSE   Aliases: F10M10.12	3.1	3.4	-0.4	-2.0	100.0%	-3.5
2667	AT2G34585.1   expressed protein   chr2:14575126-14575716 REVERSE   Aliases: None	9.3	8.8	0.6	2.0	100.0%	-3.9
2668	AT5G08420.1   expressed protein   chr5:2713414-2716180 FORWARD   Aliases: F8L15.150, F8L15_150	6.5	7.7	-1.2	-1.9	100.0%	-3.0
2669	AT1G22150.1   Symbol: SULTR1;3   sulfate transporter (Sultr1;3), identical to sulfate transporter Sultr1;3 (Arabidopsis thaliana) GI:10716805; contains Pfam profile PF00916: Sulfate transporter family; contains Pfam profile PF01740: STAS domain; contains TIGRfam profile TIGR00815: sulfate permease   chr1:7818350-7821333 FORWARD   Aliases: F2E2.22, F2E2_22, SULFATE TRANSPORTER SULTR1;3	4.2	3.7	0.5	1.9	100.0%	-3.2
2670	AT3G17000.1   ubiquitin-conjugating enzyme, putative, similar to Non-Canonical Ubiquitin Conjugating Enzyme 1 (NCUBE1) from (Gallus gallus) GI:7362937, (Mus musculus) GI:7363050, (Homo sapiens) GI:7362973; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr3:5797185-5799689 FORWARD   Aliases: K14A17.7	7.6	6.3	1.3	1.9	100.0%	-3.0
2671	AT1G79280.1   expressed protein, weak similarity to Nucleoprotein TPR (Swiss-Prot:P12270) (Homo sapiens)   chr1:29824069-29837702 REVERSE   Aliases: YUP8H12R.12, YUP8H12R_12	7.0	7.9	-0.9	-1.9	100.0%	-3.3
2672	AT1G78450.1   SOUL heme-binding family protein, weak similarity to SOUL protein (Mus musculus) GI:4886906; contains Pfam profile PF04832: SOUL heme-binding protein   chr1:29521882-29522826 REVERSE   Aliases: F3F9.4	4.5	3.6	0.9	1.9	100.0%	-2.9
2673	AT3G53730.1   histone H4, identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP:P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797	11.8	12.6	-0.8	-1.9	100.0%	-3.5
2674	ATMG00720.1   Symbol: ORF107D   hypothetical protein   chrM:209499-209822 FORWARD   Aliases: ORF107D	2.2	2.5	-0.3	-1.9	100.0%	-3.8
2675	AT1G23340.2   expressed protein, similar to At1g70550, At1g10750 contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr1:8283633-8286517 REVERSE   Aliases: F26F24.22, F26F24_22	3.6	4.2	-0.6	-1.9	100.0%	-3.2
2676	AT1G51650.1   ATP synthase epsilon chain, mitochondrial, identical to ATP synthase epsilon chain, mitochondrial SP:Q96253 from (Arabidopsis thaliana)   chr1:19156283-19157597 FORWARD   Aliases: F19C24.25, F19C24_25	12.0	12.3	-0.3	-1.9	100.0%	-3.9
2677	AT1G23560.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8352604-8354251 REVERSE   Aliases: F28C11.32	4.4	5.2	-0.8	-1.9	100.0%	-3.1
2678	AT2G20340.1   tyrosine decarboxylase, putative, similar to tyrosine/dopa decarboxylase (Papaver somniferum) GI:3282527, SP:Q06087 Tyrosine decarboxylase 3 (EC 4.1.1.25) {Petroselinum crispum}; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain   chr2:8786816-8789853 FORWARD   Aliases: F11A3.11, F11A3_11	3.2	3.9	-0.7	-1.9	100.0%	-3.2
2679	AT3G09830.2   protein kinase, putative, similar to protein kinase (Lophopyrum elongatum) gi:13022177:gb:AAK11674   chr3:3016545-3018988 FORWARD   Aliases: F8A24.12	5.2	4.5	0.7	1.9	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2680	AT1G14690.1   similar to microtubule associated protein (MAP65/ASE1) family protein [Arabidopsis thaliana] (TAIR:At5g55230.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470643.1); contains InterPro domain MAP65/ASE1 (InterPro:IPR007145)   chr1:5051758-5055247 REVERSE   Aliases: F10B6.8, F10B6_8	8.0	8.7	-0.7	-1.9	100.0%	-3.2
2681	AT5G34930.1   arogenate dehydrogenase, identical to arogenate dehydrogenase Gl:16903098 from (Arabidopsis thaliana); contains Pfam profile: PF02153: prephenate dehydrogenase   chr5:13250604-13252797 FORWARD   Aliases: T2L5.1	5.0	5.5	-0.5	-1.9	100.0%	-3.4
2682	AT3G02250.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter -related' based on similarity to axi 1 protein (GB:X80301) (Gl:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr3:423808-427068 REVERSE   Aliases: F14P3.10, F14P3_10	3.3	3.6	-0.4	-1.9	100.0%	-3.7
2683	AT5G44730.2   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:Q94915 Rhythmically expressed gene 2 protein (DREG-2) {Drosophila melanogaster}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:18062758-18064135 REVERSE   Aliases: K23L20.7, K23L20_7	6.9	6.1	0.8	1.9	100.0%	-3.1
2684	AT4G30935.1   WRKY family transcription factor, contains Pfam profile: PF03106	6.8	6.2	0.5	1.9	100.0%	-3.2
2685	ATCG00440.1   Symbol: NDHC   Encodes NADH dehydrogenase D3 subunit of the chloroplast NAD(P)H dehydrogenase complex   chrC:50001-50363 REVERSE   Aliases: NDHC	11.3	10.4	0.9	1.9	100.0%	-3.5
2686	AT5G51140.1   pseudouridine synthase family protein, low similarity to SP:P23851 Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70) (Pseudouridylate synthase) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF00849: RNA pseudouridylate synthase	8.9	8.3	0.5	1.9	100.0%	-3.2
2687	AT4G31970.1   Symbol: CYP82C2   cytochrome P450 family protein, similar to cytochrome P450 82C1 (CYP82C1p)(Gl:2739004) (Glycine max); flavonoid 3 ,5'-hydroxylase, Campanula medium, PATCHX:D1003951   chr4:15462414-15464364 FORWARD   Aliases: F11C18.12	2.7	3.0	-0.3	-1.9	100.0%	-3.9
2688	AT3G12510.1   expressed protein   chr3:3967134-3967804 FORWARD   Aliases: T2E22.17	6.9	6.2	0.7	1.9	100.0%	-3.0
2689	AT1G06570.1   Symbol: PDS1   4-hydroxyphenylpyruvate dioxygenase (HPD), identical to 4-hydroxyphenylpyruvate dioxygenase (HPD) SP:P93836 (Arabidopsis thaliana (Mouse-ear cress))   chr1:2011885-2013544 REVERSE   Aliases: 4 HYDROXYPHENYLPYRUVATE DIOXYGENASE, F12K11.9, F12K11_9, HPD, P HYDROXYPHENYLPYRUVATE DIOXYGENASE, PHYTOENE DESATURATION 1	10.1	8.9	1.2	1.9	100.0%	-3.2
2690	AT4G16630.1   DEAD/DEAH box helicase, putative (RH28), identical to cDNA DEAD box RNA helicase, RH28 Gl:3776026   chr4:9362011-9366770 REVERSE   Aliases: DL4340C, FCAALL.424	4.0	5.4	-1.4	-1.9	100.0%	-2.9
2691	AT4G02990.1   mitochondrial transcription termination factor family protein / mTERF family protein, weak similarity to mtDBP protein (Paracentrotus lividus) Gl:4584695; contains Pfam profile PF02536: mTERF   chr4:1321859-1324004 FORWARD   Aliases: T4I9.13, T4I9_13	3.8	4.3	-0.5	-1.9	100.0%	-3.3
2692	AT5G59010.1   protein kinase-related, low similarity to serine/threonine/tyrosine-specific protein kinase APK1, Arabidopsis thaliana, SP:Q06548 PIR:S28615; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr5:23837594-23840476 REVERSE   Aliases: K19M22.7, K19M22_7	3.6	4.1	-0.4	-1.9	100.0%	-3.4
2693	AT1G79350.1   Symbol: EMB1135   DNA-binding protein, putative, contains Pfam PF00628: PHD-finger domain; contains TIGRFAMS TIGR01053: zinc finger domain, LSD1 subclass; contains Pfam PF00271: Helicase conserved C-terminal domain; similar to WSSV086 (Gl:19481678)(shrimp white spot syndrome virus); similar to nuclear protein Np95 (Gl:17939938) (Mus musculus)   chr1:29849548-29858307 REVERSE   Aliases: EMB1135, EMBRYO DEFECTIVE 1135, YUP8H12R.3, YUP8H12R_3	7.4	8.2	-0.9	-1.9	100.0%	-3.3
2694	AT1G07450.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr1:2288004-2289253 REVERSE   Aliases: F22G5.20, F22G5_20	3.1	2.7	0.3	1.9	100.0%	-3.7
2695	AT5G61130.1   glycosyl hydrolase family protein 17, similar to beta-1,3-glucanase Gl:15150341 from (Camellia sinensis); C-terminal homology only   chr5:24604456-24606806 REVERSE   Aliases: MAF19.13, MAF19_13	3.8	4.4	-0.6	-1.9	100.0%	-3.2
2696	AT5G64930.1   Symbol: CPR5   CPR5 protein, putative, Constitutive expressor of Pathogenesis Related genes 5 (cpr5); regulator of disease resistance and senescence (Plant J. (2001)26(4)409-420.   chr5:25962938-25965565 REVERSE   Aliases: CONSTITUTIVE EXPRESSION OF PR GENES 5, HYS1, MXK3.16, MXK3_16	6.8	6.4	0.5	1.9	100.0%	-3.3
2697	AT2G38310.1   expressed protein, low similarity to early flowering protein 1 (Asparagus officinalis) Gl:1572683, SP:P80889 Ribonuclease 1 (EC 3.1.-.-) {Panax ginseng}	8.6	7.8	0.9	1.9	100.0%	-3.2
2698	AT2G38740.1   haloacid dehalogenase-like hydrolase family protein, similar to SP:P71447 Beta-phosphoglucomutase (EC 5.4.2.6) {Lactococcus lactis}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	7.9	8.8	-0.9	-1.9	100.0%	-3.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2699	AT3G15430.2   regulator of chromosome condensation (RCC1) family protein, low similarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)   chr3:5208766-5211752 FORWARD   Aliases: MJK13.9	7.0	6.5	0.5	1.9	100.0%	-3.2
2700	AT1G06560.1   NOL1/NOP2/sun family protein, contains Pfam profile PF01189: NOL1/NOP2/sun family   chr1:2007629-2012200 FORWARD   Aliases: F12K11.10, F12K11_10	4.7	5.3	-0.7	-1.9	100.0%	-3.2
2701	AT2G42890.2   Symbol: MEI2   RNA recognition motif (RRM)-containing protein   chr2:17857639-17861607 FORWARD   Aliases: F7D19.11, F7D19_11	6.2	5.3	0.9	1.9	100.0%	-2.9
2702	AT4G23850.1   long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase, nearly identical to acyl-CoA synthetase (MF7P) from Brassica napus (gi:1617270)   chr4:12403477-12408343 REVERSE   Aliases: T32A16.20, T32A16_20	8.0	8.7	-0.7	-1.9	100.0%	-3.3
2703	AT3G07610.1   transcription factor jumonji (jmjC) domain-containing protein, contains Pfam domain, PF02373: jmjC domain   chr3:2426154-2432882 FORWARD   Aliases: MLP3.6	3.7	4.1	-0.4	-1.9	100.0%	-3.4
2704	AT1G78995.1   expressed protein   chr1:29719972-29721004 REVERSE   Aliases: None	4.1	3.7	0.5	1.9	100.0%	-3.4
2705	AT3G16220.1   expressed protein, similar to CGI-18 protein GB:AAD27727 (Homo sapiens)   chr3:5497620-5499241 FORWARD   Aliases: MYA6.3	5.5	4.8	0.8	1.9	100.0%	-2.9
2706	AT5G28290.1   protein kinase, putative, similar to LSTK-1-like kinase (Lycopersicon esculentum) GI:15637110; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr5:10278695-10282618 REVERSE   Aliases: T8M17.60, T8M17_60	3.3	3.7	-0.4	-1.9	100.0%	-3.6
2707	AT3G28860.1   Symbol: ATMDR1/ATMDR11/PGP19   Belongs to the family of ATP-binding cassette (ABC) transporters. Also known as AtMDR11 and PGP19. Possibly regulates auxin-dependent responses by influencing basipetal auxin transport in the root. Acts upstream of phyA in regulating hypocotyl elongation and gravitropic response. Exerts nonredundant, partially overlapping functions with the ABC transporter encoded by AtPGP1.   chr3:10871275-10878743 REVERSE   Aliases: ATMDR1, ATMDR11, MLD15.2, PGP19	5.6	6.2	-0.6	-1.9	100.0%	-3.3
2708	AT5G14520.1   pescadillo-related, similar to pescadillo (Zebrafish, Danio rerio) SWISS-PROT:P79741   chr5:4680792-4684333 REVERSE   Aliases: T15N1.10, T15N1_10	7.7	8.2	-0.5	-1.9	100.0%	-3.4
2709	AT5G54760.1   eukaryotic translation initiation factor SUI1, putative, similar to SP:P32911 Protein translation factor SUI1 {Saccharomyces cerevisiae}; contains Pfam profile PF01253: Translation initiation factor SUI1   chr5:22261112-22262961 FORWARD   Aliases: MBG8.2, MBG8_2	11.3	10.7	0.7	1.9	100.0%	-3.5
2710	AT3G59430.3   expressed protein   chr3:21975042-21977324 REVERSE   Aliases: F25L23.290	2.6	2.3	0.3	1.9	100.0%	-3.9
2711	AT3G17940.1   aldose 1-epimerase family protein, similar to ALDOSE 1-EPIMERASE PRECURSOR GB:P05149 (SP:P05149) from (Acinetobacter calcoaceticus); contains Pfam profile PF01263 Aldose 1-epimerase   chr3:6143525-6145324 REVERSE   Aliases: MEB5.16	9.4	9.9	-0.5	-1.9	100.0%	-3.6
2712	AT4G35850.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to CRP1 (Zea mays) GI:3289002; contains Pfam profile PF01535: PPR repeat   chr4:16983528-16987203 FORWARD   Aliases: F4B14.120, F4B14_120	8.2	9.2	-1.0	-1.9	100.0%	-3.1
2713	AT1G80660.1   Symbol: AHA9   ATPase 9, plasma membrane-type, putative / proton pump 9, putative / proton-exporting ATPase, putative, strong similarity to SP:Q42556 ATPase 9, plasma membrane-type (EC 3.6.3.6) (Proton pump 9) {Arabidopsis thaliana}; contains InterPro accession IPR001757: ATPase, E1-E2 type   chr1:30321119-30324840 REVERSE   Aliases: F23A5.1, F23A5_1	2.5	2.7	-0.2	-1.9	100.0%	-3.8
2714	AT3G06910.1   Ulp1 protease family protein, similar to sentrin/SUMO-specific protease (Homo sapiens) GI:6906859; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr3:2178636-2181203 REVERSE   Aliases: F17A9.6	3.4	3.8	-0.4	-1.9	100.0%	-3.7
2715	AT2G41420.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr2:17273555-17275102 REVERSE   Aliases: F13H10.3, F13H10_3	7.2	5.7	1.4	1.9	100.0%	-3.1
2716	AT4G32060.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:15501084-15503599 FORWARD   Aliases: F10N7.140, F10N7_140	9.4	8.9	0.5	1.9	100.0%	-3.4
2717	AT1G11545.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endo-xyloglucan transferase GI:2244732 from (Gossypium hirsutum)   chr1:3878550-3880360 REVERSE   Aliases: T23J18.21, T23J18_21	3.4	4.1	-0.7	-1.9	100.0%	-3.4
2718	AT1G19150.1   Symbol: LHCA2*1   chlorophyll A-B binding protein, putative / LHCl type II, putative, very strong similarity to PSI type II chlorophyll a/b-binding protein Lhca2*1 GI:541565 from (Arabidopsis thaliana); contains Pfam profile: PF00504 chlorophyll A-B binding protein   chr1:6612740-6613963 FORWARD   Aliases: PSI TYPE II CHLOROPHYLL A/B BINDING PROTEIN, T29M8.2, T29M8_2	3.9	3.2	0.7	1.9	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2719	AT1G09330.1   expressed protein, contains 3 transmembrane domains; contains Pfam profile PF05832: Eukaryotic protein of unknown function   chr1:3012764-3015093 REVERSE   Aliases: T31J12.5, T31J12_5	9.9	9.3	0.6	1.9	100.0%	-3.5
2720	AT2G30490.1   Symbol: ATC4H   trans-cinnamate 4-monooxygenase / cinnamic acid 4-hydroxylase (C4H) (CA4H) / cytochrome P450 73 (CYP73) (CYP73A5), identical to SP:P92994: Trans-cinnamate 4-monooxygenase (EC 1.14.13.11) (Cinnamic acid 4-hydroxylase) (CA4H) (C4H) (P450C4H) (Cytochrome P450 73). {Arabidopsis thaliana}; molecular marker C4H (GB:U71080)   chr2:13000740-13002847 REVERSE   Aliases: C4H, CINNAMATE 4 HYDROXYLASE, CINNAMATE 4 HYDROXYLASE, CYP73A5, T6B20.16, T6B20_16	10.2	11.0	-0.8	-1.9	100.0%	-3.5
2721	AT1G77890.1   expressed protein   chr1:29297017-29301054 FORWARD   Aliases: AT1G77900, F28K19.10, F28K19_10	4.5	3.9	0.6	1.9	100.0%	-3.4
2722	AT1G50010.1   Symbol: TUA2   tubulin alpha-2/alpha-4 chain (TUA2), identical to tubulin alpha-2/alpha-4 chain SP:P29510 GB:P29510 from (Arabidopsis thaliana)	9.1	6.9	2.2	1.9	100.0%	-3.0
2723	AT2G47190.1   Symbol: MYB2   myb family transcription factor (MYB2), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:19383272-19384601 FORWARD   Aliases: ATMYB2, T8I13.3	3.4	3.0	0.4	1.9	100.0%	-3.4
2724	AT2G19760.1   Symbol: PRF1   profilin 1 (PRO1) (PFN1) (PRF1) / allergen Ara t 8, identical to profilin 1 (Allergen Ara t 8) SP:Q42449 GI:1353770 from (Arabidopsis thaliana)   chr2:8523869-8525249 REVERSE   Aliases: F6F22.21, F6F22_21, PFN1, PROFILIN 1	12.9	12.4	0.5	1.9	100.0%	-3.7
2725	AT5G11410.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:3638432-3639884 REVERSE   Aliases: F15N18.1	2.2	2.3	-0.2	-1.9	100.0%	-4.2
2726	AT5G12840.4   Symbol: HAP2A   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr5:4050808-4053591 REVERSE   Aliases: ATHAP2A, EMB2220, EMBRYO DEFECTIVE 2220, HAP2, T24H18.10, T24H18_10	4.4	4.1	0.4	1.9	100.0%	-3.5
2727	AT5G10480.1   Symbol: PAS2   protein tyrosine phosphatase-like protein, putative (PAS2), identical to PEPINO/PASTICCINO2 protein GI:24411193, GI:24575153 from (Arabidopsis thaliana); contains Pfam:04387: protein tyrosine phosphatase-like protein	4.9	5.8	-0.9	-1.9	100.0%	-3.2
2728	AT2G27000.1   Symbol: CYP705A8   cytochrome P450 family protein   chr2:11530382-11532173 REVERSE   Aliases: T20P8.5, T20P8_5	3.9	4.7	-0.8	-1.9	100.0%	-3.1
2729	AT2G04280.1   expressed protein   chr2:1479815-1482086 REVERSE   Aliases: T23O15.9, T23O15_9	7.5	8.2	-0.7	-1.9	100.0%	-3.4
2730	AT5G10190.1   transporter-related, low similarity to spinster membrane proteins from (Drosophila melanogaster) GI:12003974, GI:12003976, GI:12003972, GI:12003970; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:3199134-3201364 FORWARD   Aliases: F18D22.5	6.2	5.2	1.0	1.9	100.0%	-3.2
2731	AT1G02680.1   transcription initiation factor IID (TFIID) 18 kDa subunit (TAFII-18) family protein, similar to transcription factor TFIID (SP:Q15543) (Homo sapiens); contains Pfam PF02269: Transcription initiation factor IID, 18kD subunit	5.9	5.2	0.7	1.9	100.0%	-3.2
2732	AT2G45740.3   similar to peroxisomal biogenesis factor 11 family protein / PEX11 family protein [Arabidopsis thaliana] (TAIR:At3g61070.1); similar to peroxisomal biogenesis factor 11 protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_550574.1); contains InterPro domain Peroxisomal biogenesis factor 11 (InterPro:IPR008733)   chr2:18846662-18848414 FORWARD   Aliases: F4I18.28	7.3	6.4	1.0	1.9	100.0%	-3.0
2733	AT3G50910.1   expressed protein   chr3:18930494-18933219 FORWARD   Aliases: F18B3.190	9.9	9.3	0.6	1.9	100.0%	-3.2
2734	AT1G09320.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr1:3009943-3012354 REVERSE   Aliases: T31J12.4, T31J12_4	4.3	5.2	-0.8	-1.9	100.0%	-3.1
2735	AT2G21185.1   expressed protein   chr2:9083518-9084129 REVERSE   Aliases: None	7.6	6.9	0.7	1.9	100.0%	-3.0
2736	AT5G47670.1   CCAAT-box binding transcription factor family protein / leafy cotyledon 1-related (L1L), supporting cDNA gi:27372446:gb:AY138461.1.; contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; contains similarity to CCAAT-binding transcription factor subunit A (CBF-A) (NF-Y protein chain B) (NF-YB) (CAAT-box DNA binding protein subunit B) (Swiss-Prot:P25209) (Zea mays)   chr5:19332287-19333616 FORWARD   Aliases: MNJ7.26, MNJ7_26	3.0	2.8	0.3	1.9	100.0%	-3.8
2737	AT3G21690.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile: PF01554 MatE uncharacterized membrane protein family   chr3:7638672-7642212 FORWARD   Aliases: MIL23.25	5.0	4.5	0.5	1.9	100.0%	-3.5
2738	AT2G46100.1   expressed protein   chr2:18960353-18962069 FORWARD   Aliases: T3F17.25	9.6	8.8	0.8	1.9	100.0%	-2.9
2739	AT3G11830.1   chaperonin, putative, similar to SWISS-PROT:P80313 T-complex protein 1, eta subunit (TCP-1-eta) (Mus musculus); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr3:3732670-3736377 FORWARD   Aliases: F26K24.12	7.4	8.4	-1.0	-1.9	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2740	AT5G56190.2   WD-40 repeat family protein, contains 3 (2 significant) WD-40 repeats (PF0400); similar to beta transducin-like protein HET-E2C*40 (GI:17225208) (Podospora anserina)   chr5:22759258-22762403 FORWARD   Aliases: MDA7.25, MDA7_25	8.1	7.7	0.4	1.9	100.0%	-3.6
2741	AT2G45170.2   autophagy 8e (APG8e), identical to autophagy 8e (Arabidopsis thaliana) GI:19912159; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3   chr2:18631456-18632773 FORWARD   Aliases: T14P1.2	7.4	6.5	0.8	1.9	100.0%	-3.2
2742	AT1G12640.1   membrane bound O-acyl transferase (MBOAT) family protein, low similarity to porcupine from (Xenopus laevis) GI:6714514, GI:6714520, GI:6714518, GI:6714516; contains Pfam profile PF03062: MBOAT family   chr1:4303315-4305786 REVERSE   Aliases: T12C24.17, T12C24_17	7.7	6.5	1.3	1.9	100.0%	-3.2
2743	AT4G19100.1   expressed protein   chr4:10453464-10454370 FORWARD   Aliases: None	4.2	3.8	0.4	1.9	100.0%	-3.5
2744	AT3G09820.2   Symbol: ADK1   adenosine kinase 1 (ADK1) / adenosine 5'-phosphotransferase 1, identical to adenosine kinase 1 /adenosine 5'-phosphotransferase 1 SP:Q9SF85 from (Arabidopsis thaliana)   chr3:3012099-3014949 FORWARD   Aliases: ADENOSINE KINASE 1, F8A24.13	10.7	11.9	-1.3	-1.9	100.0%	-3.1
2745	AT5G22690.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:7541274-7545185 FORWARD   Aliases: MDJ22.11, MDJ22_11	3.5	3.2	0.3	1.9	100.0%	-3.6
2746	AT2G36010.3   Symbol: E2F3   E2F transcription factor-3 (E2F3), identical to E2F transcription factor-3 E2F3 (Arabidopsis thaliana) gi:10443853:gb:AAG17610   chr2:15126621-15130683 FORWARD   Aliases: ATE2FA, E2F TRANSCRIPTION FACTOR 3, E2F TRANSCRIPTION FACTOR 3 E2F3, F11F19.8, F11F19_8	2.5	2.7	-0.2	-1.9	100.0%	-4.1
2747	AT1G50710.1   expressed protein   chr1:18788177-18791470 REVERSE   Aliases: F17J6.23, F17J6_23	5.6	6.3	-0.6	-1.9	100.0%	-3.2
2748	AT3G21060.1   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); similar to Retinoblastoma-binding protein 5 (RBBP-5) (Homo sapiens)(RBQ-3)   chr3:7377440-7380717 FORWARD   Aliases: MSA6.10	4.1	4.7	-0.6	-1.9	100.0%	-3.4
2749	AT5G54520.1   WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to pre-mRNA splicing factor PRP17 (SP:O60508) (Homo sapiens)   chr5:22163740-22166346 REVERSE   Aliases: MRB17.2, MRB17_2	5.3	4.8	0.5	1.9	100.0%	-3.2
2750	AT5G62570.1   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum)   chr5:25131617-25134193 FORWARD   Aliases: K19B1.18, K19B1_18	6.4	5.9	0.6	1.9	100.0%	-3.2
2751	AT1G61100.1   disease resistance protein (TIR class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:22512203-22515936 REVERSE   Aliases: F11P17.17, F11P17_17	6.8	6.1	0.7	1.9	100.0%	-3.1
2752	AT1G10140.1   expressed protein, similar to EST gb:AA598098   chr1:3322804-3323550 REVERSE   Aliases: F14N23.2, F14N23_2	6.2	5.9	0.3	1.9	100.0%	-3.6
2753	AT1G72070.1   DNAJ heat shock N-terminal domain-containing protein, similar to TCJ2 (Trypanosoma cruzi) GI:886414; contains Pfam profile: PF00226: Dnaj domain	2.7	3.0	-0.3	-1.9	100.0%	-3.7
2754	AT1G49470.1   expressed protein, contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)   chr1:18314162-18315302 FORWARD   Aliases: F13F21.10, F13F21_10	6.6	6.2	0.5	1.9	100.0%	-3.4
2755	AT1G16290.1   expressed protein   chr1:5570747-5573532 REVERSE   Aliases: F3O9.9, F3O9_9	4.1	3.7	0.5	1.9	100.0%	-3.5
2756	AT2G38180.1   GDSL-motif lipase/hydrolase family protein, similar to SP:P41734 Isoamyl acetate-hydrolyzing esterase (EC 3.1.-.-) {Saccharomyces cerevisiae}; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr2:16004221-16005984 FORWARD   Aliases: F16M14.11, F16M14_11	6.8	7.3	-0.5	-1.9	100.0%	-3.5
2757	AT2G36530.1   Symbol: LOS2   enolase, identical to SWISS-PROT:P25696 enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase)(2-phospho-D- glycerate hydro-lyase) (Arabidopsis thaliana)   chr2:15327835-15330945 REVERSE   Aliases: F1O11.16, F1O11_16	11.7	12.7	-1.0	-1.9	100.0%	-3.6
2758	AT1G55960.1   expressed protein, weak similarity to SP:P53808 Phosphatidylcholine transfer protein (PC-TP) {Mus musculus}   chr1:20931308-20933682 REVERSE   Aliases: F14J16.24, F14J16_24	8.6	8.0	0.6	1.9	100.0%	-3.3
2759	AT5G62980.1   dihydroneopterin aldolase, putative, similar to SP:O33725 Dihydroneopterin aldolase (EC 4.1.2.25) (DHNA) {Streptococcus pyogenes}; contains Pfam profile PF02152: dihydroneopterin aldolase   chr5:25293260-25294418 FORWARD   Aliases: MJH22.3, MJH22_3	7.4	8.1	-0.8	-1.9	100.0%	-3.0
2760	AT1G15400.2   expressed protein, ESTs gb:H37295 and gb:R64895 come from this gene   chr1:5296220-5296897 REVERSE   Aliases: F9L1.35, F9L1_35	8.6	8.1	0.6	1.9	100.0%	-3.1
2761	AT1G19025.1   DNA cross-link repair protein-related, contains weak similarity to Swiss-Prot:P30620 DNA cross-LINK repair protein PSO2/SNM1 (Saccharomyces cerevisiae)   chr1:6568844-6570930 FORWARD   Aliases: None	2.9	3.2	-0.3	-1.9	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2762	AT3G61190.1   Symbol: BAP1   BON1-associated protein 1 (BAP1), identical to BON1-associated protein 1 (Arabidopsis thaliana) GI:15487384; contains Pfam profile PF00168: C2 domain; supporting cDNA gi:15487383:gb:AY045765.1:   chr3:22661502-22662424 REVERSE   Aliases: BON ASSOCIATION PROTEIN 1, T20K12.90	5.2	4.3	0.9	1.9	100.0%	-3.1
2763	AT3G60380.1   expressed protein   chr3:22327888-22330241 REVERSE   Aliases: T8B10.40	6.7	7.5	-0.8	-1.9	100.0%	-3.3
2764	AT1G23230.1   expressed protein   chr1:8244470-8251730 FORWARD   Aliases: F26F24.8, F26F24_8	5.3	6.0	-0.7	-1.9	100.0%	-3.2
2765	AT3G02210.1   phytochelatin synthetase family protein / COBRA cell expansion protein COBL3, similar to phytochelatin synthetase (Hordeum vulgare subsp. vulgare) GI:29570314; identified in Roudier, et al, Plant Phys. (2002) 130:538-548 (PMID:12376623); supported by cDNA: gi:26452134:dbj:AK118555.1; contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region   chr3:409208-411659 REVERSE   Aliases: F14P3.14, F14P3_14	4.5	4.9	-0.4	-1.9	100.0%	-3.4
2766	AT1G53590.1   C2 domain-containing protein   chr1:20000118-20003933 FORWARD   Aliases: F22G10.28	4.8	5.4	-0.6	-1.9	100.0%	-3.2
2767	AT2G41690.1   Symbol: AT HSF3   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr2:17388801-17389655 FORWARD   Aliases: HSF3, T32G6.21, T32G6_21	3.3	3.7	-0.4	-1.9	100.0%	-3.6
2768	AT4G00830.2   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At3g52660.1); similar to putative RNA-binding protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52145.1); contains InterPro domain RNA-binding region RNP-1	7.3	6.8	0.5	1.9	100.0%	-3.4
2769	AT5G64860.1   Symbol: DPE1   4-alpha-glucanotransferase, putative / disproportionating enzyme, putative, similar to 4-alpha-glucanotransferase SP:Q06801 from (Solanum tuberosum)   chr5:25942400-25946034 REVERSE   Aliases: DISPROPORTIONATING ENZYME, MXK3.9, MXK3_9	6.9	7.7	-0.8	-1.9	100.0%	-3.0
2770	AT3G45000.1   SNF7 family protein, contains Pfam profile PF03357: SNF7 family   chr3:16471333-16472392 FORWARD   Aliases: F14D17.70	3.0	2.7	0.3	1.9	100.0%	-4.0
2771	AT4G17520.1   nuclear RNA-binding protein, putative, similar to nuclear RNA binding protein GI:6492264 from (Arabidopsis thaliana)   chr4:9771343-9773605 FORWARD   Aliases: DL4795W, FCAALL.142	9.8	10.5	-0.7	-1.9	100.0%	-3.4
2772	AT3G19240.1   expressed protein   chr3:6664256-6666564 FORWARD   Aliases: MVI11.21	10.0	9.2	0.8	1.9	100.0%	-3.1
2773	AT2G01420.2   Symbol: PIN4   auxin transport protein, putative, similar to auxin transport protein PIN7(Arabidopsis thaliana) gi:5817305:gb:AAD52697   chr2:180104-183327 REVERSE   Aliases: AUXIN TRANSPORTER SPLICE VARIANT B, F10A8.27, PIN FORMED 4	3.4	3.8	-0.4	-1.9	100.0%	-3.5
2774	AT3G03580.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:860519-863359 REVERSE   Aliases: T12J13.14, T12J13_14	3.7	4.2	-0.5	-1.9	100.0%	-3.4
2775	AT3G62290.1   Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct.   chr3:23062627-23064719 FORWARD   Aliases: T17J13.250	12.4	11.8	0.6	1.9	100.0%	-3.7
2776	AT5G58790.1   expressed protein, ; expression supported by MPSS   chr5:23762232-23763018 FORWARD   Aliases: MZN1.28	5.2	4.6	0.6	1.9	100.0%	-3.5
2777	AT5G61960.2   Symbol: AML1   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At5g07290.1); similar to AML1 [Lycopersicon esculentum] (GB:AAT39005.1); similar to Mei2-like protein [Hordeum vulgare subsp. vulgare] (GB:AAL85701.1); contains InterPro domain RNA recognition motif 2 (InterPro:IPR007201); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr5:24895746-24901376 REVERSE   Aliases: ARABIDOPSIS MEI2 LIKE PROTEIN 1, K22G18.10, K22G18_10	6.0	7.2	-1.2	-1.9	100.0%	-3.1
2778	AT2G18790.1   Symbol: PHYB   phytochrome B (PHYB), identical to SP:P14713 Phytochrome B {Arabidopsis thaliana}   chr2:8146963-8151512 FORWARD   Aliases: HY3, MSF3.17, MSF3_17, OOP1, OUT OF PHASE 1, PHYTOCHROME B	5.7	6.6	-0.9	-1.9	100.0%	-3.3
2779	AT4G38210.1   Symbol: ATEXPA20   expansin, putative (EXP20), similar to alpha-expansin 3 GI:6942322 from (Triphysaria versicolor); alpha-expansin gene family, PMID:11641069   chr4:17922750-17923967 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A20, ATEXP20, ATHEXP ALPHA 1.23, EXP20, F20D10.330, F20D10_330	5.0	5.8	-0.9	-1.9	100.0%	-3.0
2780	AT4G20170.1   expressed protein   chr4:10896689-10899151 FORWARD   Aliases: F1C12.90, F1C12_90	7.7	7.1	0.5	1.9	100.0%	-3.3
2781	AT5G03440.2   expressed protein   chr5:856871-858404 REVERSE   Aliases: F12E4.200, F12E4_200	6.2	5.5	0.7	1.9	100.0%	-3.3
2782	AT5G07010.1   sulfotransferase family protein, similar to steroid sulfotransferase 3 (Brassica napus) GI:3420008, steroid sulfotransferase 1 (Brassica napus) GI:3420004; contains Pfam profile PF00685: Sulfotransferase domain   chr5:2174679-2176107 REVERSE   Aliases: MOJ9.18, MOJ9_18	3.3	3.0	0.3	1.9	100.0%	-3.6
2783	AT3G01015.1   expressed protein, ; expression supported by MPSS   chr3:1805-4024 REVERSE   Aliases: TEL3N.1, TEL3N_1	2.8	2.6	0.2	1.9	100.0%	-4.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2784	AT2G21710.1   Symbol: EMB2219   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr2:9277966-9280498 FORWARD   Aliases: EMB2219, EMBRYO DEFECTIVE 2219, F7D8.3, F7D8_3	3.3	3.8	-0.4	-1.9	100.0%	-3.4
2785	AT5G02290.2   Symbol: NAK   protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) SWISS-PROT:Q06548   chr5:470194-472782 REVERSE   Aliases: PROTEIN KINASE NAK, T1E22.50, T1E22_50	7.7	7.0	0.7	1.9	100.0%	-3.3
2786	AT2G05170.1   Symbol: ATVPS11   vacuolar protein sorting 11 family protein / VPS11 family protein, similar to Vacuolar protein sorting 11 (hVPS11) (PP3476) (Swiss-Prot:Q9H270) (Homo sapiens); similar to Vacuolar biogenesis protein END1 (PEP5 protein) (Vacuolar protein sorting 11) (Swiss-Prot:P12868) (Saccharomyces cerevisiae)   chr2:1869882-1873809 FORWARD   Aliases: F5G3.7, F5G3_7	3.7	4.7	-1.0	-1.9	100.0%	-3.2
2787	AT1G21650.1   preprotein translocase secA family protein, contains Pfam profiles: PF01043 SecA protein, amino terminal region, PF00400 WD domain, G-beta repeat, PF00097 zinc finger, C3HC4 type (RING finger)	2.8	3.1	-0.3	-1.9	100.0%	-3.8
2788	AT3G28970.1   expressed protein, contains Pfam domain PF03556: Domain of unknown function (DUF298)   chr3:10989024-10991122 REVERSE   Aliases: K5K13.10	8.1	8.5	-0.5	-1.9	100.0%	-3.7
2789	AT3G11590.1   expressed protein   chr3:3660383-3663740 FORWARD   Aliases: F24K9.26	6.7	7.3	-0.6	-1.9	100.0%	-3.4
2790	AT3G12360.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr3:3934085-3936701 FORWARD   Aliases: T2E22.31	8.7	8.3	0.4	1.9	100.0%	-3.7
2791	AT5G03960.1   calmodulin-binding family protein   chr5:1068275-1069977 REVERSE   Aliases: F8F6.170, F8F6_170	4.9	4.1	0.8	1.9	100.0%	-3.1
2792	AT5G25540.1   Symbol: CID6   Expressed protein contains PAM2 PABC interacting domain.	6.9	6.5	0.4	1.9	100.0%	-3.5
2793	AT5G39130.1   germin-like protein, putative, identical to germin-like protein subfamily 1 member 16 (SP:Q9FIC8)   chr5:15682730-15683667 REVERSE   Aliases: MXF12.140, MXF12_140	2.6	2.9	-0.2	-1.9	100.0%	-4.3
2794	AT4G05110.1   equilibrative nucleoside transporter, putative (ENT6), identical to putative equilibrative nucleoside transporter ENT6 (Arabidopsis thaliana) GI:16518997; contains similarity to SWISS-PROT:O54699 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptapurine riboside-insensitive nucleoside transporter, Equilibrative NBMPR-insensitive nucleoside transporter, Nucleoside transporter, ei-type) (Rattus norvegicus); contains Pfam profile PF01733: Nucleoside transporter   chr4:2626403-2628828 REVERSE   Aliases: C17L7.30, C17L7_30	4.2	3.5	0.7	1.9	100.0%	-3.0
2795	AT4G05120.1   equilibrative nucleoside transporter, putative (ENT3), identical to putative equilibrative nucleoside transporter ENT3 (Arabidopsis thaliana) GI:16518993; contains similarity to SWISS-PROT:O54699 equilibrative nucleoside transporter 2 (Equilibrative nitrobenzylmercaptapurine riboside-insensitive nucleoside transporter, Equilibrative NBMPR-insensitive nucleoside transporter, Nucleoside transporter, ei-type) (Rattus norvegicus); contains Pfam profile PF01733: Nucleoside transporter   chr4:2632884-2634822 REVERSE   Aliases: C17L7.40, C17L7_40	4.2	3.5	0.7	1.9	100.0%	-3.0
2796	AT2G19830.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr2:8564931-8566800 REVERSE   Aliases: F6F22.14, F6F22_14	7.8	7.2	0.5	1.9	100.0%	-3.4
2797	AT5G47580.1   expressed protein, strong similarity to unknown protein (pir::E71441)   chr5:19312072-19314644 REVERSE   Aliases: MNJ7.17, MNJ7_17	5.3	5.8	-0.5	-1.9	100.0%	-3.4
2798	AT2G47770.1   benzodiazepine receptor-related, contains weak similarity to Peripheral-type benzodiazepine receptor (PBR) (PKBS) (Mitochondrial benzodiazepine receptor) (Swiss-Prot:P30536) (Homo sapiens)   chr2:19575534-19576577 FORWARD   Aliases: F17A22.16	5.6	4.9	0.6	1.9	100.0%	-3.2
2799	AT2G04940.1   scramblase-related, weak similarity to Phospholipid scramblase 1 (PL scramblase 1) (Ca(2)-dependent phospholipid scramblase 1) (Transplantability associated protein 1) (TRA1) (NOR1) (Swiss-Prot:Q9JJ00) (Mus musculus); weak similarity to Phospholipid scramblase 4 (PL scramblase 4) (Ca(2)-dependent phospholipid scramblase 4) (Swiss-Prot:Q9NRQ2) (Homo sapiens)   chr2:1736482-1740385 REVERSE   Aliases: F1O13.7, F1O13_7	6.4	5.8	0.5	1.9	100.0%	-3.4
2800	AT5G01210.1   transferase family protein, contains Pfam profile PF02458 transferase family   chr5:84473-86274 FORWARD   Aliases: F7J8.190, F7J8_190	11.5	10.7	0.7	1.9	100.0%	-3.5
2801	AT3G07580.1   expressed protein   chr3:2420975-2422667 REVERSE   Aliases: MLP3.3	4.6	4.1	0.4	1.9	100.0%	-3.3
2802	AT5G58120.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:23534718-23538293 FORWARD   Aliases: K21L19.1, K21L19_1	4.1	3.8	0.3	1.9	100.0%	-3.7
2803	AT2G31840.1   expressed protein   chr2:13544989-13546835 REVERSE   Aliases: F20M17.12, F20M17_12	5.6	6.2	-0.6	-1.9	100.0%	-3.3
2804	AT3G49830.1   DNA helicase-related, similar to DNA helicase GI:4521249 from (Mus musculus)   chr3:18493368-18494925 FORWARD   Aliases: T16K5.180	2.7	2.4	0.2	1.9	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2805	AT1G13160.1   SDA1 family protein, contains Pfam PF05285: SDA1 domain; similar to mystery 45A (GI:16797816){Drosophila melanogaster}   chr1:4484597-4488525 FORWARD   Aliases: F3F19.18, F3F19_18	6.6	7.2	-0.6	-1.9	100.0%	-3.4
2806	AT1G32260.1   expressed protein, identical to hypothetical protein GB:AAF81322 GI:8920600 from (Arabidopsis thaliana)   chr1:11640562-11641764 REVERSE   Aliases: F27G20.13	4.8	5.2	-0.4	-1.9	100.0%	-3.4
2807	AT2G01610.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:Q42534 Pectinesterase 2 precursor (EC 3.1.1.11) (Pectin methylesterase 2) (PE 2) {Arabidopsis thaliana}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr2:274123-274819 REVERSE   Aliases: T8O11.22, T8O11_22	2.9	3.4	-0.4	-1.9	100.0%	-3.4
2808	AT5G49660.1   leucine-rich repeat transmembrane protein kinase, putative, contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:20178432-20181955 REVERSE   Aliases: MNI5.4, MNI5_4	6.1	6.6	-0.5	-1.9	100.0%	-3.3
2809	AT5G58660.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to ACC oxidase, Lycopersicon esculentum (SP:P05116), gibberellin 3B-hydroxylase, Lactuca sativa (gi:4164145); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily	4.7	4.1	0.6	1.9	100.0%	-3.2
2810	AT2G42240.1   RNA recognition motif (RRM)-containing protein, similar to RNA-binding protein (Hermes) from {Gallus gallus} SP:Q9W6I1, {Xenopus laevis} SP:Q9YGP5, {Mus musculus} SP:Q9WVB0; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:17603967-17604642 FORWARD   Aliases: T24P15.15, T24P15_15	3.3	3.0	0.3	1.9	100.0%	-3.7
2811	AT5G46420.1   16S rRNA processing protein RimM family, contains weak similarity to Swiss-Prot:O74933 UDP-N-acetylglucosamine pyrophosphorylase (Candida albicans); contains Pfam profiles PF01782: 16S rRNA processing protein RimM, PF05239: PRC-barrel domain   chr5:18847182-18850180 FORWARD   Aliases: K11I1.1, K11I1_1	6.0	6.5	-0.6	-1.9	100.0%	-3.3
2812	AT2G39090.2   similar to cell division cycle family protein / CDC family protein [Arabidopsis thaliana] (TAIR:At3g48150.1); similar to IVR-like protein [Nicotiana tabacum] (GB:CAA08776.1); contains InterPro domain TPR repeat (InterPro:IPR001440)   chr2:16319760-16324378 REVERSE   Aliases: T7F6.26, T7F6_26	3.3	3.9	-0.6	-1.9	100.0%	-3.5
2813	AT3G04340.1   Symbol: EMB2458   FtsH protease family protein, similar to chloroplast FtsH protease (Arabidopsis thaliana) GI:1483215; contains Pfam profiles PF01434: Peptidase family M41, PF00004: ATPase AAA family   chr3:1146807-1152455 REVERSE   Aliases: EMB2458, EMBRYO DEFECTIVE 2458, T6K12.4, T6K12_4	4.3	4.7	-0.5	-1.9	100.0%	-3.3
2814	AT4G36680.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat; identical to cDNA membrane-associated salt-inducible protein like GI:2632060	6.8	7.5	-0.7	-1.9	100.0%	-3.1
2815	AT3G15810.1   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr3:5347833-5349295 REVERSE   Aliases: MSJ11.21	7.0	6.6	0.5	1.9	100.0%	-3.5
2816	AT3G11745.1   expressed protein   chr3:3713769-3714585 REVERSE   Aliases: None	4.4	3.9	0.5	1.9	100.0%	-3.4
2817	AT3G21240.1   Symbol: 4CL2   4-coumarate--CoA ligase 2 / 4-coumaroyl-CoA synthase 2 (4CL2), identical to SP:Q9S725 4-coumarate--CoA ligase 2 (EC 6.2.1.12) (4CL2) (4-coumaroyl-CoA synthase 2) {Arabidopsis thaliana}   chr3:7454282-7457385 REVERSE   Aliases: COUMARATE:COA LIGASE, AT4CL2, MXL8.10	10.7	11.7	-1.0	-1.9	100.0%	-3.7
2818	AT3G16290.1   Symbol: EMB2083   FtsH protease, putative, contains similarity to cell division protein FtsH GI:1652085 from (Synechocystis sp. PCC 6803)   chr3:5521193-5525001 REVERSE   Aliases: EMB2083, EMBRYO DEFECTIVE 2083, MYA6.12	5.5	6.0	-0.5	-1.9	100.0%	-3.5
2819	AT4G15260.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr4:8713689-8715339 FORWARD   Aliases: DL3675W, FCAALL.250	5.3	4.3	1.0	1.9	100.0%	-3.2
2820	AT2G31390.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr2:13390140-13393286 REVERSE   Aliases: T28P16.12, T28P16_12	11.2	11.7	-0.5	-1.9	100.0%	-3.7
2821	AT1G08840.1   Symbol: EMB2411   DNA replication helicase, putative, similar to helicase (Xenopus laevis) gi:18845092:gb:AAL79550   chr1:2829582-2838372 REVERSE   Aliases: EMB2411, EMBRYO DEFECTIVE 2411, F7G19.26	2.8	3.1	-0.2	-1.9	100.0%	-4.0
2822	AT5G13220.3   expressed protein   chr5:4218920-4220770 FORWARD   Aliases: T31B5.40, T31B5_40	4.1	2.5	1.6	1.9	100.0%	-3.6
2823	AT1G77660.1   MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related, low similarity to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profile PF02493: MORN repeat   chr1:29190967-29192394 REVERSE   Aliases: T5M16.25, T5M16_25	3.7	3.2	0.5	1.9	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2824	AT1G43000.1   zinc-binding family protein, similar to zinc-binding protein (Pisum sativum) GI:16117799; contains Pfam profile PF04640 : Protein of unknown function, DUF597   chr1:16143256-16144095 FORWARD   Aliases: F13A11.6, F13A11_6	3.0	3.3	-0.3	-1.9	100.0%	-3.7
2825	AT3G08880.1   expressed protein   chr3:2703175-2703598 FORWARD   Aliases: T16O11.19	3.1	3.4	-0.3	-1.9	100.0%	-3.9
2826	AT1G13890.1   Symbol: SNAP30	2.9	2.6	0.3	1.9	100.0%	-4.0
2827	AT3G03570.1   expressed protein, similar to hypothetical protein GB:CAB38918 (Arabidopsis thaliana)   chr3:856903-860476 FORWARD   Aliases: T12J13.15, T12J13_15	3.5	3.9	-0.4	-1.9	100.0%	-3.4
2828	AT1G30040.2   similar to gibberellin 2-oxidase / GA2-oxidase (GA2OX3) [Arabidopsis thaliana] (TAIR:At2g34555.1); similar to GA 2-oxidase 2 [Nerium oleander] (GB:AAT92094.1); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)   chr1:10537632-10539172 FORWARD   Aliases: T1P2.6, T1P2_6	5.6	6.4	-0.8	-1.9	100.0%	-3.0
2829	AT3G11530.2   vacuolar protein sorting 55 family protein / VPS55 family protein, contains Pfam domain PF04133: Vacuolar protein sorting 55   chr3:3628599-3630416 REVERSE   Aliases: F24K9.21	7.7	7.1	0.6	1.9	100.0%	-3.3
2830	AT1G70090.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr1:26404453-26406060 FORWARD   Aliases: F20P5.18, F20P5_18	5.2	4.7	0.5	1.9	100.0%	-3.3
2831	AT1G22800.1   expressed protein, similar to Biotin synthesis protein bioC. {Serratia marcescens} (SP:P36571); ESTs gb:Z34075, gb:Z34835 and gb:AA404888 come from this gene   chr1:8071924-8074346 FORWARD   Aliases: T22J18.3, T22J18_3	6.7	7.5	-0.7	-1.9	100.0%	-3.0
2832	AT4G24270.2   RNA recognition motif (RRM)-containing protein, low similarity to tumor-rejection antigen SART3 (Mus musculus) GI:7637845; contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain   chr4:12581611-12587394 REVERSE   Aliases: T22A6.100, T22A6_100	4.7	5.1	-0.4	-1.9	100.0%	-3.4
2833	AT5G45610.1   expressed protein   chr5:18513538-18516900 REVERSE   Aliases: MRA19.1, MRA19_1	4.2	4.6	-0.4	-1.9	100.0%	-3.4
2834	AT1G42540.1   Symbol: ATGLR3.3   glutamate receptor family protein (GLR3.3), plant glutamate receptor family, PMID:11379626   chr1:15975929-15979143 FORWARD   Aliases: GLR3.3, T8D8.1, T8D8_1	5.0	5.5	-0.6	-1.9	100.0%	-3.3
2835	AT5G65750.1   2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative, similar to SP:P20967 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase) {Saccharomyces cerevisiae}; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF00676: Dehydrogenase E1 component   chr5:26320932-26325415 FORWARD   Aliases: MPA24.10, MPA24_10	8.3	8.9	-0.7	-1.9	100.0%	-3.0
2836	AT5G11710.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Af10-protein (GI:1724114) (Avena fatua); similar to clathrin assembly protein AP180 (GI:6492344) (Xenopus laevis); Af10-protein, Avena fatua, EMBL:U80041   chr5:3772865-3776663 FORWARD   Aliases: T22P22.100, T22P22_100	6.1	5.7	0.4	1.9	100.0%	-3.4
2837	AT1G66980.1   protein kinase family protein / glycerophosphoryl diester phosphodiesterase family protein, similar to leaf rust resistance kinase Lr10 GI:1680685 from (Triticum aestivum); contains Pfam profiles PF03009: Glycerophosphoryl diester phosphodiesterase family, PF00069: Protein kinase domain   chr1:25000972-25005624 REVERSE   Aliases: F1O19.6, F1O19_6	3.5	3.2	0.4	1.9	100.0%	-3.5
2838	AT1G08700.1   presenilin family protein, similar to SP:P52166 Presenilin sel-12 {Caenorhabditis elegans}; contains Pfam profile PF01080: Presenilin   chr1:2769818-2771480 REVERSE   Aliases: F22O13.18, F22O13_18	8.5	8.9	-0.4	-1.9	100.0%	-3.6
2839	AT5G14030.1   translocon-associated protein beta (TRAPB) family protein, low similarity to SP:P23438 Translocon-associated protein, beta subunit precursor (TRAP-beta) (Signal sequence receptor beta subunit) {Canis familiaris}; contains Pfam profile PF05753: Translocon-associated protein beta (TRAPB)   chr5:4526813-4528411 FORWARD   Aliases: MUA22.2, MUA22_2	9.9	10.5	-0.6	-1.9	100.0%	-3.4
2840	AT4G09490.1   RNase H domain-containing protein, contains Pfam profile PF00075: RNase H   chr4:6015559-6016572 REVERSE   Aliases: T15G18.90, T15G18_90	4.1	3.4	0.7	1.9	100.0%	-3.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2841	AT1G11280.4   similar to S-locus protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g61390.1); similar to S-locus protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g61480.1); similar to S-locus protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g61490.1); similar to S-locus lectin protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g61370.1); similar to S-locus protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g61380.1); similar to receptor kinase 5 [Brassica rapa] (GB:BAB69683.1); similar to KI domain interacting kinase 1 [Zea mays] (GB:AAB93834.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Apple-like (InterPro:IPR003609); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Curculin-like (mannose-binding) lectin (InterPro:IPR001480); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain S-locus glycoprotein (InterPro:IPR000858)   chr1:3787334-3790812 REVERSE   Aliases: T28P6.7, T28P6_7	6.4	7.1	-0.7	-1.9	100.0%	-3.3
2842	AT4G26110.1   nucleosome assembly protein (NAP), putative, similar to nucleosome assembly protein 1 (Glycine max) GI:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP)	6.8	7.4	-0.6	-1.9	100.0%	-3.4
2843	AT5G64330.1   Symbol: NPH3   non-phototropic hypocotyl 3 (NPH3), identical to non-phototropic hypocotyl 3 (Arabidopsis thaliana) gi:6224712:gb:AAF05914, PMID:10542152   chr5:25744563-25748328 FORWARD   Aliases: JK218, MSJ1.17, MSJ1_17, NON PHOTOTROPIC HYPOCOTYL 3, ROOT PHOTOTROPISM 3, RPT3	4.9	5.4	-0.5	-1.9	100.0%	-3.3
2844	AT5G36160.1   aminotransferase-related, similar to nicotianamine aminotransferase B GI:6469087 from (Hordeum vulgare subsp. vulgare)   chr5:14250343-14252364 REVERSE   Aliases: MAB16.11, MAB16_11	6.8	8.0	-1.2	-1.9	100.0%	-3.3
2845	AT5G02740.2   expressed protein   chr5:616492-618595 FORWARD   Aliases: F9G14.50, F9G14_50	5.7	6.6	-0.9	-1.9	100.0%	-3.3
2846	AT3G62560.1   GTP-binding protein, putative, similar to GTP-binding protein SAR1A (SP:O04834) (Arabidopsis thaliana); small GTP-binding protein Bsar1a - Brassica campestris, EMBL:U55035   chr3:23148459-23150021 FORWARD   Aliases: T12C14.260	9.3	8.4	0.9	1.9	100.0%	-3.3
2847	AT2G24970.1   expressed protein   chr2:10627198-10628386 REVERSE   Aliases: F27C12.11, F27C12_11	4.8	6.1	-1.2	-1.9	100.0%	-3.0
2848	AT1G21680.1   expressed protein, similar to TolB protein precursor (SP:Q9ZDM5) {Rickettsia prowazekii}; ESTs gb:N96028, gb:F14286, gb:T20680, gb:F14443, gb:AA657300 and gb:N65244 come from this gene	9.8	8.5	1.2	1.9	100.0%	-3.3
2849	AT1G09560.1   Symbol: GLP5   germin-like protein (GLP4) (GLP5), identical to Arabidopsis germin-like protein subfamily 2 member 1 (SP:P94014); Location of EST 180L10T7, gi:906417   chr1:3093841-3094864 FORWARD   Aliases: F14J9.22, F14J9_22, GERMIN LIKE PROTEIN 5, GLP5	8.0	8.9	-0.9	-1.9	100.0%	-3.0
2850	AT3G20100.1   Symbol: CYP705A19   cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) (Glycine max); contains Pfam profile: PF00067 cytochrome P450; supported by full-length cDNA: Ceres:149380.   chr3:7019001-7020907 FORWARD   Aliases: MAL21.14	7.8	7.4	0.4	1.9	100.0%	-3.4
2851	AT4G13280.1   terpene synthase/cyclase family protein, predicted protein, Arabidopsis thaliana	2.9	3.2	-0.4	-1.9	100.0%	-3.6
2852	AT1G80160.1   lactoylglutathione lyase family protein / glyoxalase I family protein, contains glyoxalase family protein domain, Pfam:PF00903   chr1:30155895-30157082 FORWARD   Aliases: F18B13.24, F18B13_24	2.9	2.7	0.2	1.9	100.0%	-4.0
2853	AT3G55605.1   mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	6.7	7.4	-0.6	-1.9	100.0%	-3.1
2854	AT2G38060.1   transporter-related, low similarity to vesicular glutamate transporter 3 (Homo sapiens) GI:21213895, brain specific Na+-dependent inorganic phosphate cotransporter (Rattus norvegicus) GI:507415; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:15929805-15932701 REVERSE   Aliases: T8P21.3, T8P21_3	4.4	4.9	-0.5	-1.9	100.0%	-3.3
2855	AT1G76185.1   expressed protein   chr1:28595219-28596412 FORWARD   Aliases: None	5.3	4.5	0.8	1.9	100.0%	-3.1
2856	AT1G55210.1   disease resistance response protein-related/ dirigent protein-related, smimilar to dirigent protein (Thuja plicata) gi:6694699:gb:AAF25360; similar to pathogenesis-related protein (Pisum sativum) gi:4585273:gb:AAD25355   chr1:20601536-20602375 REVERSE   Aliases: F7A10.7, F7A10_7	6.3	7.2	-0.8	-1.9	100.0%	-3.4
2857	AT1G09340.1   expressed protein   chr1:3015388-3018236 FORWARD   Aliases: None	8.1	7.2	0.9	1.9	100.0%	-2.9
2858	AT4G01026.1   expressed protein   chr4:447090-448510 FORWARD   Aliases: None	5.6	4.9	0.6	1.9	100.0%	-3.3
2859	AT1G77250.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr1:29025201-29028349 REVERSE   Aliases: T14N5.11, T14N5_11	5.3	6.1	-0.7	-1.9	100.0%	-3.3
2860	AT2G29260.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12589600-12591178 FORWARD   Aliases: F16P2.36, F16P2_36	4.2	4.7	-0.5	-1.9	100.0%	-3.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2861	AT2G26600.2   glycosyl hydrolase family 17 protein   chr2:11323530-11325561 FORWARD   Aliases: T9J22.27, T9J22_27	7.5	7.1	0.4	1.9	100.0%	-3.5
2862	AT5G47210.1   nuclear RNA-binding protein, putative, similar to nuclear RNA binding protein GI:6492264 from (Arabidopsis thaliana)   chr5:19186249-19188446 REVERSE   Aliases: MQL5.6, MQL5_6	11.5	12.0	-0.6	-1.9	100.0%	-3.9
2863	AT5G42980.1   Symbol: ATTRX3	13.4	13.1	0.3	1.9	100.0%	-4.0
2864	AT1G75690.1   chaperone protein dnaJ-related, contains Pfam PF00684 : DnaJ central domain (4 repeats); similar to bundle sheath defective protein 2 (GI:4732091) (Zea mays)   chr1:28425771-28426880 REVERSE   Aliases: F10A5.12, F10A5_12	6.7	5.7	1.0	1.9	100.0%	-3.0
2865	AT5G49840.1   ATP-dependent Clp protease ATP-binding subunit ClpX, putative, similar to CLP protease regulatory subunit CLPX GI:2674203 from (Arabidopsis thaliana); non-consensus splice donor GC at exon 4; non-consensus splice donor AA at exon 7   chr5:20272469-20276261 FORWARD   Aliases: K21G20.5, K21G20_5	5.9	5.4	0.5	1.9	100.0%	-3.2
2866	AT2G37420.1   kinesin motor protein-related   chr2:15707410-15712422 FORWARD   Aliases: F3G5.21, F3G5_21	4.4	5.4	-1.0	-1.9	100.0%	-3.2
2867	AT3G11840.1   U-box domain-containing protein, low similarity to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain	4.6	4.0	0.6	1.9	100.0%	-3.2
2868	AT2G45960.1   Symbol: PIP1B   plasma membrane intrinsic protein 1B (PIP1B) / aquaporin PIP1.2 (PIP1.2) / transmembrane protein A (TMPA), identical to plasma membrane intrinsic protein 1B SP:Q06611 from (Arabidopsis thaliana)   chr2:18917384-18919035 FORWARD   Aliases: ATHH2, F4I18.6, PIP1;2, PIP1B, TMP A	6.4	5.5	0.9	1.9	100.0%	-3.0
2869	AT1G21560.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At4g01170.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAV24769.1)   chr1:7554829-7557014 FORWARD   Aliases: F24J8.19, F24J8_19	6.0	6.6	-0.6	-1.9	100.0%	-3.2
2870	AT5G55660.1   expressed protein, similar to unknown protein (pir::T08929)   chr5:22556601-22560700 FORWARD   Aliases: MDF20.10, MDF20_10	5.3	6.5	-1.2	-1.9	100.0%	-3.2
2871	AT5G51440.1   23.5 kDa mitochondrial small heat shock protein (HSP23.5-M), similar to heat shock 22 kDa protein, mitochondrial precursor SP:Q96331 from (Arabidopsis thaliana); identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.   chr5:20908389-20909437 FORWARD   Aliases: MFG13.15, MFG13_15	3.5	3.2	0.3	1.9	100.0%	-3.7
2872	AT2G26730.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:11395485-11398719 FORWARD   Aliases: F18A8.10, F18A8_10	4.0	4.6	-0.6	-1.9	100.0%	-3.2
2873	AT5G13770.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:4445426-4447839 FORWARD   Aliases: MXE10.6, MXE10_6	8.6	7.2	1.4	1.9	100.0%	-3.2
2874	AT4G05020.1   NADH dehydrogenase-related, similar to alternative NADH-dehydrogenase (Yarrowia lipolytica) GI:3718005, 64 kDa mitochondrial NADH dehydrogenase (Neurospora crassa) GI:4753821; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr4:2572693-2576593 FORWARD   Aliases: C17L7.11	5.2	6.8	-1.5	-1.9	100.0%	-3.2
2875	AT3G18295.1   expressed protein   chr3:6281210-6282087 FORWARD   Aliases: MIE15.10	3.5	3.3	0.3	1.9	100.0%	-3.8
2876	AT1G74420.2   Symbol: FUT3   xyloglucan fucosyltransferase, putative (FUT3), identical to SP:Q9CA71 Probable fucosyltransferase 3 (EC 2.4.1.-) (AtFUT3) {Arabidopsis thaliana}; similar to SP:Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}   chr1:27971555-27973464 REVERSE   Aliases: ATFUT3, F1M20.10, F1M20_10	3.1	3.7	-0.5	-1.9	100.0%	-3.5
2877	AT3G11440.1   Symbol: ATMYB65   myb family transcription factor (MYB65), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:3602100-3605110 FORWARD   Aliases: F24K9.11, MYB65	5.3	4.8	0.5	1.9	100.0%	-3.5
2878	AT2G24940.1   cytochrome b5 domain-containing protein, similar to SP:P70580 Membrane associated progesterone receptor component 1 {Rattus norvegicus}; contains Pfam profile PF00173: Heme/Steroid binding domain   chr2:10616473-10619311 FORWARD   Aliases: F27C12.14, F27C12_14	12.8	12.0	0.8	1.9	100.0%	-3.4
2879	AT2G24945.1   expressed protein   chr2:10616492-10619311 FORWARD   Aliases: None	12.8	12.0	0.8	1.9	100.0%	-3.4
2880	AT2G45140.1   vesicle-associated membrane protein, putative / VAMP, putative, similar to VAP27 GI:6688926 (Nicotiana glauca)   chr2:18617881-18620365 FORWARD   Aliases: T14P1.5	7.9	7.4	0.5	1.9	100.0%	-3.4
2881	AT1G10020.1   expressed protein   chr1:3269606-3271989 REVERSE   Aliases: T27I1.4, T27I1_4	4.5	3.9	0.5	1.9	100.0%	-3.4
2882	AT1G20480.1   4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein, similar to SP:Q9S725 from Arabidopsis thaliana and SP:P17814 from Oryza sativa; contains Pfam AMP-binding enzyme domain PF00501   chr1:7094250-7097104 REVERSE   Aliases: F5M15.29, F5M15_29	4.8	4.3	0.4	1.9	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2883	AT4G24290.2   expressed protein   chr4:12594349-12598038 FORWARD   Aliases: T22A6.120, T22A6_120	3.3	3.0	0.3	1.9	100.0%	-3.8
2884	AT3G25160.1   ER lumen protein retaining receptor family protein, similar to SP:P24390 ER lumen protein retaining receptor 1 (KDEL receptor 1) {Homo sapiens}; contains Pfam profile PF00810: ER lumen protein retaining receptor   chr3:9160175-9162074 REVERSE   Aliases: MJL12.10	3.2	2.7	0.5	1.9	100.0%	-3.4
2885	AT4G40070.1   similar to zinc finger (C3HC4-type RING finger) family protein (ATL6) [Arabidopsis thaliana] (TAIR:At3g05200.1); similar to RING/C3HC4/PHD zinc finger-like protein [Cucumis melo] (GB:AAO45753.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr4:18576412-18577768 FORWARD   Aliases: T5J17.240, T5J17_240	6.3	5.7	0.6	1.9	100.0%	-3.4
2886	AT2G01640.1   expressed protein   chr2:283003-284124 FORWARD   Aliases: T8O11.19, T8O11_19	5.0	5.6	-0.6	-1.9	100.0%	-3.4
2887	AT1G45976.1   Symbol: SBP1   expressed protein   chr1:17201791-17203173 FORWARD   Aliases: F2G19.22, F2G19_22, S RIBONUCLEASE BINDING PROTEIN 1	7.7	7.1	0.5	1.9	100.0%	-3.5
2888	AT5G65520.1   expressed protein   chr5:26206951-26207817 REVERSE   Aliases: K21L13.2, K21L13_2	4.1	3.7	0.4	1.9	100.0%	-3.8
2889	AT2G31740.1   expressed protein   chr2:13497985-13502187 REVERSE   Aliases: F20M17.22, F20M17_22	6.8	7.3	-0.5	-1.9	100.0%	-3.4
2890	AT3G53650.1   histone H2B, putative, similar to histone H2B from Lycopersicon esculentum, PIR:T06389 GI:3021483, Gossypium hirsutum SP:O22582, Capsicum annuum SP:O49118; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr3:19900336-19900752 FORWARD   Aliases: F4P12.350	6.5	7.7	-1.2	-1.9	100.0%	-3.0
2891	AT5G25210.1   expressed protein   chr5:8723961-8725774 FORWARD   Aliases: F21J6.105, F21J6_105	3.3	3.0	0.3	1.9	100.0%	-3.7
2892	AT4G24060.1   Dof-type zinc finger domain-containing protein, Dof zinc finger protein - Oryza sativa,PID:d1042342   chr4:12503821-12505656 FORWARD   Aliases: T19F6.50, T19F6_50	5.2	4.6	0.6	1.9	100.0%	-3.5
2893	AT3G02650.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:566278-570110 FORWARD   Aliases: F16B3.28, F16B3_28	6.7	7.6	-0.9	-1.9	100.0%	-3.2
2894	AT3G17860.2   expressed protein   chr3:6121059-6123017 FORWARD   Aliases: MEB5.8	4.6	4.2	0.4	1.9	100.0%	-3.4
2895	AT2G29050.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr2:12485223-12487449 FORWARD   Aliases: T9I4.13, T9I4_13	3.8	4.4	-0.6	-1.9	100.0%	-3.2
2896	AT1G30570.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:10828915-10831464 FORWARD   Aliases: T5I8.2, T5I8_2	3.6	4.1	-0.5	-1.9	100.0%	-3.6
2897	AT2G13540.1   Symbol: ABH1   mRNA cap-binding protein (ABH1), identical to mRNA cap binding protein (Arabidopsis thaliana) GI:15192738; contains Pfam profile PF02854: MIF4G domain; identical to cDNA nuclear cap-binding protein CBP80 GI:8515770   chr2:5643966-5650039 FORWARD   Aliases: ABA HYPERSENSITIVE 1, CBP80, NUCLEAR CAP BINDING PROTEIN CBP80, T10F5.8, T10F5_8	6.2	6.7	-0.5	-1.9	100.0%	-3.4
2898	AT5G39350.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:15768157-15770190 FORWARD   Aliases: MUL8.30, MUL8_30	4.5	5.0	-0.5	-1.9	100.0%	-3.3
2899	AT1G57680.2   expressed protein   chr1:21366153-21368351 REVERSE   Aliases: T8L23.15, T8L23_15	6.5	5.3	1.2	1.9	100.0%	-3.2
2900	AT1G54720.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD6 protein (Arabidopsis thaliana) GI:3123712	2.2	2.0	0.2	1.9	100.0%	-4.3
2901	AT1G11940.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr1:4031578-4034076 REVERSE   Aliases: F12F1.19, F12F1_19	4.6	5.2	-0.6	-1.9	100.0%	-3.3
2902	ATCG00160.1   Symbol: RPS2   Chloroplast ribosomal protein S2	6.6	7.5	-0.9	-1.9	100.0%	-3.4
2903	AT5G54580.1   RNA recognition motif (RRM)-containing protein, low similarity to RNA-binding protein RGP-3 (Nicotiana glauca) GI:1009363; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	8.7	8.1	0.6	1.9	100.0%	-3.3
2904	AT3G11880.1   expressed protein   chr3:3751666-3754066 FORWARD   Aliases: F26K24.17	6.7	6.3	0.4	1.9	100.0%	-3.5
2905	AT1G14260.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:4872900-4874821 FORWARD   Aliases: F14L17.2, F14L17_2	3.3	2.9	0.4	1.9	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2906	AT5G65950.2   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD33026.1)   chr5:26398945-26402447 FORWARD   Aliases: K14B20.12, K14B20_12	8.1	8.7	-0.6	-1.9	100.0%	-3.3
2907	AT5G54780.1   similar to RabGAP/TBC domain-containing protein [Arabidopsis thaliana] (TAIR:At4g27100.1); similar to putative GTPase activating protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468334.1); contains InterPro domain RabGAP/TBC domain (InterPro:IPR000195)   chr5:22265673-22269089 REVERSE   Aliases: MBG8.4, MBG8_4	3.5	3.9	-0.4	-1.9	100.0%	-3.4
2908	AT4G08150.1   Symbol: KNAT1   homeobox protein knotted-1 like 1 (KNAT1), identical to homeobox protein knotted-1 like 1 (KNAT1) SP:P46639 from (Arabidopsis thaliana)   chr4:5147697-5150963 REVERSE   Aliases: BP, BP1, BREVIPEDICELLUS, BREVIPEDICELLUS 1, F9M13.2, F9M13_2, KNOTTED LIKE HOMEBOX PROTEIN	3.3	2.9	0.4	1.9	100.0%	-3.6
2909	AT4G37410.1   Symbol: CYP81F4   cytochrome P450, putative, similar to cytochrome p450 SP:O65790 from (Arabidopsis thaliana)   chr4:17590766-17592914 FORWARD   Aliases: F6G17.60, F6G17_60	6.2	7.2	-1.0	-1.9	100.0%	-3.4
2910	AT1G19850.1   Symbol: MP   transcription factor MONOPTEROS (MP) / auxin-responsive protein (IAA24) / auxin response factor 5 (ARF5), identical to transcription factor MONOPTEROS (MP/IAA24/ARF5) SP:P93024 from (Arabidopsis thaliana)   chr1:6886870-6891365 FORWARD   Aliases: ARF5, F6F9.10, F6F9_10, IAA24, MONOPTEROS, MP, TRANSCRIPTION FACTOR IAA24	3.9	4.3	-0.3	-1.9	100.0%	-3.6
2911	AT2G35900.1   expressed protein   chr2:15077076-15078732 REVERSE   Aliases: F11F19.19, F11F19_19	7.8	6.8	1.0	1.9	100.0%	-3.0
2912	AT5G45680.1   FK506-binding protein 1 (FKBP13), identical to Probable FKBP-type peptidyl-prolyl cis-trans isomerase 3, chloroplast precursor (Ppiase) (Rotamase) (SP:Q9SCY2) / FK506 binding protein 1 (GI:21535744) (Arabidopsis thaliana); contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr5:18548107-18549508 FORWARD   Aliases: MRA19.7, MRA19_7	4.8	4.2	0.5	1.9	100.0%	-3.3
2913	AT4G25390.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:12977351-12979578 FORWARD   Aliases: T30C3.60, T30C3_60	5.7	4.8	0.9	1.9	100.0%	-3.2
2914	AT1G23280.1   MAK16 protein-related, contains similarity to MAK16 protein SP:P10962 from (Saccharomyces cerevisiae)   chr1:8260854-8262639 REVERSE   Aliases: F26F24.12, F26F24_12	5.1	6.3	-1.2	-1.9	100.0%	-3.2
2915	AT1G20900.1   Symbol: ESC   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr1:7272545-7274061 FORWARD   Aliases: ESC, ESCAROLA, F9H16.12, F9H16_12	5.6	5.0	0.6	1.9	100.0%	-3.1
2916	AT3G23250.2   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At1g06180.1); similar to myb-related transcription factor LBM4 [Nicotiana tabacum] (GB:BAA88224.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)	5.9	5.1	0.8	1.9	100.0%	-3.1
2917	AT3G21390.1   mitochondrial substrate carrier family protein   chr3:7531408-7534544 FORWARD   Aliases: MHC9.7	8.3	7.6	0.7	1.9	100.0%	-3.2
2918	AT5G66470.1   expressed protein   chr5:26558965-26561585 REVERSE   Aliases: K1F13.13, K1F13_13	4.8	5.5	-0.7	-1.9	100.0%	-3.1
2919	AT4G31580.1   Symbol: SRZ 22	7.8	7.1	0.8	1.9	100.0%	-3.1
2920	AT4G17830.1   peptidase M20/M25/M40 family protein, similar to acetylornithine deacetylase (Acetylornithinase, AO; N-acetylornithinase, NAO) (Dictyostelium discoideum) SWISS-PROT:P54638   chr4:9915893-9918256 FORWARD   Aliases: T6K21.10	5.7	6.4	-0.7	-1.9	100.0%	-3.3
2921	AT2G13820.2   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:5782333-5783371 REVERSE   Aliases: F17L24.13, F17L24_13	6.0	6.6	-0.6	-1.9	100.0%	-3.2
2922	AT5G43870.1   expressed protein   chr5:17649573-17653125 REVERSE   Aliases: F6B6.1, F6B6_1	3.6	4.1	-0.6	-1.9	100.0%	-3.2
2923	AT3G51550.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:19128563-19131840 REVERSE   Aliases: F26O13.190	5.6	4.8	0.8	1.9	100.0%	-3.3
2924	AT1G52630.2   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;   chr1:19610003-19612215 REVERSE   Aliases: F6D8.15, F6D8_15	3.6	3.3	0.3	1.9	100.0%	-3.7
2925	AT3G04610.1   Symbol: FLK   KH domain-containing protein, similar putative nucleic acid binding protein GB:CAB39665 (Arabidopsis thaliana); Pfam HMM hit: KH domain family of RNA binding proteins   chr3:1250568-1254878 REVERSE   Aliases: F7O18.9, F7O18_9, FLK, FLOWERING LOCUS KH DOMAIN	7.1	7.6	-0.5	-1.9	100.0%	-3.4
2926	AT2G01190.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, Pfam profile PF00564: PB1 domain   chr2:114974-117639 FORWARD   Aliases: F10A8.7, F10A8_7	5.2	4.7	0.4	1.9	100.0%	-3.5
2927	AT4G23885.1   expressed protein   chr4:12419404-12420477 FORWARD   Aliases: None	9.1	9.7	-0.5	-1.9	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2928	AT2G23470.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g49820.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82127.1); contains InterPro domain Protein of unknown function DUF647 (InterPro:IPR006968)	3.3	3.9	-0.6	-1.9	100.0%	-3.5
2929	AT5G46070.1   guanylate-binding family protein, contains Pfam domains PF02263: Guanylate-binding protein, N-terminal domain and PF02841: Guanylate-binding protein, C-terminal domain   chr5:18700695-18705934 FORWARD   Aliases: MCL19.12, MCL19_12	4.6	5.0	-0.5	-1.9	100.0%	-3.5
2930	AT3G56040.1   expressed protein   chr3:20803052-20808551 REVERSE   Aliases: F27K19.220	4.2	4.7	-0.5	-1.9	100.0%	-3.3
2931	AT1G67910.1   expressed protein   chr1:25474972-25476008 REVERSE   Aliases: T23K23.24, T23K23_24	4.2	4.9	-0.7	-1.9	100.0%	-3.3
2932	AT3G07760.2   expressed protein   chr3:2476450-2478204 FORWARD   Aliases: MLP3.21	7.4	6.5	0.9	1.9	100.0%	-3.4
2933	AT3G52430.1   Symbol: PAD4   phytoalexin-deficient 4 protein (PAD4), identical to phytoalexin-deficient 4 protein (Arabidopsis thaliana) GI:6457331; contains Pfam profile PF01764: Lipase   chr3:19442349-19445381 FORWARD   Aliases: F22O6.190, PAD4, PHYTOALEXIN DEFICIENT 4, PHYTOALEXIN DEFICIENT 4	4.3	5.0	-0.8	-1.9	100.0%	-3.3
2934	AT1G22530.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; similar to SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP) (bTAP) (Fragment) (SP:P58875) {Bos taurus}   chr1:7955482-7958431 REVERSE   Aliases: F12K8.13, F12K8_13	8.6	7.2	1.5	1.9	100.0%	-3.1
2935	AT3G56730.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr3:21025166-21026053 FORWARD   Aliases: T8M16.60	8.3	7.6	0.7	1.9	100.0%	-3.5
2936	AT5G11670.1   malate oxidoreductase, putative, similar to NADP-dependent malic enzyme (EC 1.1.1.40) (NADP-ME) (SP:P12628) {Phaseolus vulgaris}	10.4	11.0	-0.6	-1.9	100.0%	-3.8
2937	AT5G09410.1   Symbol: EICBP.B   calmodulin-binding protein, similar to another ethylene-upregulated calmodulin-binding protein ER1 GI:11612392 from (Nicotiana tabacum)   chr5:2921458-2927417 FORWARD   Aliases: EICBP.B, ETHYLENE INDUCED CALMODULIN BINDING PROTEIN, T5E8.210, T5E8_210	8.2	8.9	-0.7	-1.9	100.0%	-3.8
2938	AT3G13140.1   hydroxyproline-rich glycoprotein family protein   chr3:4226661-4227384 REVERSE   Aliases: MJG19.9	2.5	2.8	-0.3	-1.9	100.0%	-4.0
2939	AT1G62640.2   Symbol: KAS III   similar to beta-ketoacyl-acyl carrier protein synthase III [Glycine max] (GB:AAF70509.1); contains InterPro domain Beta-ketoacyl-acyl carrier protein synthase III (FabH) (InterPro:IPR004655)   chr1:23195909-23198740 FORWARD   Aliases: 3 KETOACYL ACYL CARRIER PROTEIN SYNTHASE III, T3P18.20, T3P18_20	8.2	8.6	-0.5	-1.9	100.0%	-3.6
2940	AT5G07870.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:2513795-2515419 FORWARD   Aliases: F13G24.70, F13G24_70	3.5	4.0	-0.4	-1.9	100.0%	-3.4
2941	AT5G66980.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:26758789-26760052 FORWARD   Aliases: K8A10.5, K8A10_5	3.4	3.0	0.4	1.9	100.0%	-3.7
2942	AT2G31190.1   expressed protein, contains Pfam domain, PF04884: Protein of unknown function, DUF647   chr2:13298303-13300839 REVERSE   Aliases: F16D14.3, F16D14_3	5.4	5.9	-0.6	-1.9	100.0%	-3.3
2943	AT5G23850.1   expressed protein   chr5:8038129-8040934 FORWARD   Aliases: MRO11.11, MRO11_11	6.6	7.3	-0.7	-1.9	100.0%	-3.1
2944	AT5G10170.1   inositol-3-phosphate synthase, putative / myo-inositol-1-phosphate synthase, putative / MI-1-P synthase, putative, very strong similarity to SP:Q38862 Myo-inositol-1-phosphate synthase isozyme 2 (EC 5.5.1.4) (MI-1-P synthase 2) (IPS 2) {Arabidopsis thaliana}; identical to SP:Q9LX12: Probable inositol-3-phosphate synthase isozyme 3 (EC 5.5.1.4) (Myo- inositol-1-phosphate synthase 3) (MI-1-P synthase 3) (IPS 3) {Arabidopsis thaliana}; contains Pfam profile PF01658: Myo-inositol-1-phosphate synthase   chr5:3187278-3190252 REVERSE   Aliases: T31P16.160, T31P16_160	4.0	4.5	-0.5	-1.9	100.0%	-3.4
2945	AT1G66480.1   expressed protein   chr1:24809433-24811129 REVERSE   Aliases: F28G11.8, F28G11_8	4.3	3.9	0.4	1.9	100.0%	-3.5
2946	AT5G62670.1   ATPase, plasma membrane-type, putative / proton pump, putative, strong similarity to P-type H(+)-transporting ATPase from Nicotiana plumbaginifolia (SP:Q08435, SP:Q08436), Lycopersicon esculentum (GI:5901757, SP:P22180), Solanum tuberosum (GI:435003); contains InterPro accession IPR001757: ATPase, E1-E2 type   chr5:25176456-25183574 FORWARD   Aliases: MRG21.9, MRG21_9	8.2	9.2	-1.0	-1.9	100.0%	-3.0
2947	AT5G36890.2   similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At1g26560.1); similar to putative latex cyanogenic beta glucosidase [Oryza sativa (japonica cultivar-group)] (GB:BAD82183.1); contains InterPro domain Glycoside hydrolase, family 1 (InterPro:IPR001360)   chr5:14558580-14563459 REVERSE   Aliases: MLF18.1, MLF18_1	7.1	8.2	-1.1	-1.9	100.0%	-3.4
2948	AT3G09000.1   proline-rich family protein   chr3:2745649-2748464 FORWARD   Aliases: T16O11.4	5.1	5.5	-0.4	-1.9	100.0%	-3.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2949	AT2G17720.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus (GI:212530), Rattus norvegicus (GI:474940), Mus musculus (SP:Q60715); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr2:7704418-7706636 FORWARD   Aliases: T17A5.10, T17A5_10	7.4	8.0	-0.6	-1.9	100.0%	-3.5
2950	AT3G29030.1   Symbol: ATEXPA5   expansin, putative (EXP5), identical to expansin At-EXP5 GB:AAB38071 from (Arabidopsis thaliana); alpha-expansin gene family, PMID:11641069   chr3:11012545-11014595 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A5, ATEXP5, ATHEXP ALPHA 1.4, EXPANSIN 5, K5K13.14	4.2	3.6	0.5	1.9	100.0%	-3.4
2951	AT2G48020.2   sugar transporter, putative, similar to ERD6 protein {Arabidopsis thaliana} GI:3123712, sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:19651325-19654250 FORWARD   Aliases: T9J23.17	8.0	7.4	0.6	1.9	100.0%	-3.3
2952	AT4G16150.1   calmodulin-binding protein, similar to anther ethylene-upregulated calmodulin-binding protein ER1 GI:11612392 from (Nicotiana tabacum)   chr4:9148239-9153064 FORWARD   Aliases: DL4115W, FCAALL.291	6.5	7.4	-0.9	-1.9	100.0%	-3.5
2953	AT5G62710.1   leucine-rich repeat family protein / protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr5:25204529-25207826 FORWARD   Aliases: MQB2.1, MQB2_1	3.5	3.8	-0.3	-1.9	100.0%	-3.6
2954	AT1G05060.1   expressed protein   chr1:1451057-1452871 REVERSE   Aliases: T7A14.7, T7A14_7	6.3	5.3	1.0	1.8	100.0%	-3.1
2955	AT1G49860.1   Symbol: ATGSTF14   glutathione S-transferase, putative, similar to GI:860955 from (Hyoscyamus muticus) (Plant Physiol. 109 (1), 253-260 (1995))	2.5	3.5	-1.0	-1.8	100.0%	-2.9
2956	AT4G19810.1   glycosyl hydrolase family 18 protein, similar to chitinase/lysozyme GI:467689 from (Nicotiana tabacum)   chr4:10764046-10765763 REVERSE   Aliases: T16H5.170, T16H5_170	3.5	4.4	-0.9	-1.8	100.0%	-3.2
2957	AT1G16610.2   Symbol: SR45   arginine/serine-rich protein, putative (SR45), similar to arginine/serine-rich protein GI:6601502 from (Arabidopsis thaliana)   chr1:5675723-5678734 REVERSE   Aliases: ARGININE/SERINE RICH PROTEIN SR45, F19K19.9, F19K19_9	7.5	8.3	-0.8	-1.8	100.0%	-3.1
2958	AT5G51100.1   Symbol: FSD2   superoxide dismutase (Fe), putative / iron superoxide dismutase, putative, similar to Fe-superoxide dismutase precursor (Medicago sativa) gi:16974682:gb:AAL32441   chr5:20790522-20792898 REVERSE   Aliases: FE SUPEROXIDE DISMUTASE 2, MWD22.4, MWD22_4	4.1	4.8	-0.8	-1.8	100.0%	-3.2
2959	AT4G35620.1   Symbol: CYCB2;2   cyclin 2b (CYC2b), identical to cyclin 2b protein (Arabidopsis thaliana) GI:509423   chr4:16901647-16903916 FORWARD   Aliases: CYCB2;2, Cyclin B2;2, F8D20.130, F8D20_130	4.1	4.6	-0.5	-1.8	100.0%	-3.4
2960	AT2G22230.1   beta-hydroxyacyl-ACP dehydratase, putative, similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii (GI:3850997); contains Pfam profile PF01377 Thioester dehydratase	5.3	6.1	-0.8	-1.8	100.0%	-3.2
2961	AT4G15430.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr4:8827876-8831503 FORWARD   Aliases: DL3760W, FCAALL.292	4.5	4.1	0.4	1.8	100.0%	-3.5
2962	AT4G37780.1   myb family transcription factor (MYB87), identical to AtMYB87 R2R3-MYB transcription factor GI:2832559 from (Arabidopsis thaliana); contains Pfam profile: PF00249 myb-like DNA-binding domain   chr4:17758237-17759493 REVERSE   Aliases: T28I19.60, T28I19_60	3.7	4.5	-0.8	-1.8	100.0%	-3.1
2963	AT4G20230.1   terpene synthase/cyclase family protein, vetispiradiene synthase, Hyoscyamus muticus, PATX:G763421   chr4:10924221-10926761 REVERSE   Aliases: F1C12.150, F1C12_150	2.4	2.8	-0.4	-1.8	100.0%	-3.7
2964	AT2G27710.3   60S acidic ribosomal protein P2 (RPP2B)   chr2:11823868-11824944 FORWARD   Aliases: F15K20.19, F15K20_19	9.6	10.6	-0.9	-1.8	100.0%	-3.2
2965	AT3G48150.1   Symbol: APC8   cell division cycle family protein / CDC family protein, similar to cell division cycle protein 23 (Homo sapiens) GI:3283051, anaphase-promoting complex subunit 8 (Homo sapiens) GI:6180017; contains Pfam profile PF00515: TPR Domain   chr3:17790641-17793630 REVERSE   Aliases: CDC23, T24C20.30	6.2	6.8	-0.6	-1.8	100.0%	-3.4
2966	AT5G54130.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:21981074-21982505 FORWARD   Aliases: MJP23.11, MJP23_11	4.3	3.6	0.7	1.8	100.0%	-3.1
2967	AT4G28050.1   senescence-associated protein, putative, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr4:13942013-13943738 REVERSE   Aliases: T13J8.160, T13J8_160	3.9	4.3	-0.4	-1.8	100.0%	-3.6
2968	AT1G61667.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:22771328-22772160 FORWARD   Aliases: None	6.0	5.1	1.0	1.8	100.0%	-3.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2969	AT3G54050.1   fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative, strong similarity to fructose-1,6-bisphosphatase (Brassica napus) GI:289367; identical to SP:P25851 Fructose-1,6-bisphosphatase, chloroplast precursor (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) {Arabidopsis thaliana}; contains Pfam profile PF00316: fructose-1,6-bisphosphatase   chr3:20027891-20029726 FORWARD   Aliases: F24B22.10	3.8	3.4	0.4	1.8	100.0%	-3.4
2970	AT5G47870.1   expressed protein   chr5:19401600-19403095 REVERSE   Aliases: MCA23.21, MCA23_21	7.7	8.1	-0.4	-1.8	100.0%	-3.5
2971	AT3G53020.1   60S ribosomal protein L24 (RPL24B), 60S ribosomal protein L24, Arabidopsis thaliana, EMBL:AC006282   chr3:19671545-19673003 REVERSE   Aliases: F8J2.190	11.8	12.1	-0.3	-1.8	100.0%	-3.9
2972	AT2G42210.4   expressed protein, similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_450480.1); contains InterPro domain Mitochondrial import inner membrane translocase, subunit Tim17/22 (InterPro:IPR003397)   chr2:17597291-17598930 FORWARD   Aliases: T24P15.12, T24P15_12	10.9	11.5	-0.6	-1.8	100.0%	-3.6
2973	AT1G71010.1   phosphatidylinositol-4-phosphate 5-kinase family protein, low similarity to phosphatidylinositol 3,5-kinase (Candida albicans) GI:14571648; contains Pfam profile PF01504: Phosphatidylinositol-4-phosphate 5-Kinase   chr1:26786501-26792630 FORWARD   Aliases: F23N20.21	8.3	7.9	0.4	1.8	100.0%	-3.5
2974	AT2G34040.2   apoptosis inhibitory 5 (API5) family protein, contains Pfam domain PF05918 Apoptosis inhibitory protein 5 (API5)	6.4	7.1	-0.7	-1.8	100.0%	-3.4
2975	AT3G11420.1   fringe-related protein, similar to hypothetical protein GB:AAC23643 (Arabidopsis thaliana) + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr3:3591481-3594539 FORWARD   Aliases: F24K9.9	5.0	4.5	0.4	1.8	100.0%	-3.4
2976	AT1G14460.1   DNA polymerase-related, weak similarity to DNA polymerase III holoenzyme tau subunit (Thermus thermophilus) GI:2583049   chr1:4948743-4952922 REVERSE   Aliases: F14L17.24, F14L17_24	5.0	5.4	-0.4	-1.8	100.0%	-3.5
2977	AT1G74950.1   expressed protein   chr1:28152236-28154055 REVERSE   Aliases: F25A4.8, F25A4_8	6.8	5.5	1.3	1.8	100.0%	-3.1
2978	AT5G17280.1   expressed protein, similar to unknown protein (pir::T41692)   chr5:5686301-5686889 FORWARD   Aliases: MKP11.13, MKP11_13	6.8	6.0	0.8	1.8	100.0%	-3.3
2979	AT1G53140.1   dynamin family protein, low similarity to dynamin-like protein E (Arabidopsis thaliana) GI:19423872; contains Pfam profile PF00350: Dynamin family   chr1:19802906-19806262 FORWARD   Aliases: F8L10.1, F8L10_1	5.2	5.5	-0.3	-1.8	100.0%	-3.8
2980	AT3G01210.1   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At1g14340.1); similar to hypothetical protein [Solanum demissum] (GB:AAT40482.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)	6.2	5.3	0.9	1.8	100.0%	-3.4
2981	AT3G07370.1   tetratricopeptide repeat (TPR)-containing protein / U-box domain-containing protein, similar to serologically defined colon cancer antigen 7 GB:5031963 GI:3170178 (Homo sapiens);   chr3:2358091-2360555 REVERSE   Aliases: F21O3.8	4.9	4.5	0.4	1.8	100.0%	-3.6
2982	AT2G18660.1   expansin family protein (EXPR3), identical to Expansin-related protein 3 precursor (Ath-ExpGamma-1.2) (Swiss-Prot:Q9ZV52) (Arabidopsis thaliana); contains Prosite PS00092: N-6 Adenine-specific DNA methylases signature;   chr2:8097740-8098738 REVERSE   Aliases: MSF3.4, MSF3_4	3.1	2.6	0.5	1.8	100.0%	-3.7
2983	AT3G62680.1   Symbol: PRP3   proline-rich family protein, contains proline-rich region, INTERPRO:IPR000694   chr3:23193698-23194970 FORWARD   Aliases: ATPRP3, F26K9.110, PROLINE RICH PROTEIN 3	4.6	5.3	-0.7	-1.8	100.0%	-3.2
2984	AT1G13120.1   Symbol: EMB1745   expressed protein, contains Prosite PS00012: Phosphopantetheine attachment site; similar to GLE1 (GI:3288817) {Homo sapiens}; EST gb:N37870 comes from this gene   chr1:4469181-4473211 REVERSE   Aliases: EMB1745, EMBRYO DEFECTIVE 1745, F3F19.14, F3F19_14	6.1	6.7	-0.5	-1.8	100.0%	-3.4
2985	AT5G22710.1   expressed protein   chr5:7547800-7549372 REVERSE   Aliases: MDJ22.13, MDJ22_13	4.0	3.5	0.5	1.8	100.0%	-3.4
2986	AT5G04020.1   calmodulin-binding protein-related (PICBP), contains similarity to potato calmodulin-binding protein PCBP GI:17933110 from (Solanum tuberosum)   chr5:1081610-1086545 REVERSE   Aliases: F8F6.230, F8F6_230	5.7	6.2	-0.5	-1.8	100.0%	-3.4
2987	AT5G09990.1   expressed protein   chr5:3124569-3125073 FORWARD   Aliases: MYH9.1	3.6	3.1	0.5	1.8	100.0%	-3.8
2988	AT5G08470.1   Symbol: PEX1   peroxisome biogenesis protein (PEX1), identical to peroxisome biogenesis protein PEX1 (Arabidopsis thaliana) gi:12006272:gb:AAG44817; contains Pfam profile PF00004: ATPase, AAA family; identical to cDNA peroxisome biogenesis protein PEX1 (PEX1) mRNA, partial cds GI:12006271   chr5:2735926-2743057 FORWARD   Aliases: F8L15.15, PEROXISOME 1	3.5	3.9	-0.4	-1.8	100.0%	-3.6
2989	AT2G29990.1   pyridine nucleotide-disulphide oxidoreductase family protein, similar to SP:P32340 Rotenone-insensitive NADH-ubiquinone oxidoreductase, mitochondrial precursor (EC 1.6.5.3) (Internal NADH dehydrogenase) {Saccharomyces cerevisiae} ; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr2:12800639-12802990 REVERSE   Aliases: F23F1.9, F23F1_9	6.8	6.1	0.7	1.8	100.0%	-3.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
2990	AT2G06530.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr2:2588542-2590442 REVERSE   Aliases: T12H3.8, T12H3_8	9.7	9.0	0.7	1.8	100.0%	-3.4
2991	AT2G19990.1   Symbol: PR 1 LIKE   pathogenesis-related protein 1 (PR-1), identical to pathogenesis-related protein 1 {Arabidopsis thaliana} GI:166805; contains an extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature (PDOC00772)   chr2:8637146-8637676 REVERSE   Aliases: PATHOGENESIS RELATED PROTEIN 1 LIKE, PR 1 LIKE, T2G17.21, T2G17_21	2.6	2.9	-0.3	-1.8	100.0%	-3.7
2992	AT1G10490.1   expressed protein, contains Pfam profile PF05127: Putative ATPase (DUF699)   chr1:3453230-3460621 FORWARD   Aliases: T10O24.10, T10O24_10	3.5	3.9	-0.4	-1.8	100.0%	-3.6
2993	AT2G45160.1   scarecrow transcription factor family protein   chr2:18624937-18627225 REVERSE   Aliases: T14P1.3	4.9	5.3	-0.4	-1.8	100.0%	-3.7
2994	AT4G24740.2   Symbol: AFC2   protein kinase (AFC2), identical to protein kinase AFC2 (Arabidopsis thaliana) SWISS-PROT:P51567	7.1	6.5	0.6	1.8	100.0%	-3.3
2995	AT2G30460.1   expressed protein, contains 4 predicted transmembrane domains; similar to c_pp004044298r (GI:14597790) (Physcomitrella patens)   chr2:12983526-12985566 REVERSE   Aliases: T6B20.18, T6B20_18	3.8	4.5	-0.7	-1.8	100.0%	-3.2
2996	AT5G56150.2   ubiquitin-conjugating enzyme, putative, strong similarity to ubiquitin-conjugating enzyme UBC2 (Mesembryanthemum crystallinum) GI:5762457, UBC4 (Pisum sativum) GI:456568; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr5:22746408-22748409 FORWARD   Aliases: MDA7.21, MDA7_21	11.1	11.5	-0.4	-1.8	100.0%	-3.9
2997	AT5G13560.1   expressed protein, weak similarity to SP:O42184 Restin (Cytoplasmic linker protein-170) (CLIP-170) {Gallus gallus}   chr5:4360634-4366413 REVERSE   Aliases: T6I14.4	7.6	6.8	0.8	1.8	100.0%	-3.3
2998	AT5G19200.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to follicular variant translocation protein 1 precursor (FVT-1) SP:Q06136 from (Homo sapiens)   chr5:6458997-6460858 FORWARD   Aliases: T24G5.100, T24G5_100	4.3	4.0	0.3	1.8	100.0%	-3.7
2999	AT4G28940.1   nucleosidase-related, contains weak similarity to MTA/SAH nucleosidase (P46). (Swiss-Prot:P24247) (Shigella flexneri)   chr4:14275811-14277101 FORWARD   Aliases: F25O24.60, F25O24_60	3.0	3.3	-0.3	-1.8	100.0%	-3.8
3000	AT4G02430.2   pre-mRNA splicing factor, putative / SR1 protein, putative, strong similarity to SP:O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}; cDNA NCBI_gi:15810292 supports a truncated version while protein evidence supports a longer model.	5.4	4.6	0.8	1.8	100.0%	-3.4
3001	AT2G28130.1   expressed protein   chr2:11995753-11998694 FORWARD   Aliases: F24D13.8, F24D13_8	4.6	5.0	-0.4	-1.8	100.0%	-3.7
3002	AT3G18524.1   Symbol: MSH2   DNA mismatch repair protein MSH2 (MSH2), identical to SP:O24617 DNA mismatch repair protein MSH2 (AtMsh2) {Arabidopsis thaliana}	3.8	4.3	-0.5	-1.8	100.0%	-3.4
3003	AT1G62870.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g12380.1); similar to OSJNBa0013A04.12 [Oryza sativa (japonica cultivar-group)] (GB:CAE05175.2); contains domain HIS_RICH (PS50316)	3.3	4.1	-0.7	-1.8	100.0%	-3.3
3004	AT3G02070.1   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr3:360928-363336 FORWARD   Aliases: F1C9.14, F1C9_14	5.1	4.5	0.6	1.8	100.0%	-3.1
3005	AT2G45980.1   expressed protein   chr2:18924425-18926182 REVERSE   Aliases: F4I18.37, F4I18_37	8.2	7.3	0.9	1.8	100.0%	-3.2
3006	AT3G49010.3   Symbol: ATBBC1	12.6	13.2	-0.5	-1.8	100.0%	-3.9
3007	AT3G44590.2   60S acidic ribosomal protein P2 (RPP2D), acidic ribosomal protein P2, maize, PIR:S54179	9.9	10.4	-0.5	-1.8	100.0%	-3.4
3008	AT5G45280.2   pectinacylesterase, putative, similar to pectinacylesterase precursor GI:1431629 from (Vigna radiata)   chr5:18362822-18366919 FORWARD   Aliases: K9E15.6, K9E15_6	4.9	5.3	-0.4	-1.8	100.0%	-3.4
3009	AT1G68550.2   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr1:25729118-25731049 REVERSE   Aliases: T26J14.12, T26J14_12	4.6	5.0	-0.4	-1.8	100.0%	-3.5
3010	AT3G12750.1   Symbol: ZIP1   zinc transporter (ZIP1), identical to putative zinc transporter GB:AAC24197 from (Arabidopsis thaliana), ( Proc. Natl. Acad. Sci. U.S.A. 95 (12), 7220-7224 (1998)); member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563   chr3:4051658-4053187 REVERSE   Aliases: MBK21.8, ZRT, IRT LIKE PROTEIN	4.7	4.2	0.6	1.8	100.0%	-3.4
3011	AT5G09980.1   expressed protein   chr5:3122757-3123909 FORWARD   Aliases: MYH9.20, MYH9_20	4.3	3.6	0.7	1.8	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3012	AT5G18470.1   curculin-like (mannose-binding) lectin family protein, contains Pfam profile: PF01453 lectin (probable mannose binding)   chr5:6127799-6129679 FORWARD   Aliases: T28N17.6	3.9	4.4	-0.5	-1.8	100.0%	-3.5
3013	AT2G29080.1   Symbol: FTSH3   encodes an FtsH protease that is localized to the mitochondrion	7.2	8.2	-1.0	-1.8	100.0%	-3.4
3014	AT4G27750.1   expressed protein   chr4:13841694-13843639 FORWARD   Aliases: T29A15.240, T29A15_240	10.3	9.5	0.8	1.8	100.0%	-3.3
3015	AT1G16060.2   ovule development protein, putative, similar to ovule development protein AINTEGUMENTA (GI:1209099)(Arabidopsis thaliana)   chr1:5508537-5511729 FORWARD   Aliases: T24D18.16, T24D18_16	3.0	3.7	-0.6	-1.8	100.0%	-3.3
3016	AT2G37110.1   expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614   chr2:15599636-15601072 FORWARD   Aliases: T2N18.13, T2N18_13	9.2	8.5	0.7	1.8	100.0%	-3.6
3017	AT1G09430.1   Symbol: ACLA 3	8.4	9.0	-0.6	-1.8	100.0%	-3.6
3018	AT1G50575.1   lysine decarboxylase family protein, contains Pfam profile PF03641: lysine decarboxylase family   chr1:18732387-18734055 REVERSE   Aliases: None	6.8	7.5	-0.7	-1.8	100.0%	-3.1
3019	AT3G06450.1   anion exchange family protein, similar to putative Anion exchanger family members: GB:AAD39673, GB:AAD55295 (Arabidopsis thaliana)   chr3:1975965-1980042 REVERSE   Aliases: F24P17.6, F24P17_6	7.1	7.7	-0.6	-1.8	100.0%	-3.2
3020	AT1G23890.2   NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	6.3	5.3	1.0	1.8	100.0%	-3.3
3021	AT1G16870.1   mitochondrial 28S ribosomal protein S29-related, contains weak similarity to Swiss-Prot:P51398 mitochondrial 28S ribosomal protein S29 (MRP-S29, Death-associated protein 3, DAP-3) (Homo sapiens)   chr1:5770728-5773241 REVERSE   Aliases: F17F16.14	7.5	8.5	-0.9	-1.8	100.0%	-3.2
3022	AT4G32970.1   expressed protein, low similarity to SP:Q13061 Triadin {Homo sapiens}   chr4:15910348-15914328 REVERSE   Aliases: F26P21.90, F26P21_90	4.9	5.9	-0.9	-1.8	100.0%	-3.1
3023	AT4G38920.1   vacuolar ATP synthase 16 kDa proteolipid subunit 3 / V-ATPase 16 kDa proteolipid subunit 3 (AVAP3) (AVA-P3), identical to SP:P59227 Vacuolar ATP synthase 16 kDa proteolipid subunit 1/3/5 (EC 3.6.3.14) (V-ATPase 16 kDa proteolipid subunit 1/3/5) {Arabidopsis thaliana}; contains Pfam profile PF00137: ATP synthase subunit C   chr4:18147205-18149261 FORWARD   Aliases: F19H22.20	11.0	10.3	0.8	1.8	100.0%	-3.7
3024	AT4G30440.1   Symbol: GAE1   NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	8.1	7.6	0.6	1.8	100.0%	-3.5
3025	AT5G13120.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr5:4162506-4164787 REVERSE   Aliases: T19L5.80, T19L5_80	9.0	9.6	-0.5	-1.8	100.0%	-3.8
3026	AT4G34555.1   40S ribosomal protein S25, putative   chr4:16504235-16505477 REVERSE   Aliases: None	7.7	8.6	-0.9	-1.8	100.0%	-3.1
3027	AT3G25660.1   glutamyl-tRNA(Gln) amidotransferase, putative, similar to SP:O06491 Glutamyl-tRNA(Gln) amidotransferase subunit A (EC 6.3.5.-) {Bacillus subtilis}; contains Pfam profile PF01425: Amidase   chr3:9340678-9343441 REVERSE   Aliases: T5M7.15, T5M7_15	6.9	7.3	-0.4	-1.8	100.0%	-3.5
3028	AT3G05040.1   Symbol: HST   similar to P0503E05.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_918909.1)   chr3:1401322-1408101 REVERSE   Aliases: HASTY, T9J14.1, T9J14_1	4.0	4.6	-0.5	-1.8	100.0%	-3.3
3029	AT4G15530.3   similar to pyruvate,orthophosphate dikinase [Flaveria brownii] (GB:CAA55784.1); similar to pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum] (GB:CAA57872.1); similar to pyruvate,orthophosphate dikinase [Mesembryanthemum crystallinum] (GB:CAA55143.1); similar to cold stable pyruvate, orthophosphate dikinase (GB:AAA86940.1); similar to pyruvate, phosphate dikinase (EC 2.7.9.1) precursor, chloroplast - Flaveria brownii (GB:S56649); contains InterPro domain Pyruvate phosphate dikinase, PEP/pyruvate-binding (InterPro:IPR002192); contains InterPro domain PEP-utilizing enzyme (InterPro:IPR000121); contains InterPro domain PEP-utilizing enzyme, mobile region (InterPro:IPR008279)   chr4:8864826-8870905 REVERSE   Aliases: DL3805C, FCAALL.325	5.7	5.0	0.7	1.8	100.0%	-3.1
3030	AT3G06350.1   Symbol: EMB3004   dehydroquinase dehydratase, putative / shikimate dehydrogenase, putative, similar to dehydroquinase dehydratase/shikimate dehydrogenase (Nicotiana tabacum)(GI:535771), dehydroquinase dehydratase/shikimate:NADP oxidoreductase (Lycopersicon esculentum)(GI:3169883)   chr3:1924368-1927759 REVERSE   Aliases: EMB3004, EMBRYO DEFECTIVE 3004, F24P17.18, F24P17_18	9.5	10.1	-0.7	-1.8	100.0%	-3.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3031	AT2G19730.2   similar to 60S ribosomal protein L28 (RPL28C) [Arabidopsis thaliana] (TAIR:At4g29410.1); similar to putative 60S ribosomal L28 protein [Oryza sativa (japonica cultivar-group)] (GB:AAV67824.1); contains InterPro domain Ribosomal L28e protein (InterPro:IPR002672)   chr2:8518589-8520303 FORWARD   Aliases: F6F22.24, F6F22_24	11.2	11.7	-0.5	-1.8	100.0%	-3.5
3032	AT5G03490.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:871459-873046 FORWARD   Aliases: F12E4.260, F12E4_260	6.8	6.2	0.6	1.8	100.0%	-3.5
3033	AT4G15120.1   VQ motif-containing protein, contains PF05678: VQ motif   chr4:8634722-8635558 FORWARD   Aliases: DL3605W, FCAALL.67	3.0	3.4	-0.4	-1.8	100.0%	-3.5
3034	AT5G55920.1   nucleolar protein, putative, similar to SP:P46087 Proliferating-cell nucleolar antigen p120 (Proliferation-associated nucleolar protein p120) {Homo sapiens}, SP:P40991 Nucleolar protein NOP2 {Saccharomyces cerevisiae}; contains Pfam profile PF01189: NOL1/NOP2/sun family   chr5:22662709-22666673 REVERSE   Aliases: None	9.2	9.9	-0.6	-1.8	100.0%	-3.4
3035	AT1G51140.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.5	4.9	0.7	1.8	100.0%	-3.3
3036	AT5G53920.1   ribosomal protein L11 methyltransferase-related, similar to ribosomal protein L11 methyltransferase; PrmA (Escherichia coli) GI:455655   chr5:21909350-21911493 FORWARD   Aliases: K19P17.9, K19P17_9	2.7	3.0	-0.3	-1.8	100.0%	-3.9
3037	AT3G55370.2   Symbol: OBP3   Dof-type zinc finger domain-containing protein   chr3:20538053-20540268 FORWARD   Aliases: OBF BINDING PROTEIN 3, T22E16.30, ZINC FINGER PROTEIN OBP3	3.3	3.0	0.4	1.8	100.0%	-3.7
3038	AT4G37610.1   TAZ zinc finger family protein / BTB/POZ domain-containing protein, contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 : TAZ zinc finger; similar to Speckle-type POZ protein (SP:O43791) (Homo sapiens)   chr4:17670475-17672334 REVERSE   Aliases: F19F18.100, F19F18_100	7.6	6.9	0.7	1.8	100.0%	-3.4
3039	AT4G14200.1   expressed protein   chr4:8185365-8188719 REVERSE   Aliases: DL3140C, FCAALL.116	2.9	3.2	-0.3	-1.8	100.0%	-3.6
3040	AT4G28740.1   expressed protein   chr4:14200995-14202651 FORWARD   Aliases: F16A16.150, F16A16_150	8.1	7.5	0.6	1.8	100.0%	-3.4
3041	AT1G06180.1   Symbol: ATMYB13   myb family transcription factor, identical to	2.5	2.9	-0.4	-1.8	100.0%	-3.7
3042	AT1G74020.1   Symbol: SS2   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088   chr1:27838792-27840970 REVERSE   Aliases: ATSS 2 STRICTOSIDINE SYNTHASE, F2P9.11, F2P9_11, STRICTOSIDINE SYNTHASE 2	11.0	11.4	-0.4	-1.8	100.0%	-3.7
3043	AT4G03070.1   Symbol: AOP1   2-oxoglutarate-dependent dioxygenase (AOP1.2), identical to GI:16118887; contains PF03171: 2OG-Fe(II) oxygenase superfamily domain   chr4:1358432-1359644 FORWARD   Aliases: AOP, AOP1.1, T4I9.5, T4I9_5	3.3	2.9	0.4	1.8	100.0%	-3.6
3044	AT3G21220.1   Symbol: ATMKK5	4.5	4.1	0.4	1.8	100.0%	-3.7
3045	AT4G26780.1   Symbol: AR192   co-chaperone grpE family protein, similar to chaperone GrpE type 2 (Nicotiana tabacum) GI:3851640; contains Pfam profile PF01025: co-chaperone GrpE   chr4:13484845-13486777 REVERSE   Aliases: F10M23.120, F10M23_120	7.5	8.3	-0.7	-1.8	100.0%	-3.3
3046	AT2G29760.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:12719961-12722177 FORWARD   Aliases: T27A16.14, T27A16_14	4.5	4.9	-0.4	-1.8	100.0%	-3.6
3047	AT1G47900.1   expressed protein   chr1:17650813-17654704 REVERSE   Aliases: T6B12.1, T6B12_1	6.0	6.7	-0.7	-1.8	100.0%	-3.4
3048	AT1G07030.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:2158419-2160808 REVERSE   Aliases: F10K1.26, F10K1_26	5.1	5.5	-0.4	-1.8	100.0%	-3.6
3049	AT2G32380.1   expressed protein   chr2:13753688-13754868 REVERSE   Aliases: T32F6.10, T32F6_10	3.6	4.2	-0.5	-1.8	100.0%	-3.5
3050	AT3G15530.2   expressed protein   chr3:5252882-5254465 REVERSE   Aliases: MJK13.19	7.5	6.9	0.6	1.8	100.0%	-3.5
3051	AT1G29710.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:10387659-10389086 FORWARD   Aliases: T3M22.4, T3M22_4	3.2	3.4	-0.2	-1.8	100.0%	-4.0
3052	AT2G40330.1   Bet v I allergen family protein, contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr2:16851942-16853012 REVERSE   Aliases: T7M7.15	4.6	3.9	0.7	1.8	100.0%	-3.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3053	AT3G62030.1   Symbol: ROC4   peptidyl-prolyl cis-trans isomerase, chloroplast / cyclophilin / rotamase / cyclosporin A-binding protein (ROC4), identical to peptidyl-prolyl cis-trans isomerase, chloroplast precursor, PPlase (cyclophilin, cyclosporin A-binding protein) (Arabidopsis thaliana) SWISS-PROT:P34791; identical to cDNA nuclear-encoded chloroplast stromal cyclophilin (ROC4) GI:405130   chr3:22984585-22986345 FORWARD   Aliases: PEPTIDYLPROLYL ISOMERASE ROC4, ROTAMASE CYCLOPHILIN 4, ROTAMASE CYP 4, T17J13.1	9.0	9.9	-0.9	-1.8	100.0%	-3.1
3054	AT2G19430.1   transducin family protein / WD-40 repeat family protein, similar to WD-repeat protein 5 (SP:Q9UGP9) (Homo sapiens); contains 7 Trp-Asp WD-40 repeats   chr2:8422241-8424998 FORWARD   Aliases: F27F23.25	5.1	4.6	0.6	1.8	100.0%	-3.4
3055	AT3G07210.1   expressed protein, predicted using genefinder   chr3:2292804-2295458 REVERSE   Aliases: T1B9.12	3.4	3.9	-0.5	-1.8	100.0%	-3.4
3056	AT5G13100.1   expressed protein   chr5:4156663-4158539 FORWARD   Aliases: T19L5.60, T19L5_60	6.1	5.5	0.6	1.8	100.0%	-3.2
3057	AT1G51660.1   Symbol: ATMKK4	4.3	3.9	0.4	1.8	100.0%	-3.7
3058	AT2G32030.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:13639545-13640412 REVERSE   Aliases: F22D22.22, F22D22_22	4.1	3.7	0.4	1.8	100.0%	-3.6
3059	AT5G47800.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr5:19371053-19373526 FORWARD   Aliases: MCA23.12, MCA23_12	3.2	3.5	-0.3	-1.8	100.0%	-3.8
3060	AT1G11420.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr1:3844581-3846872 REVERSE   Aliases: T23J18.9, T23J18_9	5.0	6.0	-1.0	-1.8	100.0%	-3.3
3061	AT4G38470.1   protein kinase family protein, similar to protein kinase (gi:170047) from Glycine max; contains Pfam protein kinase domain PF00069   chr4:17999426-18003675 FORWARD   Aliases: F20M13.30, F20M13_30	6.1	6.8	-0.7	-1.8	100.0%	-3.5
3062	AT1G12030.1   expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506)   chr1:4064749-4066317 REVERSE   Aliases: F12F1.10, F12F1_10	3.8	4.5	-0.7	-1.8	100.0%	-3.3
3063	AT4G38670.1   pathogenesis-related thaumatin family protein, similar to receptor serine/threonine kinase PR5K (Arabidopsis thaliana) GI:1235680; contains Pfam profile PF00314: Thaumatin family   chr4:18069610-18071346 REVERSE   Aliases: T9A14.1	3.9	3.1	0.8	1.8	100.0%	-3.5
3064	AT2G45130.1   SPX (SYG1/Pho81/XPR1) domain-containing protein, weak similarity to NUC-2 (Neurospora crassa) GI:1399532, xenotropic and polytropic murine leukemia virus receptor (Mus musculus castaneus) GI:6093320; contains Pfam profile PF03105: SPX domain   chr2:18613485-18614928 FORWARD   Aliases: T14P1.6	4.1	3.4	0.7	1.8	100.0%	-3.5
3065	AT5G13840.1   WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to Fzr1 (GI:6463679){Homo sapiens}   chr5:4468519-4470994 REVERSE   Aliases: MAC12.21, MAC12_21	7.0	7.7	-0.7	-1.8	100.0%	-3.5
3066	AT4G10790.1   UBX domain-containing protein, low similarity to SP:Q9UNN5 FAS-associated factor 1 (FAF1 protein) {Homo sapiens}; contains Pfam profile PF00789: UBX domain   chr4:6640609-6643058 REVERSE   Aliases: T12H20.9, T12H20_9	7.1	6.4	0.6	1.8	100.0%	-3.3
3067	AT1G71400.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596   chr1:26913497-26916259 FORWARD   Aliases: F3I17.30, F3I17_30	5.0	5.5	-0.5	-1.8	100.0%	-3.3
3068	AT5G04790.1   expressed protein   chr5:1388156-1388320 REVERSE   Aliases: MUK11.11	7.5	6.5	1.0	1.8	100.0%	-3.0
3069	AT5G15750.1   RNA-binding S4 domain-containing protein, 40S RIBOSOMAL PROTEINs - different species   chr5:5141194-5142861 FORWARD   Aliases: F14F8.130, F14F8_130	8.3	8.7	-0.4	-1.8	100.0%	-3.4
3070	AT5G65020.1   Symbol: ANNAT2	12.1	12.9	-0.8	-1.8	100.0%	-3.5
3071	AT3G09210.1   KOW domain-containing transcription factor family protein, ; est match   chr3:2825290-2826886 REVERSE   Aliases: F3L24.8	8.0	8.7	-0.7	-1.8	100.0%	-3.1
3072	AT3G08940.2   Symbol: LHCB4.2   chlorophyll A-B binding protein (LHCB4.2), contains Pfam profile: PF00504 chlorophyll A-B binding protein; identical to Lhcb4.2 protein GB:AAD28774 (Arabidopsis thaliana)   chr3:2717681-2718874 FORWARD   Aliases: T16O11.12	8.2	7.2	1.0	1.8	100.0%	-3.2
3073	AT1G64405.1   expressed protein   chr1:23927395-23927999 FORWARD   Aliases: None	2.9	3.5	-0.7	-1.8	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3074	AT5G44800.1   chromodomain-helicase-DNA-binding family protein / CHD family protein, similar to chromatin remodeling factor CHD3 (PICKLE) (Arabidopsis thaliana) GI:6478518; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00628: PHD-finger, PF00385: 'chromo' (CHRromatin Organization MOdifier)   chr5:18100886-18109347 REVERSE   Aliases: K23L20.15, K23L20_15	3.5	3.8	-0.3	-1.8	100.0%	-3.9
3075	AT1G03350.1   BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	7.4	7.0	0.4	1.8	100.0%	-3.7
3076	AT3G59660.1   C2 domain-containing protein / GRAM domain-containing protein, low similarity to GLUT4 vesicle protein (Rattus norvegicus) GI:4193489; contains Pfam profiles PF00168: C2 domain, PF02893: GRAM domain   chr3:22045155-22049634 REVERSE   Aliases: T16L24.210	5.3	5.9	-0.6	-1.8	100.0%	-3.2
3077	AT1G22550.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:7966522-7968630 REVERSE   Aliases: F12K8.11, F12K8_11	6.9	6.3	0.6	1.8	100.0%	-3.2
3078	AT2G30390.1   ferrochelatase II, identical to Swiss-Prot:O04921 ferrochelatase II, chloroplast precursor (EC 4.99.1.1) (Protoheme ferro-lyase) (Heme synthetase) (Arabidopsis thaliana)   chr2:12958104-12961167 REVERSE   Aliases: T9D9.1	7.7	8.4	-0.7	-1.8	100.0%	-3.2
3079	AT4G32730.2   Symbol: PC MYB1   myb family transcription factor, identical to PC-MYB1 GI:5678826 from (Arabidopsis thaliana);	3.5	3.9	-0.4	-1.8	100.0%	-3.9
3080	AT4G11550.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.1	3.3	-0.3	-1.8	100.0%	-3.9
3081	AT5G28650.1   Symbol: WRKY74	5.1	5.6	-0.5	-1.8	100.0%	-3.4
3082	AT4G37640.1   Symbol: ACA2   calcium-transporting ATPase 2, plasma membrane-type / Ca(2+)-ATPase isoform 2 (ACA2), identical to SP:O81108 Calcium-transporting ATPase 2, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 2) {Arabidopsis thaliana}   chr4:17682971-17686935 REVERSE   Aliases: CALCIUM ATPASE 2, F19F18.130, F19F18_130	6.2	6.9	-0.8	-1.8	100.0%	-3.6
3083	AT3G13000.2   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr3:4157975-4161948 REVERSE   Aliases: MGH6.15, MGH6_15	3.2	2.8	0.3	1.8	100.0%	-3.8
3084	AT1G70560.1   alliinase C-terminal domain-containing protein, contains Pfam profiles: PF04864 alliinase C-terminal domain, PF04863 alliinase EGF-like domain   chr1:26608518-26611166 FORWARD   Aliases: F24J13.13, F24J13_13	6.0	7.0	-0.9	-1.8	100.0%	-3.0
3085	AT5G25820.1   exostosin family protein, contains Pfam profile: PF03016 exostosin family   chr5:8997186-9000318 REVERSE   Aliases: F18A17.70, F18A17_70	4.4	3.5	0.8	1.8	100.0%	-3.0
3086	AT2G02850.1   Symbol: ARPN   plastocyanin-like domain-containing protein / plantacyanin, putative, similar to plantacyanin GI:3395754 from (Spinacia oleracea)   chr2:826542-827785 REVERSE   Aliases: PLANTACYANIN, T17M13.2, T17M13_2	3.6	4.6	-0.9	-1.8	100.0%	-3.2
3087	AT4G31600.2   similar to integral membrane family protein [Arabidopsis thaliana] (TAIR:At5g19980.1); similar to hypothetical protein DDB0202972 [Dictyostelium discoideum] (GB:EAL69125.1)   chr4:15314891-15317141 REVERSE   Aliases: F28M20.210, F28M20_210	4.1	4.5	-0.4	-1.8	100.0%	-3.7
3088	AT1G70890.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294062) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:26729288-26730206 REVERSE   Aliases: F15H11.12, F15H11_12	4.6	5.2	-0.7	-1.8	100.0%	-3.4
3089	AT1G04530.1   expressed protein   chr1:1234198-1236033 REVERSE   Aliases: T1G11.22, T1G11_22	5.4	6.1	-0.7	-1.8	100.0%	-3.3
3090	AT1G08830.1   Symbol: CSD1   superoxide dismutase (Cu-Zn) (SODCC) / copper/zinc superoxide dismutase (CSD1), identical to SWISS-PROT: P24704   chr1:2827089-2829260 FORWARD   Aliases: F22O13.32, F22O13_32	12.0	12.8	-0.8	-1.8	100.0%	-4.3
3091	AT5G47990.1   Symbol: CYP705A5   cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) (Glycine max);   chr5:19452053-19453915 FORWARD   Aliases: MDN11.4, MDN11_4	2.5	2.8	-0.3	-1.8	100.0%	-3.7
3092	AT5G66090.1   expressed protein   chr5:26442962-26444394 FORWARD   Aliases: K2A18.17, K2A18_17	4.4	3.9	0.5	1.8	100.0%	-3.5
3093	AT5G42880.1   expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827)   chr5:17208986-17211319 FORWARD   Aliases: MBD2.7, MBD2_7	4.7	5.6	-0.9	-1.8	100.0%	-3.5
3094	AT1G54680.1   expressed protein   chr1:20416721-20418149 FORWARD   Aliases: T22H22.11, T22H22_11	9.3	8.5	0.8	1.8	100.0%	-3.4
3095	AT3G04260.1   SAP domain-containing protein, contains Pfam domain PF02037: SAP domain   chr3:1123030-1127522 REVERSE   Aliases: T6K12.12, T6K12_12	4.8	5.5	-0.6	-1.8	100.0%	-3.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3096	AT5G47180.2   vesicle-associated membrane family protein / VAMP family protein, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia), to VAMP-associated protein B GI:4240464 (Rattus norvegicus) and to Vesicle-associated membrane protein/synaptobrevin binding protein (VAP-33) (SP:Q16943)(Aplysia californica)   chr5:19178372-19181010 REVERSE   Aliases: MQL5.3, MQL5_3	5.7	5.0	0.7	1.8	100.0%	-3.5
3097	AT3G02760.1   histidyl-tRNA synthetase, putative / histidine--tRNA ligase, putative, similar to SP:P12081 Histidyl-tRNA synthetase (EC 6.1.1.21) (Histidine--tRNA ligase) (HisRS) {Homo sapiens}; contains Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF03129: Anticodon binding domain   chr3:597366-599445 REVERSE   Aliases: F13E7.30, F13E7_30	8.1	9.1	-1.0	-1.8	100.0%	-3.7
3098	AT5G65640.1   basic helix-loop-helix (bHLH) family protein   chr5:26254285-26256310 FORWARD   Aliases: K21L13.16, K21L13_16	3.5	4.2	-0.7	-1.8	100.0%	-3.3
3099	AT5G50010.1   expressed protein   chr5:20365841-20367936 FORWARD   Aliases: K9P8.17	3.6	4.2	-0.6	-1.8	100.0%	-3.4
3100	AT1G71020.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:26794259-26796837 REVERSE   Aliases: F23N20.1, F23N20_1	3.5	3.9	-0.3	-1.8	100.0%	-3.7
3101	AT4G17190.2   Symbol: FPS2   farnesyl pyrophosphate synthetase 2 (FPS2) / FPP synthetase 2 / farnesyl diphosphate synthase 2, identical to SP:Q43315 Farnesyl pyrophosphate synthetase 2 (FPP synthetase 2) (FPS 2) (Farnesyl diphosphate synthetase 2) (Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)) {Arabidopsis thaliana}   chr4:9648552-9650857 REVERSE   Aliases: DL4630C, FARNESYL DIPHOSPHATE SYNTHASE 2, FCAALL.91	6.3	7.2	-1.0	-1.8	100.0%	-3.0
3102	AT4G07400.1   Symbol: VFB3   F-box family protein (FBL8) (FBL24), contains similarity to SKP1 interacting partner 2 GI:10716949 from (Arabidopsis thaliana); contains Pfam PF00646: F-box domain   chr4:4197844-4199508 REVERSE   Aliases: F28D6.13, F28D6_13, VFB3, VIER F BOX PROTEINE 3	4.6	5.4	-0.7	-1.8	100.0%	-3.4
3103	AT5G46210.1   Symbol: CUL4   cullin, putative, similar to SP:Q13619 Cullin homolog 4A (CUL-4A) {Homo sapiens}; contains Pfam profile PF00888: Cullin family   chr5:18748645-18754037 REVERSE   Aliases: CUL4, MDE13.3, MDE13_3	9.4	10.0	-0.5	-1.8	100.0%	-3.6
3104	AT2G05620.1   Symbol: PGR5   expressed protein   chr2:2081050-2081837 REVERSE   Aliases: T20G20.3, T20G20_3	9.2	8.3	0.9	1.8	100.0%	-3.3
3105	AT4G26840.1   Symbol: SUM1   ubiquitin-like protein (SMT3), identical to Ubiquitin-like protein SMT3 SP:P55852 from(Arabidopsis thaliana); identical to cDNA SMT3 protein GI:1707371   chr4:13497334-13498733 FORWARD   Aliases: F10M23.180, F10M23_180, SMALL UBIQUITIN LIKE MODIFIER 1, SUMO 1, SUMO1	9.6	8.9	0.7	1.8	100.0%	-3.8
3106	AT5G38700.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g02170.1); similar to disease resistance gene [Pinus sylvestris] (GB:AAR36911.1)   chr5:15506825-15507468 FORWARD   Aliases: MBB18.26, MBB18_26	3.1	2.7	0.4	1.8	100.0%	-3.5
3107	AT2G45530.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:18763552-18765002 FORWARD   Aliases: F17K2.6	8.0	7.4	0.5	1.8	100.0%	-3.4
3108	AT5G11510.2   Symbol: MYB3R 4   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At4g32730.1); similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At4g32730.2); similar to Myb [Nicotiana tabacum] (GB:BAB70510.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)   chr5:3680453-3683634 FORWARD   Aliases: F15N18.100, F15N18_100	3.5	3.9	-0.5	-1.8	100.0%	-3.6
3109	AT1G55090.1   carbon-nitrogen hydrolase family protein, low similarity to SP:P71911 Glutamine-dependent NAD(+) synthetase (EC 6.3.5.1) {Mycobacterium tuberculosis}; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family   chr1:20558104-20561855 FORWARD   Aliases: T7N22.4, T7N22_4	4.5	5.0	-0.5	-1.8	100.0%	-3.5
3110	AT4G26850.1   Symbol: VTC2   expressed protein   chr4:13499016-13501654 REVERSE   Aliases: F10M23.190, F10M23_190, VITAMIN C DEFECTIVE 2	8.7	7.8	0.9	1.8	100.0%	-3.3
3111	AT5G53750.1   similar to CBS domain-containing protein [Arabidopsis thaliana] (TAIR:At4g27460.1); similar to OSJNBb0017101.11 [Oryza sativa (japonica cultivar-group)] (GB:XP_474370.1); contains InterPro domain CBS domain (InterPro:IPR000644)   chr5:21834593-21836064 FORWARD   Aliases: MGN6.11, MGN6_11	6.0	5.5	0.5	1.8	100.0%	-3.4
3112	AT1G73180.1   eukaryotic translation initiation factor-related, similar to eukaryotic translation initiation factor 2A (GI:21956484) (Homo sapiens); similar to Eukaryotic translation initiation factor 3 subunit 9 (eIF-3 eta) (eIF3 p116) (eIF3 p110) (eIF3b) (Swiss-Prot:P55884) (Homo sapiens)   chr1:27521577-27525290 FORWARD   Aliases: T18K17.15, T18K17_15	7.6	8.1	-0.5	-1.8	100.0%	-3.3
3113	AT2G22620.1   expressed protein   chr2:9611881-9617675 REVERSE   Aliases: T9I22.6, T9I22_6	2.9	3.6	-0.7	-1.8	100.0%	-3.3
3114	AT5G17170.1   rubredoxin family protein, contains Pfam profile PF00301: Rubredoxin   chr5:5649205-5651160 FORWARD   Aliases: MKP11.2, MKP11_2	8.8	8.0	0.7	1.8	100.0%	-3.1
3115	AT5G06370.1   NC domain-containing protein, contains Pfam domain, PF04970: NC domain   chr5:1947140-1948574 REVERSE   Aliases: MHF15.11, MHF15_11	7.9	7.3	0.6	1.8	100.0%	-3.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3116	AT5G60340.1   maoC-like dehydratase domain-containing protein, contains similarity to (R)-specific enoyl-CoA hydratase Phaj1 (Pseudomonas oleovorans) gi:22506675:gb:AAM97601; contains Pfam domain PF01575: MaoC like domain   chr5:24291105-24293117 REVERSE   Aliases: K9B18.5, K9B18_5	2.7	2.9	-0.3	-1.8	100.0%	-4.0
3117	AT4G21110.1   G10 family protein, contains Pfam profile: PF01125 G10 protein   chr4:11267196-11268968 FORWARD   Aliases: F7J7.50, F7J7_50	10.7	10.2	0.5	1.8	100.0%	-3.6
3118	AT2G31350.2   hydroxyacylglutathione hydrolase, putative / glyoxalase II, putative, similar to glyoxalase II isozyme (Arabidopsis thaliana) gi:2570338:gb:AAC49865   chr2:13375370-13378070 FORWARD   Aliases: T28P16.16, T28P16_16	9.4	8.8	0.6	1.8	100.0%	-3.6
3119	AT1G67630.1   DNA polymerase alpha subunit B family, contains Pfam profile: PF04058 DNA polymerase alpha subunit B   chr1:25348103-25352069 REVERSE   Aliases: F12B7.19, F12B7_19	4.3	4.9	-0.6	-1.8	100.0%	-3.5
3120	AT4G26720.1   Symbol: PPX1   serine/threonine protein phosphatase PP-X isozyme 1 (PPX1), identical to SP:P48529 Serine/threonine protein phosphatase PP-X isozyme 1 (EC 3.1.3.16) {Arabidopsis thaliana}; contains Pfam profile PF00149: Ser/Thr protein phosphatase   chr4:13470040-13472326 REVERSE   Aliases: EP124, EP129, F10M23.60, F10M23_60, PPX 1	6.0	5.7	0.3	1.8	100.0%	-3.8
3121	AT3G17010.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain. Activated by AGAMOUS in a cal-1, ap1-1 background. Expressed in stamen primordia, the placental region of developing carpels and the ovary.   chr3:5800466-5802474 FORWARD   Aliases: K14A17.8	4.4	3.9	0.5	1.8	100.0%	-3.9
3122	AT1G13700.1   glucosamine/galactosamine-6-phosphate isomerase family protein, similar to SP:O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) {Homo sapiens}; contains Pfam profile PF01182: Glucosamine-6-phosphate isomerase/6-phosphogluconolactonase   chr1:4693959-4695979 REVERSE   Aliases: F21F23.14, F21F23_14	3.6	4.1	-0.6	-1.8	100.0%	-3.6
3123	AT5G14270.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr5:4604735-4608908 FORWARD   Aliases: F18O22.60, F18O22_60	7.5	6.9	0.7	1.8	100.0%	-3.3
3124	AT3G56690.1   Symbol: CIP111	4.8	5.4	-0.6	-1.8	100.0%	-3.4
3125	AT1G72480.1   expressed protein   chr1:27289727-27292001 REVERSE   Aliases: T10D10.5, T10D10_5	4.7	5.2	-0.6	-1.8	100.0%	-3.4
3126	AT2G21950.1   SKP1 interacting partner 6 (SKIP6), identical to SKP1 interacting partner 6 GI:10716957 from (Arabidopsis thaliana)   chr2:9360254-9361725 REVERSE   Aliases: F7D8.27, F7D8_27	7.1	6.6	0.5	1.8	100.0%	-3.6
3127	AT2G39880.1   Symbol: MYB25   myb family transcription factor (MYB25), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:16655023-16656557 REVERSE   Aliases: T28M21.4, T28M21_4	5.1	5.5	-0.4	-1.8	100.0%	-3.4
3128	AT1G03830.1   guanylate-binding family protein, contains Pfam domains PF02263: Guanylate-binding protein, N-terminal domain and PF02841: Guanylate-binding protein, C-terminal domain   chr1:962127-966621 REVERSE   Aliases: F21M11.26, F21M11_26	4.9	5.7	-0.8	-1.8	100.0%	-3.7
3129	AT3G26560.1   ATP-dependent RNA helicase, putative, similar to SP:Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain, PF00575: S1 RNA binding domain   chr3:9751166-9755009 REVERSE   Aliases: MFE16.8	6.5	7.4	-0.9	-1.8	100.0%	-3.2
3130	AT2G26380.1   disease resistance protein-related / LRR protein-related, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-2A (Lycopersicon pimpinellifolium) gi:3894389:gb:AAC78594   chr2:11233693-11235135 REVERSE   Aliases: T9J22.5, T9J22_5	3.5	3.1	0.4	1.8	100.0%	-3.6
3131	AT1G76130.1   Symbol: ATAMY2	4.8	4.2	0.6	1.8	100.0%	-3.2
3132	AT3G62700.1   Symbol: ATMRP10   glutathione-conjugate transporter, putative, similar to glutathione-conjugate transporter AtMRP4 GI:2959767 from (Arabidopsis thaliana)   chr3:23201243-23206738 REVERSE   Aliases: F26K9.130	7.0	7.8	-0.8	-1.8	100.0%	-3.5
3133	AT5G17000.1   NADP-dependent oxidoreductase, putative, strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana   chr5:5584804-5587066 REVERSE   Aliases: F2K13.150, F2K13_150	9.0	8.2	0.8	1.8	100.0%	-3.3
3134	AT5G22300.1   Symbol: NIT4   nitrilase 4 (NIT4), identical to SP:P46011 Nitrilase 4 (EC 3.5.5.1) {Arabidopsis thaliana}   chr5:7379221-7381928 FORWARD   Aliases: NITRILASE 4, T6G21.6	5.6	4.9	0.7	1.8	100.0%	-3.1
3135	AT3G56760.1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK3 (Nicotiana tabacum) gi:16904226:gb:AAL30820   chr3:21031537-21034735 REVERSE   Aliases: T8M16.90	6.3	6.8	-0.5	-1.8	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3136	AT5G07220.1   BAG domain-containing protein, contains Pfam:PF02179 BAG domain   chr5:2265257-2266968 REVERSE   Aliases: T28J14.160, T28J14_160	5.8	5.1	0.7	1.8	100.0%	-3.2
3137	AT4G35020.1   Symbol: ROP6   Rac-like GTP-binding protein (ARAC3) / Rho-like GTP-binding protein (ROP6), identical to SP:Q38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) {Arabidopsis thaliana}; identical to cDNA Rho-like GTP binding protein (Rop6) GI:2645642   chr4:16672945-16674776 FORWARD   Aliases: ATROP6, M4E13.80, M4E13_80, RHO1PS	6.7	7.2	-0.6	-1.8	100.0%	-3.3
3138	AT2G15690.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:6838077-6840859 REVERSE   Aliases: F9O13.34	5.8	6.6	-0.8	-1.8	100.0%	-3.1
3139	AT5G10770.1   chloroplast nucleoid DNA-binding protein, putative, similar to CND41, chloroplast nucleoid DNA binding protein (Nicotiana tabacum) GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease   chr5:3403120-3405449 REVERSE   Aliases: T30N20.40, T30N20_40	4.1	3.4	0.8	1.8	100.0%	-3.6
3140	AT3G10190.1   calmodulin, putative, similar to calmodulin NtCaM13 (Nicotiana tabacum) GI:14625425, calmodulin GB:AAA34015 (Glycine max); contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr3:3155303-3156145 FORWARD   Aliases: F14P13.21	4.2	3.6	0.6	1.8	100.0%	-3.5
3141	AT1G16750.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr1:5729090-5731863 REVERSE   Aliases: F19K19.16	7.5	6.5	1.0	1.8	100.0%	-3.0
3142	AT2G28650.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit   chr2:12296229-12298122 REVERSE   Aliases: T8O18.6, T8O18_6	5.8	5.2	0.6	1.8	100.0%	-3.6
3143	AT5G12340.1   expressed protein, ; expression supported by MPSS   chr5:3992949-3993611 REVERSE   Aliases: None	3.4	4.0	-0.6	-1.8	100.0%	-3.4
3144	AT1G62250.2   expressed protein   chr1:22999169-23001221 REVERSE   Aliases: F19K23.17, F19K23_17	6.7	5.9	0.8	1.8	100.0%	-3.4
3145	AT3G55280.1   60S ribosomal protein L23A (RPL23aB), various ribosomal L23a proteins   chr3:20511312-20512686 FORWARD   Aliases: T26I12.160	9.0	9.9	-0.9	-1.8	100.0%	-3.2
3146	AT3G51270.1   RIO1 family protein, contains Pfam profile PF01163: RIO1 family   chr3:19044830-19047751 FORWARD   Aliases: F24M12.310	7.0	7.8	-0.8	-1.8	100.0%	-3.3
3147	AT4G14680.1   Symbol: APS3   sulfate adenylyltransferase 3 / ATP-sulfurylase 3 (APS3), identical to ATP sulfurylase (APS3) (Arabidopsis thaliana) GI:1575327   chr4:8413286-8415349 REVERSE   Aliases: DL3380C, FCAALL.128	8.4	9.6	-1.2	-1.8	100.0%	-3.3
3148	AT1G16920.1   Symbol: RAB11   Ras-related GTP-binding protein, putative, similar to GTP binding protein GI:218228 from (Vicia faba); identical to cDNA small GTP-binding protein (Rab11) GI:451859   chr1:5787323-5789242 REVERSE   Aliases: ATRABA4B, F17F16.26, RAB11	7.8	8.9	-1.0	-1.8	100.0%	-3.2
3149	AT3G51880.2   Symbol: HMGB1   high mobility group protein alpha (HMGalpha) / HMG protein alpha, nearly identical to HMG protein (HMGalpha) (Arabidopsis thaliana) GI:2832357; contains Pfam profile PF00505: HMG (high mobility group) box   chr3:19257980-19260072 REVERSE   Aliases: ATEM1.13, HIGH MOBILITY GROUP B 1, HMG ALPHA, NFD1	9.1	8.5	0.6	1.8	100.0%	-3.5
3150	AT5G08610.1   DEAD box RNA helicase (RH26), strong similarity to RNA helicase RH26 (Arabidopsis thaliana) GI:3776025; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain; identical to cDNA DEAD box RNA helicase, RH26 GI:3776024   chr5:2790296-2794216 FORWARD   Aliases: MAH20.17, MAH20_17	6.1	6.9	-0.8	-1.8	100.0%	-3.1
3151	AT2G22250.3   similar to aminotransferase class I and II family protein [Arabidopsis thaliana] (TAIR:At1g77670.1); similar to aspartate aminotransferase [Pinus pinaster] (GB:CAF31327.1); contains InterPro domain Aminotransferase, class I and II (InterPro:IPR004839); contains InterPro domain Aminotransferases class-I pyridoxal-phosphate-binding site (InterPro:IPR004838)   chr2:9464890-9467999 REVERSE   Aliases: T26C19.9, T26C19_9	8.1	9.1	-1.0	-1.8	100.0%	-3.4
3152	AT1G55680.1   WD-40 repeat family protein, contains 2 (1 significant) WD-40 repeats (PF0400); similar to Trp-Asp repeat protein (PIR:T40094) (Schizosaccharomyces)   chr1:20808258-20811544 REVERSE   Aliases: F20N2.10	5.3	4.6	0.6	1.8	100.0%	-3.4
3153	AT1G28200.1   Symbol: FIP1   GRAM domain-containing protein / ABA-responsive protein-related, similar to ABA-responsive protein (Hordeum vulgare) GI:4103635; contains Pfam profile PF02893: GRAM domain   chr1:9850134-9852353 REVERSE   Aliases: F3H9.14, F3H9_14, FH INTERACTING PROTEIN 1, VIRF INTERACTING PROTEIN 1	8.5	7.7	0.8	1.8	100.0%	-3.4
3154	AT5G48800.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr5:19803990-19806733 FORWARD   Aliases: K24G6.13, K24G6_13	3.7	4.3	-0.5	-1.8	100.0%	-3.5
3155	AT2G32090.2   lactoylglutathione lyase family protein / glyoxalase I family protein, contains glyoxalase family protein domain, Pfam:PF00903   chr2:13651704-13652906 FORWARD   Aliases: F22D22.16, F22D22_16	10.6	9.8	0.8	1.8	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3156	AT5G65450.1   ubiquitin carboxyl-terminal hydrolase family protein / zinc finger (MYND type) family protein, similar to ubiquitin-specific protease 16 (UBP16) (Arabidopsis thaliana) GI:11993477; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF01753: MYND finger	6.5	7.2	-0.6	-1.8	100.0%	-3.3
3157	AT5G40610.1   glycerol-3-phosphate dehydrogenase (NAD+) / GPDH, strong similarity to SP:P52425 Glycerol-3-phosphate dehydrogenase (NAD+) (EC 1.1.1.8) {Cuphea lanceolata}; contains Pfam profile PF01210: NAD-dependent glycerol-3-phosphate dehydrogenase   chr5:16282090-16284520 REVERSE   Aliases: MNF13.130, MNF13_130	7.1	7.8	-0.7	-1.8	100.0%	-3.2
3158	AT2G41120.1   expressed protein   chr2:17147973-17149497 REVERSE   Aliases: T3K9.11, T3K9_11	4.0	3.5	0.5	1.8	100.0%	-3.4
3159	AT5G53180.1   polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative, similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) from {Rattus norvegicus} SP:Q00438, {Homo sapiens} SP:P26599; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:21585426-21589115 REVERSE   Aliases: MFH8.12, MFH8_12	8.1	7.6	0.5	1.8	100.0%	-3.4
3160	AT2G25140.1   heat shock protein 100, putative / HSP100, putative / heat shock protein clpB, putative / HSP100/ClpB, putative, similar to HSP100/ClpB GI:9651530 (Phaseolus lunatus)   chr2:10704782-10709231 REVERSE   Aliases: F13D4.100, F13D4_100	6.0	6.5	-0.4	-1.8	100.0%	-3.5
3161	AT1G18290.1   expressed protein   chr1:6297429-6297959 FORWARD   Aliases: F15H18.19	3.2	2.8	0.3	1.8	100.0%	-3.7
3162	AT5G55180.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr5:22406012-22407938 FORWARD   Aliases: MCO15.13, MCO15_13	8.5	8.1	0.5	1.8	100.0%	-3.5
3163	AT1G76120.2   tRNA pseudouridine synthase family protein, similar to SP:Q9Y606 tRNA pseudouridine synthase A (EC 4.2.1.70) (Uracil hydrolyase) {Homo sapiens}; contains Pfam profile PF01416: tRNA pseudouridine synthase   chr1:28563568-28565330 REVERSE   Aliases: T23E18.5, T23E18_5	4.3	4.7	-0.4	-1.8	100.0%	-3.4
3164	AT2G26390.1   serpin, putative / serine protease inhibitor, putative, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr2:11236165-11237569 REVERSE   Aliases: T9J22.6, T9J22_6	3.3	3.6	-0.3	-1.8	100.0%	-4.0
3165	AT3G10940.1   protein phosphatase-related, similar to protein phosphatase PTPKIS1 protein (GI:11595504) (Arabidopsis thaliana)	6.3	6.8	-0.5	-1.8	100.0%	-3.5
3166	AT1G16520.1   expressed protein   chr1:5648763-5651160 FORWARD   Aliases: F3O9.32	6.5	7.3	-0.8	-1.8	100.0%	-3.3
3167	AT1G67330.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr1:25217515-25218834 FORWARD   Aliases: F1N21.15	3.3	4.5	-1.2	-1.8	100.0%	-3.2
3168	AT2G37500.1   arginine biosynthesis protein Argj family, contains Pfam profile: PF01960 Argj family   chr2:15746418-15749836 REVERSE   Aliases: F3G5.29, F3G5_29	7.7	8.5	-0.8	-1.8	100.0%	-3.3
3169	AT5G16920.1   expressed protein   chr5:5567014-5568131 FORWARD   Aliases: F2K13.70, F2K13_70	1.9	2.0	-0.1	-1.8	100.0%	-4.7
3170	AT1G69210.1   expressed protein   chr1:26021765-26023721 REVERSE   Aliases: F4N2.17, F4N2_17	3.6	4.0	-0.4	-1.8	100.0%	-3.7
3171	AT2G20080.2   expressed protein   chr2:8670011-8672107 REVERSE   Aliases: T2G17.12, T2G17_12	2.3	2.6	-0.2	-1.8	100.0%	-4.3
3172	AT1G67560.1   lipoxygenase family protein, similar to 13-lipoxygenase GB:CAA65269 (Solanum tuberosum), gi:1654140 (Lycopersicon esculentum)   chr1:25323562-25327927 FORWARD   Aliases: F12B7.11, F12B7_11	7.9	7.3	0.6	1.8	100.0%	-3.4
3173	AT1G28050.1   zinc finger (B-box type) family protein   chr1:9775515-9777797 REVERSE   Aliases: F13K9.15, F13K9_15	5.2	4.7	0.5	1.8	100.0%	-3.6
3174	AT5G61620.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:24789609-24790733 FORWARD   Aliases: K11J9.15, K11J9_15	3.2	2.9	0.3	1.8	100.0%	-3.8
3175	AT5G65460.1   kinesin motor protein-related, contains similarity to kinesin heavy chain   chr5:26179057-26186227 REVERSE   Aliases: MNA5.20, MNA5_20	3.2	3.7	-0.5	-1.8	100.0%	-3.7
3176	AT4G27440.2   Symbol: PORB   similar to protochlorophyllide reductase A, chloroplast / PCR A / NADPH-protochlorophyllide oxidoreductase A (PORA) [Arabidopsis thaliana] (TAIR:At5g54190.1); similar to NADPH-protochlorophyllide oxidoreductase [Cucumis sativus] (GB:BAA21089.1); similar to protochlorophyllide reductase (EC 1.3.1.33) precursor - garden pea (GB:S20941); similar to protochlorophyllide reductase [Pisum sativum] (GB:CAA44786.1); similar to NADPH:protochlorophyllide oxidoreductase [Nicotiana tabacum] (GB:BA93003.1); similar to NADPH:protochlorophyllide oxidoreductase [Daucus carota] (GB:AAF20949.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Light-dependent protochlorophyllide reductase (InterPro:IPR005979); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)	6.4	7.3	-0.9	-1.8	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3177	AT3G49690.1   myb family transcription factor, contains Pfam profile: myb DNA binding domain PF00249   chr3:18438821-18440186 FORWARD   Aliases: T16K5.40	5.0	5.9	-0.9	-1.8	100.0%	-3.3
3178	AT1G08770.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr1:2808886-2809747 FORWARD   Aliases: F22O13.26, F22O13_26	4.8	4.5	0.4	1.8	100.0%	-3.8
3179	AT5G63905.1   expressed protein   chr5:25588084-25588812 REVERSE   Aliases: None	5.6	4.7	0.8	1.8	100.0%	-3.3
3180	AT2G36270.1   Symbol: ABI5   bZIP transcription factor family protein / ABA-responsive element-binding protein, putative, similar to ABA-responsive element binding protein 1 (AREB1) GI:9967417 from (Arabidopsis thaliana); contains a bZIP transcription factor basic domain signature (PDOC00036)	5.5	4.8	0.7	1.8	100.0%	-3.4
3181	AT3G56800.1   Symbol: CAM3   calmodulin-2/3/5 (CAM3), identical to calmodulin GI:474183 from (Arabidopsis thaliana); almost identical to calmodulin-2/3/5 SP:P25069 (Arabidopsis thaliana)   chr3:21045656-21047053 REVERSE   Aliases: ACAM 3, CALMODULIN 3, T8M16.130	11.4	10.9	0.5	1.8	100.0%	-3.6
3182	AT5G40520.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g07170.1); similar to B1158C05.16 [Oryza sativa (japonica cultivar-group)] (GB:NP_917835.1)   chr5:16248482-16251536 REVERSE   Aliases: MNF13.3, MNF13_3	3.8	4.2	-0.4	-1.8	100.0%	-3.7
3183	AT4G26870.1   aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative, simialr to aspartate-tRNA ligase (EC 6.1.1.12) from Drosophila melanogaster GI:4512034, Homo sapiens SP:P14868, Rattus norvegicus SP:P15178; contains Pfam profile PF00152 tRNA synthetases class II (D, K and N)	6.4	7.0	-0.6	-1.8	100.0%	-3.5
3184	AT1G80070.1   Symbol: SUS2   splicing factor, putative, strong similarity to splicing factor Prp8 (Homo sapiens) GI:3661610; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr1:30122945-30132704 FORWARD   Aliases: ABNORMAL SUSPENSOR 2, EMB14, EMB158, EMB177, EMB33, EMBRYO DEFECTIVE 14, EMBRYO DEFECTIVE 177, EMBRYO DEFECTIVE 33, F18B13.15, F18B13_15	8.3	9.1	-0.8	-1.8	100.0%	-3.3
3185	AT5G35180.1   expressed protein   chr5:13441648-13450248 FORWARD   Aliases: T25C13.60, T25C13_60	6.3	7.2	-0.9	-1.8	100.0%	-3.3
3186	AT1G80750.1   60S ribosomal protein L7 (RPL7A), similar to ribosomal protein L7 GB:AAA03081 GI:307388 from (Homo sapiens)   chr1:30353715-30355456 FORWARD   Aliases: F23A5.10, F23A5_10	7.9	8.8	-0.9	-1.8	100.0%	-3.2
3187	AT5G19180.1   Symbol: ECR1   ubiquitin activating enzyme, putative (ECR1), identical to putative ubiquitin activating enzyme E1 (Arabidopsis thaliana) GI:2952433; similar to NEDD8 activating enzyme (Mus musculus) GI:17061821   chr5:6453279-6456016 FORWARD   Aliases: E1 C TERMINAL RELATED 1, T24G5.80, T24G5_80	5.9	6.8	-0.9	-1.8	100.0%	-3.4
3188	AT3G30220.1   expressed protein   chr3:11880345-11880937 REVERSE   Aliases: MIL15.3	2.0	2.1	-0.1	-1.8	100.0%	-4.6
3189	AT2G44850.1   expressed protein   chr2:18505747-18507898 FORWARD   Aliases: T13E15.14	4.0	3.6	0.4	1.8	100.0%	-3.7
3190	AT4G26710.2   ATP synthase subunit H family protein, contains similarity to Swiss-Prot:O15342 Vacuolar ATP synthase subunit H (V-ATPase H subunit) (Vacuolar proton pump H subunit) (V-ATPase M9.2 subunit) (V-ATPase 9.2 kDa membrane accessory protein) (Homo sapiens)   chr4:13468603-13469941 FORWARD   Aliases: F10M23.50, F10M23_50	10.6	9.9	0.7	1.8	100.0%	-4.0
3191	AT2G46690.1   auxin-responsive family protein, similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) (Phaseolus aureus)   chr2:19187800-19188537 FORWARD   Aliases: T3A4.7	8.9	8.4	0.5	1.8	100.0%	-3.5
3192	AT5G60940.2   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to cleavage stimulation factor 50K chain Homo sapiens, PIR:A45142   chr5:24540247-24543038 FORWARD   Aliases: MSL3.60, MSL3_60	3.9	4.3	-0.4	-1.8	100.0%	-3.7
3193	AT5G19430.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:6553827-6555833 FORWARD   Aliases: F7K24.180, F7K24_180	6.3	5.7	0.7	1.8	100.0%	-3.6
3194	AT2G03760.1   Symbol: ST   steroid sulfotransferase, putative, strong similarity to steroid sulfotransferases from (Brassica napus) GI:3420008, GI:3420004, GI:3420006; contains Pfam profile PF00685: Sulfotransferase domain   chr2:1149334-1150660 REVERSE   Aliases: F19B11.21, F19B11_21, RAR047, SULFOTRANSFERASE, SULFURTRANSFERASE	3.5	4.0	-0.5	-1.8	100.0%	-3.4
3195	AT5G63200.1   tetratricopeptide repeat (TPR)-containing protein, low similarity to SP:P28290 Sperm-specific antigen 2 (Cleavage signal-1 protein) (CS-1) Homo sapiens; contains Pfam profile PF00515: TPR Domain   chr5:25366237-25370228 FORWARD   Aliases: AT5G63210, MDC12.17, MDC12_17	5.7	5.4	0.3	1.8	100.0%	-3.9
3196	AT1G77590.1   Symbol: LACS9   long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS9), similar to LACS 3 (SP:O95573) from Homo Sapiens, LACS 3 (SP:Q63151) from Rattus norvegicus; contains Pfam HMM hit: AMP-binding enzymes PF00501   chr1:29153150-29156670 REVERSE   Aliases: LONG CHAIN ACYL COA SYNTHETASE 9, T5M16.18, T5M16_18	4.9	5.5	-0.6	-1.8	100.0%	-3.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3197	AT4G12120.1   Symbol: SEC1B   cytokinesis-related Sec1 protein, putative, similar to cytokinesis-related Sec1 protein KEULE (Arabidopsis thaliana) gi:12659318:gb:AAK01291; contains Pfam domain, PF00995: Sec1 family   chr4:7256532-7261174 REVERSE   Aliases: ATSEC1B, F16J13.190, F16J13_190, SEC1B	5.4	5.8	-0.4	-1.8	100.0%	-3.6
3198	AT1G55265.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:20620980-20621668 FORWARD   Aliases: None	4.6	4.1	0.5	1.8	100.0%	-3.3
3199	AT5G27110.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:9538575-9540650 REVERSE   Aliases: T21B4.20, T21B4_20	5.2	5.7	-0.5	-1.8	100.0%	-3.4
3200	AT1G35780.1   expressed protein   chr1:13278486-13281472 REVERSE   Aliases: F14D7.8, F14D7_8	5.2	5.7	-0.5	-1.8	100.0%	-3.6
3201	AT1G30890.1   integral membrane HRF1 family protein, contains Pfam domain PF03878: Hrf1 family	7.2	6.6	0.6	1.8	100.0%	-3.5
3202	AT5G44240.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from {Mus musculus} SP:P70704, {Bos taurus} SP:Q29449; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:17834846-17840933 FORWARD   Aliases: MLN1.17, MLN1_17	5.6	6.3	-0.6	-1.8	100.0%	-3.3
3203	AT3G28900.1   60S ribosomal protein L34 (RPL34C), similar to 60S ribosomal protein L34 GB:P41098 (Nicotiana tabacum)   chr3:10903924-10905686 REVERSE   Aliases: MLD15.7	7.7	8.8	-1.1	-1.8	100.0%	-3.2
3204	AT5G12150.1   pleckstrin homology (PH) domain-containing protein / RhoGAP domain-containing protein, weak similarity to glucocorticoid receptor DNA binding factor 1 (Canis familiaris) GI:23266717; contains Pfam profiles PF00169: PH domain, PF00620: RhoGAP domain	6.7	7.3	-0.6	-1.8	100.0%	-3.4
3205	AT1G53280.1   DJ-1 family protein, similar to DJ-1 protein (Homo sapiens) GI:1780755; similar to DJ-1 beta (GI:18642508) (Drosophila melanogaster); contains Pfam profile: PF01965 Thij/Pfpl family; TIGRFAM TIGR01383: DJ-1 family protein   chr1:19867968-19871057 REVERSE   Aliases: F12M16.18, F12M16_18	10.1	10.5	-0.4	-1.8	100.0%	-3.8
3206	AT2G33450.1   50S ribosomal protein L28, chloroplast (CL28)   chr2:14180655-14181609 FORWARD   Aliases: F4P9.22, F4P9_22	5.6	6.5	-0.9	-1.8	100.0%	-3.1
3207	AT3G13222.1   Symbol: GIP1   expressed protein   chr3:4251021-4254244 REVERSE   Aliases: GBF INTERACTING PROTEIN 1, MJG19.5	3.9	4.4	-0.5	-1.8	100.0%	-3.5
3208	AT3G53240.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.1 (Lycopersicon pimpinellifolium) gi:1184075:gb:AAC15779   chr3:19744791-19750159 FORWARD   Aliases: T4D2.170	4.5	4.0	0.4	1.8	100.0%	-3.5
3209	AT2G30600.4   similar to BTB/POZ domain-containing protein [Arabidopsis thaliana] (TAIR:At2g46260.1); similar to similar to Dictyostelium discoideum (Slime mold). MigA (GB:AAS45368.1); contains InterPro domain BTB/POZ domain (InterPro:IPR000210)   chr2:13043953-13048761 FORWARD   Aliases: AT2G30610, T6B20.5, T6B20_5	6.5	5.8	0.7	1.8	100.0%	-3.9
3210	AT3G61610.1   aldose 1-epimerase family protein, similar to apospory-associated protein C; APOC (Chlamydomonas reinhardtii) GI:6970044; contains Pfam profile PF01263: Aldose 1-epimerase   chr3:22810002-22812180 FORWARD   Aliases: F15G16.1	3.1	3.4	-0.3	-1.8	100.0%	-3.8
3211	AT5G52920.1   pyruvate kinase, putative, similar to pyruvate kinase isozyme G, chloroplast precursor (Nicotiana tabacum) SWISS-PROT:Q40546   chr5:21480769-21484043 FORWARD   Aliases: MXC20.15, MXC20_15	9.8	10.5	-0.7	-1.8	100.0%	-3.8
3212	AT1G02020.2   nitroreductase family protein, contains Pfam PF00881: nitroreductase family protein profile; contains Prosite PS00343: Gram-positive cocci surface proteins 'anchoring' hexapeptide   chr1:352637-354969 REVERSE   Aliases: T7I23.2, T7I23_2	6.2	5.6	0.6	1.8	100.0%	-3.3
3213	AT1G75040.1   Symbol: PR5   pathogenesis-related protein 5 (PR-5), identical to SP:P28493 Pathogenesis-related protein 5 precursor (PR-5) {Arabidopsis thaliana}; contains Pfam profile: PF00314 Thaumatin family   chr1:28181364-28182601 FORWARD   Aliases: PATHOGENESIS RELATED GENE 5, PATHOGENESIS RELATED PROTEIN 5	3.9	4.4	-0.6	-1.8	100.0%	-3.4
3214	AT5G46570.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:18911629-18914633 FORWARD   Aliases: F10E10.4, F10E10_4	5.2	6.0	-0.7	-1.8	100.0%	-3.2
3215	AT3G12640.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:4014462-4017851 FORWARD   Aliases: T2E22.5	5.2	5.8	-0.6	-1.8	100.0%	-3.5
3216	AT1G53560.1   expressed protein   chr1:19988423-19989649 REVERSE   Aliases: F22G10.10	5.8	5.2	0.6	1.8	100.0%	-3.5
3217	AT2G24762.1   expressed protein   chr2:10566463-10567213 FORWARD   Aliases: None	4.3	4.9	-0.6	-1.8	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3218	AT4G17760.2   similar to Rad1-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_550603.1)   chr4:9871803-9873411 FORWARD   Aliases: DL4915W, FCAALL.108	3.2	3.5	-0.4	-1.8	100.0%	-3.8
3219	AT1G36310.2   similar to hypothetical protein LOC67667 [Mus musculus] (GB:NP_080579.1); similar to unnamed protein product [Mus musculus] (GB:BAC38223.1); contains InterPro domain Generic methyltransferase (InterPro:IPR001601); contains InterPro domain SAM (and some other nucleotide) binding motif (InterPro:IPR000051)   chr1:13670711-13672337 FORWARD   Aliases: F7F23.3, F7F23_3	6.6	7.4	-0.7	-1.8	100.0%	-3.2
3220	AT3G59360.2   nucleotide-sugar transporter family protein, low similarity to SP:P78382 CMP-sialic acid transporter {Homo sapiens}; contains Pfam profile PF04142: Nucleotide-sugar transporter	4.5	3.9	0.6	1.8	100.0%	-3.4
3221	AT4G34680.2   similar to zinc finger (GATA type) family protein [Arabidopsis thaliana] (TAIR:At4g36240.1); similar to zinc finger (GATA type) family protein [Arabidopsis thaliana] (TAIR:At5g66320.1); similar to zinc finger (GATA type) family protein [Arabidopsis thaliana] (TAIR:At5g66320.2); similar to AG-motif binding protein-3 [Nicotiana tabacum] (GB:BAC98493.1); contains InterPro domain Zn-finger, GATA type (InterPro:IPR000679)   chr4:16553395-16554735 FORWARD   Aliases: T4L20.260, T4L20_260	5.9	5.6	0.3	1.8	100.0%	-3.7
3222	AT4G13270.1   expressed protein   chr4:7731276-7733162 FORWARD   Aliases: T9E8.10, T9E8_10	5.1	4.6	0.6	1.8	100.0%	-3.6
3223	AT4G12800.1   photosystem I reaction center subunit XI, chloroplast (PSI-L) / PSI subunit V, identical to Photosystem I reaction center subunit XI, chloroplast precursor (PSI-L) (PSI subunit V) (Swiss-Prot:Q9SUI4) (Arabidopsis thaliana); contains Pfam profile PF02605: photosystem I reaction center subunit XI; contains 2 transmembrane domains   chr4:7521319-7522667 FORWARD   Aliases: T20K18.150, T20K18_150	8.8	8.0	0.9	1.8	100.0%	-3.1
3224	AT5G48810.1   Symbol: ATB5 B	11.7	11.3	0.5	1.8	100.0%	-3.7
3225	AT1G62085.1   mitochondrial transcription termination factor family protein / mTERF family protein, contains Pfam profile PF02536: mTERF   chr1:22952422-22953807 REVERSE   Aliases: None	2.7	3.0	-0.3	-1.8	100.0%	-4.1
3226	AT1G60190.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:22202068-22204343 FORWARD   Aliases: T13D8.8, T13D8_8	6.8	6.3	0.5	1.8	100.0%	-3.5
3227	AT1G19690.1   expressed protein, similar to (SP:P76370) Protein yeeZ precursor. {Escherichia coli O157:H7}   chr1:6807706-6809560 REVERSE   Aliases: F14P1.35, F14P1_35	6.8	6.1	0.7	1.8	100.0%	-3.2
3228	AT1G60380.1   apical meristem formation protein-related, contains similarity to CUC1 (Arabidopsis thaliana) gi:12060422:dbj:BAB20598 and NAM (Petunia x hybrida) gi:1279640:emb:CAA63101   chr1:22250120-22251076 REVERSE   Aliases: T13D8.25, T13D8_25	2.6	2.8	-0.2	-1.8	100.0%	-4.2
3229	AT5G05840.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620); expression supported by MPSS   chr5:1757269-1760459 REVERSE   Aliases: MJJ3.26, MJJ3_26	3.5	3.9	-0.4	-1.8	100.0%	-3.8
3230	AT5G18170.1   Symbol: GDH1   glutamate dehydrogenase 1 (GDH1), identical to glutamate dehydrogenase 1 (GDH 1) (Arabidopsis thaliana) SWISS-PROT:Q43314   chr5:6006046-6008451 FORWARD   Aliases: GLUTAMATE DECARBOXYLASE 1, GLUTAMATE DEHYDROGENASE 1, GLUTAMATE DEHYDROGENASE DEFICIENT 1, MRG7.13, MRG7_13	7.6	6.8	0.8	1.8	100.0%	-3.4
3231	AT1G44100.1   Symbol: AAP5   amino acid permease 5, putative (AAP5), nearly identical to amino acid permease (AAP5) GI:608673 from (Arabidopsis thaliana)   chr1:16766845-16769973 REVERSE   Aliases: T7O23.19, T7O23_19	5.5	4.8	0.7	1.8	100.0%	-3.3
3232	AT3G61650.1   tubulin gamma-1 chain / gamma-1 tubulin (TUBG1), identical to SP:P38557 Tubulin gamma-1 chain (Gamma-1 tubulin) {Arabidopsis thaliana}   chr3:22823576-22825986 REVERSE   Aliases: F15G16.40	4.2	4.9	-0.7	-1.8	100.0%	-3.2
3233	AT5G05620.1   tubulin gamma-2 chain / gamma-2 tubulin (TUBG2), identical to SP:P38558 Tubulin gamma-2 chain (Gamma-2 tubulin) {Arabidopsis thaliana}   chr5:1679341-1681720 FORWARD   Aliases: MJJ3.10, MJJ3_10	4.2	4.9	-0.7	-1.8	100.0%	-3.2
3234	AT5G05160.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:1528001-1530063 FORWARD   Aliases: K2A11.3, K2A11_3	9.1	9.7	-0.5	-1.8	100.0%	-3.6
3235	AT4G24260.1   endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-1,4-beta-D-glucanase; cellulase GI:5689613 from (Brassica napus)   chr4:12577881-12580143 REVERSE   Aliases: T22A6.90, T22A6_90	6.7	7.7	-1.0	-1.8	100.0%	-3.1
3236	AT1G03040.1   basic helix-loop-helix (bHLH) family protein, component of the pyruvate dehydrogenase complex E3, contains PF:00010 helix-loop-helix DNA-binding domain. ESTs gb:T45640 and gb:T22783 come from this gene   chr1:703906-706631 REVERSE   Aliases: F10O3.14, F10O3_14	8.2	6.9	1.3	1.8	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3237	AT5G25510.1   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative, similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) ( <i>Oryctolagus cuniculus</i> ); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)   chr5:8882471-8884837 REVERSE   Aliases: T14C9.50, T14C9_50	4.9	5.4	-0.5	-1.8	100.0%	-3.4
3238	AT4G21940.1   Symbol: CPK15   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase ( <i>Nicotiana tabacum</i> ) gi:3283996:gb:AAC25423   chr4:11640819-11643653 FORWARD   Aliases: F1N20.5	3.4	3.8	-0.4	-1.8	100.0%	-3.8
3239	AT4G26230.1   60S ribosomal protein L31 (RPL31B), ribosomal protein L31, <i>Nicotiana glutinosa</i> , U23784   chr4:13285837-13286800 FORWARD   Aliases: T25K17.40, T25K17_40	11.6	12.0	-0.4	-1.8	100.0%	-3.8
3240	AT1G80360.1   aminotransferase class I and II family protein, low similarity to GI:14278621 Aromatic Aminotransferase from <i>Pyrococcus horikoshii</i>   chr1:30213391-30215579 REVERSE   Aliases: F5I6.11, F5I6_11	7.7	8.4	-0.6	-1.8	100.0%	-3.4
3241	AT1G79590.2   Symbol: SYP52   similar to syntaxin 51 (SYP51) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g16240.1); similar to putative syntaxin of plants 52 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_463898.1); contains InterPro domain Target SNARE coiled-coil domain (InterPro:IPR000727)   chr1:29951130-29953667 FORWARD   Aliases: ATSYP52, F20B17.2, F20B17_2, SYNTAXIN OF PLANTS 52	7.5	6.7	0.8	1.8	100.0%	-3.3
3242	AT2G16880.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:7319228-7321615 REVERSE   Aliases: F12A24.6, F12A24_6	3.6	3.9	-0.3	-1.8	100.0%	-4.0
3243	AT5G37830.1   hydantoinase/oxoprolinase family protein, contains Pfam profiles: PF02538 hydantoinase B/oxoprolinase, PF01968 hydantoinase/oxoprolinase, PF05378 hydantoinase/oxoprolinase N-terminal region   chr5:15073551-15078007 REVERSE   Aliases: K22F20.70, K22F20_70	5.8	6.2	-0.4	-1.8	100.0%	-3.7
3244	AT2G43030.1   ribosomal protein L3 family protein, contains Pfam profile PF00297: ribosomal protein L3	7.9	8.8	-1.0	-1.8	100.0%	-3.2
3245	AT3G61250.1   myb family transcription factor (MYB17), contains PFAM profile: Myb-like DNA-binding domain PF00249   chr3:22681977-22683713 FORWARD   Aliases: T20K12.150	2.9	3.1	-0.3	-1.8	100.0%	-3.9
3246	AT4G21430.1   similar to transcription factor jumonji (jmc) domain-containing protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g62310.1); similar to putative DNA-binding protein PD3, chloroplast [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_468520.1); contains InterPro domain Transcription factor jumonji, jmc (InterPro:IPR003347)	5.4	5.9	-0.5	-1.8	100.0%	-3.7
3247	AT5G06960.2   Symbol: OBF5   bZIP family transcription factor (OBF5), identical to bZIP family transcription factor (OBF5) GI:414615 from ( <i>Arabidopsis thaliana</i> )   chr5:2154823-2157647 FORWARD   Aliases: MOJ9.13, MOJ9_13, OBF5, OCS ELEMENT BINDING FACTOR 5, TGA5	6.1	5.6	0.5	1.8	100.0%	-3.3
3248	AT3G02860.2   expressed protein   chr3:625187-627374 REVERSE   Aliases: F13E7.20, F13E7_20	6.0	5.6	0.4	1.8	100.0%	-3.6
3249	AT1G73970.1   expressed protein   chr1:27820475-27823735 FORWARD   Aliases: F2P9.16, F2P9_16	5.9	6.3	-0.5	-1.8	100.0%	-3.4
3250	AT1G12800.1   S1 RNA-binding domain-containing protein, contains Pfam domain, PF00575: S1 RNA binding domain   chr1:4361549-4365314 REVERSE   Aliases: F13K23.5, F13K23_5	6.5	7.4	-0.9	-1.8	100.0%	-3.2
3251	AT2G30550.2   lipase class 3 family protein, similar to DEFECTIVE IN ANOTHER DEHISCENCE1 ( <i>Arabidopsis thaliana</i> ) GI:16215706; contains Pfam profile PF01764: Lipase   chr2:13021925-13024230 FORWARD   Aliases: T6B20.10, T6B20_10	7.0	6.1	0.9	1.8	100.0%	-3.4
3252	AT3G58700.1   60S ribosomal protein L11 (RPL11B), ribosomal protein L11, cytosolic, <i>Arabidopsis thaliana</i> , PIR:S49033   chr3:21722540-21723930 FORWARD   Aliases: T20N10.50	9.9	10.3	-0.4	-1.7	100.0%	-3.5
3253	AT5G07240.1   calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr5:2271920-2274288 FORWARD   Aliases: T28J14.180, T28J14_180	3.9	3.4	0.5	1.7	100.0%	-3.4
3254	AT1G01820.1   peroxisomal biogenesis factor 11 family protein / PEX11 family protein, contains Pfam PF05648: Peroxisomal biogenesis factor 11 (PEX11)   chr1:296001-298109 REVERSE   Aliases: T1N6.24, T1N6_24	7.8	7.4	0.4	1.7	100.0%	-3.7
3255	AT3G26085.1   CAAX amino terminal protease family protein, contains Pfam profile PF02517 CAAX amino terminal protease family protein   chr3:9532006-9533850 FORWARD   Aliases: None	5.8	5.4	0.4	1.7	100.0%	-3.5
3256	AT2G30400.1   ovate family protein, 57% similar to ovate protein (GI:23429649) ( <i>Lycopersicon esculentum</i> ); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.2	3.5	0.7	1.7	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3257	AT1G31020.1   thioredoxin o (TRXO2), similar to thioredoxin 2 from Saccharomyces cerevisiae GI:173050, 3'-end of protein contains similarity to thioredoxins; contains Pfam profile: PF00085 Thioredoxin; identical to cDNA thioredoxin o (TRXO2) GI:15081458	6.7	6.2	0.5	1.7	100.0%	-3.6
3258	AT3G63440.1   similar to FAD-binding domain-containing protein / cytokinin oxidase family protein [Arabidopsis thaliana] (TAIR:At2g41510.1); similar to putative cytokinin oxidase [Oryza sativa (japonica cultivar-group)] (GB:XP_463696.1); similar to putative cytokinin dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:BAD87612.1); similar to cytokinin oxidase 3 [Zea mays] (GB:CAE55201.1); contains InterPro domain FAD linked oxidase, N-terminal (InterPro:IPR006094)   chr3:23435132-23437240 FORWARD   Aliases: MAA21.70	6.7	5.8	0.9	1.7	100.0%	-3.1
3259	AT5G59440.2   thymidylate kinase family protein, similar to thymidylate kinase GI:291900   chr5:23988461-23990097 FORWARD   Aliases: F2O15.12, F2O15_12	6.5	5.7	0.8	1.7	100.0%	-3.2
3260	AT2G24100.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g30780.1); similar to hypothetical protein [Pinus pinaster] (GB:CAC84497.1)   chr2:10251966-10253999 FORWARD   Aliases: F27D4.1, F27D4_1	6.1	5.0	1.1	1.7	100.0%	-3.3
3261	AT3G03970.3   expressed protein   chr3:1028004-1030612 REVERSE   Aliases: T11I18.8, T11I18_8	4.2	4.6	-0.5	-1.7	100.0%	-3.6
3262	AT2G20240.1   expressed protein   chr2:8734713-8737581 REVERSE   Aliases: F11A3.21, F11A3_21	2.7	2.9	-0.2	-1.7	100.0%	-4.0
3263	AT3G06040.2   ribosomal protein L12 family protein, contains similarity to 50S ribosomal protein L12-C, chloroplast precursor GB:P36212 from (Arabidopsis thaliana)   chr3:1824382-1825634 REVERSE   Aliases: F24F17.2, F24F17_2	5.1	6.0	-0.9	-1.7	100.0%	-3.3
3264	AT3G03060.1   AAA-type ATPase family protein, contains a ATP/GTP-binding site motif A (P-loop), PROSITE:PS00017   chr3:692195-695431 FORWARD   Aliases: T17B22.25, T17B22_25	4.6	5.2	-0.6	-1.7	100.0%	-3.4
3265	AT3G05430.1   PWWP domain-containing protein, contains Pfam profile:PF00855 PWWP domain   chr3:1567631-1571078 FORWARD   Aliases: F22F7.12, F22F7_12	3.8	4.1	-0.3	-1.7	100.0%	-4.0
3266	AT3G57540.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr3:21312374-21314038 REVERSE   Aliases: T8H10.140	8.7	7.6	1.1	1.7	100.0%	-3.6
3267	AT1G27200.1   expressed protein, contains Pfam PF01697: Domain of unknown function   chr1:9449536-9451737 REVERSE   Aliases: T7N9.26, T7N9_26	3.5	3.3	0.2	1.7	100.0%	-4.1
3268	AT1G61920.1   expressed protein   chr1:22892122-22892433 FORWARD   Aliases: F8K4.11, F8K4_11	7.6	6.7	0.8	1.7	100.0%	-3.5
3269	AT5G64550.1   loricrin-related, contains weak similarity to Loricrin (Swiss-Prot:P23490) (Homo sapiens)   chr5:25818754-25822206 REVERSE   Aliases: MUB3.7, MUB3_7	5.5	5.1	0.4	1.7	100.0%	-3.6
3270	AT1G06630.1   F-box family protein, contains F-box domain Pfam:PF00646	4.6	4.2	0.4	1.7	100.0%	-3.6
3271	AT3G10860.1   ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative, similar to ubiquinol--cytochrome c reductase GI:633687 from (Solanum tuberosum)   chr3:3399741-3400732 FORWARD   Aliases: T7M13.6	13.2	13.4	-0.2	-1.7	100.0%	-4.7
3272	AT5G40450.1   expressed protein   chr5:16202027-16212756 REVERSE   Aliases: MPO12.160, MPO12_160	9.4	8.6	0.7	1.7	100.0%	-3.7
3273	AT2G20550.2   similar to DNAJ heat shock family protein [Arabidopsis thaliana] (TAIR:At2g20560.1); similar to DnaJ like protein [Lycopersicon esculentum] (GB:CAC16088.2); contains InterPro domain Heat shock protein DnaJ (InterPro:IPR003095); contains InterPro domain Chaperone DnaJ, C-terminal (InterPro:IPR002939)   chr2:8852883-8854392 REVERSE   Aliases: T13C7.14, T13C7_14	4.7	4.3	0.4	1.7	100.0%	-3.5
3274	AT1G56690.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:21257482-21259596 FORWARD   Aliases: F25P12.87, F25P12_87	2.6	2.9	-0.2	-1.7	100.0%	-4.1
3275	AT1G80440.1   kelch repeat-containing F-box family protein, similar to SP:Q9ER30 Kelch-related protein 1 (Sarcosin) {Rattus norvegicus}; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:30246499-30247956 FORWARD   Aliases: T21F11.23, T21F11_23	5.4	4.5	0.9	1.7	100.0%	-3.3
3276	AT3G44750.1   Symbol: HD2A   histone deacetylase, putative (HD2A), contains Pfam domain, PF00096: Zinc finger, C2H2 type; identical to cDNA putative histone deacetylase (HD2A) GI:11066134   chr3:16308970-16310733 FORWARD   Aliases: ATHD2A, HDA3, HDT1, HISTONE DEACETYLASE 2A, T32N15.8	7.7	8.5	-0.8	-1.7	100.0%	-3.2
3277	AT4G12550.1   Symbol: AIR1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234; identical to cDNA AIR1 mRNA, partial cds GI:3695016	2.2	3.4	-1.2	-1.7	100.0%	-3.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3278	AT4G19500.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. A false intron was added between exons 2 and 3 to circumvent a frameshift caused by a sequencing error, as per Blake Meyers (bcmeyers@vegmail.ucdavis.edu)   chr4:10625798-10630150 FORWARD   Aliases: F24J7.60, F24J7_60	5.7	6.3	-0.6	-1.7	100.0%	-3.5
3279	AT2G25270.1   expressed protein   chr2:10766828-10769797 FORWARD   Aliases: T22F11.14, T22F11_14	6.7	7.5	-0.8	-1.7	100.0%	-3.1
3280	AT4G20980.3   similar to eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative [Arabidopsis thaliana] (TAIR:At5g44320.1); similar to ENSANGP00000015368 [Anopheles gambiae str. PEST] (GB:XP_312631.2); contains InterPro domain Eukaryotic translation initiation factor 3, subunit 7 (InterPro:IPR007783)   chr4:11216955-11219330 FORWARD   Aliases: T13K14.140, T13K14_140	7.3	8.2	-0.9	-1.7	100.0%	-3.4
3281	AT5G43990.2   SET domain-containing protein, identical to SET domain protein SUVR2 (Arabidopsis thaliana) GI:15290521; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif; identical to cDNA SET domain protein SUVR2 GI:15290520   chr5:17715116-17719190 FORWARD   Aliases: MRH10.10, MRH10_10	4.5	5.1	-0.6	-1.7	100.0%	-3.4
3282	AT3G20330.1   aspartate carbamoyltransferase, chloroplast / aspartate transcarbamylase / ATCase (PYRB), identical to SP:P49077 Aspartate carbamoyltransferase, chloroplast precursor (EC 2.1.3.2) (Aspartate transcarbamylase) (ATCase) {Arabidopsis thaliana}	7.9	9.0	-1.1	-1.7	100.0%	-3.3
3283	AT4G23750.2   encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	3.4	3.9	-0.5	-1.7	100.0%	-3.6
3284	AT3G11964.1   S1 RNA-binding domain-containing protein, similar to SP:Q05022 rRNA biogenesis protein RRP5 {Saccharomyces cerevisiae}; contains Pfam profile PF00575: S1 RNA binding domain   chr3:3793963-3806632 REVERSE   Aliases: MEC18.13	5.7	6.6	-0.9	-1.7	100.0%	-3.2
3285	AT5G24930.1   zinc finger (B-box type) family protein, similar to CONSTANS-like protein 1 GI:4091804 from (Malus x domestica)   chr5:8589237-8591239 FORWARD   Aliases: F6A4.140, F6A4_140	8.5	8.0	0.5	1.7	100.0%	-3.7
3286	AT4G27180.1   Symbol: ATK2   kinesin-like protein B (KATB)   chr4:13614866-13619162 REVERSE   Aliases: ARABIDOPSIS THALIANA KINESIN 2, KATB, KINESIN LIKE PROTEIN B, T24A18.130, T24A18_130	5.5	6.3	-0.8	-1.7	100.0%	-3.5
3287	AT5G25890.1   Symbol: IAA28   auxin-responsive protein / indoleacetic acid-induced protein 28 (IAA28), identical to SP:Q9XFM0:AXIS_ARATH Auxin-responsive protein IAA28 (Indoleacetic acid-induced protein 28) {Arabidopsis thaliana}	6.0	5.4	0.6	1.7	100.0%	-3.4
3288	AT1G53160.2   Symbol: SPL4   squamosa promoter-binding protein-like 4 (SPL4), nearly identical to squamosa promoter binding protein-like 4 (Arabidopsis thaliana) GI:5931657; contains Pfam profile PF03110: SBP domain   chr1:19810087-19811276 FORWARD   Aliases: F8L10.12, F8L10_12, SQUAMOSA PROMOTER BINDING PROTEIN LIKE 4	3.5	3.2	0.2	1.7	100.0%	-4.1
3289	AT4G28390.1   Symbol: AAC3   ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative, similar to mitochondrial ADP,ATP carrier protein SP:P12857 from (Zea mays)   chr4:14040745-14043251 REVERSE   Aliases: ADP/ATP CARRIER 3, ATAAC3, F20O9.60, F20O9_60	7.4	6.6	0.8	1.7	100.0%	-3.2
3290	AT5G06820.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:2112995-2116664 FORWARD   Aliases: MPH15.19, MPH15_19	3.0	2.8	0.3	1.7	100.0%	-4.0
3291	AT1G75180.3   expressed protein   chr1:28219134-28222046 REVERSE   Aliases: F22H5.9, F22H5_9	5.0	4.6	0.4	1.7	100.0%	-3.9
3292	AT5G61590.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr5:24781664-24782550 REVERSE   Aliases: K11J9.4, K11J9_4	6.6	5.7	0.9	1.7	100.0%	-3.5
3293	AT3G13030.2   similar to hAT dimerisation domain-containing protein [Arabidopsis thaliana] (TAIR:At3g13020.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910050.1); contains InterPro domain HAT dimerisation (InterPro:IPR008906); contains InterPro domain Protein of unknown function DUF659 (InterPro:IPR007021)   chr3:4169548-4171785 REVERSE   Aliases: MGH6.16	4.1	4.5	-0.4	-1.7	100.0%	-3.7
3294	AT5G27380.1   Symbol: GSH2   glutathione synthetase (GSH2), non-consensus AT donor splice site at exon 6, AC acceptor splice site at exon 7; identical to Swiss-Prot:P46416 glutathione synthetase, chloroplast precursor (Glutathione synthase) (GSH synthetase) (GSH-S) (Arabidopsis thaliana)   chr5:9668039-9670858 REVERSE   Aliases: F21A20.90, F21A20_90, GLUTATHIONE SYNTHETASE, GSHB	10.1	10.4	-0.3	-1.7	100.0%	-4.1
3295	AT2G40010.1   60S acidic ribosomal protein P0 (RPP0A)   chr2:16715457-16717526 REVERSE   Aliases: T28M21.17, T28M21_17	7.3	5.8	1.5	1.7	100.0%	-3.2
3296	AT2G43535.1   Encodes a defensin-like (DEFL) family protein.   chr2:18078050-18078739 FORWARD   Aliases: None	3.7	4.7	-1.1	-1.7	100.0%	-3.3
3297	AT1G24260.2   Symbol: SEP3   MADS-box protein (AGL9), strongly similar to GB:O22456, MADS-box protein, Location of EST gb:H37053   chr1:8593631-8595857 REVERSE   Aliases: AGAMOUS LIKE 9, AGL9, F3I6.19, F3I6_19, SEPALLATA3, TRANSCRIPTION FACTOR AGL9	2.3	2.2	0.1	1.7	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3298	AT5G20850.1   Symbol: ATRAD51   DNA repair protein RAD51, putative, identical to Rad51-like protein (Arabidopsis thaliana) GI:2388778; strong similarity to SP:Q06609 DNA repair protein RAD51 homolog 1 {Homo sapiens}; contains Pfam profile PF00633: Helix-hairpin-helix motif   chr5:7070588-7072953 REVERSE   Aliases: F22D1.20, F22D1_20, RAD51	3.6	4.0	-0.4	-1.7	100.0%	-3.9
3299	AT1G03620.1   phagocytosis and cell motility protein ELMO1-related, contains weak similarity to ELMO1 (Mus musculus) gi:16118551:gb:AAL14464   chr1:904318-906012 REVERSE   Aliases: F21B7.23	3.7	3.1	0.5	1.7	100.0%	-3.5
3300	AT3G62380.1   expressed protein, weak similarity to S locus F-box (SLF)-S2 protein (Antirrhinum hispanicum) GI:13161526   chr3:23094584-23095827 REVERSE   Aliases: T12C14.80	2.8	2.6	0.2	1.7	100.0%	-4.1
3301	AT5G20430.1   mob1/phocein family protein, contains Pfam profile: PF03637 mob1/phocein family   chr5:6904707-6905393 FORWARD   Aliases: F7C8.20, F7C8_20	3.0	2.6	0.4	1.7	100.0%	-3.8
3302	AT5G20440.1   similar to mob1/phocein family protein [Arabidopsis thaliana] (TAIR:At5g45550.1); similar to putative Mob1-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_463026.1); similar to putative Mob1/phocein family protein [Oryza sativa (japonica cultivar-group)] (GB:AAT76373.1); contains InterPro domain Mob1/phocein family (InterPro:IPR005301)   chr5:6908668-6909998 FORWARD   Aliases: F7C8.30, F7C8_30	3.0	2.6	0.4	1.7	100.0%	-3.8
3303	AT1G45000.1   26S proteasome regulatory complex subunit p42D, putative, similar to 26S proteasome regulatory complex subunit p42D (Drosophila melanogaster) gi:6434958:gb:AAF08391   chr1:17011584-17014326 FORWARD   Aliases: F27F5.8, F27F5_8	10.1	10.6	-0.5	-1.7	100.0%	-3.7
3304	AT1G78370.1   Symbol: ATGSTU20   glutathione S-transferase, putative, similar to 2,4-D inducible glutathione S-transferase GI:2920666 from (Glycine max)   chr1:29489165-29490183 REVERSE   Aliases: F3F9.23, F3F9_23	3.3	3.8	-0.5	-1.7	100.0%	-3.5
3305	AT1G75100.1   expressed protein, low similarity to SP:O14976 Cyclin G-associated kinase (EC 2.7.1.-) {Homo sapiens}   chr1:28194604-28197461 REVERSE   Aliases: F9E10.5, F9E10_5	4.4	3.9	0.5	1.7	100.0%	-3.5
3306	AT3G11150.1   expressed protein   chr3:3492873-3494655 REVERSE   Aliases: F11B9.8	3.7	3.3	0.4	1.7	100.0%	-3.7
3307	AT3G60900.1   Symbol: FLA10   fasciclin-like arabinogalactan-protein (FLA10)   chr3:22510335-22512214 REVERSE   Aliases: T4C21.310	2.1	2.2	-0.2	-1.7	100.0%	-4.4
3308	AT3G62010.1   expressed protein   chr3:22975652-22982754 FORWARD   Aliases: F21F14.180	6.2	5.6	0.6	1.7	100.0%	-3.6
3309	AT2G18730.1   diacylglycerol kinase, putative, contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain   chr2:8125912-8129003 FORWARD   Aliases: MSF3.11, MSF3_11	4.8	4.4	0.4	1.7	100.0%	-3.7
3310	AT5G64580.1   AAA-type ATPase family protein, similar to zinc dependent protease (Arabidopsis thaliana) GI:7650138; contains Pfam profile PF00004: ATPase AAA family   chr5:25834318-25838691 REVERSE   Aliases: MUB3.10, MUB3_10	4.6	5.3	-0.7	-1.7	100.0%	-3.3
3311	AT3G48750.1   Symbol: CDC2A   A-type cyclin-dependent kinase. Together with its specific inhibitor, the Kip-related protein, KRP2 they regulate the mitosis-to-endocycle transition during leaf development.   chr3:18082533-18085626 FORWARD   Aliases: CDC2AAT, CDK2, CDKA;1, CELL DIVISION CONTROL 2, CYCLIN DEPENDENT KINASE A;1, P34CDC2, T21J18.20	6.7	7.7	-1.1	-1.7	100.0%	-3.2
3312	AT5G49460.1   Symbol: ACLB 2	5.4	6.3	-1.0	-1.7	100.0%	-3.5
3313	AT1G74160.1   expressed protein   chr1:27890797-27895084 FORWARD   Aliases: F9E11.1, F9E11_1	3.8	4.3	-0.5	-1.7	100.0%	-3.5
3314	AT5G54260.1   Symbol: MRE11   DNA repair and meiosis protein (Mre11), identical to DNA repair and meiosis protein (Mre11) GI:5524769 from (Arabidopsis thaliana)   chr5:22049295-22055217 FORWARD   Aliases: MDK4.8, MDK4_8	2.8	3.1	-0.3	-1.7	100.0%	-4.0
3315	AT2G45540.1   WD-40 repeat family protein / beige-related, contains Pfam PF02138: Beige/BEACH domain; contains Pfam PF00400: WD domain, G-beta repeat (3 copies)   chr2:18763579-18779303 REVERSE   Aliases: F17K2.7	4.2	4.9	-0.7	-1.7	100.0%	-3.4
3316	AT1G32760.1   glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	5.3	4.9	0.4	1.7	100.0%	-3.8
3317	AT3G13760.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	5.2	4.6	0.6	1.7	100.0%	-3.2
3318	AT3G13845.1   expressed protein   chr3:4557333-4558586 REVERSE   Aliases: None	9.6	10.2	-0.5	-1.7	100.0%	-3.8
3319	AT4G28290.1   expressed protein   chr4:14011875-14012589 REVERSE   Aliases: F26K10.170, F26K10_170	5.4	4.5	0.9	1.7	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3320	AT1G26230.1   chaperonin, putative, similar to SWISS-PROT:P08927- RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta) (Pisum sativum); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr1:9072375-9075266 REVERSE   Aliases: F28B23.11, F28B23_11	4.8	4.2	0.6	1.7	100.0%	-3.2
3321	AT5G62580.1   Symbol: VEX1   Encodes a protein that is expressed in vegetative cells of pollen.   chr5:25137089-25139752 FORWARD   Aliases: K19B1.19, K19B1_19, VEGETATIVE CELL EXPRESSED1, VEX1	5.0	5.4	-0.5	-1.7	100.0%	-3.5
3322	AT4G24630.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr4:12714929-12717121 FORWARD   Aliases: F22K18.170, F22K18_170	3.3	3.0	0.3	1.7	100.0%	-4.0
3323	AT5G50335.1   expressed protein   chr5:20506320-20506953 REVERSE   Aliases: None	2.7	2.6	0.2	1.7	100.0%	-4.5
3324	AT1G55050.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g09040.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g09050.1); similar to hypothetical protein DDB0188541 [Dictyostelium discoideum] (GB:EAL62571.1)	2.4	2.6	-0.2	-1.7	100.0%	-4.3
3325	AT2G37510.1   RNA-binding protein, putative, similar to SP:P10979 Glycine-rich RNA-binding, abscisic acid-inducible protein {Zea mays}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:15750070-15751619 REVERSE   Aliases: F3G5.30, F3G5_30	4.9	5.6	-0.6	-1.7	100.0%	-3.3
3326	AT1G09740.1   ethylene-responsive protein, putative, similar to ER6 protein (Lycopersicon esculentum) GI:5669654; contains Pfam profile PF00582: universal stress protein family   chr1:3154534-3156252 FORWARD   Aliases: F21M12.12, F21M12_12	6.9	5.6	1.3	1.7	100.0%	-3.3
3327	AT1G65220.1   eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein, low similarity to SP:P47823 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) {Oryctolagus cuniculus}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon   chr1:24229774-24232633 FORWARD   Aliases: T23K8.13, T23K8_13	8.6	8.2	0.4	1.7	100.0%	-3.9
3328	AT3G16730.1   expressed protein, ; expression supported by MPSS   chr3:5695639-5698869 REVERSE   Aliases: MGL6.20	3.5	3.9	-0.3	-1.7	100.0%	-3.8
3329	AT1G35310.1   Bet v I allergen family protein, similar to Csf-2 (Cucumis sativus)(GI:5762258)(J Am Soc Hortic Sci 124, 136-139 (1999)) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:12956137-12957048 REVERSE   Aliases: T9I1.8, T9I1_8	3.0	2.9	0.1	1.7	100.0%	-4.5
3330	AT4G01560.1   brix domain-containing protein, contains Pfam domain, PF04427: Brix domain   chr4:677054-679229 REVERSE   Aliases: F11O4.6, F11O4_6	4.6	5.3	-0.6	-1.7	100.0%	-3.7
3331	AT3G12160.1   Ras-related GTP-binding family protein, similar to ras-related GTP-binding protein RGP1 SP:P25766 from (Oryza sativa);contains Pfam profile: PF00071 Ras family   chr3:3879502-3880444 REVERSE   Aliases: T21B14.2	3.0	2.7	0.3	1.7	100.0%	-4.1
3332	AT1G74470.1   geranylgeranyl reductase, identical to geranylgeranyl reductase GB:Y14044 (Arabidopsis thaliana) (involvement: chlorophyll, the tocopherol and the phylloquinone pathways Eur J Biochem 1998 Jan 15;251(1-2):413-7)   chr1:27994826-27996667 FORWARD   Aliases: F1M20.15, F1M20_15	11.2	9.9	1.3	1.7	100.0%	-3.3
3333	AT5G01790.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g40475.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475660.1)   chr5:304894-305693 REVERSE   Aliases: T20L15.60, T20L15_60	3.7	3.3	0.4	1.7	100.0%	-3.5
3334	AT5G65670.2   Symbol: IAA9   auxin-responsive protein / indoleacetic acid-induced protein 9 (IAA9), identical to SP:Q38827 Auxin-responsive protein IAA9 (Indoleacetic acid-induced protein 9) {Arabidopsis thaliana}	6.0	6.9	-0.9	-1.7	100.0%	-3.5
3335	AT4G37740.1   Symbol: AtGRF2	3.7	4.5	-0.8	-1.7	100.0%	-3.4
3336	AT4G09140.1   Symbol: ATMLH1	3.9	4.2	-0.4	-1.7	100.0%	-3.9
3337	AT3G13640.1   Symbol: ATRLI1	4.3	3.9	0.5	1.7	100.0%	-3.7
3338	AT3G55060.1   expressed protein, contains weak similarity to intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae); expression supported by MPSS	3.5	4.0	-0.5	-1.7	100.0%	-3.8
3339	AT3G10350.1   anion-transporting ATPase family protein, similar to SP:O43681 Arsenical pump-driving ATPase (EC 3.6.3.16) (Arsenite-translocating ATPase) (Arsenical resistance ATPase) (Arsenite-transporting ATPase) (ARSA) (ASNA-I) {Homo sapiens}; contains Pfam profile PF02374: Anion-transporting ATPase; contains non-consensus GA donor splice site at intron 5   chr3:3208244-3211299 FORWARD   Aliases: F14P13.5	7.8	7.3	0.5	1.7	100.0%	-3.4
3340	AT4G31070.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:15118702-15120543 REVERSE   Aliases: F6I18.20, F6I18_20	2.9	3.0	-0.1	-1.7	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3341	AT3G23410.1   alcohol oxidase-related, similar to long chain fatty alcohol oxidase from <i>Candida cloacae</i> (GI:6983581), <i>Candida tropicalis</i> (GI:6983594)   chr3:8382818-8386155 FORWARD   Aliases: MLM24.14	6.7	5.9	0.8	1.7	100.0%	-3.4
3342	AT5G46250.2   RNA recognition motif (RRM)-containing protein, contains similarity to RNA-binding protein; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:18772535-18775505 FORWARD   Aliases: MPL12.3, MPL12_3	10.4	10.0	0.4	1.7	100.0%	-3.9
3343	AT3G60470.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr3:22355788-22357859 FORWARD   Aliases: T8B10.130	3.0	2.7	0.3	1.7	100.0%	-3.8
3344	AT2G31090.1   expressed protein   chr2:13263215-13263788 FORWARD   Aliases: T16B12.10, T16B12_10	9.9	9.4	0.5	1.7	100.0%	-3.8
3345	AT5G01450.1   expressed protein   chr5:183329-186444 REVERSE   Aliases: T1008.160, T1008_160	5.8	4.9	0.9	1.7	100.0%	-3.5
3346	AT2G27980.1   expressed protein   chr2:11920706-11926818 REVERSE   Aliases: T1E2.10, T1E2_10	3.4	3.1	0.3	1.7	100.0%	-3.8
3347	AT3G57010.1   strictosidine synthase family protein, similar to strictosidine synthase ( <i>Rauvolfia serpentina</i> )(SP:P15324)   chr3:21106633-21108430 REVERSE   Aliases: F24I3.90	9.0	9.9	-0.9	-1.7	100.0%	-3.3
3348	AT1G75800.1   pathogenesis-related thaumatin family protein, similar to receptor serine/threonine kinase PR5K ( <i>Arabidopsis thaliana</i> ) GI:1235680; contains Pfam profile: PF00314 Thaumatin family   chr1:28462443-28464515 FORWARD   Aliases: T4O12.3, T4O12_3	6.2	5.5	0.7	1.7	100.0%	-3.8
3349	AT5G12160.1   expressed protein, similar to unknown protein (pir::T09909)   chr5:3931650-3932090 FORWARD   Aliases: MXC9.12, MXC9_12	3.7	3.3	0.4	1.7	100.0%	-3.9
3350	AT2G24050.1   MIF4G domain-containing protein / MA3 domain-containing protein, similar to SP:Q03387 Eukaryotic initiation factor (iso)4F subunit P82-34 (eIF-(iso)4F P82-34) { <i>Triticum aestivum</i> }; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain   chr2:10232305-10235718 REVERSE   Aliases: T29E15.25, T29E15_25	6.5	7.0	-0.5	-1.7	100.0%	-3.7
3351	AT3G54130.1   josephin family protein, contains Pfam domain PF02099: Josephin   chr3:20053683-20055504 REVERSE   Aliases: F24B22.90	4.4	4.7	-0.3	-1.7	100.0%	-3.8
3352	AT5G16760.1   Encodes a inositol 1,3,4-trisphosphate 5/6-kinase.   chr5:5509677-5511235 FORWARD   Aliases: F5E19.100, F5E19_100, INOSITOL 1,3,4 TRISPHOSPHATE 5/6 KINASE	7.7	8.2	-0.5	-1.7	100.0%	-3.6
3353	AT3G09085.1   expressed protein   chr3:2782156-2782688 FORWARD   Aliases: None	7.8	6.9	0.9	1.7	100.0%	-3.4
3354	AT3G14200.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:O75190:DJB6_HUMAN Dnaj homolog subfamily B member 6 (Heat shock protein J2) { <i>Homo sapiens</i> }; contains Pfam profile PF00226 Dnaj domain	5.6	5.1	0.4	1.7	100.0%	-3.7
3355	AT1G70660.1   ubiquitin-conjugating enzyme family protein, similar to TRAF6-regulated IKK activator 1 beta Uev1A ( <i>Homo sapiens</i> ) GI:10880969; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr1:26644258-26645810 FORWARD   Aliases: F5A18.16, F5A18_16	7.8	8.4	-0.6	-1.7	100.0%	-3.3
3356	AT5G39900.1   similar to GTP-binding protein LepA, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g08650.1); similar to hypothetical protein LOC231279 isoform a [ <i>Mus musculus</i> ] (GB:NP_766299.1); similar to PREDICTED: similar to Hypothetical protein FLJ13220 [ <i>Canis familiaris</i> ] (GB:XP_539246.1); similar to PREDICTED: similar to expressed sequence AA407526 isoform a [ <i>Rattus norvegicus</i> ] (GB:XP_223381.3); similar to unnamed protein product [ <i>Homo sapiens</i> ] (GB:BAB14507.1); similar to Hypothetical protein FLJ13220 [ <i>Homo sapiens</i> ] (GB:AAH36768.1); contains InterPro domain GTP-binding protein LepA (InterPro:IPR006297); contains InterPro domain Small GTP-binding protein domain (InterPro:IPR005225); contains InterPro domain Elongation factor G, C-terminal (InterPro:IPR000640); contains InterPro domain Elongation factor, GTP-binding (InterPro:IPR000795)   chr5:15993775-15996229 REVERSE   Aliases: MYH19.60, MYH19_60	3.4	3.7	-0.3	-1.7	100.0%	-4.2
3357	AT4G22010.1   Symbol: SKS4   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)( <i>Brassica napus</i> ); contains Pfam profile: PF00394 Multicopper oxidase   chr4:11663336-11666727 FORWARD   Aliases: F1N20.110, F1N20_110, SKS4	2.7	3.3	-0.5	-1.7	100.0%	-3.5
3358	AT2G23120.1   expressed protein   chr2:9849123-9849714 FORWARD   Aliases: F21P24.18, F21P24_18	11.6	12.1	-0.5	-1.7	100.0%	-4.4
3359	AT3G46210.4   similar to hypothetical protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g07110.1); similar to putative exosome component [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_470449.1); contains InterPro domain 3' exoribonuclease (InterPro:IPR001247)   chr3:16987739-16989877 REVERSE   Aliases: F12M12.180	5.3	5.8	-0.6	-1.7	100.0%	-3.5
3360	AT3G47380.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:Q42534 Pectinesterase 2 precursor (EC 3.1.1.11) (Pectin methylesterase 2) (PE 2) { <i>Arabidopsis thaliana</i> }; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr3:17468780-17469555 FORWARD   Aliases: T21L8.130	3.1	3.5	-0.4	-1.7	100.0%	-3.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3361	AT3G20475.1   similar to DNA mismatch repair protein MSH3 (MSH3) [Arabidopsis thaliana] (TAIR:At4g25540.1); similar to hypothetical protein [Neurospora crassa] (GB:XP_332076.1); contains InterPro domain DNA mismatch repair protein MutS, C-terminal (InterPro:IPR000432)   chr3:7148223-7150943 FORWARD   Aliases: MQC12.27	2.4	2.6	-0.2	-1.7	100.0%	-4.1
3362	AT1G76660.1   expressed protein   chr1:28773774-28776260 REVERSE   Aliases: F28O16.3, F28O16_3	4.0	4.4	-0.4	-1.7	100.0%	-3.8
3363	AT3G56370.1   leucine-rich repeat transmembrane protein kinase, putative, leucine-rich receptor-like protein kinase - Malus domestica, EMBL:AF053127   chr3:20910078-20913960 REVERSE   Aliases: T5P19.20	3.1	3.4	-0.4	-1.7	100.0%	-3.7
3364	AT2G31970.1   Symbol: RAD50   DNA repair-recombination protein (RAD50), identical to DNA repair-recombination protein GI:7110148 from (Arabidopsis thaliana)   chr2:13607589-13616146 FORWARD   Aliases: ATRAD50, DNA REPAIR RECOMBINATION PROTEIN, F22D22.28, F22D22_28	3.4	3.8	-0.4	-1.7	100.0%	-3.8
3365	AT3G11650.1   Symbol: NHL2   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein / NDR1/HIN1-like protein 2, identical to NDR1/HIN1-Like protein 2 (GP:9502174) (Arabidopsis thaliana); similar to hin1 GB:CAA68848 (Nicotiana tabacum)   chr3:3676152-3677043 REVERSE   Aliases: T19F11.5	3.9	3.5	0.4	1.7	100.0%	-3.9
3366	AT1G07240.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:2223690-2225447 FORWARD   Aliases: F10K1.5, F10K1_5	5.6	5.1	0.5	1.7	100.0%	-3.4
3367	AT1G69930.1   Symbol: ATGSTU11   glutathione S-transferase, putative, similar to glutathione transferase GB:CAA09188 (Alopecurus myosuroides)	5.9	6.9	-1.0	-1.7	100.0%	-3.0
3368	AT5G47830.2   expressed protein   chr5:19390124-19391557 REVERSE   Aliases: MCA23.17, MCA23_17	6.0	5.6	0.5	1.7	100.0%	-3.5
3369	AT3G18170.1   expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)   chr3:6228348-6229668 FORWARD   Aliases: MRC8.17	5.2	4.0	1.1	1.7	100.0%	-3.1
3370	AT5G49900.1   expressed protein, contains Pfam domain PF04685: Protein of unknown function, DUF608   chr5:20314349-20319572 REVERSE   Aliases: K9P8.4, K9P8_4	7.8	8.2	-0.4	-1.7	100.0%	-3.6
3371	AT1G06490.1   Symbol: ATGSL07   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr1:1978761-1989045 FORWARD   Aliases: ATGSL7, F12K11.17, F12K11_17, GLUCAN SYNTHASE LIKE 7, GSL07	4.7	4.3	0.4	1.7	100.0%	-3.7
3372	AT5G26850.3   similar to cyclin-related [Arabidopsis thaliana] (TAIR:At2g41830.1); similar to cyclin-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477071.1); similar to cyclin-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464126.1)   chr5:9445443-9450822 FORWARD   Aliases: F2P16.24, F2P16_24	4.4	4.9	-0.5	-1.7	100.0%	-3.6
3373	AT1G26750.1   expressed protein   chr1:9246774-9248261 FORWARD   Aliases: T24P13.13, T24P13_13	7.1	7.9	-0.8	-1.7	100.0%	-3.2
3374	AT1G26790.1   Dof-type zinc finger domain-containing protein, similar to H-protein promoter binding factor-2b GI:3386548 from (Arabidopsis thaliana)   chr1:9273844-9275299 REVERSE   Aliases: T24P13.17, T24P13_17	2.9	2.6	0.3	1.7	100.0%	-3.9
3375	AT3G58120.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor ;supported by cDNA gi:15100054:gb:AF401300.1:AF401300	3.1	2.8	0.3	1.7	100.0%	-3.9
3376	AT5G17410.2   tubulin family protein, similar to spindle pole body protein (Homo sapiens)(GI:2801701)(PMID:9566967), gamma-tubulin ring protein Dgrip84 (Drosophila melanogaster)(GI:4689225)(PMID: 10037793)   chr5:5730612-5737366 FORWARD   Aliases: T10B6.70, T10B6_70	3.2	3.6	-0.4	-1.7	100.0%	-3.8
3377	AT5G40500.1   expressed protein   chr5:16245062-16245839 FORWARD   Aliases: MNF13.2, MNF13_2	4.7	4.2	0.5	1.7	100.0%	-3.4
3378	AT3G18750.2   Symbol: WNK6   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g49160.2); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g49160.1); similar to putative MAP kinase [Oryza sativa (japonica cultivar-group)] (GB:BAD27820.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:6454116-6457503 REVERSE   Aliases: MVE11.20, ZIK5	3.6	4.4	-0.7	-1.7	100.0%	-3.4
3379	AT5G61560.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:24770094-24773944 FORWARD   Aliases: K11J9.9, K11J9_9	4.6	5.1	-0.5	-1.7	100.0%	-3.5
3380	AT3G27080.1   Symbol: TOM20 3   mitochondrial import receptor subunit TOM20-3 / translocase of outer membrane 20 kDa subunit 3 (TOM20-3), identical to mitochondrial import receptor subunit TOM20-3 SP:P82874 from (Arabidopsis thaliana)   chr3:9986319-9987866 REVERSE   Aliases: MOJ10.22, TRANSLOCASE OUTER MEMBRANE 20 3	9.0	9.6	-0.6	-1.7	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3381	AT5G01220.1   Symbol: SQD2   UDP-sulfoquinovose:DAG sulfoquinovosyltransferase / sulfolipid synthase (SQD2), identical to GI:20302857	3.9	3.6	0.3	1.7	100.0%	-3.9
3382	AT3G04820.1   expressed protein, contains Pfam profile PF01142: Uncharacterized protein family UPF0024; expression supported by MPSS   chr3:1321537-1325955 REVERSE   Aliases: T9J14.23, T9J14_23	3.4	3.8	-0.4	-1.7	100.0%	-3.8
3383	AT4G36830.1   GNS1/SUR4 membrane family protein, weak similarity to long chain polyunsaturated fatty acid elongation enzyme (Isochrysis galbana) GI:17226123; contains Pfam profile PF01151: GNS1/SUR4 family   chr4:17349488-17350384 FORWARD   Aliases: AP22.81, AP22_81	4.5	3.7	0.8	1.7	100.0%	-3.3
3384	AT5G62490.1   Symbol: ATHVA22B   ABA-responsive protein (HVA22b), identical to AtHVA22b (Arabidopsis thaliana) GI:4884934   chr5:25107356-25108781 FORWARD   Aliases: ATHVA22B, K19B1.10, K19B1_10	4.1	3.7	0.4	1.7	100.0%	-3.7
3385	AT2G43660.2   glycosyl hydrolase family protein 17, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum); C terminal homology only	6.5	7.4	-0.9	-1.7	100.0%	-3.2
3386	AT1G59700.1   Symbol: ATGSTU16   glutathione S-transferase, putative, similar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum)   chr1:21940094-21941624 FORWARD   Aliases: F23H11.1, F23H11_1	4.0	3.5	0.5	1.7	100.0%	-3.7
3387	AT5G47790.1   forkhead-associated domain-containing protein / FHA domain-containing protein   chr5:19368531-19370670 FORWARD   Aliases: MCA23.11, MCA23_11	5.1	4.8	0.4	1.7	100.0%	-3.8
3388	AT1G71990.1   Symbol: FUT13   alpha-(1,4)-fucosyltransferase / galactoside 3(4)-L-fucosyltransferase (FUT13) (FucTC), identical to SP:Q9C8W3 Alpha-(1,4)-fucosyltransferase (EC 2.4.1.-) (FT4-M) (Galactoside 3(4)- L-fucosyltransferase) (FucTC) (AtFUT13) {Arabidopsis thaliana}; identical to cDNA alpha1,3-fucosyltransferase homologue (FucTC) GI:13992485   chr1:27103946-27105924 FORWARD   Aliases: ATFUT13, F17M19.14, F17M19_14, FT4 M, FUCTC	5.7	5.0	0.6	1.7	100.0%	-3.4
3389	AT5G63980.1   Symbol: SAL1   3'(2'),5'-bisphosphate nucleotidase / inositol polyphosphate 1-phosphatase / FIERY1 protein (FRY1) (SAL1), identical to SP:Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (3'(2'),5- bisphosphonucleoside 3'(2')-phosphohydrolase) (DPNPase) {Arabidopsis thaliana}; identical to cDNA inositol polyphosphate 1-phosphatase FIERY1 (FRY1) GI:15281147   chr5:25627089-25629157 FORWARD   Aliases: ATSAL1, FIERY 1, FRY1, HIGH EXPRESSION OF OSMOTICALLY RESPONSIVE GENES, HOS2, MBM17.8, MBM17_8	6.3	7.2	-0.9	-1.7	100.0%	-3.6
3390	AT1G69530.3   Symbol: ATEXPA1   expansin, putative (EXP1), identical to expansin (At-EXP1) (Arabidopsis thaliana) GI:1041702; alpha-expansin gene family, PMID:11641069   chr1:26145499-26147159 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A1, AT EXP1, ATEXP1, ATHEXP ALPHA 1.2, EXP1, F10D13.18, F10D13_18	8.9	6.9	2.0	1.7	100.0%	-3.1
3391	AT4G39170.1   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus) and phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus   chr4:18240667-18243772 FORWARD   Aliases: T22F8.70, T22F8_70	6.6	7.5	-0.9	-1.7	100.0%	-3.5
3392	AT3G04600.2   tRNA synthetase class I (W and Y) family protein, contains Pfam profile: PF00579 tRNA synthetases class I (W and Y)   chr3:1242993-1246184 FORWARD   Aliases: F7O18.7, F7O18_7	5.6	6.1	-0.5	-1.7	100.0%	-3.5
3393	AT1G17280.1   ubiquitin-conjugating enzyme, putative, similar to ubiquitin conjugating enzyme 6 from (Homo sapiens) GI:14029267, (Mus musculus) GI:14029263; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr1:5916864-5920051 REVERSE   Aliases: F20D23.1, F20D23_1	5.8	4.5	1.3	1.7	100.0%	-3.3
3394	AT5G50430.3   similar to ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] (TAIR:At1g17280.1); similar to probable ubiquitin-conjugating enzyme E2 [Picea mariana] (GB:AAC32141.1); contains InterPro domain Ubiquitin-conjugating enzymes (InterPro:IPR000608)   chr5:20551399-20554343 REVERSE   Aliases: MXI22.15, MXI22_15	5.8	4.5	1.3	1.7	100.0%	-3.3
3395	AT1G29340.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:10264381-10266804 FORWARD   Aliases: F15D2.34, F15D2_34	7.1	6.6	0.5	1.7	100.0%	-3.6
3396	AT3G21540.1   transducin family protein / WD-40 repeat family protein, contains Pfam profile: PF00400 WD domain, G-beta repeat (10 copies); similar to WD-repeat protein 3 (SP:Q9UNX4) (Homo sapiens)   chr3:7585952-7590862 REVERSE   Aliases: MIL23.11	5.0	5.7	-0.7	-1.7	100.0%	-3.4
3397	AT4G26530.2   similar to fructose-bisphosphate aldolase, cytoplasmic [Arabidopsis thaliana] (TAIR:At4g26520.1); similar to fructose-bisphosphate aldolase [Glycine max] (GB:AAR86689.1); similar to fructose 1,6, bisphosphate aldolase [Salicornia herbacea] (GB:AAR84667.1); contains InterPro domain Fructose-bisphosphate aldolase, class-I (InterPro:IPR000741)   chr4:13391351-13393126 FORWARD   Aliases: M3E9.40, M3E9_40	2.3	2.1	0.1	1.7	100.0%	-4.5
3398	AT3G08710.1   thioredoxin family protein, similar to thioredoxin H-type GB:P29448 SP:P29448 (Arabidopsis thaliana), Thioredoxin H-type 2 (TRX-H2) SP:Q07090 {Nicotiana tabacum}; contains Pfam profile: PF00085 Thioredoxin   chr3:2645223-2646496 FORWARD   Aliases: F17O14.18	10.4	9.7	0.7	1.7	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3399	AT1G14345.1   expressed protein, contains one transmembrane domain   chr1:4899141-4899974 FORWARD   Aliases: None	4.2	3.9	0.4	1.7	100.0%	-3.8
3400	AT1G30400.2   Symbol: ATMRP1	5.6	6.3	-0.7	-1.7	100.0%	-3.4
3401	AT2G35710.3   glycogenin glucosyltransferase (glycogenin)-related, low similarity to glycogenin-2 from Homo sapiens (SP:O15488)   chr2:15020656-15021226 REVERSE   Aliases: T20F21.27	4.1	3.8	0.3	1.7	100.0%	-4.1
3402	AT2G47200.1   expressed protein   chr2:19384799-19385401 REVERSE   Aliases: T8I13.4	2.8	3.6	-0.8	-1.7	100.0%	-3.2
3403	AT2G29700.1   Symbol: ATPH1   pleckstrin homology (PH) domain-containing protein (PH1), identical to AtPH1 (Arabidopsis thaliana) GI:5926716; contains Pfam profile PF00169: PH domain   chr2:12704497-12705244 FORWARD   Aliases: ARABIDOPSIS THALIANA PLECKSTRIN HOMOLOGUE 1, T27A16.20, T27A16_20	10.6	9.7	1.0	1.7	100.0%	-3.9
3404	AT2G23380.1   Symbol: CLF   curly leaf protein (CURLY LEAF) / polycomb-group protein, identical to polycomb group (Arabidopsis thaliana) GI:1903019 (curly leaf); contains Pfam profile PF00856: SET domain   chr2:9962650-9967197 FORWARD   Aliases: CLF, CURLY LEAF, F26B6.3, F26B6_3, ICU1, INCURVATA 1	4.7	5.3	-0.5	-1.7	100.0%	-3.6
3405	AT1G30820.1   CTP synthase, putative / UTP--ammonia ligase, putative, similar to SP:P17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) {Homo sapiens}; contains Pfam profile PF00117: glutamine amidotransferase class-I; similar to ESTs gb:AA660762, gb:AA220982, dbj:AU008137, gb:AI054783, and gb:AA100804   chr1:10944894-10949431 REVERSE   Aliases: T17H7.12, T17H7_12	6.5	5.6	0.9	1.7	100.0%	-3.4
3406	AT4G09340.1   SP1a/Ryanodine receptor (SPRY) domain-containing protein, low similarity to RanBPM (Homo sapiens) GI:15080674; contains Pfam profile PF00622: SPRY domain   chr4:5924599-5927632 REVERSE   Aliases: AT4G09330, T30A10.100, T30A10_100	6.0	7.0	-0.9	-1.7	100.0%	-3.5
3407	AT3G55830.1   Symbol: EPC1   glycosyltransferase family protein 47, similar to exostose-related protein 2, Homo sapiens, PIR:JC5935 (SP:Q93063), EXTL2, Mus musculus (GI:10443633)   chr3:20726080-20729017 FORWARD   Aliases: ECTOPICALLY PARTING CELLS, F27K19.10	7.6	7.0	0.6	1.7	100.0%	-3.3
3408	AT5G07390.1   Symbol: ATRBOHA   respiratory burst oxidase protein A (RbohA) / NADPH oxidase, identical to respiratory burst oxidase protein A from Arabidopsis thaliana (gi:3242781)   chr5:2335896-2339914 REVERSE   Aliases: ATRBOHA, RESPIRATORY BURST OXIDASE HOMOLOG A, T2I1.100, T2I1_100	3.4	4.4	-1.0	-1.7	100.0%	-3.2
3409	AT3G16770.1   Symbol: ATEBP/RAP2.3   Encodes a member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family (RAP2.3). The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12.   chr3:5705721-5707029 FORWARD   Aliases: ATEBP, MGL6.1, RAP2.3, RELATED TO AP2 3	11.4	10.5	0.8	1.7	100.0%	-3.8
3410	AT2G47010.2   expressed protein   chr2:19324195-19326467 FORWARD   Aliases: F14M4.16	3.1	3.3	-0.2	-1.7	100.0%	-4.3
3411	AT5G47220.1   Symbol: ATERF 2/ATERF2/ERF2   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ATERF-2). The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5. Functions as activator of GCC box??dependent transcription.   chr5:19189089-19190050 REVERSE   Aliases: ATERF 2, ATERF2, ERF2, ETHYLENE RESPONSE FACTOR 2, ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 2, MQL5.7, MQL5_7	4.2	3.8	0.4	1.7	100.0%	-3.6
3412	AT1G21590.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:7566221-7569890 REVERSE   Aliases: F24J8.18, F24J8_18	3.5	4.0	-0.5	-1.7	100.0%	-3.7
3413	AT2G40290.3   similar to eukaryotic translation initiation factor 2 subunit 1, putative / eIF-2A, putative / eIF-2-alpha, putative [Arabidopsis thaliana] (TAIR:At5g05470.1); similar to hypothetical protein [Neurospora crassa] (GB:XP_328983.1); contains InterPro domain RNA binding S1 (InterPro:IPR003029)   chr2:16835844-16838132 REVERSE   Aliases: T7M7.14	7.1	8.1	-1.1	-1.7	100.0%	-3.3
3414	AT5G18830.2   Symbol: SPL7   squamosa promoter-binding protein-like 7 (SPL7), identical to squamosa promoter binding protein-like 7 (Arabidopsis thaliana) GI:5931635; contains Pfam profile PF03110: SBP domain   chr5:6276024-6280683 FORWARD   Aliases: F17K4.80, F17K4_80, SQUAMOSA PROMOTER BINDING PROTEIN LIKE 7	3.9	4.5	-0.6	-1.7	100.0%	-3.5
3415	AT5G20740.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Arabidopsis thaliana SP:Q42534, Lycopersicon esculentum SP:Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:7025688-7026534 REVERSE   Aliases: T1M15.140, T1M15_140	5.2	6.4	-1.2	-1.7	100.0%	-3.0
3416	AT1G23480.3   Symbol: ATCSLA03   similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At5g03760.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At1g24070.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At4g13410.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At3g56000.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At5g16190.1); similar to glycosyltransferase 10 [Ipomoea trifida] (GB:AAQ62572.1); similar to glycosyltransferase 5 [Ipomoea trifida] (GB:AAQ62571.1); similar to glycosyltransferase 1 [Ipomoea trifida] (GB:AAQ62570.1); similar to TPA: cellulose synthase-like A1 [Oryza sativa (japonica cultivar-group)] (GB:DAA01743.1); contains InterPro domain Glycosyl transferase, family 2 (InterPro:IPR001173)   chr1:8333685-8336374 FORWARD   Aliases: ATCSLA3, CSLA03, F28C11.11	3.0	3.6	-0.6	-1.7	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3417	AT1G12990.1   glycosyl transferase family 17 protein, low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from <i>Mus musculus</i> (SP:Q10470), <i>Rattus norvegicus</i> (SP:Q02527), <i>Homo sapiens</i> (SP:Q09327); contains Pfam profile PF04724 :Glycosyltransferase family 17   chr1:4433638-4436068 FORWARD   Aliases: F3F19.2, F3F19_2	3.2	2.9	0.3	1.7	100.0%	-3.9
3418	AT3G09850.1   D111/G-patch domain-containing protein, contains Pfam profile PF01585: G-patch domain   chr3:3023216-3025856 REVERSE   Aliases: F8A24.10	8.1	8.4	-0.4	-1.7	100.0%	-3.6
3419	AT1G22290.1   14-3-3 protein GF14, putative (GRF10), similar to 14-3-3 protein GF14 epsilon GI:5802798 from ( <i>Arabidopsis thaliana</i> )   chr1:7876955-7877904 REVERSE   Aliases: T16E15.9, T16E15_9	2.2	2.4	-0.2	-1.7	100.0%	-4.4
3420	AT3G50080.1   Symbol: VFB2   F-box family protein (FBL16), contains similarity to SKP1 interacting partner 2 GI:10716949 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile: PF00646 F-box domain   chr3:18583719-18585497 FORWARD   Aliases: F3A4.160, VFB2, VIER F BOX PROTEINE 2	6.7	6.1	0.6	1.7	100.0%	-3.4
3421	AT4G12890.1   gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein, similar to SP:P13284 Gamma-interferon inducible lysosomal thiol reductase precursor { <i>Homo sapiens</i> }; contains Pfam profile PF03227: Gamma interferon inducible lysosomal thiol reductase (GILT)   chr4:7546375-7547569 FORWARD   Aliases: T20K18.240, T20K18_240	3.1	2.8	0.3	1.7	100.0%	-4.0
3422	AT2G16600.1   Symbol: ROC3   peptidyl-prolyl cis-trans isomerase, cytosolic / cyclophilin / rotamase (ROC3), identical to cytosolic cyclophilin ( <i>Arabidopsis thaliana</i> ) GI:1305455   chr2:7207889-7208650 FORWARD   Aliases: CYCLOPHILIN, T24I21.1, T24I21_1	8.3	9.9	-1.6	-1.7	100.0%	-3.2
3423	AT2G29360.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from ( <i>Datura stramonium</i> )   chr2:12610902-12612312 FORWARD   Aliases: F16P2.26, F16P2_26	3.6	3.2	0.4	1.7	100.0%	-3.8
3424	AT3G05560.2   60S ribosomal protein L22-2 (RPL22B), identical to 60S ribosomal protein L22-2 SP:Q9M9W1 from ( <i>Arabidopsis thaliana</i> )   chr3:1614221-1615449 FORWARD   Aliases: F18C1.17, F18C1_17	12.2	12.6	-0.4	-1.7	100.0%	-4.2
3425	AT2G27510.1   ferredoxin, putative, similar to non-photosynthetic ferredoxin from <i>Citrus sinensis</i> (GI:1360725), Ferredoxin, root R-B2 from <i>Raphanus sativus</i> (SP:P14937); contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain   chr2:11765157-11766554 REVERSE   Aliases: F10A12.19, F10A12_19	11.8	11.4	0.5	1.7	100.0%	-3.8
3426	AT4G28950.1   Symbol: ARAC7   Rac-like GTP-binding protein (ARAC7), identical to rac GTP binding protein Arac7 GI:3702962 from ( <i>Arabidopsis thaliana</i> )	3.4	3.8	-0.3	-1.7	100.0%	-4.0
3427	AT5G37730.1   expressed protein   chr5:15003263-15004147 REVERSE   Aliases: K12B20.20, K12B20_20	2.3	2.1	0.2	1.7	100.0%	-4.7
3428	AT5G55190.1   Symbol: RAN3   Ras-related GTP-binding protein (RAN3), identical to atran3 ( <i>Arabidopsis thaliana</i> ) GI:2058280   chr5:22409402-22411392 FORWARD   Aliases: MCO15.14, MCO15_14	10.9	11.3	-0.4	-1.7	100.0%	-3.8
3429	AT2G02800.2   Symbol: APK2B   protein kinase (APK2b), identical to protein kinase APK2b ( <i>Arabidopsis thaliana</i> ) gi:2852449:dbj:BAA24695   chr2:795514-799441 REVERSE   Aliases: PROTEIN KINASE 2B, T20F6.6, T20F6_6	9.0	8.2	0.9	1.7	100.0%	-3.5
3430	AT5G63290.1   coproporphyrinogen oxidase-related, low similarity to coproporphyrinogen III oxidase from <i>Geobacillus stearothermophilus</i> (GI:2104798); contains Pfam profile PF04055: radical SAM domain protein	4.2	4.7	-0.5	-1.7	100.0%	-3.4
3431	AT1G61370.1   S-locus lectin protein kinase family protein, contains Pfam domains, PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain, and PF01453: Lectin (probable mannose binding)   chr1:22645761-22648812 REVERSE   Aliases: T1F9.14, T1F9_14	5.9	5.3	0.5	1.7	100.0%	-3.5
3432	AT5G38140.1   histone-like transcription factor (CBF/NF-Y) family protein, similar to CCAAT-binding transcription factor subunit AAB-1 (GI:2583171) ( <i>Neurospora crassa</i> ); contains a CBF/NF-Y subunit signature (PDOC00578) present in members of histone-like transcription factor family; contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone	3.6	4.1	-0.5	-1.7	100.0%	-3.5
3433	AT5G57360.1   Symbol: ZTL   F-box family protein / LOV kelch protein 1 (LKP1), E3 ubiquitin ligase SCF complex F-box subunit; identical to clock-associated PAS protein ZTL; ZEITLUPE GI:7839456, LOV kelch protein 1 GI:11610573, Adagio 1 GI:13487068 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF01344: Kelch motif; identical to cDNA Adagio 1 (ADO1) GI:13487067; identical to cDNA LKP1 mRNA for LOV kelch protein 1, GI:11610572   chr5:23258653-23261777 FORWARD   Aliases: ADO1, FKF1 LIKE PROTEIN 2, FKL2, LKP1, LOV KELCH PROTEIN 1, MSF19.2, MSF19_2, ZEITLUPE, ZTL	4.1	3.7	0.4	1.7	100.0%	-3.9
3434	AT1G70950.1   expressed protein   chr1:26756351-26759011 FORWARD   Aliases: F15H11.15, F15H11_15	3.8	4.1	-0.3	-1.7	100.0%	-4.0
3435	AT2G24390.1   similar to avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g31310.1); similar to avrRpt2-induced protein 2-like [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_464100.1)   chr2:10380811-10382032 FORWARD   Aliases: T28I24.12, T28I24_12	3.7	3.4	0.3	1.7	100.0%	-3.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3436	AT5G16715.1   Symbol: EMB2247   tRNA synthetase class I (I, L, M and V) family protein, similar to SP:P11931 Valyl-tRNA synthetase (EC 6.1.1.9) (Valine--tRNA ligase) (VALRS) {Bacillus stearothermophilus}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)   chr5:5485356-5493407 FORWARD   Aliases: EMB2247, EMBRYO DEFECTIVE 2247	4.7	5.3	-0.6	-1.7	100.0%	-3.4
3437	AT5G20790.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:7039913-7040656 REVERSE   Aliases: T1M15.190, T1M15_190	4.6	3.9	0.7	1.7	100.0%	-3.3
3438	AT1G09510.1   similar to Eucalyptus gunnii alcohol dehydrogenase of unknown physiological function (GI:1143445), Vigna unguiculata (gi:1854445), NOT a cinnamyl-alcohol dehydrogenase   chr1:3069387-3072052 FORWARD   Aliases: F14J9.17, F14J9_17	2.5	2.7	-0.2	-1.7	100.0%	-4.2
3439	AT4G30830.1   expressed protein, weak similarity to M protein type 1 (Streptococcus pyogenes) GI:311758; contains Pfam profile PF04576: Protein of unknown function, DUF593   chr4:15015276-15016983 REVERSE   Aliases: F6I18.260, F6I18_260	4.4	3.8	0.6	1.7	100.0%	-3.7
3440	AT1G76790.1   O-methyltransferase family 2 protein, similar to caffeic acid O-methyltransferase (Catharanthus roseus)(GI:18025321), catechol O-methyltransferase GB:CAA55358 (Vanilla planifolia)   chr1:28827080-28828567 REVERSE   Aliases: F28O16.16, F28O16_16	9.8	9.0	0.8	1.7	100.0%	-3.7
3441	AT1G55450.1   embryo-abundant protein-related, similar to embryo-abundant protein GI:1350531 from (Picea glauca)   chr1:20708593-20710556 REVERSE   Aliases: T5A14.14, T5A14_14	5.2	5.8	-0.6	-1.7	100.0%	-3.6
3442	AT3G51240.1   Symbol: F3H   naringenin 3-dioxygenase / flavanone 3-hydroxylase (F3H), identical to GI:3790548	7.6	8.4	-0.8	-1.7	100.0%	-3.7
3443	AT1G59650.1   Symbol: CW14   expressed protein, ; supporting cDNA gi:6520232:dbj:AB028233.1:   chr1:21923410-21926588 FORWARD   Aliases: CW14, T30E16.22, T30E16_22	7.2	7.6	-0.4	-1.7	100.0%	-3.7
3444	AT2G36480.1   zinc finger (C2H2-type) family protein, weak similarity to S-locus protein 4 (GI:6069478) (Brassica rapa); weak similarity to Pre-mRNA cleavage complex II protein Pcf11 (Fragment) (Swiss-Prot:O94913) (Homo sapiens); contains Prosite PS00028: Zinc finger, C2H2 type, domain	5.6	5.9	-0.4	-1.7	100.0%	-3.8
3445	AT3G05320.1   expressed protein   chr3:1513456-1514688 REVERSE   Aliases: T12H1.29, T12H1_29	5.5	4.6	0.9	1.7	100.0%	-3.5
3446	AT4G34120.1   CBS domain-containing protein, contains Pfam profile PF00571: CBS domain	8.0	7.3	0.7	1.7	100.0%	-3.4
3447	AT3G12530.2   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAD38294.1); contains InterPro domain Protein of unknown function DUF392 (InterPro:IPR007257)	3.3	3.7	-0.4	-1.7	100.0%	-3.7
3448	AT2G36330.1   integral membrane protein, putative, contains 4 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)   chr2:15239349-15242377 FORWARD   Aliases: F2H17.6, F2H17_6	6.1	5.5	0.7	1.7	100.0%	-3.6
3449	AT1G11100.1   SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related, similar to RUSH-1alpha (Oryctolagus cuniculus) GI:1655930; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr1:3703358-3709302 REVERSE   Aliases: T19D16.2, T19D16_2	4.7	5.2	-0.5	-1.7	100.0%	-3.6
3450	AT1G07570.2   Symbol: APK1A   protein kinase (APK1a), identical to Protein kinase APK1A from (Arabidopsis thaliana) SWISS-PROT:Q06548	4.9	4.5	0.5	1.7	100.0%	-3.5
3451	AT4G38270.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr4:17938366-17941547 FORWARD   Aliases: F22I13.40, F22I13_40	6.4	6.9	-0.5	-1.7	100.0%	-3.6
3452	AT2G01250.1   60S ribosomal protein L7 (RPL7B)	11.5	11.9	-0.5	-1.7	100.0%	-4.1
3453	AT1G67110.1   Symbol: CYP735A2   cytochrome P450, putative, similar to Cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus);   chr1:25065394-25069080 REVERSE   Aliases: F5A8.3, F5A8_3	6.5	7.2	-0.7	-1.7	100.0%	-3.4
3454	AT2G37920.1   Symbol: EMB1513   expressed protein   chr2:15876187-15877149 REVERSE   Aliases: EMB1513, EMBRYO DEFECTIVE 1513, T8P21.17, T8P21_17	5.1	4.6	0.4	1.7	100.0%	-3.8
3455	AT1G05910.1   cell division cycle protein 48-related / CDC48-related, similar to SP:P54609 Cell division cycle protein 48 homolog {Arabidopsis thaliana}; contains Pfam profiles PF00004: ATPase AAA family, PF00439: Bromodomain   chr1:1790223-1796646 FORWARD   Aliases: T20M3.19, T20M3_19	5.4	5.9	-0.5	-1.7	100.0%	-3.6
3456	AT3G14075.1   lipase class 3 family protein, low similarity to calmodulin-binding heat-shock protein CaMBP (Nicotiana tabacum) GI:1087073; contains Pfam profile PF01764: Lipase, PF03893: Lipase 3 N-terminal region   chr3:4663609-4666975 REVERSE   Aliases: None	6.8	6.3	0.5	1.7	100.0%	-3.7
3457	AT1G34380.1   5'-3' exonuclease family protein, similar to DNA polymerase type I (Rhodothermus sp. 'ITI 518') gi:4090935:gb:AAC98908 ; contains Pfam profile PF02739: 5'-3' exonuclease, N-terminal resolvase-like domain   chr1:12552633-12554298 REVERSE   Aliases: F7P12.3, F7P12_3	4.0	4.6	-0.7	-1.7	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3458	AT5G02570.1   histone H2B, putative, similar to histone H2B-2 <i>Lycopersicon esculentum</i> GI:3021483, <i>Gossypium hirsutum</i> SP:O22582, <i>Asparagus officinalis</i> GI:563329; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:576740-577138 REVERSE   Aliases: T22P11.160, T22P11_160	6.9	8.1	-1.2	-1.7	100.0%	-3.2
3459	AT4G01970.1   similar to raffinose synthase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g40390.1); similar to raffinose synthase [ <i>Cucumis sativus</i> ] (GB:AAD02832.1); similar to galactinol-raffinose galactosyltransferase [ <i>Vigna angularis</i> ] (GB:CAB64363.1); similar to putative alkaline alpha galactosidase I [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_550270.1); similar to putative raffinose synthase [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:NP_909442.1); similar to stachyose synthase [ <i>Pisum sativum</i> ] (GB:CAD55555.1); contains InterPro domain Raffinose synthase (InterPro:IPR008811)   chr4:853927-857358 REVERSE   Aliases: T7B11.23, T7B11_23	2.9	3.3	-0.4	-1.7	100.0%	-3.8
3460	AT4G10710.1   transcriptional regulator-related, similar to chromatin-specific transcription elongation factor FACT 140 kDa subunit (GI:5499741) ( <i>Homo sapiens</i> )   chr4:6601985-6606350 REVERSE   Aliases: T12H20.3, T12H20_3	7.1	7.6	-0.5	-1.7	100.0%	-3.8
3461	AT1G66830.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profiles: PF00069: Eukaryotic protein kinase domain, multiple PF00560: Leucine Rich Repeat   chr1:24934328-24936581 REVERSE   Aliases: F4N21.23, F4N21_23	3.4	3.8	-0.4	-1.7	100.0%	-3.6
3462	AT2G27830.1   expressed protein   chr2:11867295-11868552 FORWARD   Aliases: F15K20.7, F15K20_7	4.2	3.3	0.9	1.7	100.0%	-3.1
3463	AT5G28840.1   NAD-dependent epimerase/dehydratase family protein, similar to sugar epimerase BlmG from <i>Streptomyces verticillus</i> GI:9937230; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family   chr5:10862177-10864906 REVERSE   Aliases: F7P1.20, F7P1_20	8.0	9.0	-1.0	-1.7	100.0%	-3.3
3464	AT2G39750.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein ( <i>Arabidopsis thaliana</i> ) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr2:16585902-16589482 REVERSE   Aliases: T5I7.5, T5I7_5	7.8	8.1	-0.4	-1.7	100.0%	-3.6
3465	AT2G23050.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr2:9817737-9819740 FORWARD   Aliases: F21P24.11, F21P24_11	2.7	3.1	-0.4	-1.7	100.0%	-3.8
3466	AT1G04560.1   AWPM-19-like membrane family protein, contains Pfam PF05512: AWPM-19-like family; similar to late embryogenesis abundant protein, (Lea) with hydrophobic domain, high pI value (11.6); 15kD protein; putative (GI:310570) {Glycine max}   chr1:1244986-1246057 FORWARD   Aliases: T1G11.19, T1G11_19	3.4	3.1	0.4	1.7	100.0%	-3.9
3467	AT5G13330.1   encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	6.5	5.9	0.6	1.7	100.0%	-3.5
3468	AT5G43700.1   Symbol: ATAUX2 11   auxin-responsive protein / indoleacetic acid-induced protein 4 (IAA4) / auxin-induced protein (AUX2-11), identical to SP:P33077 Auxin-responsive protein IAA4 (Indoleacetic acid-induced protein 4) (Auxin-induced protein AUX2-11) { <i>Arabidopsis thaliana</i> }   chr5:17567460-17568808 FORWARD   Aliases: IAA4, MQD19.3, MQD19_3	5.1	5.3	-0.2	-1.7	100.0%	-4.2
3469	AT5G65840.1   expressed protein   chr5:26360956-26363289 REVERSE   Aliases: K14B20.1, K14B20_1	4.2	3.8	0.4	1.7	100.0%	-3.7
3470	AT1G68460.1   Symbol: ATIPT1	3.1	3.6	-0.5	-1.7	100.0%	-3.5
3471	AT2G47780.1   rubber elongation factor (REF) protein-related, similar to Small rubber particle protein (SRPP) (22 kDa rubber particle protein) (22 kDa RPP) (Latex allergen Hev b 3) (27 kDa natural rubber allergen) (Swiss-Prot:O82803) ( <i>Hevea brasiliensis</i> ); similar to Stress-related protein (Swiss-Prot:Q9SW70) ( <i>Vitis riparia</i> )   chr2:19577132-19578494 FORWARD   Aliases: F17A22.17	7.2	6.3	0.9	1.7	100.0%	-3.1
3472	AT5G35750.1   Symbol: AHK2   histidine kinase (AHK2), identical to histidine kinase AHK2 ( <i>Arabidopsis thaliana</i> ) gi:13537196:dbj:BAB40774   chr5:13928601-13933567 REVERSE   Aliases: ARABIDOPSIS HISTIDINE KINASE 2, MXH1.16, MXH1_16	4.4	3.7	0.7	1.7	100.0%	-3.3
3473	AT4G13020.3   Symbol: MHK   similar to protein kinase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g19110.1); similar to protein kinase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g19110.2); similar to putative Cdc2-related protein kinase CRK2 [ <i>Beta vulgaris</i> ] (GB:CAB90209.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:7603823-7607152 FORWARD   Aliases: F25G13.110, F25G13_110, PROTEIN KINASE	5.2	5.8	-0.6	-1.7	100.0%	-3.4
3474	AT2G32910.1   expressed protein   chr2:13966127-13969195 FORWARD   Aliases: T21L14.15, T21L14_15	6.4	7.1	-0.7	-1.7	100.0%	-3.7
3475	AT2G37080.1   myosin heavy chain-related, low similarity to myosin heavy chain ( <i>Rana catesbeiana</i> ) GI:4249701   chr2:15588486-15592265 REVERSE   Aliases: T2N18.16, T2N18_16	6.3	7.2	-0.8	-1.7	100.0%	-3.6
3476	AT5G27240.1   DNAJ heat shock N-terminal domain-containing protein   chr5:9597555-9600869 FORWARD   Aliases: T21B4.150, T21B4_150	3.1	3.3	-0.2	-1.7	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3477	AT1G61680.1   terpene synthase/cyclase family protein, similar to 1,8-cineole synthase (GI:3309117)(Salvia officinalis); contains Pfam profile: PF01397 terpene synthase family   chr1:22776120-22778352 REVERSE   Aliases: T13M11.3, T13M11_3	2.2	2.4	-0.2	-1.7	100.0%	-4.6
3478	AT3G22840.1   Symbol: ELIP1   chlorophyll A-B binding family protein / early light-induced protein (ELIP), identical to early light-induced protein; ELIP (Arabidopsis thaliana) GI:1872544; contains Pfam profile: PF00504 chlorophyll A-B binding protein; identical to cDNA early light-induced protein GI:1872543	10.1	9.0	1.1	1.7	100.0%	-3.1
3479	AT5G56710.1   60S ribosomal protein L31 (RPL31C)   chr5:22961062-22962196 REVERSE   Aliases: MIK19.16, MIK19_16	11.7	12.3	-0.6	-1.7	100.0%	-3.7
3480	AT3G22780.1   Symbol: TSO1   CXC domain protein (TSO1), identical to CXC domain protein TSO1 (Arabidopsis thaliana) GI:7767425   chr3:8048809-8052819 FORWARD   Aliases: MWI23.15	6.6	7.4	-0.8	-1.7	100.0%	-3.6
3481	AT4G11010.1   Symbol: NDPK3   nucleoside diphosphate kinase 3, mitochondrial (NDK3), identical to Nucleoside diphosphate kinase III, mitochondrial precursor (NDK III) (NDP kinase III) (NDPK III) (SP:O49203) (Arabidopsis thaliana); contains Pfam PF00334 : Nucleoside diphosphate kinase domain;	10.3	11.0	-0.7	-1.7	100.0%	-3.6
3482	AT5G09670.2   loricrin-related, contains weak similarity to Loricrin (Swiss-Prot:P23490) (Homo sapiens)   chr5:2995913-2998917 REVERSE   Aliases: F17I14.140, F17I14_140	7.9	7.5	0.5	1.7	100.0%	-3.6
3483	AT4G26260.1   Symbol: MIOX4   expressed protein, similar to myo-inositol oxygenase (Sus scrofa) gi:17432544:gb:AAL39076   chr4:13297948-13300186 FORWARD   Aliases: MYO INOSITOL OXYGENASE 4, T25K17.70, T25K17_70	8.3	7.1	1.2	1.7	100.0%	-3.0
3484	AT5G01710.1   expressed protein   chr5:263516-265613 REVERSE   Aliases: F7A7.230, F7A7_230	9.0	8.6	0.4	1.7	100.0%	-3.9
3485	AT3G62890.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At5g48910.1); similar to pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:NP_919101.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr3:23257132-23259036 FORWARD   Aliases: F26K9.320	3.5	3.9	-0.4	-1.7	100.0%	-3.7
3486	AT5G67100.1   DNA-directed DNA polymerase alpha catalytic subunit, putative, similar to SP:O48653 DNA polymerase alpha catalytic subunit (EC 2.7.7.7) {Oryza sativa}; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain   chr5:26794220-26802330 FORWARD   Aliases: K21H1.14, K21H1_14	3.1	3.4	-0.3	-1.7	100.0%	-4.1
3487	AT5G48360.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr5:19612883-19615718 FORWARD   Aliases: K23F3.8, K23F3_8	3.1	3.7	-0.6	-1.7	100.0%	-3.7
3488	AT4G13780.1   methionine--tRNA ligase, putative / methionyl-tRNA synthetase, putative / MetRS, putative, similar to methionyl-tRNA synthetase (Oryza sativa) GI:4091008; contains Pfam profiles PF00133: tRNA synthetases class I (I, L, M and V), PF01588: Putative tRNA binding domain   chr4:7993198-7998511 REVERSE   Aliases: F18A5.170, F18A5_170	9.3	9.9	-0.5	-1.7	100.0%	-3.8
3489	AT5G61140.1   DEAD box RNA helicase, putative, similar to ASC-1 complex subunit P200 (Homo sapiens) GI:12061185; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF02889: Sec63 domain   chr5:24607225-24620740 FORWARD   Aliases: MAF19.14, MAF19_14	5.6	6.1	-0.5	-1.7	100.0%	-3.7
3490	AT3G14980.1   PHD finger transcription factor, putative, contains Pfam profile: PF00628 PHD-finger   chr3:5039938-5044818 REVERSE   Aliases: K15M2.12	5.1	5.6	-0.5	-1.7	100.0%	-3.5
3491	AT5G42440.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:16990532-16991802 REVERSE   Aliases: MDH9.13, MDH9_13	3.7	3.4	0.3	1.7	100.0%	-4.0
3492	AT4G27010.1   expressed protein, ; expression supported by MPSS   chr4:13558472-13568302 FORWARD   Aliases: F10M23.350, F10M23_350	3.9	4.5	-0.6	-1.7	100.0%	-3.6
3493	AT1G03687.2   DTW domain-containing protein, contains Pfam PF03942: DTW domain	4.8	5.3	-0.5	-1.7	100.0%	-3.4
3494	AT5G19110.1   extracellular dermal glycoprotein-related / EDGP-related, similar to extracellular dermal glycoprotein EDGP precursor (Daucus carota) GI:285741   chr5:6411563-6413172 REVERSE   Aliases: T24G5.10, T24G5_10	6.3	5.3	1.0	1.7	100.0%	-3.2
3495	AT5G61900.3   Symbol: BON1   copine BONZAI1 (BON1), nearly identical to BONZAI1 (Arabidopsis thaliana) GI:15487382; contains Pfam profile PF00168: C2 domain   chr5:24872887-24876453 REVERSE   Aliases: BON, BONSAI, BONZAI1, COPINE 1, CPN1, K22G18.2, K22G18_2	6.5	6.1	0.5	1.7	100.0%	-3.7
3496	AT1G06110.1   F-box family protein, contains similarity to F-box protein FBX3 GI:6103643 from (Homo sapiens) ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:1853076-1855021 REVERSE   Aliases: T21E18.16, T21E18_16	6.4	6.0	0.4	1.7	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3497	AT1G71980.1   protease-associated zinc finger (C3HC4-type RING finger) family protein, identical to ReMembR-H2 protein JR702 (Arabidopsis thaliana) gi:6942149:gb:AAF32326; contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); identical to cDNA ReMembR-H2 protein JR702 mRNA, partial cds GI:6942148   chr1:27101628-27103801 FORWARD   Aliases: F17M19.13, F17M19_13	5.7	4.9	0.7	1.7	100.0%	-3.4
3498	AT1G50630.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g20300.1); similar to OSJNBa0064H22.7 [Oryza sativa (japonica cultivar-group)] (GB:XP_462655.1)   chr1:18755124-18757337 REVERSE   Aliases: F11F12.5, F11F12_5	4.5	3.8	0.7	1.7	100.0%	-3.4
3499	AT5G24740.1   expressed protein   chr5:8469954-8489706 REVERSE   Aliases: T4C12.10	5.2	5.8	-0.7	-1.7	100.0%	-3.6
3500	AT5G15170.1   tyrosyl-DNA phosphodiesterase-related, similar to Chain A, Crystal Structure Of Human Tyrosyl-Dna Phosphodiesterase (Tdp1) (Homo sapiens) GI:20150581   chr5:4926097-4929505 REVERSE   Aliases: F8M21.60, F8M21_60	4.3	4.8	-0.6	-1.7	100.0%	-3.5
3501	AT1G67920.1   expressed protein   chr1:25477207-25477803 FORWARD   Aliases: T23K23.23, T23K23_23	3.9	4.9	-0.9	-1.7	100.0%	-3.4
3502	AT3G48610.1   phosphoesterase family protein, low similarity to SP:P95246 Phospholipase C 2 precursor (EC 3.1.4.3) {Mycobacterium tuberculosis}; contains Pfam profile PF04185: Phosphoesterase family	7.7	8.5	-0.8	-1.7	100.0%	-3.3
3503	AT5G42520.1   expressed protein   chr5:17017511-17019835 FORWARD   Aliases: MDH9.22, MDH9_22	8.8	9.2	-0.4	-1.7	100.0%	-3.8
3504	AT3G44600.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, similar to SP:P87051 Peptidyl-prolyl cis-trans isomerase cyp2 (EC 5.2.1.8) (Cyclophilin cyp2) {Schizosaccharomyces pombe}; contains Pfam profiles PF00160: peptidyl-prolyl cis-trans isomerase cyclophilin-type, PF00400: WD domain G-beta repeat   chr3:16175922-16180249 REVERSE   Aliases: F14L2.150	5.1	5.6	-0.5	-1.7	100.0%	-3.4
3505	AT2G21170.1   Symbol: TIM   triosephosphate isomerase, chloroplast, putative, similar to Triosephosphate isomerase, chloroplast precursor: SP:P48496 from Spinacia oleracea, SP:P46225 from Secale cereale   chr2:9077835-9080304 REVERSE   Aliases: F26H11.7, F26H11_7, TRIOSEPHOSPHATE ISOMERASE	11.0	11.7	-0.6	-1.7	100.0%	-3.9
3506	AT5G63700.1   zinc finger (C3HC4 type RING finger) family protein, contains Pfam PF03126: Plus-3 domain; contains Pfam PF02201: BAF60b domain of the SWIB complex; contains Pfam PF00628: PHD-finger domain; contains Prosite Zinc finger, C3HC4 type (RING finger), signature; similar to CPRF interacting protein (GI:9588690) (Petroselinum crispum)   chr5:25511160-25514858 REVERSE   Aliases: MBK5.18, MBK5_18	5.4	6.1	-0.7	-1.7	100.0%	-3.5
3507	AT5G35910.1   3'-5' exonuclease domain-containing protein / helicase and RNase D C-terminal domain-containing protein / HRDC domain-containing protein, low similarity to SP:Q01780 Polymyositis/scleroderma autoantigen 2 {Homo sapiens}; contains Pfam profiles PF00570: HRDC domain, PF01612: 3'-5' exonuclease   chr5:14046916-14052635 REVERSE   Aliases: MIK22.22, MIK22_22	4.2	4.7	-0.5	-1.7	100.0%	-4.0
3508	AT1G22750.3   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD68607.1)   chr1:8050851-8052893 FORWARD   Aliases: T22J18.8, T22J18_8	5.6	4.9	0.7	1.7	100.0%	-3.4
3509	AT1G07150.1   Symbol: MAPKKK13   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719	4.7	4.2	0.5	1.7	100.0%	-3.6
3510	AT3G49810.1   U-box domain-containing protein, contains Pfam profile PF04564: U-box domain   chr3:18485522-18487819 REVERSE   Aliases: T16K5.160	3.2	3.5	-0.2	-1.7	100.0%	-4.2
3511	AT5G54900.1   Symbol: ATRBP45A   RNA-binding protein 45 (RBP45), putative, contains similarity to polyadenylate-binding protein 5   chr5:22312609-22315572 FORWARD   Aliases: ATRBP45A, MBG8.17, MBG8_17	10.2	10.9	-0.7	-1.7	100.0%	-3.7
3512	AT1G01100.2   60S acidic ribosomal protein P1 (RPP1A), similar to 60S ACIDIC RIBOSOMAL PROTEIN P1 GB:O23095 from (Arabidopsis thaliana)   chr1:50091-51182 REVERSE   Aliases: T25K16.9, T25K16_9	11.6	12.1	-0.5	-1.7	100.0%	-4.0
3513	AT2G28740.1   Symbol: HIS4   histone H4, identical to histone H4 from Lycopersicon esculentum GI:297150, Lolium temulentum SP:P02308, Acropora formosa GI:455652, Citrus jambhiri GI:16797797	8.2	9.0	-0.8	-1.7	100.0%	-3.2
3514	AT3G03210.1   expressed protein   chr3:740777-742316 FORWARD   Aliases: T17B22.10, T17B22_10	6.2	5.7	0.6	1.7	100.0%	-3.6
3515	AT4G17610.1   tRNA/rRNA methyltransferase (SpoU) family protein, similar to TAR RNA loop binding protein (Homo sapiens) GI:1184692; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family   chr4:9805665-9814923 REVERSE   Aliases: DL4840C, FCAALL.71	7.5	6.9	0.6	1.7	100.0%	-3.5
3516	AT3G14120.2   expressed protein, similar to Nuclear pore complex protein Nup107 (Nucleoporin Nup107) (107 kDa nucleoporin) (p105) (Swiss-Prot:P52590) (Rattus norvegicus)   chr3:4677821-4685645 FORWARD   Aliases: MAG2.8	5.1	5.5	-0.5	-1.7	100.0%	-3.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3517	AT5G51590.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr5:20973793-20976339 REVERSE   Aliases: K17N15.14, K17N15_14	6.1	6.9	-0.8	-1.7	100.0%	-3.3
3518	AT3G10480.2   Symbol: ANAC050   no apical meristem (NAM) family protein, similar to to NAC2 (GI:645671) (Arabidopsis thaliana); contains Pfam PF02365: No apical meristem (NAM) protein; N-terminus similar to unknown protein GB:AAD25613 (Arabidopsis thaliana)   chr3:3264362-3267068 FORWARD   Aliases: ANAC050, F13M14.24	3.3	2.9	0.4	1.7	100.0%	-3.7
3519	AT3G10490.2   Symbol: ANAC051/ANAC052   no apical meristem (NAM) family protein, similar to to NAC2 (GI:645671) (Arabidopsis thaliana); contains Pfam PF02365: No apical meristem (NAM) protein   chr3:3267877-3270888 FORWARD   Aliases: ANAC051, ANAC052, F13M14.23	3.3	2.9	0.4	1.7	100.0%	-3.7
3520	AT4G38060.2   expressed protein   chr4:17873003-17874801 REVERSE   Aliases: F20D10.180, F20D10_180	7.6	6.6	1.0	1.7	100.0%	-3.4
3521	AT5G41970.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g49320.1); similar to LOC496075 protein [Xenopus laevis] (GB:AAH87491.1); contains InterPro domain Metal-dependent protein hydrolase (InterPro:IPR003226)   chr5:16808411-16810485 FORWARD   Aliases: MJC20.7, MJC20_7	7.8	8.3	-0.6	-1.7	100.0%	-3.6
3522	AT5G35980.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At2g40120.1); similar to putative protein kinase YakA [Oryza sativa (japonica cultivar-group)] (GB:XP_467340.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:14145214-14151682 FORWARD   Aliases: MEE13.9, MEE13_9	4.9	5.4	-0.5	-1.7	100.0%	-3.8
3523	AT5G12980.1   rcd1-like cell differentiation protein, putative, similar to protein involved in sexual development (Schizosaccharomyces pombe) GI:1620896; contains Pfam profile PF04078: Cell differentiation family, Rcd1-like   chr5:4105386-4108179 REVERSE   Aliases: T24H18.150, T24H18_150	6.2	7.1	-0.8	-1.7	100.0%	-3.3
3524	AT1G76405.2   expressed protein   chr1:28666817-28668683 FORWARD   Aliases: None	5.9	6.8	-0.8	-1.7	100.0%	-3.3
3525	AT4G16720.1   60S ribosomal protein L15 (RPL15A)   chr4:9399987-9401404 REVERSE   Aliases: DL4385C, FCAALL.416	11.7	12.0	-0.3	-1.7	100.0%	-4.1
3526	AT2G01200.2   Symbol: IAA32   auxin-responsive AUX/IAA family protein, contains Pfam profile: PF02309 AUX/IAA family   chr2:118017-119341 FORWARD   Aliases: F10A8.8, F10A8_8	4.9	3.6	1.3	1.7	100.0%	-3.1
3527	AT1G75780.1   Symbol: TUB1   tubulin beta-1 chain (TUB1), nearly identical to SP:P12411 Tubulin beta-1 chain {Arabidopsis thaliana}   chr1:28454802-28457301 REVERSE   Aliases: F10A5.3, F10A5_3	4.3	4.8	-0.5	-1.7	100.0%	-3.6
3528	AT2G29350.3   Symbol: SAG13   similar to tropinone reductase, putative / tropine dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At2g29290.1); similar to putative pfam00106, adh_short, short chain dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:NP_912375.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)	2.9	3.3	-0.4	-1.7	100.0%	-3.7
3529	AT5G40060.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. False intron created at intron 2 to escape a frameshift in the BAC sequence.   chr5:16051816-16055861 FORWARD   Aliases: MUD12.40, MUD12_40	2.9	2.6	0.2	1.7	100.0%	-4.2
3530	AT1G66070.1   translation initiation factor-related, similar to Eukaryotic translation initiation factor 3 subunit 1 (eIF-3 alpha) (eIF3 p35) (eIF3j) (Swiss-Prot:O75822) (Homo sapiens)   chr1:24599549-24602181 REVERSE   Aliases: F15E12.10, F15E12_10	5.1	5.5	-0.4	-1.7	100.0%	-3.8
3531	AT4G03100.1   rac GTPase activating protein, putative, similar to rac GTPase activating protein 3 (Lotus japonicus) GI:3695063; contains Pfam profile PF00620: RhoGAP domain   chr4:1374281-1376231 FORWARD   Aliases: F4C21.2	3.0	3.3	-0.3	-1.7	100.0%	-4.1
3532	AT3G50830.1   Symbol: COR413 PM2   stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi:18449100:gb:AAL69988; similar to stress-regulated protein SAP1 (Xerophyta viscosa) gi:21360378:gb:AAM47505; identical to cDNA cold acclimation protein WCOR413-like protein beta form GI:10121842   chr3:18904826-18906476 REVERSE   Aliases: ATCOR413 PM2, F18B3.110, F18B3_110	7.5	6.0	1.5	1.7	100.0%	-3.5
3533	AT5G08560.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to will die slowly protein (WDS) (SP:Q9V3J8) (Drosophila melanogaster)   chr5:2770875-2774673 REVERSE   Aliases: MAH20.12, MAH20_12	8.9	9.2	-0.4	-1.7	100.0%	-3.8
3534	AT3G60245.1   60S ribosomal protein L37a (RPL37aC)   chr3:22279721-22280981 FORWARD   Aliases: None	13.6	13.9	-0.3	-1.7	100.0%	-4.1
3535	AT1G23440.2   pyrrolidone-carboxylate peptidase family protein, similar to Pyrrolidone-carboxylate peptidase (Swiss-Prot:O58321) (Pyrococcus horikoshii); contains Prosite PS00141: Eukaryotic and viral aspartyl proteases active site   chr1:8321694-8323359 FORWARD   Aliases: F28C11.26, F28C11_26	7.4	6.7	0.7	1.7	100.0%	-3.7
3536	AT3G12400.1   tumour susceptibility gene 101 (TSG101) family protein, contains Pfam profile PF05743: Tumour susceptibility gene 101 protein (TSG101); similar to Tumor susceptibility gene 101 protein (Swiss-Prot:Q99816) (Homo sapiens)   chr3:3944303-3945858 REVERSE   Aliases: T2E22.28	7.1	6.7	0.4	1.7	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3537	AT2G48040.1   expressed protein   chr2:19658266-19659835 REVERSE   Aliases: T9J23.19	5.5	6.1	-0.6	-1.7	100.0%	-3.5
3538	AT5G41620.1   expressed protein, weak similarity to microtubule binding protein D-CLIP-190 (GI:2773363) (Drosophila melanogaster); weak similarity to Synaptonemal complex protein 1 (SCP-1 protein) (Swiss-Prot:Q15431) (Homo sapiens); weak similarity to DNA double-strand break repair rad50 ATPase. (Swiss-Prot:P58301) (Pyrococcus furiosus)   chr5:16663666-16666196 FORWARD   Aliases: MBK23.17, MBK23_17	6.1	6.8	-0.7	-1.7	100.0%	-3.6
3539	AT4G01730.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr4:749922-752034 FORWARD   Aliases: T15B16.11, T15B16_11	4.8	4.4	0.4	1.7	100.0%	-3.7
3540	AT2G47000.1   multidrug resistant (MDR) ABC transporter, putative, similar to multidrug-resistant protein CjMDR1 (Coptis japonica) GI:14715462, MDR-like p-glycoprotein (Arabidopsis thaliana) GI:24324262; contains Pfam profiles PF00005: ABC transporter, PF00664: ABC transporter transmembrane region   chr2:19316937-19321819 REVERSE   Aliases: F14M4.17	4.4	5.1	-0.7	-1.7	100.0%	-3.4
3541	AT5G04510.2   Symbol: PDK1   3-phosphoinositide-dependent protein kinase, putative, similar to 3-phosphoinositide-dependent protein kinase-1 (Oryza sativa) gi:5001830:gb:AAD37166   chr5:1286938-1289903 FORWARD   Aliases: 3 PHOSPHOINOSITIDE DEPENDENT PROTEIN KINASE 1, ATPDK1, T32M21.110, T32M21_110	4.3	4.9	-0.6	-1.7	100.0%	-3.5
3542	AT4G13640.2   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At3g24120.2); similar to transfactor-like [Oryza sativa (japonica cultivar-group)] (GB:XP_481813.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005); contains InterPro domain Myb-like DNA-binding domain, SHAQKYF class (InterPro:IPR006447)   chr4:7936602-7938626 REVERSE   Aliases: F18A5.30, F18A5_30	6.3	5.9	0.4	1.7	100.0%	-3.7
3543	AT4G30380.1   expansin-related, similar to blight-associated protein p12 precursor (Citrus jambhiri) gi:4102727:gb:AAD03398; similar to beta-expansin (Oryza sativa) gi:8118428:gb:AAF72986; expansin-related gene, PMID:11641069, www.bio.psu.edu/expansins   chr4:14860492-14861000 FORWARD   Aliases: F17I23.280, F17I23_280	2.3	2.1	0.2	1.7	100.0%	-4.6
3544	AT5G61600.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr5:24783612-24784656 REVERSE   Aliases: K11J9.13, K11J9_13	6.3	5.5	0.8	1.7	100.0%	-3.5
3545	AT5G06770.1   KH domain-containing protein / zinc finger (CCCH type) family protein, contains Pfam domains PF00013: KH domain and PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr5:2090704-2092951 REVERSE   Aliases: MPH15.13, MPH15_13	4.6	4.3	0.3	1.7	100.0%	-4.0
3546	AT1G68410.2   similar to protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] (TAIR:At1g09160.2); similar to protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] (TAIR:At1g09160.1); similar to protein phosphatase 2C-like [Oryza sativa (japonica cultivar-group)] (GB:XP_479610.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr1:25653662-25656682 REVERSE   Aliases: T2E12.9, T2E12_9	7.1	6.6	0.5	1.7	100.0%	-3.5
3547	AT1G50200.1   Symbol: ALATS   aminoacyl-tRNA synthetase family protein, contains Pfam profiles: PF01411 tRNA synthetases class II (A), PF02272 DHHA1 domain   chr1:18594882-18602149 REVERSE   Aliases: ACD, ALANYL TRNA SYNTHETASE, ALARS, F14I3.17, F14I3_17	9.8	10.1	-0.4	-1.7	100.0%	-3.9
3548	AT3G17250.1   protein phosphatase 2C-related / PP2C-related, similar to protein phosphatase-2C GB:AAC36698 from (Mesembryanthemum crystallinum)   chr3:5892567-5894452 REVERSE   Aliases: MGD8.13	5.2	4.7	0.5	1.7	100.0%	-3.5
3549	AT2G20710.2   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr2:8933087-8935297 FORWARD   Aliases: F5H14.32, F5H14_32	4.5	5.2	-0.7	-1.7	100.0%	-3.4
3550	AT5G48350.1   expressed protein   chr5:19610792-19611391 FORWARD   Aliases: K23F3.7, K23F3_7	2.7	2.3	0.3	1.7	100.0%	-4.4
3551	AT2G21900.1   Symbol: WRKY59	2.3	2.1	0.2	1.7	100.0%	-4.1
3552	AT3G47520.1   Symbol: MDH   malate dehydrogenase (NAD), chloroplast (MDH), identical to chloroplast NAD-malate dehydrogenase (Arabidopsis thaliana) GI:3256066; contains InterPro entry IPR001236: Lactate/malate dehydrogenase; contains Pfam profiles PF00056: lactate/malate dehydrogenase, NAD binding domain and PF02866: lactate/malate dehydrogenase, alpha/beta C-terminal domain   chr3:17524259-17526026 FORWARD   Aliases: F1P2.70, MALATE DEHYDROGENASE	9.8	10.5	-0.7	-1.7	100.0%	-3.6
3553	AT3G48210.1   expressed protein   chr3:17860344-17862663 FORWARD   Aliases: T24C20.90	3.0	3.3	-0.3	-1.7	100.0%	-4.1
3554	AT3G44140.1   expressed protein   chr3:15896064-15896367 REVERSE   Aliases: F26G5.90	9.1	8.4	0.6	1.7	100.0%	-3.6
3555	AT3G06130.1   heavy-metal-associated domain-containing protein, contains Pfam heavy metal associated domain PF00403   chr3:1852899-1855035 REVERSE   Aliases: F28L1.7, F28L1_7	5.4	6.0	-0.6	-1.7	100.0%	-3.5
3556	AT3G21430.1   expressed protein   chr3:7544634-7550830 REVERSE   Aliases: MHC9.11	5.2	5.7	-0.5	-1.7	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3557	AT4G26240.1   expressed protein   chr4:13286786-13288980 REVERSE   Aliases: T25K17.50, T25K17_50	6.5	6.1	0.5	1.7	100.0%	-3.7
3558	AT1G26180.1   expressed protein   chr1:9054738-9056837 FORWARD   Aliases: F28B23.14, F28B23_14	6.0	5.3	0.7	1.7	100.0%	-3.3
3559	AT2G27180.1   expressed protein   chr2:11627311-11628252 FORWARD   Aliases: T22O13.5, T22O13_5	4.0	3.5	0.5	1.7	100.0%	-3.8
3560	AT3G52640.3   expressed protein, similar to hypothetical protein DDB0187645 [Dictyostelium discoideum] (GB:EAL63547.1)	5.5	5.9	-0.4	-1.7	100.0%	-3.8
3561	AT5G49580.1   DNAJ heat shock N-terminal domain-containing protein, contains similarity to S-locus protein 5 GI:6069485 from (Brassica rapa); contains Pfam profile PF00226 DnaJ domain   chr5:20141049-20144039 REVERSE   Aliases: K6M13.13, K6M13_13	7.8	8.4	-0.5	-1.7	100.0%	-3.7
3562	AT3G01780.1   expressed protein, est hit,   chr3:279067-283554 FORWARD   Aliases: F28J7.11, F28J7_11	8.2	9.0	-0.8	-1.7	100.0%	-3.6
3563	AT4G32760.1   similar to VHS domain-containing protein / GAT domain-containing protein [Arabidopsis thaliana] (TAIR:At3g08790.1); similar to putative VHS domain-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464916.1); contains InterPro domain GAT domain (InterPro:IPR004152); contains InterPro domain VHS (InterPro:IPR002014)   chr4:15799144-15804180 FORWARD   Aliases: F4D11.40, F4D11_40	6.3	5.7	0.6	1.7	100.0%	-3.6
3564	AT5G58670.1   Symbol: ATPLC1	5.5	5.9	-0.4	-1.7	100.0%	-3.7
3565	AT1G06950.1   Symbol: ATTIC110/TIC110   Encodes a protein thought to be a part of the translocon at the chloroplast inner envelope. Involved in protein import into the chloroplast and chloroplast biogenesis.   chr1:2130154-2135664 REVERSE   Aliases: ATTIC110, F10K1.33, TIC110	8.0	8.9	-1.0	-1.7	100.0%	-3.5
3566	AT3G22980.1   elongation factor Tu family protein, similar to eukaryotic translation elongation factor 2 GB:NP_001952 (Homo sapiens)   chr3:8160276-8163323 REVERSE   Aliases: MXC7.1	4.1	4.4	-0.3	-1.7	100.0%	-4.0
3567	AT1G70985.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:26768334-26768947 REVERSE   Aliases: None	3.5	3.2	0.3	1.7	100.0%	-3.9
3568	AT1G76810.1   eukaryotic translation initiation factor 2 family protein / eIF-2 family protein, similar to IF2 protein (Drosophila melanogaster) GI:7108770; contains Pfam profile PF03144: Elongation factor Tu domain 2   chr1:28835900-28841480 REVERSE   Aliases: F28O16.18, F28O16_18	6.0	7.0	-1.0	-1.7	100.0%	-3.3
3569	AT1G58440.1   Symbol: XF1   squalene monooxygenase, putative / squalene epoxidase, putative, similar to SP:O65404 (SE 1,1), SP:O65402 (SE 1,2) 6566341 dbj AB008021.1 AB008021   chr1:21717507-21720955 REVERSE   Aliases: F9K23.3, F9K23_3, XF1	3.8	4.4	-0.5	-1.7	100.0%	-3.4
3570	AT5G25800.1   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr5:8979625-8982876 REVERSE   Aliases: F18A17.50, F18A17_50	4.5	4.9	-0.4	-1.7	100.0%	-3.6
3571	AT5G65040.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana)   chr5:25994847-25995643 REVERSE   Aliases: MXK3.29, MXK3_29	7.4	6.7	0.7	1.7	100.0%	-3.4
3572	AT2G40660.1   tRNA-binding region domain-containing protein, similar to SP:Q12904 Multisynthetase complex auxiliary component p43 (Contains: Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1)) {Homo sapiens}; contains Pfam profile PF01588: Putative tRNA binding domain   chr2:16973011-16976075 FORWARD   Aliases: T7D17.16, T7D17_16	8.1	8.7	-0.7	-1.7	100.0%	-3.6
3573	AT5G59845.1   gibberellin-regulated family protein, similar to SP:P27057 GAST1 protein precursor {Lycopersicon esculentum}; contains Pfam profile PF02704: Gibberellin regulated protein   chr5:24128550-24129238 FORWARD   Aliases: None	4.0	4.7	-0.7	-1.7	100.0%	-3.6
3574	AT3G51600.1   Symbol: LTP5   nonspecific lipid transfer protein 5 (LTP5), identical to SP:Q9XFS7 Nonspecific lipid-transfer protein 5 (LTP 5) {Arabidopsis thaliana}   chr3:19149373-19150231 REVERSE   Aliases: LIPID TRANSFER PROTEIN 5, T18N14.5	3.2	3.5	-0.3	-1.7	100.0%	-4.0
3575	AT5G35170.2   similar to adenylate kinase, chloroplast, putative / ATP-AMP transphosphorylase, putative [Arabidopsis thaliana] (TAIR:At5g47840.1); similar to putative adenylate kinase, chloroplast (ATP-AMP transphosphorylase) [Oryza sativa (japonica cultivar-group)] (GB:XP_479721.1); contains InterPro domain Adenylate kinase, subfamily (InterPro:IPR006259); contains InterPro domain Adenylate kinase (InterPro:IPR000850)	4.2	4.8	-0.5	-1.7	100.0%	-3.5
3576	AT3G12110.1   Symbol: ACT11   actin 11 (ACT11), identical to SP:P53496 Actin 11 {Arabidopsis thaliana}   chr3:3857860-3859804 FORWARD   Aliases: ACTIN 11, T21B14.7	8.2	7.4	0.8	1.7	100.0%	-3.3
3577	AT5G47530.1   auxin-responsive protein, putative, similar to auxin-induced protein AIR12 (GI:11357190) (Arabidopsis thaliana); similar to stromal cell derived factor receptor 2 (GI:20381292) (Mus musculus)   chr5:19298601-19300288 FORWARD   Aliases: MNJ7.12, MNJ7_12	2.7	3.2	-0.5	-1.7	100.0%	-3.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3578	AT5G18660.1   Symbol: PCB2   Encodes a protein with 3,8-divinyl protochlorophyllide a 8-vinyl reductase activity. Mutants accumulate divinyl chlorophyll rather than monovinyl chlorophyll.   chr5:6220783-6222230 REVERSE   Aliases: DVR, PALE GREEN AND CHLOROPHYLL B REDUCED 2, T1A4.40, T1A4_40	5.9	6.7	-0.8	-1.7	100.0%	-3.1
3579	AT4G21720.1   expressed protein   chr4:11542573-11544286 FORWARD   Aliases: F17L22.180, F17L22_180	4.5	4.1	0.4	1.7	100.0%	-3.8
3580	AT3G27660.1   glycine-rich protein / oleosin, identical to oleosin isoform GB:S71286 from (Arabidopsis thaliana); identical to cDNA oleosin (isoform Ato12) GI:987013   chr3:10244995-10246260 FORWARD   Aliases: MGF10.3	5.2	4.7	0.5	1.7	100.0%	-3.8
3581	AT3G17300.1   expressed protein   chr3:5907240-5908898 FORWARD   Aliases: MGD8.14	9.3	9.8	-0.6	-1.7	100.0%	-3.5
3582	AT3G12120.1   Symbol: FAD2   omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) / delta-12 desaturase, identical to omega-6 fatty acid desaturase, endoplasmic reticulum (FAD2) SP:P46313 (Arabidopsis thaliana (Mouse-ear cress)) (Plant Cell 6:147-158(1994))   chr3:3860291-3863036 REVERSE   Aliases: DELTA 12 DESATURASE, FATTY ACID DESATURASE 2, T21B14.6	12.2	11.2	1.0	1.7	100.0%	-4.0
3583	AT5G02580.2   expressed protein   chr5:579850-580785 FORWARD   Aliases: T22P11.170, T22P11_170	3.7	3.4	0.3	1.7	100.0%	-4.0
3584	AT5G26110.1   expressed protein   chr5:9117910-9119809 REVERSE   Aliases: T1N24.12, T1N24_12	5.0	5.8	-0.8	-1.7	100.0%	-3.4
3585	AT1G74840.1   myb family transcription factor, similar to myb-related transcription activator GI:9279717 from (Arabidopsis thaliana)   chr1:28119558-28121066 REVERSE   Aliases: F25A4.19, F25A4_19	9.2	8.5	0.7	1.7	100.0%	-3.8
3586	AT5G09270.2   expressed protein   chr5:2878885-2880817 FORWARD   Aliases: T2K12.7	6.5	7.0	-0.5	-1.7	100.0%	-3.7
3587	AT5G46860.1   Symbol: VAM3   syntaxin 22 (SYP22) (VAM3), identical to GP:8809669: syntaxin related protein AtVam3p (Arabidopsis thaliana)   chr5:19029248-19031194 REVERSE   Aliases: ATSYP22, ATVAM3, SYP22	6.5	6.0	0.4	1.7	100.0%	-3.8
3588	AT2G43810.1   small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative, similar to SWISS-PROT:Q9Y4Y8 U6 snRNA-associated Sm-like protein LSm6 (Mus musculus)   chr2:18156388-18158371 FORWARD   Aliases: F18O19.8	8.3	7.5	0.7	1.7	100.0%	-3.4
3589	AT1G60650.2   glycine-rich RNA-binding protein, putative, similar to RNA binding protein(RZ-1) GI:1435061 from (Nicotiana glauca); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:22343552-22346002 FORWARD   Aliases: F8A5.17, F8A5_17	6.6	6.0	0.6	1.7	100.0%	-3.5
3590	AT2G35750.1   expressed protein   chr2:15036908-15037369 REVERSE   Aliases: T20F21.6, T20F21_6	4.6	3.7	0.9	1.7	100.0%	-3.5
3591	AT4G29660.1   Symbol: EMB2752   expressed protein, predicted proteins, Arabidopsis thaliana   chr4:14534269-14535298 REVERSE   Aliases: EMB2752, EMBRYO DEFECTIVE 2752, T16L4.170, T16L4_170	8.6	8.1	0.5	1.7	100.0%	-3.6
3592	AT4G18990.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endotransglycosylase-related protein XTR4 GI:1244754 from (Arabidopsis thaliana)   chr4:10401921-10404259 REVERSE   Aliases: F13C5.160, F13C5_160	2.3	2.1	0.2	1.7	100.0%	-4.4
3593	AT5G11580.1   UVB-resistance protein-related / regulator of chromosome condensation (RCC1) family protein, contains Pfam PF00415 : Regulator of chromosome condensation (RCC1); similar to rjs protein (GI:3414809) (Mus musculus); similar to HERC2 (GI:4079809) (Homo sapiens);similar to UVB-resistance protein UVR8 (GI:10177674) {Arabidopsis thaliana}   chr5:3718811-3721335 FORWARD   Aliases: F15N18.170, F15N18_170	5.9	5.4	0.5	1.7	100.0%	-3.7
3594	AT2G28670.1   disease resistance-responsive family protein / fibroin-related, contains similarity to silk fibroin heavy chain (Bombyx mori) gi:765323:gb:AAB31861; contains disease resistance response protien domain Pfam:FP03018   chr2:12307336-12308859 REVERSE   Aliases: T8O18.4, T8O18_4	5.8	6.4	-0.7	-1.7	100.0%	-3.3
3595	AT3G10530.1   transducin family protein / WD-40 repeat family protein, contains 2 WD-40 repeats (PF00400); BING4 (gi:3811380) {Mus musculus}; similar to hypothetical protein GB:P40055 (Saccharomyces cerevisiae)   chr3:3286018-3288885 FORWARD   Aliases: F13M14.19	6.4	7.1	-0.7	-1.7	100.0%	-3.4
3596	AT4G25470.1   Symbol: CBF2   encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF2). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to low temperature and abscisic acid.   chr4:13015287-13016230 REVERSE   Aliases: DRE/CRT BINDING PROTEIN, DREB1C, T30C3.12	4.4	3.9	0.5	1.7	100.0%	-3.5
3597	AT5G58570.1   expressed protein   chr5:23689929-23690513 REVERSE   Aliases: MZN1.2, MZN1_2	2.6	2.3	0.2	1.7	100.0%	-4.3
3598	AT3G16890.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:5768407-5770386 REVERSE   Aliases: K14A17.14	2.6	2.8	-0.2	-1.7	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3599	AT3G28780.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28840.1); similar to unnamed protein product [Yarrowia lipolytica CLIB99] (GB:CAG83749.1); similar to unnamed protein product [Candida glabrata CBS138] (GB:CAG60731.1); contains domain GLY_RICH (PS50315); contains domain SER_RICH (PS50324)   chr3:10807155-10809695 REVERSE   Aliases: T19N8.7	3.6	3.4	0.2	1.7	100.0%	-4.3
3600	AT3G63300.2   expressed protein   chr3:23395963-23398817 FORWARD   Aliases: MAA21.9	3.7	4.3	-0.7	-1.7	100.0%	-3.5
3601	AT3G04580.2   Symbol: EIN4   ethylene receptor, putative (EIN4), similar to ethylene receptor GB:AAC31123 (Malus domestica), identical to putative ethylene receptor GB:AAD02485 (Arabidopsis thaliana); Pfam HMM hit: response regulator receiver domain, signal C terminal domain   chr3:1235289-1238499 REVERSE   Aliases: ETHYLENE INSENSITIVE 4, F7O18.5, F7O18_5	4.6	5.0	-0.4	-1.7	100.0%	-3.7
3602	AT1G08230.1   amino acid transporter family protein, low similarity to amino acid permease (Oryza sativa) GI:7415521; contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:2583712-2585216 REVERSE   Aliases: T23G18.9, T23G18_9	3.5	3.2	0.4	1.7	100.0%	-3.9
3603	AT2G28755.1   UDP-D-glucuronate carboxy-lyase-related, contains similarity to UDP-D-glucuronate carboxy-lyase GI:13591616 from (Pisum sativum)	2.7	2.9	-0.2	-1.7	100.0%	-4.2
3604	AT3G63170.1   expressed protein   chr3:23345327-23347732 FORWARD   Aliases: F16M2.20	6.7	7.3	-0.6	-1.7	100.0%	-3.6
3605	AT2G19750.1   40S ribosomal protein S30 (RPS30A)   chr2:8522119-8522888 FORWARD   Aliases: F6F22.22, F6F22_22	7.5	8.2	-0.7	-1.7	100.0%	-3.4
3606	AT3G15980.3   coatomer protein complex, subunit beta 2 (beta prime), putative, contains 7 WD-40 repeats (PF00400) (1 weak); identical to coatomer protein complex, beta prime (beta'-COP) protein {Arabidopsis thaliana} (GI:9294445); similar to Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) (SP:P35606) (Homo sapiens)   chr3:5411678-5418451 REVERSE   Aliases: MSL1.4	5.8	6.7	-0.9	-1.7	100.0%	-3.5
3607	AT3G19270.1   Symbol: CYP707A4   cytochrome P450 family protein, similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum};	7.4	6.4	1.1	1.7	100.0%	-3.3
3608	AT5G05320.1   monooxygenase, putative (MO3), similar to GI:3426064; identical to cDNA monooxygenase 3, partial GI:3426065   chr5:1575007-1576732 REVERSE   Aliases: K18I23.12, K18I23_12	6.7	6.2	0.5	1.7	100.0%	-3.7
3609	AT3G03250.1   Symbol: UGP   Is thought to encodes a cytosolic UDP-glucose pyrophosphorylase with strong similarity to UTP--glucose-1-phosphate uridylyltransferase (SwissProt P19595, EC 2.7.7.9, UDP-glucose pyrophosphorylase <i>Solanum tuberosum</i>).   chr3:749486-754166 REVERSE   Aliases: T17B22.6, T17B22_6, UGP, UGPASE	9.1	10.3	-1.2	-1.7	100.0%	-3.6
3610	AT1G61400.1   S-locus protein kinase, putative, similar to KI domain interacting kinase 1 (Zea mays) gi:2735017:gb:AAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954	3.5	3.8	-0.2	-1.7	100.0%	-4.2
3611	AT3G57480.1   zinc finger (C2H2 type, AN1-like) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type; contains Pfam domain, PF01428: AN1-like Zinc finger   chr3:21288917-21290331 REVERSE   Aliases: T8H10.80	5.8	5.4	0.4	1.7	100.0%	-3.8
3612	AT3G49250.1   expressed protein   chr3:18269246-18271983 REVERSE   Aliases: F2K15.110	4.4	4.8	-0.4	-1.7	100.0%	-3.6
3613	AT5G01750.2   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr5:289762-291323 FORWARD   Aliases: T20L15.20, T20L15_20	9.1	8.1	1.0	1.7	100.0%	-3.6
3614	AT4G22840.1   bile acid:sodium symporter family protein, low similarity to SP:Q12908 Ileal sodium/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family   chr4:11991508-11993781 REVERSE   Aliases: F7H19.20	4.7	4.3	0.4	1.6	100.0%	-3.8
3615	AT3G57300.1   transcriptional activator, putative, similar to transcriptional activator SRCAP (Homo sapiens) GI:5106572; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr3:21210591-21218864 FORWARD   Aliases: F28O9.150	7.3	8.1	-0.7	-1.6	100.0%	-3.5
3616	AT5G23070.1   thymidine kinase, putative, similar to thymidine kinase (Oryza sativa) SWISS-PROT:O81263	6.3	6.8	-0.4	-1.6	100.0%	-3.5
3617	AT4G38810.2   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:18115277-18119071 REVERSE   Aliases: T9A14.90, T9A14_90	5.9	5.4	0.5	1.6	100.0%	-3.5
3618	AT3G53200.1   myb family transcription factor (MYB27), similar to myb-related DNA-binding protein GI:6467223 from (Arabidopsis thaliana); contains PFAM profile: myb DNA binding domain PF00249   chr3:19729260-19730440 REVERSE   Aliases: T4D2.130	3.5	3.9	-0.4	-1.6	100.0%	-4.0
3619	AT4G17410.1   expressed protein   chr4:9717226-9721937 FORWARD   Aliases: DL4740W, FCAALL.426	3.0	2.7	0.2	1.6	100.0%	-4.0
3620	AT5G48470.1   expressed protein   chr5:19658987-19661588 FORWARD   Aliases: MJE7.11, MJE7_11	4.9	5.3	-0.4	-1.6	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3621	AT3G50900.1   expressed protein   chr3:18929000-18929599 FORWARD   Aliases: F18B3.180	4.0	4.8	-0.8	-1.6	100.0%	-3.4
3622	AT1G03850.2   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	4.1	4.9	-0.8	-1.6	100.0%	-3.2
3623	AT5G45130.1   Symbol: RHA1   Ras-related protein (RHA1) / small GTP-binding protein, identical to Ras-related protein RHA1 SP:P31582 from (Arabidopsis thaliana)   chr5:18261493-18263670 FORWARD   Aliases: K17O22.15, K17O22_15	11.3	10.8	0.5	1.6	100.0%	-4.0
3624	AT5G67200.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:26830951-26833792 REVERSE   Aliases: K21H1.16, K21H1_16	3.6	4.0	-0.4	-1.6	100.0%	-3.7
3625	AT5G20320.1   DEAD/DEAH box helicase, putative, similar to CAF protein (Arabidopsis thaliana) GI:6102610; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF03368: Domain of unknown function, PF00636: RNase3 domain, PF00035: Double-stranded RNA binding motif   chr5:6859342-6869070 REVERSE   Aliases: F5O24.210, F5O24_210	6.5	7.2	-0.7	-1.6	100.0%	-3.5
3626	AT1G06190.1   expressed protein   chr1:1892272-1894137 REVERSE   Aliases: F9P14.5, F9P14_5	5.2	4.8	0.4	1.6	100.0%	-3.6
3627	AT5G15920.1   structural maintenance of chromosomes (SMC) family protein (MSS2), similar to SMC-related protein MSS2 (Arabidopsis thaliana) GI:9965743; contains Pfam profiles PF02483: SMC family C-terminal domain, PF02463: RecF/RecN/SMC N terminal domain	3.8	4.2	-0.5	-1.6	100.0%	-3.7
3628	AT5G60990.1   DEAD/DEAH box helicase, putative (RH10), probable replication protein A1, Oryza sativa, EMBL:AF009179   chr5:24563658-24566565 REVERSE   Aliases: MSL3.110, MSL3_110	6.3	7.1	-0.8	-1.6	100.0%	-3.4
3629	AT3G45140.1   Symbol: LOX2   lipoxygenase (LOX2), identical to SP:P38418   chr3:16536395-16540337 FORWARD   Aliases: ATLOX2, LIPOXYGENASE 2, T14D3.80	2.8	3.1	-0.3	-1.6	100.0%	-4.1
3630	AT5G39720.1   avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related, similar to SP:P54121 AIG2 protein {Arabidopsis thaliana}   chr5:15916874-15917881 FORWARD   Aliases: MKM21.1	7.1	6.2	0.9	1.6	100.0%	-3.2
3631	AT1G52720.1   expressed protein   chr1:19644567-19645333 FORWARD   Aliases: F6D8.3, F6D8_3	7.0	6.3	0.7	1.6	100.0%	-3.6
3632	AT3G48710.1   expressed protein, putative protein - Arabidopsis thaliana, EMBL:AL078465.1   chr3:18051962-18055173 FORWARD   Aliases: T8P19.220	5.4	6.6	-1.2	-1.6	100.0%	-3.5
3633	AT2G43140.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile PF00010: Helix-loop-helix DNA-binding domain	3.5	3.1	0.4	1.6	100.0%	-3.8
3634	AT3G29610.1   hypothetical protein   chr3:11412081-11412569 FORWARD   Aliases: MTO24.8	2.5	2.7	-0.2	-1.6	100.0%	-4.3
3635	AT2G23620.1   esterase, putative, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:10054459-10056371 REVERSE   Aliases: F26B6.27, F26B6_27	7.9	6.7	1.2	1.6	100.0%	-3.5
3636	AT2G04240.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:1461627-1462934 REVERSE   Aliases: T23O15.13, T23O15_13	6.2	5.6	0.6	1.6	100.0%	-3.6
3637	AT3G58570.1   DEAD box RNA helicase, putative, similar to SP:O00571 DEAD-box protein 3 (Helicase-like protein 2) {Homo sapiens}, DEAD box RNA helicase DDX3 (Homo sapiens) GI:3523150; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr3:21667481-21671509 FORWARD   Aliases: F14P22.160	6.5	6.1	0.4	1.6	100.0%	-4.1
3638	AT2G32790.1   ubiquitin-conjugating enzyme, putative, similar to ubiquitin conjugating enzyme from (Oryza sativa) GI:1373001, {Arabidopsis thaliana} SP:P35134, SP:P35131; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	4.1	3.7	0.4	1.6	100.0%	-3.7
3639	AT1G22985.1   encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	6.6	6.0	0.6	1.6	100.0%	-3.7
3640	AT3G10780.1   emp24/gp25L/p24 family protein, similar to SP:O35587 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Mesocricetus auratus}; contains Pfam profile: PF01105 emp24/gp25L/p24 family; contains non-consensus TG acceptor splice site at exon 3   chr3:3375166-3376339 FORWARD   Aliases: T7M13.14	3.9	3.5	0.5	1.6	100.0%	-3.7
3641	AT5G39590.1   expressed protein   chr5:15868639-15871194 FORWARD   Aliases: MIJ24.8, MIJ24_8	6.7	7.7	-0.9	-1.6	100.0%	-3.5
3642	AT2G16640.1   Symbol: ATTOC132/TOC132   chloroplast outer membrane protein, putative, similar to chloroplast protein import component Toc159 (Pisum sativum) GI:8489806, chloroplast outer envelope protein 86 (Pisum sativum) GI:599958, GTP-binding protein (Pisum sativum) GI:576509   chr2:7218194-7222612 REVERSE   Aliases: ATTOC132, T24I21.5, T24I21_5, TOC132	6.7	7.3	-0.6	-1.6	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3643	AT2G13440.1   glucose-inhibited division family A protein, similar to GidA from Pseudomonas syringae (GI:10764670); contains Pfam profile PF01134 Glucose inhibited division protein A	4.5	4.9	-0.3	-1.6	100.0%	-3.8
3644	AT1G04780.1   ankyrin repeat family protein, contains Pfam PF00023: Ankyrin repeat   chr1:1340668-1343583 REVERSE   Aliases: F13M7.23	7.1	8.0	-0.9	-1.6	100.0%	-3.4
3645	AT2G17420.1   Symbol: NTRA   similar to thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1) [Arabidopsis thaliana] (TAIR:At4g35460.1); similar to NADPH-thioredoxin reductase [Triticum aestivum] (GB:CAD19162.1); contains InterPro domain Thioredoxin reductase (InterPro:IPR005982); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class I (InterPro:IPR001100); contains InterPro domain FAD-dependent pyridine nucleotide-disulphide oxidoreductase (InterPro:IPR001327); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class-II, active site (InterPro:IPR008255); contains InterPro domain Adrenodoxin reductase (InterPro:IPR000759); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class-II (InterPro:IPR000103)   chr2:7571427-7573621 FORWARD   Aliases: ATNTRA, F5J6.18, F5J6_18	12.2	12.5	-0.3	-1.6	100.0%	-4.6
3646	AT4G35460.1   Symbol: NTR1   thioredoxin reductase 1 / NADPH-dependent thioredoxin reductase 1 (NTR1), identical to SP:Q39243	12.2	12.5	-0.3	-1.6	100.0%	-4.6
3647	AT1G13410.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:4601636-4603171 FORWARD   Aliases: T6J4.15, T6J4_15	3.0	3.3	-0.3	-1.6	100.0%	-4.1
3648	AT5G18090.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:5985390-5987163 FORWARD   Aliases: MRG7.5, MRG7_5	3.5	3.2	0.3	1.6	100.0%	-4.0
3649	AT1G52700.1   phospholipase/carboxylesterase family protein, similar to lysophospholipase I (Mus musculus) GI:1864159; contains Pfam profile PF02230: Phospholipase/Carboxylesterase family   chr1:19634794-19637108 REVERSE   Aliases: F6D8.5, F6D8_5	3.8	3.4	0.3	1.6	100.0%	-3.8
3650	AT5G43790.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:17609234-17610708 REVERSE   Aliases: MQD19.14, MQD19_14	4.5	4.9	-0.4	-1.6	100.0%	-3.8
3651	AT3G11820.2   Symbol: SYP121	6.4	5.7	0.7	1.6	100.0%	-3.4
3652	AT2G29590.1   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein   chr2:12661533-12662525 REVERSE   Aliases: F16P2.3, F16P2_3	7.6	7.2	0.4	1.6	100.0%	-3.8
3653	AT3G04680.2   pre-mRNA cleavage complex family protein, similar to Pre-mRNA cleavage complex II protein Clp1 (Swiss-Prot:Q92989) (Homo sapiens)   chr3:1269859-1272922 REVERSE   Aliases: F7O18.15, F7O18_15	6.4	6.8	-0.5	-1.6	100.0%	-3.6
3654	AT2G38340.1   encodes a member of the DREB subfamily A-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are eight members in this subfamily including DREB2A AND DREB2B that are involved in response to drought.   chr2:16074474-16075369 REVERSE   Aliases: T19C21.17, T19C21_17	2.9	2.7	0.2	1.6	100.0%	-4.4
3655	AT5G20570.1   Symbol: RBX1   ring-box protein-related, similar to ring-box protein 1 GI:4769004 from (Homo sapiens)   chr5:6956662-6958313 REVERSE   Aliases: F7C8.160, F7C8_160, HRT1, ROC1	10.5	10.0	0.6	1.6	100.0%	-3.7
3656	AT2G27360.1   lipase, putative, similar to lipase (Arabidopsis thaliana) GI:1145627; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr2:11713276-11715120 FORWARD   Aliases: F12K2.6, F12K2_6	4.6	3.9	0.7	1.6	100.0%	-3.4
3657	AT3G29140.1   hypothetical protein   chr3:11107042-11107381 FORWARD   Aliases: MXE2.16	6.1	5.0	1.1	1.6	100.0%	-3.4
3658	AT4G39090.1   Symbol: RD19   cysteine proteinase RD19a (RD19A) / thiol protease, identical to cysteine proteinase RD19a, thiol protease SP:P43296, GI:435618 from (Arabidopsis thaliana)   chr4:18214569-18217476 REVERSE   Aliases: EMB3005, EMBRYO DEFECTIVE 3005, F19H22.190, F19H22_190, RD19A, RESPONSIVE TO DEHYDRATION 19	11.5	10.5	1.0	1.6	100.0%	-3.8
3659	AT5G61290.1   flavin-containing monooxygenase family protein / FMO family protein, low similarity to FMO3 from Homo sapiens (SP:P31513); contains Pfam profile: PF00743 Flavin-binding monooxygenase-like; supported by full-length cDNA Ceres:14492   chr5:24665784-24668492 FORWARD   Aliases: MFB13.9, MFB13_9	3.0	3.3	-0.3	-1.6	100.0%	-4.0
3660	AT1G74460.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile: PF00657 lipase/acylhydrolase with GDSL-like motif   chr1:27991622-27993462 REVERSE   Aliases: F1M20.14, F1M20_14	3.7	4.4	-0.6	-1.6	100.0%	-3.3
3661	AT4G29010.1   Symbol: AIM1   abnormal inflorescence meristem 1 / fatty acid multifunctional protein (AIM1), identical to gi:4337025; contains Pfam profiles PF02737 (3-hydroxyacyl-CoA dehydrogenase, NAD binding domain), PF00378 (enoyl-CoA hydratase/isomerase family protein), PF00725 (3-hydroxyacyl-CoA dehydrogenase)   chr4:14296679-14302066 REVERSE   Aliases: ABNORMAL INFLORESCENCE MERISTEM, F19B15.40, F19B15_40	8.9	9.7	-0.8	-1.6	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3662	AT2G04790.3   expressed protein   chr2:1679525-1680540 FORWARD   Aliases: F28I8.17, F28I8_17	3.1	2.8	0.3	1.6	100.0%	-4.0
3663	AT4G36730.2   Symbol: GBF1   G-box binding factor 1 (GBF1), identical to G-box binding factor 1 SP:P42774 from (Arabidopsis thaliana); contains Pfam profile: PF00170 bZIP transcription factor   chr4:17309623-17312480 REVERSE   Aliases: AP22.21, AP22_21	8.1	7.4	0.8	1.6	100.0%	-3.7
3664	AT3G50790.1   late embryogenesis abundant protein, putative / LEA protein, putative, similar to Picea glauca late embryogenesis abundant protein (EMB8), PID:g1350545 SP:Q40863; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr3:18890904-18892963 REVERSE   Aliases: F18B3.70	5.8	6.4	-0.6	-1.6	100.0%	-3.5
3665	AT1G74390.1   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr1:27965198-27967508 REVERSE   Aliases: F1M20.7, F1M20_7	5.4	4.9	0.5	1.6	100.0%	-3.5
3666	AT5G62390.1   calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612   chr5:25069275-25071515 REVERSE   Aliases: MMI9.22, MMI9_22	6.6	7.3	-0.8	-1.6	100.0%	-3.5
3667	AT3G18870.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr3:6508226-6509349 REVERSE   Aliases: MCB22.4	3.1	2.8	0.3	1.6	100.0%	-4.0
3668	AT1G25375.1   metallo-beta-lactamase family protein   chr1:8900189-8903244 REVERSE   Aliases: None	6.3	6.7	-0.4	-1.6	100.0%	-4.0
3669	AT3G52105.1   expressed protein   chr3:19334310-19334805 FORWARD   Aliases: None	5.7	4.5	1.1	1.6	100.0%	-3.2
3670	AT2G23700.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr2:10083449-10087312 REVERSE   Aliases: F27L4.12, F27L4_12	3.4	4.1	-0.7	-1.6	100.0%	-3.8
3671	AT4G18480.1   Symbol: CHLI1   magnesium-chelatase subunit chlI, chloroplast / Mg-protoporphyrin IX chelatase (CHLI) (CS) (CH42), identical to SP:P161127 Magnesium-chelatase subunit chlI, chloroplast precursor (Mg-protoporphyrin IX chelatase) (Protein CS/CH-42) {Arabidopsis thaliana}   chr4:10201683-10203454 REVERSE   Aliases: CH 42, CH42, CHLORATA, CHLORINA 42, F28J12.140, F28J12_140, PROTOPORPHYRIN IX MG CHELATASE	8.2	9.0	-0.8	-1.6	100.0%	-3.4
3672	AT5G26980.2   Symbol: SYP41   similar to syntaxin, putative [Arabidopsis thaliana] (TAIR:At3g05710.2); similar to putative syntaxin protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910328.1); contains InterPro domain Target SNARE coiled-coil domain (InterPro:IPR000727); contains InterPro domain Syntaxin, N-terminal (InterPro:IPR006011)   chr5:9488153-9490819 REVERSE   Aliases: ATSYP41, ATTLG2A, F2P16.16, F2P16_16, SYNTAXIN OF PLANTS 41	5.2	4.8	0.4	1.6	100.0%	-3.7
3673	AT4G16566.1   histidine triad family protein / HIT family protein, contains Pfam domain, PF01230: HIT family (histidine triad protein family)   chr4:9334648-9335980 REVERSE   Aliases: None	7.2	6.5	0.7	1.6	100.0%	-3.5
3674	AT3G16620.1   Symbol: ATTOC120   chloroplast outer membrane protein, putative, similar to chloroplast protein import component Toc159 (Pisum sativum) GI:8489806, chloroplast outer envelope protein 86 (Pisum sativum) GI:599958, GTP-binding protein (Pisum sativum) GI:576509   chr3:5658475-5661969 REVERSE   Aliases: MGL6.15	4.7	5.2	-0.5	-1.6	100.0%	-3.5
3675	AT3G06740.1   zinc finger (GATA type) family protein   chr3:2126425-2127473 FORWARD   Aliases: F3E22.12	6.1	6.9	-0.8	-1.6	100.0%	-3.5
3676	AT4G24710.1   similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At2g03670.1); similar to Hypothetical protein MGC76197 [Xenopus tropicalis] (GB:AAH63217.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain Chaperonin clpA/B (InterPro:IPR001270); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr4:12745557-12749005 REVERSE   Aliases: F22K18.90, F22K18_90	3.6	3.9	-0.3	-1.6	100.0%	-3.8
3677	AT1G68590.1   plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative, similar to SP:P82412 Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3) {Spinacia oleracea}; contains Pfam profile PF04839: Plastid and cyanobacterial ribosomal protein (PSRP-3 / Ycf65)   chr1:25761072-25761890 REVERSE   Aliases: F24J5.17, F24J5_17	5.4	6.2	-0.8	-1.6	100.0%	-3.2
3678	AT1G47240.1   Symbol: NRAMP2	6.9	6.3	0.6	1.6	100.0%	-3.6
3679	AT2G28910.1   Symbol: CXIP4   CAX-interacting protein 4 (CAXIP4), contains Pfam domain PF00098: Zinc knuckle; identical to cDNA CAX-interacting protein 4 GI:27651998	12.2	11.7	0.5	1.6	100.0%	-4.3
3680	AT5G14610.1   similar to DEAD box RNA helicase (DRH1) [Arabidopsis thaliana] (TAIR:At3g01540.2); similar to DEAD box RNA helicase (DRH1) [Arabidopsis thaliana] (TAIR:At3g01540.1); similar to DEAD box RNA helicase (DRH1) [Arabidopsis thaliana] (TAIR:At3g01540.3); similar to putative RNA helicase, DRH1 [Oryza sativa (japonica cultivar-group)] (GB:XP_462826.1); similar to ATP-dependent RNA helicase DB10 - wood tobacco (GB:S42639); similar to putative p68 RNA helicase [Oryza sativa (japonica cultivar-group)] (GB:XP_550287.1); contains InterPro domain WW/Rsp5/WWP domain (InterPro:IPR001202); contains InterPro domain ATP-dependent helicase, DEAD-box (InterPro:IPR000629); contains InterPro domain Helicase, C-terminal (InterPro:IPR001650); contains InterPro domain DEAD/DEAH box helicase (InterPro:IPR001410)   chr5:4710575-4715072 FORWARD   Aliases: T15N1.100, T15N1_100	6.5	6.9	-0.4	-1.6	100.0%	-3.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3681	AT2G25570.1   expressed protein   chr2:10892776-10894999 REVERSE   Aliases: F3N11.2, F3N11_2	7.2	7.9	-0.7	-1.6	100.0%	-3.5
3682	AT5G10160.1   beta-hydroxyacyl-ACP dehydratase, putative, similar to beta-hydroxyacyl-ACP dehydratase from Toxoplasma gondii (GI:3850997); contains Pfam profile PF01377 Thioester dehydratase	7.0	8.1	-1.1	-1.6	100.0%	-3.3
3683	AT2G39460.1   Symbol: ATRPL23A   60S ribosomal protein L23A (RPL23aA), identical to GB:AF034694   chr2:16482001-16483163 FORWARD   Aliases: F12L6.12, F12L6_12, RIBOSOMAL PROTEIN L23A, RPL23A	10.5	11.2	-0.8	-1.6	100.0%	-3.4
3684	AT5G53650.1   expressed protein   chr5:21808403-21809666 FORWARD   Aliases: MNC6.19, MNC6_19	8.7	8.1	0.6	1.6	100.0%	-3.9
3685	AT3G49500.1   Symbol: RDR6   RNA-dependent RNA polymerase (SDE1), identical to RNA-dependent RNA polymerase (Arabidopsis thaliana) gi:8248473:gb:AAF74208   chr3:18360178-18364190 REVERSE   Aliases: RNA DEPENDENT RNA POLYMERASE 6, SDE1, SGS2, SILENCING DEFECTIVE 1, SUPPRESSOR OF GENE SILENCING 2, T9C5.95	5.6	6.1	-0.6	-1.6	100.0%	-3.7
3686	AT5G23920.1   expressed protein   chr5:8073227-8074173 REVERSE   Aliases: MRO11.4, MRO11_4	6.2	6.9	-0.6	-1.6	100.0%	-3.5
3687	AT5G56640.1   Symbol: MIOX5   expressed protein, similar to myo-inositol oxygenase (Sus scrofa) gi:17432544:gb:AAL39076   chr5:22944555-22946869 REVERSE   Aliases: MIK19.9, MIK19_9	11.3	10.6	0.7	1.6	100.0%	-3.3
3688	AT2G17300.1   expressed protein   chr2:7529547-7530018 REVERSE   Aliases: F5J6.6, F5J6_6	4.1	3.8	0.3	1.6	100.0%	-3.8
3689	AT2G18120.1   lateral root primordium (LRP) protein-related, similar to lateral root primordium 1 (LRP1) (Arabidopsis thaliana) GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702)   chr2:7883697-7884763 REVERSE   Aliases: F8D23.10, F8D23_10	2.8	2.4	0.4	1.6	100.0%	-4.1
3690	AT5G55310.1   Symbol: TOP1   DNA topoisomerase I, putative, similar to Swiss-Prot:P30181 DNA topoisomerase I (Arabidopsis thaliana)   chr5:22447615-22452285 REVERSE   Aliases: MTE17.2, MTE17_2, TOPOISOMERASE I	7.8	8.5	-0.7	-1.6	100.0%	-3.9
3691	AT2G42980.1   aspartyl protease family protein, contains pfam profile: PF00026 eukaryotic aspartyl protease   chr2:17882082-17883665 REVERSE   Aliases: F23E6.3, F23E6_3	2.5	2.7	-0.3	-1.6	100.0%	-4.3
3692	AT3G54040.1   photoassimilate-responsive protein-related, contains weak similarity to mRNA inducible by sucrose and salicylic acid expressed in sugar-accumulating tobacco plants (GI:871487) (Nicotiana tabacum)   chr3:20024739-20026415 REVERSE   Aliases: F5K20.340	3.4	4.5	-1.0	-1.6	100.0%	-3.3
3693	AT1G26920.1   expressed protein, Location of EST 228A16T7A, gb:N65686   chr1:9329499-9330385 FORWARD   Aliases: T2P11.11, T2P11_11	5.0	4.6	0.4	1.6	100.0%	-3.8
3694	AT1G16070.2   similar to F-box family protein / tubby family protein [Arabidopsis thaliana] (TAIR:At1g47270.1); similar to tubby like protein 3 [Homo sapiens] (GB:AAC95431.1); contains InterPro domain Tubby (InterPro:IPR000007)   chr1:5511868-5513890 REVERSE   Aliases: T24D18.17, T24D18_17	2.5	2.7	-0.2	-1.6	100.0%	-4.3
3695	AT5G16000.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:5224146-5227291 FORWARD   Aliases: F1N13.140, F1N13_140	5.3	5.8	-0.5	-1.6	100.0%	-3.6
3696	AT3G15030.2   Symbol: TCP4   TCP family transcription factor, putative, similar to TCP3 GB:AAC24010 (Arabidopsis thaliana)   chr3:5062026-5064045 FORWARD   Aliases: K15M2.17	3.9	4.2	-0.4	-1.6	100.0%	-3.7
3697	AT4G09900.1   hydrolase, alpha/beta fold family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393, SP:Q40708 PIR7A protein {Oryza sativa}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:6221661-6224130 REVERSE   Aliases: AT4G09910, T5L19.30, T5L19_30	3.7	3.3	0.4	1.6	100.0%	-3.9
3698	AT5G66200.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr5:26470686-26473048 REVERSE   Aliases: K2A18.28, K2A18_28	6.3	5.8	0.5	1.6	100.0%	-3.8
3699	AT4G22920.1   expressed protein   chr4:12016536-12018503 REVERSE   Aliases: F7H19.100, F7H19_100	6.2	5.8	0.4	1.6	100.0%	-3.9
3700	AT1G16530.1   LOB domain protein 3 / lateral organ boundaries domain protein 3 (LBD3), identical to SP:Q9SA51 LOB domain protein 3 {Arabidopsis thaliana}; identical to ASYMMETRIC LEAVES2-like protein 9 (Arabidopsis thaliana) GI:19918989   chr1:5651463-5652832 REVERSE   Aliases: F3O9.33, F3O9_33	4.1	4.7	-0.6	-1.6	100.0%	-3.5
3701	AT3G03120.1   Symbol: ATARFB1C   Gene encoding ADP-ribosylation factor and similar to ADP-ribosylation factor 1; ARF 1 (GP:385340) {Drosophila melanogaster}, other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding.   chr3:717186-719322 FORWARD   Aliases: ATARFB1C, T17B22.19, T17B22_19	6.1	5.8	0.3	1.6	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3702	AT1G62670.1   pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR repeats Pfam Profile: PF01535   chr1:23208438-23210330 REVERSE   Aliases: F23N19.4, F23N19_4	3.1	3.6	-0.5	-1.6	100.0%	-4.0
3703	AT4G38090.2   expressed protein, contains Pfam PF01205: Uncharacterized protein family UPF0029	6.6	6.0	0.6	1.6	100.0%	-3.6
3704	AT4G18465.1   RNA helicase, putative, similar to SP:Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr4:10197067-10201622 FORWARD   Aliases: None	3.6	4.1	-0.5	-1.6	100.0%	-3.6
3705	AT3G17120.2   expressed protein   chr3:5841323-5843491 FORWARD   Aliases: K14A17.19	5.7	5.0	0.7	1.6	100.0%	-3.3
3706	AT5G28740.1   transcription-coupled DNA repair protein-related, similar to XAB2 (XPA-binding protein 2) (Homo sapiens) GI:10566459   chr5:10780778-10783915 FORWARD   Aliases: T32B20.1, T32B20_1	6.2	7.0	-0.8	-1.6	100.0%	-3.6
3707	AT5G10970.1   zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type domain, Prosite:PS00028   chr5:3469269-3470087 FORWARD   Aliases: T30N20.240, T30N20_240	2.9	2.7	0.3	1.6	100.0%	-4.0
3708	AT1G31335.1   expressed protein   chr1:11216895-11217374 REVERSE   Aliases: None	5.4	4.7	0.7	1.6	100.0%	-3.5
3709	AT3G14050.1   Symbol: RSH2   RelA/SpoT protein, putative (RSH2), nearly identical to RelA/SpoT homolog RSH2 (Arabidopsis thaliana) GI:7141306; contains Pfam profiles PF01966: HD domain, PF04607: Region found in RelA / SpoT proteins   chr3:4650768-4653921 REVERSE   Aliases: AT RSH2, MDC16.19, RELA SPOT HOMOLOG	7.1	6.6	0.5	1.6	100.0%	-3.5
3710	AT3G19553.1   amino acid permease family protein, weak similarity to aspartate/glutamate transporter 1 (Mus musculus) GI:21322754; contains Pfam profile PF00324: Amino acid permease   chr3:6790748-6792827 REVERSE   Aliases: T31J18.6	5.6	4.8	0.8	1.6	100.0%	-3.6
3711	AT3G63060.1   circadian clock coupling factor, putative, similar to gb:AAK56924 circadian clock coupling factor ZGT {Nicotiana tabacum}   chr3:23311265-23312448 REVERSE   Aliases: T20O10.160	3.3	3.1	0.2	1.6	100.0%	-4.3
3712	AT2G22500.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr2:9570304-9571831 REVERSE   Aliases: F14M13.10, F14M13_10	7.1	6.3	0.8	1.6	100.0%	-3.9
3713	AT5G05950.1   expressed protein   chr5:1788768-1789439 FORWARD   Aliases: K18J17.12, K18J17_12	4.9	4.4	0.5	1.6	100.0%	-3.7
3714	AT5G26040.2   Symbol: HDA2   histone deacetylase family protein (HDA2), identical to HDA2 (Arabidopsis thaliana) GI:21105771; similar to SP:Q96DB2 Histone deacetylase 11 (HD11) {Homo sapiens}; contains Pfam profile PF00850: Histone deacetylase family   chr5:9098557-9101639 REVERSE   Aliases: HISTONE DEACETYLASE, T1N24.9, T1N24_9	3.9	3.5	0.4	1.6	100.0%	-3.8
3715	AT5G64180.1   expressed protein   chr5:25694306-25695518 FORWARD   Aliases: MSJ1.2, MSJ1_2	5.6	5.0	0.5	1.6	100.0%	-3.7
3716	AT2G18220.1   expressed protein, contains Pfam domain PF03715: Uncharacterised protein family (UPF0120)   chr2:7935336-7938933 FORWARD   Aliases: T30D6.27, T30D6_27	4.9	6.1	-1.2	-1.6	100.0%	-3.5
3717	AT1G63290.1   ribulose-phosphate 3-epimerase, cytosolic, putative / pentose-5-phosphate 3-epimerase, putative, strong similarity to D-ribulose-5-phosphate 3-epimerase (Oryza sativa) GI:6007803; contains Pfam profile PF00834: Ribulose-phosphate 3 epimerase family	8.6	9.2	-0.7	-1.6	100.0%	-3.8
3718	AT1G50910.1   expressed protein   chr1:18870751-18873507 REVERSE   Aliases: F8A12.13, F8A12_13	2.5	2.7	-0.2	-1.6	100.0%	-4.3
3719	AT5G65930.2   Symbol: ZWI   kinesin-like calmodulin-binding protein (ZWICHEL), identical to kinesin-like protein GI:2224925 from (Arabidopsis thaliana)   chr5:26387427-26393746 REVERSE   Aliases: K14B20.10, K14B20_10, KCBP, KINESIN LIKE CALMODULIN BINDING PROTEIN, PKCBP, ZWICHEL	4.3	5.0	-0.6	-1.6	100.0%	-3.6
3720	AT2G35010.1   thioredoxin family protein, similar to SP:Q42443 Thioredoxin H-type (TRX-H) {Oryza sativa}; contains Pfam profile: PF00085 Thioredoxin   chr2:14761415-14763122 FORWARD   Aliases: F19I3.24, F19I3_24	6.4	7.2	-0.8	-1.6	100.0%	-3.7
3721	AT1G01570.1   fringe-related protein, + similar to hypothetical protein GB:AAC23643 (Arabidopsis thaliana) + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr1:205176-207435 FORWARD   Aliases: F22L4.11, F22L4_11	4.2	4.7	-0.5	-1.6	100.0%	-3.8
3722	AT4G17970.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	5.2	4.5	0.7	1.6	100.0%	-3.2
3723	AT5G13470.1   expressed protein   chr5:4318565-4319834 FORWARD   Aliases: T6I14.1	5.3	4.8	0.4	1.6	100.0%	-3.6
3724	AT1G80170.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase GI:7381227 from (Lycopersicon esculentum); contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:30158300-30160584 REVERSE   Aliases: F18B13.25, F18B13_25	5.2	5.8	-0.6	-1.6	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3725	AT3G05390.1   expressed protein, ; expression supported by MPSS   chr3:1546591-1547982 REVERSE   Aliases: F22F7.17, F22F7_17	4.5	5.1	-0.6	-1.6	100.0%	-3.6
3726	AT1G30220.1   sugar transporter family protein, similar to SP:Q96QE2 Proton myo-inositol co-transporter (Hmit) (Homo sapiens); contains Pfam profile PF00083: major facilitator superfamily protein   chr1:10632805-10635455 REVERSE   Aliases: F12P21.2, F12P21_2	5.0	4.2	0.8	1.6	100.0%	-3.5
3727	AT2G46800.2   Symbol: ZAT1   zinc transporter (ZAT), identical to zinc transporter ZAT (Arabidopsis thaliana) gi:4206640:gb:AAD11757; member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr2:19244503-19246474 FORWARD   Aliases: ATMTP1, F19D11.8, MTP1, ZINC TRANSPORTER OF ARABIDOPSIS THALIANA, ZINC TRANSPORTER ZAT	10.6	10.0	0.5	1.6	100.0%	-4.0
3728	AT4G39720.1   VQ motif-containing protein, contains PF05678: VQ motif   chr4:18429886-18430858 REVERSE   Aliases: T19P19.110, T19P19_110	4.2	3.9	0.3	1.6	100.0%	-4.0
3729	AT3G24340.1   SNF2 domain-containing protein / helicase domain-containing protein, similar to SP:P41410 DNA repair protein rhp54 (RAD54 homolog) {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr3:8832092-8835729 REVERSE   Aliases: K7M2.11	2.5	2.8	-0.3	-1.6	100.0%	-4.3
3730	AT1G29880.1   glycyl-tRNA synthetase / glycine--tRNA ligase, identical to SP:O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}	8.1	8.8	-0.6	-1.6	100.0%	-3.4
3731	AT2G39000.3   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:16293414-16295045 REVERSE   Aliases: T7F6.17, T7F6_17	7.6	6.9	0.7	1.6	100.0%	-3.6
3732	AT4G14630.1   Symbol: GLP9   germin-like protein (GLP9), identical to germin-like protein subfamily 1 member 8 (SP:Q9LEA7)   chr4:8392915-8393802 FORWARD   Aliases: DL3355W, FCAALL.278, GERMIN LIKE PROTEIN 9	2.4	2.9	-0.6	-1.6	100.0%	-3.7
3733	AT1G05290.1   expressed protein   chr1:1539151-1540545 REVERSE   Aliases: YUP8H12.10, YUP8H12_10	2.7	2.9	-0.2	-1.6	100.0%	-4.4
3734	AT5G66570.1   Symbol: PSBO 1	8.4	7.0	1.4	1.6	100.0%	-3.3
3735	AT2G41880.1   Symbol: GK 1   guanylate kinase 1 (GK-1), identical to guanylate kinase (GK-1) (Arabidopsis thaliana) gi:7861795:gb:AAF70408   chr2:17481713-17484301 FORWARD   Aliases: AGK1, GUANYLATE KINASE 1, T11A7.23	6.6	5.8	0.7	1.6	100.0%	-3.5
3736	AT5G09770.1   ribosomal protein L17 family protein, contains Pfam profile: PF01196 ribosomal protein L17   chr5:3035047-3036543 REVERSE   Aliases: F17I14.40, F17I14_40	8.6	9.2	-0.6	-1.6	100.0%	-3.5
3737	AT4G16390.1   chloroplastic RNA-binding protein P67, putative, nearly identical to 67kD chloroplastic RNA-binding protein, P67 (Arabidopsis thaliana) GI:9755842   chr4:9257980-9260300 FORWARD   Aliases: DL4225W, FCAALL.354	6.6	7.2	-0.6	-1.6	100.0%	-3.6
3738	AT1G55500.1   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr1:20723241-20726399 FORWARD   Aliases: T5A14.10, T5A14_10	5.3	5.7	-0.4	-1.6	100.0%	-3.7
3739	AT2G16250.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:7046764-7050015 REVERSE   Aliases: F16F14.25, F16F14_25	3.9	3.5	0.3	1.6	100.0%	-3.9
3740	AT3G56640.1   exocyst complex subunit Sec15-like family protein, contains Pfam profile PF04091: Exocyst complex subunit Sec15-like   chr3:20992946-20995315 FORWARD   Aliases: T5P19.290	3.6	3.8	-0.2	-1.6	100.0%	-4.1
3741	AT2G39730.3   Symbol: RCA   ribulose biphosphate carboxylase/oxygenase activase / RuBisCO activase, identical to SWISS-PROT:P10896 ribulose biphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase, RA)(Arabidopsis thaliana)   chr2:16577824-16580597 REVERSE   Aliases: RUBISCO ACTIVASE, T5I7.18	9.5	8.1	1.5	1.6	100.0%	-3.4
3742	AT4G04470.1   Symbol: PMP22   peroxisomal membrane protein 22 kDa (PMP22), identical to peroxisomal membrane protein (Arabidopsis thaliana) gi:3980254:emb:CAA06834   chr4:2227659-2229256 REVERSE   Aliases: 22 KD PEROXISOMAL MEMBRANE PROTEIN, T26N6.9, T26N6_9	7.7	8.2	-0.5	-1.6	100.0%	-3.8
3743	AT3G07060.1   Symbol: EMB1974   expressed protein, ; expression supported by MPSS   chr3:2233000-2236919 FORWARD   Aliases: EMB1974, EMBRYO DEFECTIVE 1974, F17A9.23	3.5	3.8	-0.3	-1.6	100.0%	-4.0
3744	AT2G46110.1   ketopantoate hydroxymethyltransferase family protein, similar to SP:Q9Y7B6 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase) {Emericella nidulans}; contains Pfam profile PF02548: Ketopantoate hydroxymethyltransferase   chr2:18961532-18963603 REVERSE   Aliases: T3F17.24	8.2	8.9	-0.7	-1.6	100.0%	-3.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3745	AT5G02010.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr5:383150-385847 FORWARD   Aliases: KINASE PARTNER PROTEIN LIKE, KPP LIKE, T7H20.60, T7H20_60	2.9	3.3	-0.4	-1.6	100.0%	-3.8
3746	AT5G10100.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) (Arabidopsis thaliana) GI:2944180; contains Pfam profile PF02358: Trehalose-phosphatase   chr5:3157981-3160446 FORWARD   Aliases: T31P16.90, T31P16_90	3.1	2.7	0.4	1.6	100.0%	-3.8
3747	AT5G63540.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g19950.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g19950.3); similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g19950.1); similar to hypothetical protein LOC549050 [Xenopus tropicalis] (GB:NP_001016296.1)   chr5:25458009-25461649 REVERSE   Aliases: MLE2.17, MLE2_17	3.0	3.3	-0.2	-1.6	100.0%	-4.2
3748	AT3G25610.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Mus musculus (SP:P98200, SP:P70704), {Bos taurus} SP:Q29449; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr3:9310179-9314590 REVERSE   Aliases: T5M7.10	4.4	4.9	-0.6	-1.6	100.0%	-3.4
3749	AT4G26020.1   expressed protein, weak similarity to cardiac muscle factor 1 (Gallus gallus) GI:14422164   chr4:13202022-13204037 REVERSE   Aliases: F20B18.130, F20B18_130	2.5	2.7	-0.2	-1.6	100.0%	-4.6
3750	AT5G64230.1   expressed protein   chr5:25709679-25711279 FORWARD   Aliases: MSJ1.7, MSJ1_7	4.3	3.8	0.5	1.6	100.0%	-3.8
3751	AT5G45750.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303744 from (Pisum sativum)	8.7	9.4	-0.7	-1.6	100.0%	-3.7
3752	AT2G20540.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:8851241-8852845 FORWARD   Aliases: T13C7.13, T13C7_13	3.5	4.1	-0.6	-1.6	100.0%	-3.6
3753	AT2G38370.1   expressed protein   chr2:16079148-16081269 REVERSE   Aliases: T19C21.14, T19C21_14	6.7	7.8	-1.1	-1.6	100.0%	-3.8
3754	AT3G57780.1   expressed protein   chr3:21410743-21413303 REVERSE   Aliases: F15B8.30	3.0	3.2	-0.3	-1.6	100.0%	-4.0
3755	AT5G02270.1   Symbol: ATNAP9	10.2	10.6	-0.4	-1.6	100.0%	-4.3
3756	AT1G18070.2   similar to elongation factor 1-alpha / EF-1-alpha [Arabidopsis thaliana] (TAIR:At1g07930.1); similar to elongation factor 1-alpha / EF-1-alpha [Arabidopsis thaliana] (TAIR:At5g60390.1); similar to elongation factor 1-alpha / EF-1-alpha [Arabidopsis thaliana] (TAIR:At1g07920.1); similar to elongation factor 1-alpha / EF-1-alpha [Arabidopsis thaliana] (TAIR:At1g07940.1); similar to OSJNBb0067G11.10 [Oryza sativa (japonica cultivar-group)] (GB:XP_471489.1); similar to SUP2 gene product (GB:AAA79033.1); contains InterPro domain Elongation factor, GTP-binding (InterPro:IPR000795); contains InterPro domain Yeast eukaryotic release factor (InterPro:IPR003285); contains InterPro domain Elongation factor Tu, domain 2 (InterPro:IPR004161); contains InterPro domain Elongation factor Tu, C-terminal (InterPro:IPR004160)   chr1:6213736-6218328 REVERSE   Aliases: T10F20.8	6.8	7.9	-1.1	-1.6	100.0%	-3.7
3757	AT4G31050.1   lipoyltransferase (LIP2p), identical to lipoyltransferase (LIP2p) (Arabidopsis thaliana) GI:15887052; supporting cDNA gi:15887051:dbj:AB072390.1:   chr4:15114340-15115639 FORWARD   Aliases: F6I18.40, F6I18_40	3.7	3.4	0.3	1.6	100.0%	-3.8
3758	AT3G61870.2   expressed protein, hypothetical protein - Synechocystis sp. (strain PCC 6803), PIR:S75899   chr3:22913627-22915034 FORWARD   Aliases: F21F14.40	6.9	6.2	0.7	1.6	100.0%	-3.3
3759	AT3G12040.1   DNA-3-methyladenine glycosylase (MAG), identical to DNA-3-methyladenine glycosylase (MAG) SP:Q39147 from (Arabidopsis thaliana); contains Pfam profile: PF02245 methylpurine-DNA glycosylase (MPG)   chr3:3835135-3836802 REVERSE   Aliases: MEC18.4	3.8	3.3	0.4	1.6	100.0%	-3.8
3760	AT3G06780.1   glycine-rich protein   chr3:2143494-2144527 FORWARD   Aliases: F3E22.8	4.8	4.5	0.3	1.6	100.0%	-4.0
3761	AT4G32680.1   expressed protein   chr4:15763242-15765119 REVERSE   Aliases: F4D11.120, F4D11_120	4.8	4.2	0.6	1.6	100.0%	-3.9
3762	AT3G07390.1   Symbol: AIR12   auxin-responsive protein / auxin-induced protein (AIR12), identical (with 7 residue gap) to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana)   chr3:2365307-2366502 FORWARD   Aliases: F21O3.10	4.7	3.7	1.0	1.6	100.0%	-3.3
3763	AT3G25530.2   similar to 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis thaliana] (TAIR:At1g17650.1); similar to oxidoreductase-like [Oryza sativa (japonica cultivar-group)] (GB:BAD45192.1); contains InterPro domain 3-hydroxyisobutyrate dehydrogenase (InterPro:IPR002204); contains InterPro domain 6-phosphogluconate dehydrogenase, NAD binding domain (InterPro:IPR006115)   chr3:9273037-9274830 REVERSE   Aliases: MWL2.23	11.4	12.0	-0.5	-1.6	100.0%	-4.2
3764	AT1G22970.1   expressed protein   chr1:8130705-8132197 REVERSE   Aliases: F19G10.8, F19G10_8	5.0	5.5	-0.5	-1.6	100.0%	-3.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3765	AT5G62070.1   calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr5:24947145-24949802 REVERSE   Aliases: MTG10.10, MTG10_10	4.0	4.3	-0.3	-1.6	100.0%	-4.1
3766	AT1G16280.1   DEAD/DEAH box helicase, putative, similar to gb:L13612 DEAD-box protein (dbp45A) from Drosophila melanogaster and is a member of PF:00270 DEAD/DEAH box helicase family   chr1:5568476-5570481 REVERSE   Aliases: F3O9.8, F3O9_8	4.3	4.9	-0.6	-1.6	100.0%	-3.7
3767	AT4G39955.1   hydrolase, alpha/beta fold family protein, low similarity to SP:P24640:LIP3_MORSP Lipase 3 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Moraxella sp}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:18530537-18532253 FORWARD   Aliases: None	7.2	6.7	0.5	1.6	100.0%	-3.6
3768	AT1G76710.2   SET domain-containing protein (ASHH1), low similarity to huntingtin interacting protein 1 (Homo sapiens) GI:12697196; contains Pfam profile PF00856: SET domain; identical to cDNA ASH1-like protein 1 (ASHH1) partial cds GI:15488417   chr1:28794623-28797475 REVERSE   Aliases: F28O16.8, F28O16_8	5.7	6.2	-0.5	-1.6	100.0%	-3.6
3769	AT1G72190.1   oxidoreductase family protein, similar to D-3-phosphoglycerate dehydrogenase from Arabidopsis thaliana (SP:O04130), glyoxylate reductase from Homo sapiens (gi:6002730); contains Pfam D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain PF02826	6.7	6.3	0.3	1.6	100.0%	-3.8
3770	AT5G02100.1   oxysterol-binding family protein, similar to SWH1 (Saccharomyces cerevisiae) GI:402658; contains Pfam profile PF01237: Oxysterol-binding protein	8.0	8.5	-0.5	-1.6	100.0%	-3.8
3771	AT1G47670.1   amino acid transporter family protein, similar to lysine and histidine specific transporter GI:2576361 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:17539107-17541973 REVERSE   Aliases: F16N3.4, F16N3_4	4.8	5.1	-0.4	-1.6	100.0%	-3.9
3772	AT1G44770.1   expressed protein   chr1:16909979-16911903 REVERSE   Aliases: T12C22.4, T12C22_4	8.5	8.2	0.4	1.6	100.0%	-3.9
3773	AT4G01660.1   Symbol: ABC1At	7.1	7.6	-0.5	-1.6	100.0%	-3.8
3774	AT4G02070.1   Symbol: MSH6   DNA mismatch repair protein MSH6-1 (MSH6-1) (AGAA.3), identical to SP:O04716 DNA mismatch repair protein MSH6-1 (AtMsh6-1) cress) {Arabidopsis thaliana}	3.8	4.2	-0.3	-1.6	100.0%	-3.9
3775	AT5G13550.1   Symbol: SULTR4;1   sulfate transporter family protein, similar to sulfate transporter (Arabidopsis thaliana) GI:3777483; contains Pfam profiles PF00916: Sulfate transporter family, PF01740: STAS domain   chr5:4355279-4359555 REVERSE   Aliases: None	4.7	5.1	-0.4	-1.6	100.0%	-3.7
3776	AT1G80790.1   XH/XS domain-containing protein / XS zinc finger domain-containing protein, contains Pfam domains PF03469: XH domain, PF03468: XS domain and PF03470: XS zinc finger domain   chr1:30364615-30367748 FORWARD   Aliases: F23A5.14, F23A5_14	5.5	7.2	-1.7	-1.6	100.0%	-3.3
3777	AT4G34640.1   Symbol: SQS1   farnesyl-diphosphate farnesyltransferase 1 / squalene synthase 1 (SQS1), identical to SP:P53799 Farnesyl-diphosphate farnesyltransferase (EC 2.5.1.21) (Squalene synthetase) (SQS) (SS) (FPP:FPP farnesyltransferase) {Arabidopsis thaliana}; non-consensus GC donor splice site at exon 3, squalene synthase 2 (SQS2), Arabidopsis thaliana   chr4:16538287-16541913 FORWARD   Aliases: ERG9, SQUALENE SYNTHASE, SQUALENE SYNTHASE 1, T4L20.220, T4L20_220	7.7	8.3	-0.6	-1.6	100.0%	-3.7
3778	AT2G29995.1   expressed protein   chr2:12803987-12806496 REVERSE   Aliases: None	5.1	4.3	0.8	1.6	100.0%	-3.4
3779	AT5G54850.1   expressed protein   chr5:22297809-22298589 REVERSE   Aliases: MBG8.11, MBG8_11	4.3	4.6	-0.3	-1.6	100.0%	-4.0
3780	AT5G12260.1   expressed protein   chr5:3966366-3968879 FORWARD   Aliases: MXC9.22, MXC9_22	6.1	6.4	-0.2	-1.6	100.0%	-4.0
3781	AT1G72320.3   pumilio/Puf RNA-binding domain-containing protein, contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (5 copies)   chr1:27231822-27236658 REVERSE   Aliases: T9N14.7	7.4	8.4	-1.0	-1.6	100.0%	-3.5
3782	AT1G20870.1   expressed protein   chr1:7259091-7260764 REVERSE   Aliases: F9H16.15, F9H16_15	4.5	5.0	-0.5	-1.6	100.0%	-3.5
3783	AT3G15095.1   expressed protein   chr3:5081961-5084057 FORWARD   Aliases: K15M2.25	4.6	5.2	-0.6	-1.6	100.0%	-3.5
3784	AT5G53330.1   expressed protein   chr5:21656443-21658189 FORWARD   Aliases: K19E1.13, K19E1_13	7.3	6.8	0.5	1.6	100.0%	-3.8
3785	AT4G00355.4   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g45980.1); similar to OSJNBa0019G23.5 [Oryza sativa (japonica cultivar-group)] (GB:XP_474580.1)   chr4:154721-156376 FORWARD   Aliases: None	7.1	6.3	0.8	1.6	100.0%	-3.5
3786	AT2G32220.1   60S ribosomal protein L27 (RPL27A)   chr2:13685996-13686600 FORWARD   Aliases: F22D22.3, F22D22_3	7.5	6.8	0.7	1.6	100.0%	-3.4
3787	AT1G05100.1   Symbol: MAPKKK18   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:1469609-1470880 FORWARD   Aliases: T7A14.2, T7A14_2	4.6	4.2	0.4	1.6	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3788	AT1G66580.1   60S ribosomal protein L10 (RPL10C), contains Pfam profile: PF00826: Ribosomal L10   chr1:24842828-24844275 FORWARD   Aliases: T12I7.3, T12I7_3	11.7	12.1	-0.4	-1.6	100.0%	-3.8
3789	AT3G61690.1   expressed protein   chr3:22839324-22845011 FORWARD   Aliases: F15G16.80	5.1	5.6	-0.5	-1.6	100.0%	-3.7
3790	AT3G54090.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr3:20039102-20040964 FORWARD   Aliases: F24B22.50	5.4	6.2	-0.8	-1.6	100.0%	-3.4
3791	AT2G28250.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g10620.1); similar to putative receptor protein kinase PERK1 [Oryza sativa (japonica cultivar-group)] (GB:XP_463824.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr2:12050559-12053614 FORWARD   Aliases: T3B23.8, T3B23_8	3.6	4.4	-0.8	-1.6	100.0%	-3.3
3792	AT4G36970.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr4:17429739-17431680 REVERSE   Aliases: AP22.30, AP22_30	5.2	5.8	-0.6	-1.6	100.0%	-3.6
3793	AT5G64220.2   similar to ethylene-responsive calmodulin-binding protein, putative (SR1) [Arabidopsis thaliana] (TAIR:At2g22300.1); similar to calmodulin-binding protein [Arabidopsis thaliana] (TAIR:At5g09410.1); similar to putative calmodulin-binding transcription factor [Oryza sativa (japonica cultivar-group)] (GB:AAR06369.1); similar to another ethylene-upregulated protein ER1 [Nicotiana tabacum] (GB:AAG39222.1); similar to putative calmodulin binding protein similar to ER66 [Oryza sativa (japonica cultivar-group)] (GB:AAP53419.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048); contains InterPro domain CG-1 domain (InterPro:IPR005559); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr5:25703434-25709476 FORWARD   Aliases: MSJ1.6, MSJ1_6	6.4	7.3	-0.9	-1.6	100.0%	-3.6
3794	AT3G24200.2   similar to putative oxygenase [Oryza sativa (japonica cultivar-group)] (GB:XP_470364.1); contains InterPro domain Flavoprotein monooxygenase (InterPro:IPR000733); contains InterPro domain NAD-binding site (InterPro:IPR000205); contains InterPro domain Aromatic-ring hydroxylase (InterPro:IPR003042); contains InterPro domain UbiH/COQ6 monooxygenase (InterPro:IPR000689)   chr3:8747838-8751376 REVERSE   Aliases: MUJ8.10	10.2	9.5	0.7	1.6	100.0%	-3.8
3795	AT2G36870.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to cellulase (xyloglucan endo-transglycosylase) Gl:311835 from (Tropaeolum majus)   chr2:15479724-15481760 REVERSE   Aliases: T1J8.5, T1J8_5	3.0	3.5	-0.5	-1.6	100.0%	-3.8
3796	AT1G16350.1   inosine-5'-monophosphate dehydrogenase, putative, strong similarity to SP:P47996 gb:L34684 inosine monophosphate dehydrogenase (IMPDH) from Arabidopsis thaliana; member of the PF:00478 IMP dehydrogenase family   chr1:5590945-5592866 FORWARD   Aliases: F3O9.15, F3O9_15	8.1	8.9	-0.8	-1.6	100.0%	-3.7
3797	AT2G25830.1   YebC-related, contains Pfam profile PF01709: Domain of unknown function; contains TIGRFAM TIGR01033: conserved hypothetical protein; similar to YebC (Gl:5771432) (Legionella pneumophila)   chr2:11025846-11028768 REVERSE   Aliases: F17H15.14, F17H15_14	6.0	7.0	-1.0	-1.6	100.0%	-3.4
3798	AT1G63460.1   glutathione peroxidase, putative, contains Pfam profile: PF00255 glutathione peroxidases	9.8	10.2	-0.4	-1.6	100.0%	-3.9
3799	AT5G05710.1   pleckstrin homology (PH) domain-containing protein, similar to AtPH1 (Arabidopsis thaliana) Gl:5926716; contains Pfam profile PF00169: PH domain	10.5	9.9	0.6	1.6	100.0%	-3.5
3800	AT2G30590.1   Symbol: WRKY21	4.2	3.7	0.5	1.6	100.0%	-3.7
3801	AT4G22200.1   Symbol: AKT2   potassium channel protein 2 (AKT2) (AKT3), identical to potassium channel (Arabidopsis thaliana) gi:1100898:gb:AAA97865; Note: also identical to AKT3 (Arabidopsis thaliana) gi:1172218:gb:AAA96153, which is a truncated version of AKT2, PMID:10852932; member of the 1 pore, 6 transmembrane (1P/6TM- Shaker-type) K+ channel family, PMID:11500563; identical to cDNA inward-rectifying K+ channel (AKT3) Gl:1172219	2.5	2.7	-0.2	-1.6	100.0%	-4.4
3802	AT3G44850.1   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:16385602-16387916 REVERSE   Aliases: F28D10.40	4.6	5.5	-0.9	-1.6	100.0%	-3.6
3803	AT4G17890.2   Symbol: UBP20   similar to human Rev interacting-like family protein / hRIP family protein [Arabidopsis thaliana] (TAIR:At5g46750.1); similar to putative zinc finger protein [Oryza sativa (japonica cultivar-group)] (GB:AAO66537.1); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164)	7.7	8.5	-0.8	-1.6	100.0%	-3.5
3804	AT1G03980.1   phytochelatin synthase 2 (PCS2), identical to phytochelatin synthase (Arabidopsis thaliana) gi:16519291:gb:AAK94671   chr1:1018106-1022107 REVERSE   Aliases: F21M11.9, F21M11_9	3.2	3.4	-0.3	-1.6	100.0%	-4.1
3805	AT1G10210.2   Symbol: ATMPK1	3.0	2.7	0.3	1.6	100.0%	-4.1
3806	AT5G46780.2   VQ motif-containing protein, contains PF05678: VQ motif   chr5:18996204-18997283 FORWARD   Aliases: MZA15.20, MZA15_20	6.1	5.1	1.0	1.6	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3807	AT5G44610.1   DREPP plasma membrane polypeptide-related, contains Pfam profile: PF05558 DREPP plasma membrane polypeptide   chr5:18010792-18011895 REVERSE   Aliases: K15C23.5, K15C23_5	6.3	5.4	0.9	1.6	100.0%	-3.3
3808	AT1G24310.1   expressed protein   chr1:8624050-8626394 FORWARD   Aliases: F3I6.25, F3I6_25	4.1	4.4	-0.3	-1.6	100.0%	-3.9
3809	AT5G41460.1   fringe-related protein, strong similarity to unknown protein (pir::T13026) similarity to predicted proteins + similar to hypothetical protein GB:AAC23643 (Arabidopsis thaliana) + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr5:16606826-16609469 REVERSE   Aliases: MYC6.16, MYC6_16	3.0	3.2	-0.3	-1.6	100.0%	-4.0
3810	AT1G65590.1   glycosyl hydrolase family 20 protein, contains Pfam PF00728: Glycosyl hydrolase family 20, catalytic domain; contains Pfam PF02838: Glycosyl hydrolase family 20, domain 2; similar to Beta-hexosaminidase beta chain precursor (EC 3.2.1.52) (N-acetyl-beta- glucosaminidase) (Beta-N-acetylhexosaminidase) (Hexosaminidase B) (Swiss-Prot:P07686) (Homo sapiens)   chr1:24389594-24394870 FORWARD   Aliases: F5I14.12, F5I14_12	2.2	1.9	0.3	1.6	100.0%	-4.3
3811	AT3G26410.1   expressed protein   chr3:9670653-9672565 REVERSE   Aliases: F20C19.14	4.0	4.4	-0.4	-1.6	100.0%	-3.9
3812	AT1G24620.1   polcalcin, putative / calcium-binding pollen allergen, putative, similar to polcalcin Jun o 2 (calcium-binding pollen allergen Jun o 2) SP:O64943 from (Juniperus oxycedrus)   chr1:8723698-8724445 REVERSE   Aliases: F21J9.28	3.5	3.2	0.3	1.6	100.0%	-4.1
3813	AT1G52420.1   glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1   chr1:19531518-19534956 FORWARD   Aliases: F19K6.13	9.6	9.2	0.4	1.6	100.0%	-3.8
3814	AT2G14860.1   peroxisomal membrane protein 22 kDa, putative, similar to 22 kDa peroxisomal membrane protein {Mus musculus} SWISS-PROT:P42925, NCBI_gi:454833   chr2:6394902-6396645 REVERSE   Aliases: T26I20.2, T26I20_2	3.5	4.1	-0.5	-1.6	100.0%	-3.5
3815	AT4G18300.1   eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein, similar to SP:Q64350 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) {Rattus norvegicus}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon   chr4:10118863-10120992 FORWARD   Aliases: T9A21.150, T9A21_150	4.0	4.5	-0.5	-1.6	100.0%	-3.9
3816	AT1G68290.1   bifunctional nuclease, putative, similar to bifunctional nuclease (Zinnia elegans) gi:4099833:gb:AAD00694   chr1:25600334-25602101 FORWARD   Aliases: T22E19.8, T22E19_8	2.4	2.8	-0.4	-1.6	100.0%	-4.0
3817	AT4G33060.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr4:15948507-15952172 FORWARD   Aliases: F4I10.3	6.2	7.0	-0.8	-1.6	100.0%	-3.6
3818	AT5G62575.2   expressed protein   chr5:25134749-25136118 FORWARD   Aliases: None	7.2	7.7	-0.5	-1.6	100.0%	-3.5
3819	AT4G18750.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:10304861-10307476 FORWARD   Aliases: F28A21.160, F28A21_160	3.0	3.2	-0.2	-1.6	100.0%	-4.3
3820	AT3G23870.1   permease-related, low similarity to purine permease (Arabidopsis thaliana) GI:7620007; contains 9 predicted transmembrane domains; contains Pfam PF05653: Protein of unknown function (DUF803); identified as COG0697, Permeases of the drug/metabolite transporter (DMT) superfamily   chr3:8619199-8621914 FORWARD   Aliases: F14O13.5	3.7	3.3	0.5	1.6	100.0%	-3.6
3821	AT3G07690.1   similar to NAD-dependent glycerol-3-phosphate dehydrogenase family protein [Arabidopsis thaliana] (TAIR:At2g41540.1); similar to NAD-dependent glycerol-3-phosphate dehydrogenase family protein [Arabidopsis thaliana] (TAIR:At2g41540.2); similar to putative glycerol-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:NP_915827.1); similar to putative glycerol-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:AAU44049.1); contains InterPro domain NAD-dependent glycerol-3-phosphate dehydrogenase (InterPro:IPR006168)   chr3:2457114-2459700 FORWARD   Aliases: MLP3.14	5.5	6.0	-0.5	-1.6	100.0%	-3.6
3822	AT3G53400.1   expressed protein   chr3:19809129-19811114 FORWARD   Aliases: F4P12.100	6.9	7.5	-0.6	-1.6	100.0%	-3.4
3823	AT1G09300.1   metalloproteinase M24 family protein, similar to SP:P15034 Xaa-Pro aminopeptidase (EC 3.4.11.9) (X-Pro aminopeptidase) (Aminopeptidase P II) (Aminoacylproline aminopeptidase) {Escherichia coli}; contains Pfam profiles PF00557: metalloproteinase family M24, PF05195: Aminopeptidase P, N-terminal domain   chr1:3003928-3008215 FORWARD   Aliases: T31J12.2, T31J12_2	5.8	6.2	-0.4	-1.6	100.0%	-3.8
3824	AT4G27490.1   3' exoribonuclease family domain 1-containing protein, contains Pfam PF01138: 3' exoribonuclease family, domain 1   chr4:13739812-13741809 FORWARD   Aliases: F27G19.90, F27G19_90	5.8	6.7	-0.9	-1.6	100.0%	-3.3
3825	AT4G36420.1   ribosomal protein L12 family protein   chr4:17203034-17204315 REVERSE   Aliases: AP22.77, AP22_77	3.1	3.4	-0.3	-1.6	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3826	AT5G53770.1   nucleotidyltransferase family protein, contains Pfam domains PF03828: PAP/25A associated domain, PF01909: Nucleotidyltransferase domain   chr5:21843885-21847209 FORWARD   Aliases: MGN6.13, MGN6_13	4.0	5.0	-1.0	-1.6	100.0%	-3.8
3827	AT5G42850.2   expressed protein   chr5:17199108-17199807 REVERSE   Aliases: MBD2.4, MBD2_4	7.4	8.0	-0.6	-1.6	100.0%	-3.9
3828	AT1G07745.1   Symbol: ATRAD51D/RAD51D   DNA repair family protein, contains similarity to Swiss-Prot:O75771 DNA repair protein RAD51 homolog 4 (R51H3) (TRAD) (Homo sapiens)   chr1:2400794-2402477 REVERSE   Aliases: ATRAD51D, F24B9.14, F24B9_14, RAD51D	2.7	2.5	0.2	1.6	100.0%	-4.3
3829	AT1G01730.1   expressed protein   chr1:270967-272021 FORWARD   Aliases: T1N6.14, T1N6_14	7.7	7.3	0.3	1.6	100.0%	-3.9
3830	AT1G70360.1   F-box protein-related   chr1:26512441-26512988 FORWARD   Aliases: F17O7.10, F17O7_10	5.7	5.2	0.4	1.6	100.0%	-4.1
3831	AT1G52140.1   expressed protein   chr1:19411033-19411923 REVERSE   Aliases: F5F19.20, F5F19_20	3.8	3.4	0.4	1.6	100.0%	-4.0
3832	AT1G21740.1   expressed protein, contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Protein of unknown function (DUF630)   chr1:7641569-7645067 FORWARD   Aliases: F8K7.18, F8K7_18	4.3	4.7	-0.4	-1.6	100.0%	-3.8
3833	AT5G01240.2   amino acid permease, putative, strong similarity to AUX1 GI:1531758 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr5:98532-101830 FORWARD   Aliases: F7J8.220, F7J8_220	4.9	4.6	0.3	1.6	100.0%	-3.9
3834	AT1G14180.2   expressed protein   chr1:4847159-4849200 FORWARD   Aliases: F7A19.26	3.3	3.7	-0.4	-1.6	100.0%	-3.8
3835	AT1G53200.2   expressed protein   chr1:19844044-19847071 REVERSE   Aliases: F12M16.11, F12M16_11	3.9	4.3	-0.4	-1.6	100.0%	-3.8
3836	AT5G64140.1   Symbol: RPS28   40S ribosomal protein S28 (RPS28C)   chr5:25684550-25685518 REVERSE   Aliases: MHJ24.12, MHJ24_12, RIBOSOMAL PROTEIN S28	10.8	11.3	-0.5	-1.6	100.0%	-4.0
3837	AT1G69330.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:26067479-26069168 REVERSE   Aliases: F23O10.9, F23O10_9	4.4	3.8	0.6	1.6	100.0%	-3.7
3838	AT2G44360.1   expressed protein   chr2:18327499-18328766 REVERSE   Aliases: F4I1.17	6.9	7.5	-0.5	-1.6	100.0%	-3.7
3839	AT2G40490.1   uroporphyrinogen decarboxylase, putative / UPD, putative, similar to uroporphyrinogen decarboxylase (chloroplast) from Nicotiana tabacum (SP:Q42967), Hordeum vulgare (SP:Q42855), Zea mays (SP:O81220); contains Pfam domain uroporphyrinogen decarboxylase (URO-D) PF01208   chr2:16919940-16922255 FORWARD   Aliases: T2P4.16, T2P4_16	5.1	5.5	-0.5	-1.6	100.0%	-3.8
3840	AT1G12110.1   Symbol: NRT1.1	8.1	7.6	0.5	1.6	100.0%	-3.6
3841	AT1G70160.1   expressed protein, similar to hypothetical protein GI:4455225 from (Arabidopsis thaliana)   chr1:26423612-26426188 FORWARD   Aliases: F20P5.12, F20P5_12	8.1	9.0	-0.9	-1.6	100.0%	-3.6
3842	AT1G61990.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr1:22914870-22916600 FORWARD   Aliases: F8K4.18, F8K4_18	4.8	5.5	-0.8	-1.6	100.0%	-3.5
3843	AT1G32210.1   Symbol: ATDAD1	10.1	9.5	0.6	1.6	100.0%	-3.8
3844	AT1G78340.1   Symbol: ATGSTU22   glutathione S-transferase, putative, similar to glutathione transferase GI:2853219 from (Carica papaya)   chr1:29477785-29478756 REVERSE   Aliases: F3F9.13, F3F9_13	5.7	6.5	-0.8	-1.6	100.0%	-3.5
3845	AT5G54640.1   Symbol: RAT5   histone H2A, identical to histone H2A Arabidopsis thaliana GI:7595337   chr5:22213703-22214713 FORWARD   Aliases: MRB17.14, MRB17_14, RESISTANT TO AGROBACTERIUM TRANSFORMATION 5	8.8	9.7	-0.8	-1.6	100.0%	-3.8
3846	AT1G60180.1   expressed protein, similar to hypothetical protein GI:6017113 from (Arabidopsis thaliana)   chr1:22199190-22200350 REVERSE   Aliases: T13D8.7, T13D8_7	2.9	2.7	0.2	1.6	100.0%	-4.3
3847	AT5G56170.1   expressed protein, contains similarity to GPI-anchored protein   chr5:22753195-22754512 FORWARD   Aliases: MDA7.23, MDA7_23	9.1	8.6	0.5	1.6	100.0%	-4.3
3848	AT5G02460.1   Dof-type zinc finger domain-containing protein, zinc finger protein OBP3, Arabidopsis thaliana, EMBL:AF155818   chr5:539247-541056 REVERSE   Aliases: T22P11.50, T22P11_50	2.4	2.2	0.2	1.6	100.0%	-4.6
3849	AT1G53070.1   legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain   chr1:19782039-19783041 FORWARD   Aliases: F8L10.7, F8L10_7	3.0	3.2	-0.2	-1.6	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3850	AT3G21790.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:7676934-7678421 REVERSE   Aliases: MSD21.15	6.3	5.4	0.9	1.6	100.0%	-3.2
3851	AT1G48090.2   C2 domain-containing protein, contains Pfam profile: PF00168 C2 domain   chr1:17739966-17761639 REVERSE   Aliases: F21D18.22	4.6	5.5	-0.9	-1.6	100.0%	-3.6
3852	AT4G15390.1   transferase family protein, similar to alcohol acyltransferase (Fragaria x ananassa)(GI:10121328)(PMID:10810141), deacetylvindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034)   chr4:8792812-8794293 REVERSE   Aliases: DL3740C, FCAALL.282	3.4	4.1	-0.7	-1.6	100.0%	-3.3
3853	AT4G04800.1   methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein, low similarity to pilin-like transcription factor (Homo sapiens) GI:5059062, SP:P14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) {Neisseria gonorrhoeae}; contains Pfam profile PF01641: SelR domain   chr4:2439548-2441203 FORWARD   Aliases: T4B21.6, T4B21_6	6.0	5.6	0.4	1.6	100.0%	-3.9
3854	AT1G54340.1   Symbol: ICDH   isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative, strong similarity to NADP-isocitrate dehydrogenase GI:5764653 from (Citrus limon); Nicotiana tabacum SP:P50218   chr1:20287147-20290453 FORWARD   Aliases: F20D21.16, F20D21_16, isocitrate dehydrogenase	5.9	5.3	0.7	1.6	100.0%	-3.6
3855	AT2G31410.1   expressed protein   chr2:13399099-13399928 REVERSE   Aliases: T28P16.10, T28P16_10	4.8	5.4	-0.6	-1.6	100.0%	-3.5
3856	AT1G80400.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to SP:Q90972 RING finger protein 13 {Gallus gallus}; contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:30230068-30232931 FORWARD   Aliases: F5I6.15, F5I6_15	6.7	6.2	0.5	1.6	100.0%	-3.6
3857	AT1G35190.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to hyoscyamine 6-dioxygenase hydroxylase from Hyoscyamus niger (GB:P24397)(SP:P24397), Atropa belladonna (gi:4996123); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily	8.2	7.5	0.7	1.6	100.0%	-3.7
3858	AT3G13860.1   chaperonin, putative, similar to SWISS-PROT:P29197- chaperonin CPN60, mitochondrial precursor (HSP60) (Arabidopsis thaliana) ; contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr3:4561524-4565256 REVERSE   Aliases: MCP4.9	9.8	10.3	-0.6	-1.6	100.0%	-3.6
3859	AT1G76550.1   pyrophosphate--fructose-6-phosphate 1-phosphotransferase alpha subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative, strong similarity to SP:Q41140 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit (EC 2.7.1.90) (PFP) (PPI-PFK) {Ricinus communis}; contains Pfam profile PF00365: Phosphofructokinase   chr1:28727596-28731900 REVERSE   Aliases: F14G6.15, F14G6_15	7.8	9.2	-1.4	-1.6	100.0%	-3.3
3860	AT3G14920.1   expressed protein   chr3:5018282-5020280 FORWARD   Aliases: K15M2.6	7.7	8.6	-0.9	-1.6	100.0%	-3.6
3861	AT2G02480.1   Symbol: STI   DNA polymerase-related, weak similarity to DNA polymerase III holoenzyme tau subunit (Thermus thermophilus) GI:2583049   chr2:660742-665634 FORWARD   Aliases: DNA POLYMERASE III LIKE PROTEIN, GAMMA SUBUNIT, STICHEL, T8K22.22, T8K22_22	3.9	4.2	-0.3	-1.6	100.0%	-4.0
3862	AT4G02560.1   Symbol: LD   homeobox protein LUMINIDEPENDENS (LD), identical to Homeobox protein LUMINIDEPENDENS (Swiss-Prot:Q38796) (Arabidopsis thaliana)   chr4:1123492-1128397 REVERSE   Aliases: LUMINIDEPENDENS, T10P11.15, T10P11_15	5.7	6.4	-0.6	-1.6	100.0%	-3.7
3863	AT1G43710.1   Symbol: EMB1075   serine decarboxylase, identical to serine decarboxylase (Arabidopsis thaliana) GI:15011302; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain	9.2	9.6	-0.4	-1.6	100.0%	-4.0
3864	AT5G52810.1   ornithine cyclodeaminase/mu-crystallin family protein, contains Pfam PF02423: Ornithine cyclodeaminase/mu-crystallin family   chr5:21416557-21417829 FORWARD   Aliases: MXC20.2, MXC20_2	4.4	4.7	-0.3	-1.6	100.0%	-4.0
3865	AT1G50700.1   Symbol: CPK33   calcium-dependent protein kinase, putative / CDPK, putative, similar to calmodulin-domain protein kinase CDPK isoform 9 (Arabidopsis thaliana) gi:1399265:gb:AAB03242   chr1:18785882-18788053 FORWARD   Aliases: F17J6.22, F17J6_22	4.7	5.2	-0.5	-1.6	100.0%	-3.6
3866	AT5G20300.3   similar to chloroplast outer membrane protein, putative [Arabidopsis thaliana] (TAIR:At3g16620.1); similar to chloroplast Toc125 [Physcomitrella patens] (GB:AAS47583.1)	6.2	6.9	-0.7	-1.6	100.0%	-3.9
3867	AT5G18750.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain   chr5:6255179-6257934 FORWARD   Aliases: F17K4.2	4.9	5.4	-0.4	-1.6	100.0%	-3.6
3868	AT1G07230.1   phosphoesterase family protein, low similarity to SP:P95246 Phospholipase C 2 precursor (EC 3.1.4.3) {Mycobacterium tuberculosis}; contains Pfam profile PF04185: Phosphoesterase family	6.8	5.7	1.1	1.6	100.0%	-3.5
3869	AT5G50730.1   expressed protein, ; expression supported by MPSS   chr5:20653209-20653628 REVERSE   Aliases: MFB16.13, MFB16_13	6.2	7.3	-1.1	-1.6	100.0%	-3.5
3870	AT1G76510.2   ARID/BRIGHT DNA-binding domain-containing protein, contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain	6.1	6.7	-0.6	-1.6	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3871	AT3G46480.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to gibberellin 20-oxidase (gi:4678370); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr3:17114158-17116579 FORWARD   Aliases: F12A12.1	3.5	3.0	0.5	1.6	100.0%	-3.7
3872	AT3G22830.1   Symbol: AT HSFA6B   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr3:8078827-8081058 FORWARD   Aliases: HSFA6B, MWI23.20	5.4	4.6	0.8	1.6	100.0%	-3.4
3873	AT4G25730.1   FtsJ-like methyltransferase family protein, contains Pfam profile: PF01728 FtsJ-like methyltransferase   chr4:13102688-13106789 REVERSE   Aliases: F14M19.10, F14M19_10	5.2	5.7	-0.4	-1.6	100.0%	-3.7
3874	AT1G29470.2   similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At5g64030.1); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At3g51070.1); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At2g34300.1); similar to OSJNBb0020]19.14 [Oryza sativa (japonica cultivar-group)] (GB:XP_474482.1); similar to ankyrin-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82580.1); contains InterPro domain Putative methyltransferase DUF248 (InterPro:IPR004159)   chr1:10310231-10313741 REVERSE   Aliases: F15D2.5, F15D2_5	9.9	10.3	-0.4	-1.6	100.0%	-4.0
3875	AT4G18740.2   expressed protein   chr4:10303425-10304583 REVERSE   Aliases: F28A21.150, F28A21_150	3.4	3.0	0.4	1.6	100.0%	-4.0
3876	AT5G52430.1   hydroxyproline-rich glycoprotein family protein, Common family member At4g25620 (Arabidopsis thaliana)   chr5:21298999-21302431 REVERSE   Aliases: K24M7.18, K24M7_18	4.4	4.0	0.3	1.6	100.0%	-3.9
3877	AT3G17360.1   kinesin motor protein-related, similar to KLP2 protein GB:CAA63826 from (Xenopus laevis)	2.2	2.3	-0.1	-1.6	100.0%	-4.9
3878	AT3G46780.1   expressed protein   chr3:17239658-17242186 FORWARD   Aliases: T6H20.190	2.4	2.2	0.2	1.6	100.0%	-4.6
3879	AT3G47530.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:17528367-17530142 REVERSE   Aliases: F1P2.80	4.8	5.1	-0.3	-1.6	100.0%	-3.8
3880	AT3G24560.3   Symbol: RSY3   expressed protein, contains Pfam profile PF01171: PP-loop family   chr3:8963767-8966968 FORWARD   Aliases: MOB24.14, RASPBERRY 3	3.2	2.8	0.4	1.6	100.0%	-3.9
3881	AT5G06240.1   Symbol: EMB2735   expressed protein   chr5:1888314-1889697 FORWARD   Aliases: EMB2735, EMBRYO DEFECTIVE 2735, MBL20.12, MBL20_12	5.9	6.3	-0.4	-1.6	100.0%	-3.8
3882	AT2G22310.1   Symbol: ATUBP4	6.0	6.4	-0.4	-1.6	100.0%	-3.7
3883	AT3G56270.1   expressed protein, contains Pfam PF05701: Plant protein of unknown function (DUF827)   chr3:20880979-20883028 FORWARD   Aliases: F18O21.230	3.8	4.2	-0.4	-1.6	100.0%	-3.9
3884	AT5G18770.1   F-box family protein, contains F-box domain Pfam:PF00646	3.3	3.0	0.3	1.6	100.0%	-4.2
3885	AT2G47520.1   encodes a member of the ERF (ethylene response factor) subfamily B-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 5 members in this subfamily including RAP2.2 AND RAP2.12.   chr2:19509917-19510602 REVERSE   Aliases: T30B22.18	4.6	4.0	0.7	1.6	100.0%	-3.5
3886	AT1G56200.1   Symbol: EMB1303   expressed protein   chr1:21034480-21035721 FORWARD   Aliases: EMB1303, EMBRYO DEFECTIVE 1303, F14G9.26, F14G9_26	9.5	9.0	0.5	1.6	100.0%	-3.9
3887	AT5G10550.1   DNA-binding bromodomain-containing protein, low similarity to kinase (Gallus gallus) GI:1370092; contains Pfam profile PF00439: Bromodomain   chr5:3332856-3335233 REVERSE   Aliases: F12B17.100, F12B17_100	5.6	6.1	-0.6	-1.6	100.0%	-3.7
3888	AT3G15010.2   RNA recognition motif (RRM)-containing protein, similar to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:5052738-5054949 FORWARD   Aliases: K15M2.15	6.5	6.0	0.6	1.6	100.0%	-4.1
3889	AT3G53440.2   expressed protein   chr3:19821766-19823648 FORWARD   Aliases: F4P12.140	3.4	3.6	-0.2	-1.6	100.0%	-4.2
3890	AT5G03680.1   trihelix DNA-binding protein, putative, similar to DNA-binding protein DF1 (Pisum sativum) GI:13646986   chr5:957857-960759 FORWARD   Aliases: F17C15.100, F17C15_100	4.3	3.9	0.4	1.6	100.0%	-3.7
3891	AT3G09710.1   Symbol: IQD1   calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:2976669-2979274 REVERSE   Aliases: F11F8.30, IQ DOMAIN 1	3.2	3.0	0.3	1.6	100.0%	-4.1
3892	AT1G74150.1   kelch repeat-containing protein, low similarity to rngB protein, Dictyostelium discoideum, PIR:S68824; contains Pfam profile PF01344: Kelch motif   chr1:27884189-27887157 FORWARD   Aliases: F9E11.8, F9E11_8	2.6	2.9	-0.2	-1.6	100.0%	-4.5
3893	AT2G35733.1   expressed protein   chr2:15029755-15029946 REVERSE   Aliases: None	5.7	5.2	0.5	1.6	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3894	AT2G22830.1   squalene monooxygenase, putative / squalene epoxidase, putative, similar to SP:O65404 (SE 1,1), SP:O65402 (SE 1,2), SP:O65403 (SE 2)   chr2:9730768-9733350 REVERSE   Aliases: T20K9.4, T20K9_4	2.9	3.1	-0.3	-1.6	100.0%	-4.1
3895	AT4G23450.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr4:12240837-12242716 REVERSE   Aliases: F16G20.150, F16G20_150	3.9	3.5	0.4	1.6	100.0%	-3.7
3896	AT4G34138.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr4:16348110-16349986 REVERSE   Aliases: None	5.4	6.2	-0.9	-1.6	100.0%	-3.6
3897	AT4G11380.1   beta-adaptin, putative, strong similarity to SP:Q10567 Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) (Homo sapiens), beta-adaptin (Drosophila melanogaster) GI:434902; contains Pfam profile: PF01602 Adaptin N terminal region   chr4:6920503-6925964 FORWARD   Aliases: F8L21.170, F8L21_170	7.5	8.5	-1.0	-1.6	100.0%	-3.6
3898	AT3G53110.1   Symbol: LOS4   DEAD/DEAH box helicase, putative, RNA helicase, Mus musculus, PIR:I49731	9.0	9.4	-0.4	-1.6	100.0%	-4.1
3899	AT3G56710.1   Symbol: SIB1   sigA-binding protein, identical to SigA binding protein (Arabidopsis thaliana) gi:6980074:gb:AAF34713; contains Pfam PF05678: VQ motif   chr3:21017729-21018544 REVERSE   Aliases: SIGMA FACTOR BINDING PROTEIN 1, T8M16.40	4.3	3.9	0.4	1.6	100.0%	-3.6
3900	AT4G21900.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: MatE   chr4:11613291-11623531 REVERSE   Aliases: T8O5.110, T8O5_110	6.5	5.9	0.6	1.6	100.0%	-3.5
3901	AT4G21910.3   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr4:11625579-11631029 REVERSE   Aliases: T8O5.120, T8O5_120	6.5	5.9	0.6	1.6	100.0%	-3.5
3902	ATCG00480.1   Symbol: ATPB   chloroplast-encoded gene for beta subunit of ATP synthase   chrC:52660-54156 REVERSE   Aliases: ATPB	8.9	9.9	-1.0	-1.6	100.0%	-3.6
3903	AT5G66055.2   Symbol: EMB2036   ankyrin repeat protein / AKRP (AKR), identical to ankyrin repeat protein (AKRP) (Arabidopsis thaliana) SWISS-PROT:Q05753   chr5:26434382-26436490 REVERSE   Aliases: EMB2036, EMBRYO DEFECTIVE 2036	3.9	3.5	0.4	1.6	100.0%	-4.0
3904	AT1G31810.1   similar to formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g58160.1); similar to formin homology 2 domain-containing protein / FH2 domain-containing protein [Arabidopsis thaliana] (TAIR:At2g25050.1); similar to diaphanous homologue-like [Oryza sativa (japonica cultivar-group)] (GB:XP_468248.1); similar to putative diaphanous homologue [Oryza sativa (japonica cultivar-group)] (GB:XP_478998.1); similar to putative diaphanous 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_481245.1); contains InterPro domain Actin-binding FH2 (InterPro:IPR003104); contains InterPro domain RNA polymerase Rpb1, domain 5 (InterPro:IPR007081)	5.4	6.1	-0.7	-1.6	100.0%	-3.5
3905	AT1G68400.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor kinase GB:AAA33715 from (Petunia integrifolia)   chr1:25649702-25652609 REVERSE   Aliases: T2E12.5, T2E12_5	3.3	3.6	-0.3	-1.6	100.0%	-3.9
3906	AT1G52920.1   lanthionine synthetase C-like family protein, contains Pfam domain, PF05147: Lanthionine synthetase C-like protein   chr1:19713028-19714689 REVERSE   Aliases: F14G24.19, F14G24_19	6.1	5.2	0.9	1.6	100.0%	-3.4
3907	AT3G07970.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase precursor (Cucumis melo) GI:3320462; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases); contains non-consensus AA donor splice site at exon 2	2.6	2.9	-0.3	-1.6	100.0%	-4.2
3908	AT3G56310.2   alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative, similar to alpha-galactosidase SP:Q42656 from (Coffea arabica)   chr3:20893806-20897302 FORWARD   Aliases: F18O21.270	11.1	10.7	0.4	1.6	100.0%	-4.0
3909	AT2G03460.1   similar to kelch repeat-containing F-box family protein [Arabidopsis thaliana] (TAIR:At5g51250.1)   chr2:1043229-1044764 REVERSE   Aliases: T4M8.11, T4M8_11	4.1	3.6	0.5	1.6	100.0%	-3.9
3910	AT3G05675.2   expressed protein   chr3:1658277-1660312 REVERSE   Aliases: None	3.9	4.3	-0.3	-1.6	100.0%	-4.0
3911	AT1G70940.1   Symbol: PIN3   auxin transport protein, putative (PIN3), similar to auxin transport protein (Arabidopsis thaliana) gi:5817301:gb:AAD52695   chr1:26746716-26750057 FORWARD   Aliases: F15H11.14, F15H11_14, PIN FORMED 3, PIN3	4.8	5.5	-0.7	-1.6	100.0%	-3.6
3912	AT4G31500.1   Symbol: CYP83B1   cytochrome P450 83B1 (CYP83B1), identical to Cytochrome P450 (SP:O65782) (Arabidopsis thaliana)   chr4:15273477-15275316 REVERSE   Aliases: ALTERED TRYPTOPHAN REGULATION 4, ATR4, CYTOCHROME P450 MONOOXYGENASE 83B1, F3L17.70, F3L17_70, RED LIGHT ELONGATED 1, RED1, RNT1, SUPERROOT 2, SUR2	5.6	6.4	-0.8	-1.6	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3913	AT2G02090.1   SNF2 domain-containing protein / helicase domain-containing protein, similar to transcriptional activator SRCAP (Homo sapiens) GI:5106572; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr2:523283-527011 FORWARD   Aliases: F5O4.14, F5O4_14	6.7	7.2	-0.4	-1.6	100.0%	-3.9
3914	AT1G03420.1   expressed protein, similar to gb:T45484, emb:Z30724, and emb:Z30531   chr1:846790-847682 FORWARD   Aliases: F21B7.4, F21B7_4	5.4	5.1	0.4	1.6	100.0%	-3.9
3915	AT2G41620.1   nucleoporin interacting component family protein, contains Pfam profile PF04097: Nucleoporin interacting component   chr2:17357223-17362126 REVERSE   Aliases: T32G6.14, T32G6_14	5.4	6.2	-0.8	-1.6	100.0%	-3.7
3916	AT3G12650.1   expressed protein   chr3:4017837-4018638 REVERSE   Aliases: T2E22.4	9.1	8.7	0.4	1.6	100.0%	-3.9
3917	AT5G67600.1   expressed protein   chr5:26976797-26977535 REVERSE   Aliases: K9I9.17, K9I9_17	10.3	9.6	0.8	1.6	100.0%	-3.8
3918	AT3G20390.1   endoribonuclease L-PSP family protein, contains Pfam domain PF01042: Endoribonuclease L-PSP   chr3:7109955-7111830 REVERSE   Aliases: MQC12.17	11.3	11.9	-0.6	-1.6	100.0%	-3.9
3919	AT5G05610.2   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr5:1676941-1679105 REVERSE   Aliases: MOP10.15, MOP10_15	6.3	5.7	0.6	1.6	100.0%	-3.6
3920	AT4G15660.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.0	3.2	-0.2	-1.6	100.0%	-4.4
3921	AT4G32850.8   Symbol: nPAP   similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At1g17980.1); similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At2g25850.1); similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At2g25850.2); similar to putative polynucleotide adenylyltransferase [Oryza sativa (indica cultivar-group)] (GB:AAW68018.1); similar to putative polynucleotide adenylyltransferase [Oryza sativa (indica cultivar-group)] (GB:AAW68015.1); similar to putative poly(A) polymerase [Oryza sativa (japonica cultivar-group)] (GB:XP_464757.1); contains InterPro domain Poly(A) polymerase, predicted RNA-binding domain (InterPro:IPR007010); contains InterPro domain Poly(A) polymerase, central region (InterPro:IPR007012); contains InterPro domain PAP/25A core domain (InterPro:IPR001201); contains InterPro domain DNA polymerase, beta-like region (InterPro:IPR002934)   chr4:15849776-15854464 FORWARD   Aliases: NUCLEAR POLY(A) POLYMERASE, T16I18.60, T16I18_60	6.6	6.2	0.4	1.6	100.0%	-3.8
3922	AT4G26600.1   nucleolar protein, putative, similar to SP:P46087 Proliferating-cell nucleolar antigen p120 (Proliferation-associated nucleolar protein p120) {Homo sapiens}; contains Pfam profile PF01189: NOL1/NOP2/sun family   chr4:13419573-13423775 FORWARD   Aliases: T15N24.50, T15N24_50	3.2	3.8	-0.6	-1.6	100.0%	-4.2
3923	AT5G17310.2   UTP--glucose-1-phosphate uridylyltransferase, putative / UDP-glucose pyrophosphorylase, putative / UGPase, putative, strong similarity to SP:P19595 UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9) (UDP-glucose pyrophosphorylase) (UDPGP) (UGPase) {Solanum tuberosum}; contains Pfam profile PF01704: UTP--glucose-1-phosphate uridylyltransferase   chr5:5696649-5700924 REVERSE   Aliases: MKP11.26, MKP11_26	8.6	9.6	-1.0	-1.6	100.0%	-3.4
3924	AT5G45140.1   Symbol: NRPC2   similar to DNA-directed RNA polymerase II 135 kDa polypeptide / RNA polymerase II subunit 2 (RPB135) (RPB2) (RP140) [Arabidopsis thaliana] (TAIR:At4g21710.1); similar to hypothetical protein [Homo sapiens] (GB:CAD97689.1); similar to SPAC4G9.08c [Schizosaccharomyces pombe] (GB:CAA93558.1); similar to RNA polymerase III subunit RPC2 [Homo sapiens] (GB:AAM18214.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG03415.1); similar to Polymerase (RNA) III (DNA directed) polypeptide B [Homo sapiens] (GB:AAH46238.1); contains InterPro domain RNA polymerase Rpb2, domain 3 (InterPro:IPR007645); contains InterPro domain RNA polymerase Rpb2, domain 7 (InterPro:IPR007641); contains InterPro domain RNA polymerase Rpb2, domain 4 (InterPro:IPR007646); contains InterPro domain RNA polymerase beta subunit (InterPro:IPR007644); contains InterPro domain RNA polymerase Rpb2, domain 2 (InterPro:IPR007642); contains InterPro domain RNA polymerase Rpb2, domain 6 (InterPro:IPR007120); contains InterPro domain RNA polymerase Rpb2, domain 5 (InterPro:IPR007647); contains InterPro domain RNA polymerase, beta subunit (InterPro:IPR007121)   chr5:18264455-18275365 REVERSE   Aliases: K18C1.1, K18C1_1	5.8	6.4	-0.6	-1.6	100.0%	-3.5
3925	AT2G21690.1   RNA-binding protein, putative, similar to Glycine-rich RNA-binding protein from {Sinapis alba} SP:P49311, {Brassica napus} SP:Q05966, {Arabidopsis thaliana} SP:Q03251; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:9277194-9277677 REVERSE   Aliases: F7D8.1, F7D8_1	3.0	2.8	0.2	1.6	100.0%	-4.5
3926	AT2G38600.1   acid phosphatase class B family protein, similar to acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr2:16152985-16153935 FORWARD   Aliases: T6A23.20, T6A23_20	4.7	4.0	0.6	1.6	100.0%	-3.5
3927	AT4G24670.2   alliinase family protein, contains Pfam profiles: PF04864 allinase C-terminal domain, PF04863 alliinase EGF-like domain   chr4:12727844-12731284 REVERSE   Aliases: F22K18.130, F22K18_130	4.2	3.6	0.6	1.6	100.0%	-3.8
3928	AT3G17520.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to PIR:S04045:S04045 embryonic abundant protein D-29 (Gossypium hirsutum); contains Pfam profile PF02987: Late embryogenesis abundant protein   chr3:5999295-6000376 REVERSE   Aliases: MKP6.25	4.1	4.7	-0.6	-1.6	100.0%	-3.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3929	AT1G15440.2   transducin family protein / WD-40 repeat family protein, Strong similarity to gb X95263 Periodic tryptophan protein 2 gene (PWP2) from Homo sapiens and contains 6 WD40, G-beta repeat domains   chr1:5306056-5309509 REVERSE   Aliases: F9L1.40, F9L1_40	6.7	7.1	-0.4	-1.6	100.0%	-3.9
3930	AT3G46220.1   expressed protein   chr3:16990060-16995776 FORWARD   Aliases: F12M12.190	6.2	6.7	-0.5	-1.6	100.0%	-3.6
3931	AT5G15730.1   serine/threonine protein kinase, putative, similar to protein-serine/threonine kinase (Nicotiana tabacum) gi:505146:dbj:BAA06538	5.3	4.9	0.4	1.6	100.0%	-3.9
3932	AT2G31370.5   similar to bZIP transcription factor, putative (bZIP69) [Arabidopsis thaliana] (TAIR:At1g06070.1); similar to RF2a [Oryza sativa] (GB:AAC49832.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr2:13386110-13388600 FORWARD   Aliases: T28P16.14, T28P16_14	7.0	6.2	0.8	1.6	100.0%	-3.6
3933	AT5G12200.1   dihydropyrimidinase / DHPase / dihydropyrimidine amidohydrolase / hydantoinase (PYD2), identical to dihydropyrimidine amidohydrolase (PYD2) (Arabidopsis thaliana) GI:28194047; similar to SP:Q9EQF5 Dihydropyrimidinase (EC 3.5.2.2) (DHPase) (Hydantoinase) (DHP) {Mus musculus}; contains Pfam profile PF01979: Amidohydrolase family	9.3	8.7	0.6	1.6	100.0%	-3.6
3934	AT5G14960.1   Symbol: DEL2/E2FD/E2L1	3.1	3.3	-0.2	-1.6	100.0%	-4.2
3935	AT5G18490.1   expressed protein   chr5:6134154-6136767 REVERSE   Aliases: T28N17.2	4.8	4.2	0.5	1.6	100.0%	-3.5
3936	AT5G56020.1   expressed protein   chr5:22701715-22703595 FORWARD   Aliases: MDA7.6, MDA7_6	7.3	6.7	0.6	1.6	100.0%	-3.6
3937	AT3G48930.1   Symbol: EMB1080   40S ribosomal protein S11 (RPS11A)   chr3:18151756-18153251 REVERSE   Aliases: EMB1080, EMBRYO DEFECTIVE 1080, T2I13.230	11.4	11.8	-0.3	-1.6	100.0%	-4.1
3938	AT1G73800.1   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum)   chr1:27749109-27750369 REVERSE   Aliases: F25P22.22, F25P22_22	4.1	3.7	0.4	1.6	100.0%	-3.7
3939	AT5G57940.3   Symbol: ATCNGC5   cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC5), identical to cyclic nucleotide and calmodulin-regulated ion channel (cngc5) GI:4581205 from (Arabidopsis thaliana)	6.9	6.1	0.8	1.6	100.0%	-3.5
3940	AT1G13320.2   Symbol: PDF2   similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit A (RCN1) [Arabidopsis thaliana] (TAIR:At1g25490.1); similar to serine/threonine protein phosphatase 2A (PP2A) 65 KDa regulatory subunit A [Arabidopsis thaliana] (TAIR:At3g25800.1); similar to protein phosphatase [Cicer arietinum] (GB:CAA10285.1); similar to serine/threonine protein phosphatase type 2A regulatory subunit A (GB:AAB60713.1); similar to Ser/Thr specific protein phosphatase 2A A regulatory subunit beta isoform [Medicago sativa subsp. x varia] (GB:AAG29594.1); similar to protein phosphatase 2A [Nicotiana tabacum] (GB:CAA66487.1); similar to phosphatase 2A regulatory A subunit [Oryza sativa (japonica cultivar-group)] (GB:XP_450276.1); contains InterPro domain HEAT repeat (InterPro:IPR000357)   chr1:4563472-4567747 REVERSE   Aliases: PR65, T6J4.8, T6J4_8	6.9	8.3	-1.4	-1.6	100.0%	-3.4
3941	AT1G73177.1   expressed protein   chr1:27520248-27521515 REVERSE   Aliases: None	8.2	7.8	0.4	1.6	100.0%	-3.8
3942	AT5G22590.1   hypothetical protein   chr5:7504539-7505841 FORWARD   Aliases: MDJ22.1, MDJ22_1	2.9	2.7	0.2	1.6	100.0%	-4.7
3943	AT5G15510.1   expressed protein   chr5:5034123-5036798 FORWARD   Aliases: T20K14.120, T20K14_120	5.3	5.8	-0.5	-1.6	100.0%	-3.5
3944	AT1G57560.1   myb family transcription factor (MYB50), similar to DNA-binding protein GI:19058 from (Hordeum vulgare)   chr1:21320493-21321729 FORWARD   Aliases: T8L23.3, T8L23_3	3.0	3.7	-0.7	-1.6	100.0%	-3.5
3945	AT3G52140.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr3:19343907-19352635 FORWARD   Aliases: F4F15.250	5.7	6.3	-0.6	-1.6	100.0%	-3.8
3946	AT5G22640.1   Symbol: EMB1211   MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein, contains Pfam profile PF02493: MORN repeat   chr5:7529371-7533787 FORWARD   Aliases: EMB1211, EMBRYO DEFECTIVE 1211, MDJ22.6, MDJ22_6	5.6	6.2	-0.6	-1.6	100.0%	-3.9
3947	AT4G14100.1   expressed protein   chr4:8120715-8122406 FORWARD   Aliases: DL3085W, FCAALL.191	5.2	4.6	0.5	1.6	100.0%	-3.8
3948	AT5G42240.1   Symbol: SCPL42	4.3	4.7	-0.4	-1.6	100.0%	-3.6
3949	AT4G18570.1   proline-rich family protein, common family members: At3g25690, At4g04980, At5g61090 (Arabidopsis thaliana)   chr4:10231229-10234704 FORWARD   Aliases: F28J12.8	3.6	3.9	-0.3	-1.6	100.0%	-4.0
3950	AT1G31440.1   SH3 domain-containing protein 1 (SH3P1), nearly identical to SH3 domain-containing protein 1 (Arabidopsis thaliana) GI:16974676; contains Pfam profile PF00018: SH3 domain   chr1:11255817-11258685 REVERSE   Aliases: T8E3.10, T8E3_10	5.8	5.4	0.4	1.6	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3951	AT5G15400.1   U-box domain-containing protein, contains Pfam profile PF04564: U-box domain   chr5:4997716-5003143 REVERSE   Aliases: T20K14.10, T20K14_10	6.5	7.0	-0.6	-1.6	100.0%	-3.8
3952	AT1G23140.1   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr1:8202351-8203201 REVERSE   Aliases: T26J12.9, T26J12_9	6.0	5.5	0.6	1.6	100.0%	-3.5
3953	AT1G51620.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:19143798-19145455 FORWARD   Aliases: F19C24.15, F19C24_15	2.4	2.3	0.2	1.6	100.0%	-4.4
3954	AT1G18200.1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family   chr1:6264240-6266652 REVERSE   Aliases: T10F20.21	3.6	3.3	0.3	1.6	100.0%	-3.9
3955	AT1G75200.1   flavodoxin family protein / radical SAM domain-containing protein, contains Pfam profiles PF00258: Flavodoxin, PF04055: radical SAM domain protein   chr1:28224287-28227368 REVERSE   Aliases: F22H5.13, F22H5_13	5.2	5.8	-0.6	-1.6	100.0%	-3.5
3956	AT4G10450.1   60S ribosomal protein L9 (RPL90D), ribosomal protein L9, cytosolic - garden pea, PIR2:S19978   chr4:6462949-6464521 REVERSE   Aliases: F7L13.30, F7L13_30	5.5	6.1	-0.6	-1.6	100.0%	-3.5
3957	AT5G19090.2   heavy-metal-associated domain-containing protein, contains Pfam heavy-metal-associated domain PF00403; glycine-rich protein GRP22, rape, PIR:S31415; isoform contains a non-consensus TG-acceptor splice site at intron 3   chr5:6387491-6390026 FORWARD   Aliases: T16G12.130, T16G12_130	6.4	5.9	0.5	1.6	100.0%	-4.0
3958	AT2G19385.1   expressed protein, weak similarity to Cell growth regulating nucleolar protein (Swiss-Prot:Q08288) (Mus musculus)   chr2:8394117-8395794 FORWARD   Aliases: None	5.4	6.0	-0.6	-1.6	100.0%	-3.5
3959	AT1G72300.1   leucine-rich repeat transmembrane protein kinase, putative, similar to GI:3641252 from (Malus x domestica) (Plant Mol. Biol. 40 (6), 945-957 (1999))   chr1:27221162-27224738 REVERSE   Aliases: T9N14.20, T9N14_20	5.9	5.3	0.6	1.6	100.0%	-3.7
3960	AT3G13110.1   Symbol: AtSerat2;2   serine O-acetyltransferase (SAT-1), identical to serine acetyltransferase (Sat-1) GI:1184048 (Arabidopsis thaliana)   chr3:4214624-4216309 REVERSE   Aliases: MJG19.1, SAT 1, SAT A, SERINE ACETYLTRANSFERASE 1	8.6	7.7	0.9	1.6	100.0%	-3.6
3961	AT4G23920.1   UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative, similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SP:Q42605, Cyamopsis tetragonoloba GI:3021357 (AJ005082)   chr4:12431287-12433874 FORWARD   Aliases: T32A16.90, T32A16_90	4.4	4.7	-0.3	-1.6	100.0%	-4.1
3962	AT1G15830.1   expressed protein   chr1:5448721-5450172 FORWARD   Aliases: F7H2.23, F7H2_23	6.1	5.4	0.6	1.6	100.0%	-3.7
3963	AT1G26300.2   BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	5.0	4.7	0.2	1.6	100.0%	-4.4
3964	AT1G74230.1   glycine-rich RNA-binding protein, similar to RNA-binding protein GB:S46286 from (Nicotiana glauca)   chr1:27918367-27920744 FORWARD   Aliases: F1O17.10, F1O17_10	9.1	8.7	0.4	1.6	100.0%	-3.9
3965	AT1G69200.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr1:26019687-26022528 FORWARD   Aliases: F4N2.16, F4N2_16	3.7	4.3	-0.5	-1.6	100.0%	-3.5
3966	AT5G17150.1   expressed protein   chr5:5638872-5639594 REVERSE   Aliases: F2K13.300, F2K13_300	2.8	2.6	0.2	1.6	100.0%	-4.6
3967	AT5G05460.1   similar to glycosyl hydrolase family 85 protein [Arabidopsis thaliana] (TAIR:At3g11040.1); similar to PREDICTED: similar to RIKEN cDNA D230014K01 [Rattus norvegicus] (GB:XP_221141.2); contains InterPro domain Glycoside hydrolase, family 85 (InterPro:IPR005201)   chr5:1615616-1618903 FORWARD   Aliases: K18I23.27, K18I23_27	5.0	5.3	-0.3	-1.6	100.0%	-4.0
3968	AT1G08810.2   Symbol: MYB60   myb family transcription factor (MYB60)	2.1	2.0	0.1	1.6	100.0%	-4.9
3969	AT1G22850.1   expressed protein   chr1:8080191-8082864 REVERSE   Aliases: F19G10.23	6.8	6.0	0.8	1.6	100.0%	-3.6
3970	AT3G18380.2   expressed protein   chr3:6310742-6313305 REVERSE   Aliases: MYF24.10	6.0	5.3	0.7	1.6	100.0%	-3.7
3971	AT5G58310.1   hydrolase, alpha/beta fold family protein, low similarity to SP:Q40708 PIR7A protein {Oryza sativa}, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393, ethylene-induced esterase (Citrus sinensis) GI:14279437; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:23591706-23593310 REVERSE   Aliases: MCK7.18, MCK7_18	2.4	2.3	0.2	1.6	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3972	AT1G54140.1   Symbol: TAFII21   transcription initiation factor IID (TFIID) 31 kDa subunit (TAFII-31) family protein, contains Pfam profile: PF02291 transcription initiation factor IID, 31kD subunit   chr1:20217637-20218887 REVERSE   Aliases: F15I1.24, F15I1_24, TATA BINDING PROTEIN ASSOCIATED FACTOR 21KDA SUBUNIT, TATA BINDING PROTEIN ASSOCIATED FACTOR 21KDA SUBUNIT	7.2	7.8	-0.6	-1.6	100.0%	-3.5
3973	AT1G58180.3   similar to carbonic anhydrase family protein / carbonate dehydratase family protein [Arabidopsis thaliana] (TAIR:At4g33580.1); similar to carbonic anhydrase 2 [Flaveria bidentis] (GB:AAO17573.1); contains InterPro domain Carbonic anhydrase, prokaryotic (InterPro:IPR001765)   chr1:21541600-21543579 REVERSE   Aliases: T15M6.18	5.4	4.9	0.5	1.6	100.0%	-3.7
3974	AT5G14470.1   GHMP kinase-related, contains similarity to D-glycero-D-manno-heptose 7-phosphate kinase (Aneurinibacillus thermoaerophilus) gi:13491143:gb:AAK27850   chr5:4662807-4664650 REVERSE   Aliases: F18O22.260, F18O22_260	3.2	3.0	0.2	1.6	100.0%	-4.5
3975	AT4G33130.2   expressed protein, weak similarity to Max-interacting transcriptional repressor (Mus musculus) GI:1184157   chr4:15979053-15980658 REVERSE   Aliases: F4I10.60, F4I10_60	4.1	4.3	-0.2	-1.6	100.0%	-4.3
3976	AT5G17340.1   expressed protein, weak similarity to M3.4 protein (Brassica napus) GI:4574746   chr5:5715626-5716270 REVERSE   Aliases: MKP11.1, MKP11_1	2.6	2.4	0.2	1.6	100.0%	-4.7
3977	AT1G74400.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 domain of unknown function   chr1:27967614-27969002 FORWARD   Aliases: F1M20.8, F1M20_8	3.3	3.6	-0.3	-1.6	100.0%	-4.2
3978	AT5G63750.1   IBR domain-containing protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam:PF01485 IBR domain   chr5:25530220-25532164 REVERSE   Aliases: MBK5.23, MBK5_23	5.1	4.7	0.5	1.6	100.0%	-3.7
3979	AT5G10360.1   Symbol: EMB3010   40S ribosomal protein S6 (RPS6B)   chr5:3258475-3260228 REVERSE   Aliases: EMB3010, EMBRYO DEFECTIVE 3010, F12B17.290, F12B17_290	10.5	10.9	-0.4	-1.6	100.0%	-4.2
3980	AT2G39795.1   mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	6.4	6.9	-0.5	-1.6	100.0%	-3.7
3981	AT2G13500.1   hypothetical protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:5635018-5636181 FORWARD   Aliases: T10F5.4, T10F5_4	2.2	2.3	-0.1	-1.6	100.0%	-4.9
3982	AT1G34020.1   transporter-related, low similarity to UDP-sugar transporter (Drosophila melanogaster) GI:14971008, UDP-glucuronic acid transporter (Homo sapiens) GI:11463949   chr1:12366867-12369158 FORWARD   Aliases: F12G12.16, F12G12_16	5.2	5.9	-0.7	-1.6	100.0%	-3.7
3983	AT3G62910.1   Symbol: APG3   peptide chain release factor, putative, similar to peptide chain release factor 1 (Escherichia coli) GI:147567; contains Pfam profiles PF00472: Peptidyl-tRNA hydrolase domain, PF03462: PCRF domain   chr3:23268530-23271402 REVERSE   Aliases: ALBINO AND PALE GREEN, T20O10.10	4.8	5.3	-0.5	-1.6	100.0%	-3.6
3984	AT1G75500.1   nodulin MtN21 family protein, similar to MtN21 GB:CAA75575 GI:2598575 from (Medicago truncatula) (Mol. Plant Microbe Interact. 9 (4), 233-242 (1996)); contains Pfam profile PF00892: Integral membrane protein   chr1:28341453-28343821 REVERSE   Aliases: F1B16.19	3.3	4.4	-1.1	-1.6	100.0%	-3.3
3985	AT5G48960.1   5' nucleotidase family protein, low similarity to SP:P49902 Cytosolic purine 5'-nucleotidase (EC 3.1.3.5) (5'-nucleotidase cytosolic II) {Homo sapiens}; contains Pfam profile PF05761: 5' nucleotidase family   chr5:19866769-19870790 FORWARD   Aliases: K19E20.8, K19E20_8	4.7	4.2	0.4	1.6	100.0%	-3.6
3986	AT5G36950.1   DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana)   chr5:14612211-14615570 FORWARD   Aliases: MLF18.70, MLF18_70	5.6	6.2	-0.6	-1.6	100.0%	-3.4
3987	AT2G46910.1   plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin   chr2:19279350-19281071 FORWARD   Aliases: F14M4.46	4.4	4.8	-0.4	-1.6	100.0%	-3.9
3988	AT1G62930.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g63130.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g63080.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g62670.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g62910.1); similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g62590.1); similar to fertility restorer homologue [Raphanus sativus] (GB:CAD61286.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr1:23310199-23312348 FORWARD   Aliases: F16P17.7, F16P17_7	6.2	7.1	-0.8	-1.6	100.0%	-3.8
3989	AT2G16260.1   glycine-rich RNA-binding protein, putative, similar to Glycine-rich RNA-binding protein from {Daucus carota} SP:Q03878, {Sinapis alba} SP:P49311, {Brassica napus} SP:Q05966, {Arabidopsis thaliana} SP:Q03251; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:7051897-7052584 FORWARD   Aliases: F16F14.24, F16F14_24	4.8	4.3	0.4	1.6	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
3990	AT1G20370.1   tRNA pseudouridine synthase family protein, similar to SP:Q9WU56 tRNA pseudouridine synthase A (EC 4.2.1.70) (Uracil hydrolyase) {Mus musculus}; contains Pfam profile PF01416: tRNA pseudouridine synthase   chr1:7051567-7053631 REVERSE   Aliases: F14O10.3, F14O10_3	3.9	4.2	-0.4	-1.6	100.0%	-4.0
3991	AT4G11570.2   haloacid dehalogenase-like hydrolase family protein, similar to genetic modifier (Zea mays) Gl:10444400; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr4:7004329-7006075 FORWARD   Aliases: F25E4.190, F25E4_190	7.6	6.9	0.7	1.6	100.0%	-3.8
3992	AT1G32050.1   secretory carrier membrane protein (SCAMP) family protein, contains Pfam domain, PF04144: SCAMP family   chr1:11528461-11531261 FORWARD   Aliases: T12O21.5, T12O21_5	7.9	6.9	1.0	1.6	100.0%	-3.7
3993	AT2G26430.1   Symbol: RCY1   ania-6a type cyclin (RCY1), nearly identical to ania-6a type cyclin (Arabidopsis thaliana) Gl:13924511   chr2:11250297-11253107 REVERSE   Aliases: ARGININE RICH CYCLIN 1, ATRCY1, T9J22.10, T9J22_10	6.7	6.4	0.4	1.6	100.0%	-3.9
3994	AT4G02020.1   Symbol: EZA1   zeste-like protein 1 (EZA1), identical to enhancer of zeste-like protein 1(EZA1) (Gl:4185507) (Arabidopsis thaliana); similar to polycomb group (Arabidopsis thaliana) Gl:1903019 (curly leaf); contains Pfam profile PF00856: SET domain   chr4:886600-891955 FORWARD   Aliases: T10M13.3, T10M13_3	8.1	7.6	0.5	1.6	100.0%	-3.9
3995	AT4G38750.1   expressed protein   chr4:18084902-18090840 REVERSE   Aliases: T9A14.30, T9A14_30	6.7	7.0	-0.3	-1.6	100.0%	-4.2
3996	AT1G75090.1   methyladenine glycosylase family protein, similar to SP:P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) {Escherichia coli}; contains Pfam profile PF03352: Methyladenine glycosylase   chr1:28191112-28193386 REVERSE   Aliases: F9E10.6, F9E10_6	3.4	3.7	-0.3	-1.6	100.0%	-4.2
3997	AT2G45650.1   Symbol: AGL6   MADS-box protein (AGL6)   chr2:18811424-18813596 FORWARD   Aliases: F17K2.18	2.5	2.3	0.2	1.6	100.0%	-4.7
3998	AT5G04280.1   glycine-rich RNA-binding protein	5.7	5.0	0.8	1.6	100.0%	-3.6
3999	AT5G08220.1   expressed protein   chr5:2642281-2642992 REVERSE   Aliases: F8L15.7	2.9	2.7	0.2	1.6	100.0%	-4.4
4000	AT1G57943.1   Symbol: ATPUP17   purine permease-related, low similarity to purine permease (Arabidopsis thaliana) Gl:7620007; contains Pfam profile PF03151: Domain of unknown function, DUF250   chr1:21441267-21442554 REVERSE   Aliases: F13D13.4, F13D13_4	4.8	4.3	0.5	1.6	100.0%	-3.8
4001	AT1G49490.1   leucine-rich repeat family protein / extensin family protein, contains similarity to disease resistance protein Gl:3894383 from (Lycopersicon esculentum); contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965   chr1:18321231-18323774 REVERSE   Aliases: F13F21.7, F13F21_7	2.6	2.8	-0.2	-1.6	100.0%	-4.7
4002	AT1G72800.1   nuM1-related, contains similarity with nuM1 Gl:1279563 from (Medicago sativa)   chr1:27400878-27402162 FORWARD   Aliases: F28P22.1, F28P22_1	5.8	4.9	0.9	1.6	100.0%	-3.5
4003	AT3G25140.1   Symbol: QUA1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr3:9154718-9156851 FORWARD   Aliases: MJL12.8, QUASIMODO1	11.1	11.4	-0.3	-1.6	100.0%	-4.2
4004	AT3G05530.1   Symbol: RPT5A   26S proteasome AAA-ATPase subunit (RPT5a), identical to GB:AAF22525 Gl:6652886 from (Arabidopsis thaliana)   chr3:1603438-1606237 FORWARD   Aliases: 19S PROTEASOME REGULATORY COMPLEX SUBUNIT S6A, 26S PROTEASOME AAA ATPASE SUBUNIT, ATS6A.2, F22F7.1, F22F7_1	8.7	9.6	-0.9	-1.6	100.0%	-3.6
4005	AT2G34300.2   similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At1g29470.1); similar to dehydration-responsive family protein [Arabidopsis thaliana] (TAIR:At2g40280.1); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At5g64030.1); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At3g51070.1); similar to OSJNBb0020J19.14 [Oryza sativa (japonica cultivar-group)] (GB:XP_474482.1); similar to ankyrin-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82580.1); contains InterPro domain Putative methyltransferase DUF248 (InterPro:IPR004159)   chr2:14480744-14484343 REVERSE   Aliases: F13P17.14, F13P17_14	7.7	8.3	-0.6	-1.6	100.0%	-3.8
4006	AT1G78600.1   zinc finger (B-box type) family protein, similar to zinc finger protein Gl:3618316 from (Oryza sativa)   chr1:29572104-29573752 FORWARD   Aliases: T30F21.7, T30F21_7	5.9	5.6	0.3	1.6	100.0%	-4.1
4007	AT4G16250.1   Symbol: PHYD   phytochrome D (PHYD), nearly identical to SP:P42497 Phytochrome D {Arabidopsis thaliana}	3.9	4.1	-0.3	-1.6	100.0%	-4.0
4008	AT4G22950.1   Symbol: AGL19   MADS-box protein (AGL19), MADS-box protein AGL14, Arabidopsis thaliana, gb:U20184   chr4:12023926-12027432 REVERSE   Aliases: AGAMOUS LIKE 19, F7H19.130, F7H19_130, GL19	4.4	4.7	-0.3	-1.6	100.0%	-3.9
4009	AT5G39340.1   Symbol: AHP3   two-component phosphorelay mediator 2 (HP2), nearly identical to ATHP2 (Arabidopsis thaliana) Gl:4156243	9.1	8.8	0.3	1.6	100.0%	-4.0
4010	AT2G23670.1   expressed protein   chr2:10070235-10070943 REVERSE   Aliases: F26B6.28	5.9	5.4	0.5	1.6	100.0%	-3.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4011	AT1G29690.1   Symbol: CAD1   Encodes a protein containing a domain with significant homology to the MACPF (membrane attack complex and perforin) domain of complements and perforin proteins that are involved in innate immunity in animals. Transgenic <i>cad1-1</i> mutant plants show lesions seen in the hypersensitive response, as well as a spontaneous activation of expression of pathogenesis-related genes and leading to a 32-fold increase in salicylic acid (SA). CAD1 is postulated to act as a negative regulator controlling SA-mediated pathway of programmed cell death in plant immunity.   chr1:10379012-10382109 REVERSE   Aliases: CAD1, F15D2.24, F15D2_24	3.9	3.5	0.4	1.6	100.0%	-3.8
4012	AT3G10360.1   pumilio/Puf RNA-binding domain-containing protein, similar to RNA binding protein PufA GB:AAD39751 (Dictyostelium discoideum) and similar to Pumilio protein GB:A46221 (Drosophila sp.)   chr3:3211281-3215149 REVERSE   Aliases: F14P13.4	3.6	4.0	-0.4	-1.6	100.0%	-3.9
4013	AT1G11660.1   heat shock protein, putative, strong similarity to gb:Z70314 heat-shock protein from Arabidopsis thaliana and is a member of the PF:00012 Hsp70 protein family   chr1:3921056-3924507 FORWARD   Aliases: F25C20.19, F25C20_19	7.8	8.2	-0.5	-1.6	100.0%	-3.9
4014	AT2G34260.2   transducin family protein / WD-40 repeat family protein, similar to Vegetatible incompatibility protein HET-E-1 (SP:Q00808) {Podospora anserina}	7.0	7.6	-0.6	-1.6	100.0%	-3.6
4015	AT3G11900.1   Symbol: ANT1   amino acid transporter family protein, low similarity to proton/amino acid transporter 1 (Mus musculus) GI:21908024; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II   chr3:3758458-3760384 FORWARD   Aliases: AROMATIC AND NEUTRAL TRANSPORTER 1, F26K24.19, F26K24_19	6.2	5.8	0.5	1.6	100.0%	-3.8
4016	AT1G48370.1   oligopeptide transporter OPT family protein, similar to iron-phytosiderophore transporter protein yellow stripe 1 (Zea mays) GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein   chr1:17878183-17881065 FORWARD   Aliases: F11A17.8, F11A17_8	5.2	5.7	-0.5	-1.6	100.0%	-3.8
4017	AT2G15695.1   expressed protein, contains Pfam PF05705: Eukaryotic protein of unknown function (DUF829)   chr2:6840962-6843506 REVERSE   Aliases: None	6.0	5.4	0.7	1.6	100.0%	-3.8
4018	AT1G72660.3   similar to developmentally regulated GTP-binding protein (DRG1) [Arabidopsis thaliana] (TAIR:At1g17470.1); similar to developmentally regulated GTP binding protein [Pisum sativum] (GB:AAB67829.1); contains InterPro domain Small GTP-binding protein domain (InterPro:IPR005225); contains InterPro domain TGS domain (InterPro:IPR004095); contains InterPro domain GTP1/OBG domain (InterPro:IPR006074); contains InterPro domain GTP1/OBG (InterPro:IPR006073); contains InterPro domain GTP1/OBG sub-domain (InterPro:IPR006169)   chr1:27357542-27360332 FORWARD   Aliases: F28P22.15, F28P22_15	5.5	4.9	0.6	1.6	100.0%	-3.6
4019	AT1G75280.1   isoflavone reductase, putative, identical to SP:P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) {Arabidopsis thaliana}; contains Pfam profile PF02716: isoflavone reductase. Involved in response to oxidative stress.   chr1:28255622-28257280 FORWARD   Aliases: F22H5.17, F22H5_17, P3	11.1	12.4	-1.4	-1.6	100.0%	-3.9
4020	AT5G14780.1   Symbol: FDH   formate dehydrogenase (FDH), identical to GI:7677266   chr5:4776987-4779497 FORWARD   Aliases: FORMATE DEHYDROGENASE, T9L3.80, T9L3_80	9.9	9.0	0.9	1.6	100.0%	-3.5
4021	AT1G71130.1   encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	6.8	6.4	0.4	1.6	100.0%	-3.9
4022	AT3G07320.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase from GI:6714534 (Salix gilgiana)   chr3:2332077-2334057 REVERSE   Aliases: T1B9.1	4.8	5.6	-0.8	-1.6	100.0%	-3.8
4023	AT5G64510.1   expressed protein   chr5:25801630-25803533 FORWARD   Aliases: MUB3.3, MUB3_3	5.6	4.9	0.7	1.6	100.0%	-3.6
4024	AT5G02480.1   expressed protein, p   chr5:547561-549910 FORWARD   Aliases: T22P11.70, T22P11_70	7.8	7.4	0.3	1.6	100.0%	-3.9
4025	AT2G40080.1   Symbol: ELF4   expressed protein   chr2:16741372-16741990 REVERSE   Aliases: T28M21.24, T28M21_24	7.7	7.1	0.6	1.6	100.0%	-3.6
4026	AT3G13674.1   expressed protein   chr3:4474784-4475888 REVERSE   Aliases: MMM17.23	3.1	3.5	-0.4	-1.6	100.0%	-3.8
4027	AT1G21770.1   expressed protein   chr1:7651635-7652275 REVERSE   Aliases: F8K7.21, F8K7_21	10.2	9.5	0.6	1.6	100.0%	-4.0
4028	AT3G02780.1   Symbol: IPP2   isopentenyl-diphosphate delta-isomerase II / isopentenyl diphosphate:dimethylallyl diphosphate isomerase II (IPP2), identical to isopentenyl diphosphate:dimethylallyl diphosphate isomerase (IPP2) GB:U49259 (Arabidopsis thaliana)   chr3:602440-604682 REVERSE   Aliases: F13E7.28, F13E7_28, IDI2, IPIAT1, ISOPENTENYL DIPHOSPHATE ISOMERASE 2, ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE, ISOPENTENYL PYROPHOSPHATE:DIMETHYLLALLYL PYROPHOSPHATE ISOMERASE 2	11.2	11.6	-0.4	-1.6	100.0%	-4.0
4029	AT5G58650.1   expressed protein   chr5:23716934-23717452 REVERSE   Aliases: MZN1.10, MZN1_10	7.7	7.2	0.5	1.5	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4030	AT1G55000.3   expressed protein, similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAX95630.1); contains InterPro domain Peptidoglycan-binding LysM (InterPro:IPR002482)   chr1:20518304-20520116 FORWARD   Aliases: F14C21.53, F14C21_53	5.7	5.0	0.7	1.5	100.0%	-3.8
4031	AT4G21060.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr4:11240741-11244871 FORWARD   Aliases: T13K14.220, T13K14_220	4.3	5.1	-0.8	-1.5	100.0%	-3.5
4032	AT4G17330.1   Symbol: ATG2484 1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr4:9688900-9693875 REVERSE   Aliases: DL4700C, FCAALL.411	7.0	7.6	-0.6	-1.5	100.0%	-4.0
4033	AT5G17990.1   Symbol: TRP1   anthranilate phosphoribosyltransferase, identical to anthranilate phosphoribosyltransferase, chloroplast precursor (EC 2.4.2.18) SP:Q02166 from (Arabidopsis thaliana)   chr5:5957215-5959906 FORWARD   Aliases: MCM23.6, MCM23_6, PAT1, PHOSPHORIBOSYLANTHRANILATE TRANSFERASE, PHOSPHORIBOSYLANTHRANILATE TRANSFERASE 1, TRYPTOPHAN BIOSYNTHESIS 1	9.1	10.1	-0.9	-1.5	100.0%	-3.5
4034	AT2G43550.1   Encodes a defensin-like (DEFL) family protein.   chr2:18080311-18080982 FORWARD   Aliases: T1O24.29	3.9	4.4	-0.4	-1.5	100.0%	-3.7
4035	AT1G50640.1   Symbol: ATERF3/ERF3   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ATERF-3). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.   chr1:18760816-18762101 REVERSE   Aliases: ATERF 3, ATERF3, ERF3, ETHYLENE RESPONSIVE ELEMENT BINDING FACTOR 3, F11F12.4, F11F12_4	3.1	2.8	0.2	1.5	100.0%	-4.3
4036	AT5G02490.1   heat shock cognate 70 kDa protein 2 (HSC70-2) (HSP70-2), identical to SP:P22954 Heat shock cognate 70 kDa protein 2 (Hsc70.2) {Arabidopsis thaliana}   chr5:550033-552643 REVERSE   Aliases: T22P11.80, T22P11_80	7.8	8.4	-0.7	-1.5	100.0%	-3.4
4037	AT2G21960.1   expressed protein   chr2:9361999-9364499 FORWARD   Aliases: F7D8.28, F7D8_28	8.2	7.5	0.6	1.5	100.0%	-3.5
4038	AT1G28400.1   expressed protein, similar to E6 (GI:1000090) (Gossypium barbadense)   chr1:9972370-9973779 REVERSE   Aliases: F3M18.16, F3M18_16	12.8	13.1	-0.3	-1.5	100.0%	-4.1
4039	AT5G01370.1   expressed protein   chr5:152529-154350 FORWARD   Aliases: T1O08.80, T1O08_80	5.8	6.5	-0.7	-1.5	100.0%	-3.6
4040	AT5G54170.1   expressed protein, weak similarity to SP:Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) {Homo sapiens}   chr5:22002104-22004280 REVERSE   Aliases: K18G13.4, K18G13_4	4.5	4.2	0.4	1.5	100.0%	-3.9
4041	AT2G38410.1   VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate HRS isoform 2 (Homo sapiens) GI:9022389; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain   chr2:16093708-16097286 REVERSE   Aliases: T19C21.10, T19C21_10	3.9	3.4	0.5	1.5	100.0%	-3.9
4042	AT4G39780.1   encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.   chr4:18457951-18459174 REVERSE   Aliases: T19P19.170, T19P19_170	4.3	3.7	0.6	1.5	100.0%	-3.4
4043	AT2G45290.1   transketolase, putative, strong similarity to transketolase 1 (Capsicum annuum) GI:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain   chr2:18679756-18682980 FORWARD   Aliases: F4L23.20	6.2	7.4	-1.2	-1.5	100.0%	-3.5
4044	AT2G25150.1   transferase family protein, similar to 10-deacetylbaccatin III-10-O-acetyl transferase (gi:6746554), 2-debenzoyl-7,13-diacetylbaccatin III-2-O-benzoyl transferase (gi:11559716) from Taxus cuspidata; contains Pfam transferase family domain PF00248; contains EST gb:R65039   chr2:10709442-10711373 REVERSE   Aliases: F13D4.110, F13D4_110	2.5	2.3	0.2	1.5	100.0%	-4.6
4045	AT1G78660.3   gamma-glutamyl hydrolase, putative / gamma-Glu-X carboxypeptidase, putative / conjugase, putative, similar to SP:O65355 Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH) {Arabidopsis thaliana}   chr1:29590570-29593185 FORWARD   Aliases: T30F21.1, T30F21_1	7.1	8.0	-0.9	-1.5	100.0%	-3.7
4046	AT5G67240.1   similar to exonuclease family protein [Arabidopsis thaliana] (TAIR:At3g50100.1); similar to hypothetical protein AN7566.2 [Aspergillus nidulans FGSC A4] (GB:EAA62146.1); contains InterPro domain Exonuclease (InterPro:IPR006055)   chr5:26841462-26845395 REVERSE   Aliases: K21H1.20, K21H1_20	6.5	7.8	-1.3	-1.5	100.0%	-3.5
4047	AT4G17770.1   Symbol: ATTPS5	7.9	8.4	-0.5	-1.5	100.0%	-4.0
4048	AT5G23230.1   isochorismatase hydrolase family protein, low similarity to SP:P45743 Isochorismatase (EC 3.3.2.1) (2,3 dihydro-2,3 dihydroxybenzoate synthase) (Superoxide-inducible protein 1) (SOI1) {Bacillus subtilis}; contains Pfam profile PF00857: isochorismatase family protein   chr5:7825885-7826604 REVERSE   Aliases: MKD15.9, MKD15_9	3.9	3.6	0.3	1.5	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4049	AT5G47620.3   heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative   chr5:19319496-19321316 REVERSE   Aliases: MNJ7.21, MNJ7_21	10.1	9.8	0.3	1.5	100.0%	-4.1
4050	AT2G29980.2   Symbol: FAD3   omega-3 fatty acid desaturase, endoplasmic reticulum (FAD3), identical to SP:48623   chr2:12788668-12792114 REVERSE   Aliases: F23F1.10, F23F1_10, FATTY ACID DESATURASE 3, OMEGA 3 FATTY ACID DESATURASE, ENDOPLASMIC RETICULUM18:2 DESATURASE (OMEGA 3 FATTY ACID DESATURASE)	7.4	8.7	-1.3	-1.5	100.0%	-3.4
4051	AT2G33770.1   ubiquitin-conjugating enzyme family protein, low similarity to ubiquitin-conjugating BIR-domain enzyme APOLLON (Homo sapiens) GI:8489831, ubiquitin-conjugating enzyme (Mus musculus) GI:3319990; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr2:14284635-14290116 REVERSE   Aliases: T1B8.8, T1B8_8	5.7	6.8	-1.1	-1.5	100.0%	-3.8
4052	AT2G10920.1   expressed protein   chr2:4308965-4309216 REVERSE   Aliases: F16G22.2, F16G22_2	7.2	6.1	1.0	1.5	100.0%	-3.5
4053	AT4G07410.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400) (2 weak); similar to Vegetatible incompatibility protein HET-E-1 (SP:Q00808) {Podospora anserina}   chr4:4201246-4205221 REVERSE   Aliases: F28D6.14, F28D6_14	3.7	4.4	-0.6	-1.5	100.0%	-3.8
4054	AT1G69010.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	6.1	5.1	1.0	1.5	100.0%	-3.7
4055	AT4G12830.1   hydrolase, alpha/beta fold family protein, low similarity to haloalkane dehalogenase from (Mycobacterium avium subsp. avium) GI:14422311, (Pseudomonas pavonaceae) GI:6689030; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:7531138-7533584 FORWARD   Aliases: T20K18.180, T20K18_180	3.6	3.3	0.3	1.5	100.0%	-4.0
4056	AT3G63520.1   Symbol: CCD1   9-cis-epoxycarotenoid dioxygenase / neoxanthin cleavage enzyme / NCED1 / carotenoid cleavage dioxygenase 1 (CCD1), identical to putative 9-cis-epoxy-carotenoid dioxygenase (GI:3096910); contains Pfam profile PF03055: Retinal pigment epithelial membrane protein   chr3:23463915-23466871 FORWARD   Aliases: ATCCD1, ATNCED1, CAROTENOID CLEAVAGE DIOXYGENASE 1, MAA21.150	9.1	9.6	-0.5	-1.5	100.0%	-3.8
4057	AT1G09390.1   GDSL-motif lipase/hydrolase family protein, Similar to early nodulin ENOD8 (Medicago sativa) GI:304037, lanatoside 15'-O-acetylerase (Digitalis lanata) GI:3688284, elicitor-induced glycoprotein iEP4 (Daucus carota) GI:1911765; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family	5.3	5.7	-0.4	-1.5	100.0%	-3.8
4058	AT5G50280.1   Symbol: EMB1006   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:20476464-20478730 FORWARD   Aliases: EMB1006, EMBRYO DEFECTIVE 1006, K6A12.14, K6A12_14	3.9	4.4	-0.5	-1.5	100.0%	-3.7
4059	AT1G04680.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa)   chr1:1303528-1307881 REVERSE   Aliases: T1G11.7, T1G11_7	3.7	4.5	-0.8	-1.5	100.0%	-3.8
4060	AT1G13300.1   myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain   chr1:4556889-4558705 FORWARD   Aliases: T6J4.6, T6J4_6	5.2	5.7	-0.5	-1.5	100.0%	-3.6
4061	AT3G60940.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537; expression supported by MPSS   chr3:22532590-22534004 REVERSE   Aliases: T27I15.30	2.6	2.4	0.2	1.5	100.0%	-4.3
4062	AT3G18050.1   expressed protein   chr3:6180865-6182860 FORWARD   Aliases: MRC8.3	2.6	2.8	-0.3	-1.5	100.0%	-4.3
4063	AT1G69230.2   expressed protein   chr1:26029981-26031371 REVERSE   Aliases: F4N2.18	4.9	4.2	0.6	1.5	100.0%	-3.7
4064	AT1G62200.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family ; contains non-consensus GA donor site at intron 4   chr1:22985701-22988024 REVERSE   Aliases: F19K23.13, F19K23_13	7.2	6.8	0.4	1.5	100.0%	-3.8
4065	AT3G06730.1   thioredoxin family protein, contains Pfam profile: PF00085 Thioredoxin   chr3:2124240-2126148 FORWARD   Aliases: F3E22.13	4.7	5.3	-0.6	-1.5	100.0%	-3.4
4066	AT4G14960.2   Symbol: TUA6   tubulin alpha-6 chain (TUA6), nearly identical to SP:P29511 Tubulin alpha-6 chain {Arabidopsis thaliana}	7.6	4.6	3.0	1.5	100.0%	-3.6
4067	AT1G75560.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr1:28374802-28376902 REVERSE   Aliases: F10A5.22, F10A5_22	4.7	3.1	1.6	1.5	100.0%	-3.6
4068	AT3G06650.1   Symbol: ACLB 1	5.6	6.2	-0.6	-1.5	100.0%	-3.6
4069	AT1G56340.2   Symbol: CRT1   similar to calreticulin 2 (CRT2) [Arabidopsis thaliana] (TAIR:At1g09210.1); similar to calreticulin [Beta vulgaris subsp. vulgaris] (GB:CAA05161.1); similar to calreticulin [Nicotiana plumbaginifolia] (GB:CAA95999.1); similar to calreticulin (GB:AAA80652.1); similar to calcium-binding protein calreticulin [Prunus armeniaca] (GB:AAD32207.1); similar to CRTC_RICCO Calreticulin precursor (GB:P93508); contains InterPro domain Calreticulin (InterPro:IPR001580)   chr1:21093545-21096322 REVERSE   Aliases: CALRETICULIN 1, F14G9.5, F14G9_5	10.0	10.6	-0.6	-1.5	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4070	AT2G47730.1   Symbol: ATGSTF8   glutathione S-transferase 6 (GST6), identical to GB:X95295. Based on identical cDNA hits, the translation is now 40 AAs longer at the N-terminal, and start of exon2 is also corrected.   chr2:19565270-19566533 FORWARD   Aliases: ATGSTF5, F17A22.12, GLUTATHIONE S TRANSFERASE 16, GLUTATHIONE S TRANSFERASE 8, GST6, GSTF8	7.3	8.4	-1.1	-1.5	100.0%	-3.7
4071	AT3G03920.1   Gar1 RNA-binding region family protein, contains Pfam profile PF04410: Gar1 protein RNA binding region   chr3:1009005-1010477 REVERSE   Aliases: F20H23.3, F20H23_3	9.5	8.8	0.7	1.5	100.0%	-3.5
4072	AT3G24315.1   sec20 family protein, contains Pfam PF03908: Sec20   chr3:8820464-8822810 REVERSE   Aliases: None	9.6	9.1	0.5	1.5	100.0%	-3.9
4073	AT3G20780.1   Symbol: ATTOP6B   topoisomerase 6 subunit B (TOP6B), nearly identical to topoisomerase 6 subunit B (Arabidopsis thaliana) GI:12331188   chr3:7263906-7268578 REVERSE   Aliases: BIN3, BRASSINOSTEROID INSENSITIVE 3, ELONGATED HYPOCOTYL 6, HYP6, MOE17.8	3.6	4.2	-0.6	-1.5	100.0%	-3.7
4074	AT2G17630.1   phosphoserine aminotransferase, putative, similar to Phosphoserine aminotransferase, chloroplast precursor (PSAT) (SP:Q96255) (Arabidopsis thaliana); contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V   chr2:7673667-7675138 FORWARD   Aliases: T19E12.3, T19E12_3	7.4	8.3	-0.9	-1.5	100.0%	-3.6
4075	AT5G01810.2   Symbol: CIPK15	7.9	7.0	0.9	1.5	100.0%	-3.9
4076	AT1G27720.1   transcription initiation factor IID (TFIID) component TAF4 family protein, contains Pfam profile PF05236: Transcription initiation factor TFIID component TAF4 family   chr1:9643338-9647363 REVERSE   Aliases: T22C5.17, T22C5_17	3.8	4.1	-0.4	-1.5	100.0%	-4.1
4077	AT3G22060.1   contains Pfam profile: PF01657 Domain of unknown function that is usually associated with protein kinase domain Pfam:PF00069, however this protein does not have the protein kinase domain   chr3:7771023-7772347 FORWARD   Aliases: MZN24.26	2.8	3.1	-0.3	-1.5	100.0%	-4.0
4078	AT5G04360.1   pullulanase, putative / starch debranching enzyme, putative, similar to pullulanase (Spinacia oleracea) GI:634093 (EC 3.2.1.41); contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain   chr5:1221531-1228612 FORWARD   Aliases: T19N18.90, T19N18_90	4.8	4.1	0.7	1.5	100.0%	-3.7
4079	AT4G36940.1   similar to putative nicotinate phosphoribosyltransferase [Oryza sativa (japonica cultivar-group)] (GB:XP_470349.1); similar to nicotinate phosphoribosyltransferase-like protein [Oryza sativa] (GB:AAP69615.1); similar to OSJNBa0042L16.13 [Oryza sativa (japonica cultivar-group)] (GB:NP_910116.2); contains InterPro domain Nicotinate phosphoribosyltransferase related (InterPro:IPR006405); contains InterPro domain Nicotinate phosphoribosyltransferase and related (InterPro:IPR007229)   chr4:17416852-17420248 FORWARD   Aliases: AP22.31, AP22_31	4.7	5.3	-0.6	-1.5	100.0%	-3.9
4080	AT5G37020.1   Symbol: ARF8   auxin-responsive factor (ARF8), identical to auxin response factor 8 GI:4104931 from (Arabidopsis thaliana)   chr5:14647258-14651617 FORWARD   Aliases: AUXIN RESPONSE FACTOR 8, K15O15.1, K15O15_1	4.4	4.7	-0.3	-1.5	100.0%	-4.1
4081	AT4G15910.1   Symbol: ATDI21	11.2	11.7	-0.4	-1.5	100.0%	-3.7
4082	AT1G05205.1   expressed protein   chr1:1509212-1510280 REVERSE   Aliases: None	10.1	10.5	-0.4	-1.5	100.0%	-4.0
4083	AT3G19800.1   expressed protein   chr3:6876120-6878156 FORWARD   Aliases: MPN9.4	6.1	5.4	0.6	1.5	100.0%	-3.4
4084	AT5G01540.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:210978-213471 REVERSE   Aliases: F7A7.60, F7A7_60	2.6	2.9	-0.3	-1.5	100.0%	-4.3
4085	AT4G14615.1   expressed protein   chr4:8383765-8385074 FORWARD   Aliases: None	10.4	10.8	-0.4	-1.5	100.0%	-4.2
4086	AT1G67430.1   60S ribosomal protein L17 (RPL17B), similar to ribosomal protein GI:19101 from (Hordeum vulgare)	11.9	12.4	-0.5	-1.5	100.0%	-4.1
4087	AT2G41680.1   thioredoxin reductase, putative / NADPH-dependent thioredoxin reductase, putative, The last 2 exons encode thioredoxin. There is an EST match to exons 5-7, and the distance between exon 7 and exon 8 is only 90bp. It is unlikely this is two separate genes, but more likely a hybrid protein.   chr2:17383233-17386122 REVERSE   Aliases: T32G6.20, T32G6_20	7.2	7.7	-0.5	-1.5	100.0%	-3.8
4088	AT5G05420.1   immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative, contains similarity to peptidyl-prolyl cis-trans isomerase   chr5:1604041-1604824 REVERSE   Aliases: K18I23.23, K18I23_23	4.8	4.4	0.4	1.5	100.0%	-4.0
4089	AT2G01830.3   Symbol: WOL   histidine kinase (AHK4) (WOL), identical to histidine kinase AHK4 (Arabidopsis thaliana) gi:13537200:dbj:BAB40776; contains Pfam profiles PF03924: CHASE domain, PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00512: His Kinase A (phosphoacceptor) domain, PF00072: Response regulator receiver domain   chr2:362982-369706 REVERSE   Aliases: AHK4, CRE1, CYTOKININ RESPONSE 1, T23K3.2, T23K3_2, WOL, WOL1	4.6	5.2	-0.5	-1.5	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4090	AT1G48950.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g17210.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD52672.1)   chr1:18110565-18113905 FORWARD   Aliases: F27K7.14	5.9	6.4	-0.5	-1.5	100.0%	-3.6
4091	AT1G21690.2   Symbol: EMB1968   replication factor C 37 kDa, putative, Similar to SWISS-PROT:P35249 activator 1 37 kDa subunit (Replication factor C 37 kDa subunit, A1 37 kDa subunit, RF-C 37 kDa subunit, RFC37) (Homo sapiens); contains Pfam domain, PF00004: ATPase, AAA family	5.3	5.7	-0.4	-1.5	100.0%	-4.1
4092	AT3G22420.2   Symbol: WNK2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:7946533-7949081 FORWARD   Aliases: MCB17.15, PROTEIN KINASE, WITH NO K 2, ZIK3	6.3	7.1	-0.7	-1.5	100.0%	-3.3
4093	AT3G12690.3   protein kinase, putative, similar to viroid symptom modulation protein (Lycopersicon esculentum) gi:7672777:gb:AAF66637   chr3:4030462-4032820 REVERSE   Aliases: MBK21.5	4.1	3.9	0.3	1.5	100.0%	-4.1
4094	AT1G49970.1   Symbol: CLPR1   ATP-dependent Clp protease proteolytic subunit (ClpR1) (nClpP5), identical to nClpP5 GB:BAA82069 GI:5360595 from (Arabidopsis thaliana); identical to cDNA nClpP5 (nuclear encoded ClpP5) GI:5360594   chr1:18505201-18508277 REVERSE   Aliases: F2J10.14, F2J10_14, NCLPP5	10.5	10.0	0.5	1.5	100.0%	-4.0
4095	AT3G23590.1   expressed protein   chr3:8467456-8473626 FORWARD   Aliases: MDB19.7	6.0	5.6	0.4	1.5	100.0%	-3.9
4096	AT4G04180.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family   chr4:2020434-2023990 FORWARD   Aliases: T27D20.13, T27D20_13	4.5	4.9	-0.4	-1.5	100.0%	-3.7
4097	AT1G07970.1   expressed protein   chr1:2469288-2472620 REVERSE   Aliases: T6D22.6, T6D22_6	5.0	5.4	-0.4	-1.5	100.0%	-3.8
4098	AT1G50170.1   expressed protein, similar to Cbi protein (GI:3724039) (Bacillus megaterium); similar to YlnE protein (GI:2462961) (Bacillus subtilis); similar to NirR (GI:4433637) (Staphylococcus carnosus)   chr1:18585692-18587392 FORWARD   Aliases: F14I3.20, F14I3_20	6.0	5.4	0.6	1.5	100.0%	-3.8
4099	AT5G41380.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g63820.1); similar to 'unknown protein, contains CCT motif, PF06203' [Oryza sativa (japonica cultivar-group)] (GB:XP_475389.1)   chr5:16578506-16580960 REVERSE   Aliases: MYC6.9, MYC6_9	3.1	2.8	0.2	1.5	100.0%	-4.2
4100	AT5G23450.3   Symbol: ATLCBK1   similar to diacylglycerol kinase family protein [Arabidopsis thaliana] (TAIR:At4g21540.1); similar to putative sphingosine kinase [Oryza sativa (japonica cultivar-group)] (GB:AAP54628.1); similar to OSJNBb0103I08.5 [Oryza sativa (japonica cultivar-group)] (GB:XP_473364.1); contains InterPro domain Diacylglycerol kinase, catalytic domain (InterPro:IPR001206)   chr5:7904711-7909588 REVERSE   Aliases: A. THALIANA LONG CHAIN BASE (LCB) KINASE 1, K19M13.8, K19M13_8, SPHINGOSINE KINASE	4.9	4.4	0.5	1.5	100.0%	-3.7
4101	AT5G63880.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr5:25580964-25583175 FORWARD   Aliases: MGI19.8, MGI19_8	8.5	8.2	0.3	1.5	100.0%	-4.0
4102	AT4G36450.1   Symbol: ATMPK14   mitogen-activated protein kinase, putative / MAPK, putative (MPK14), mitogen-activated protein kinase (MAPK)(AtMPK14), PMID:12119167   chr4:17210248-17211416 REVERSE   Aliases: AP22.98, AP22_98	3.5	3.3	0.3	1.5	100.0%	-4.2
4103	AT4G12600.1   ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein, Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.   chr4:7453199-7454478 FORWARD   Aliases: T1P17.190, T1P17_190	9.9	10.5	-0.6	-1.5	100.0%	-3.7
4104	AT3G28730.1   Symbol: ATHMG   structure-specific recognition protein 1 / high mobility group protein / HMG protein, nearly identical to SP:Q05153 Structure-specific recognition protein 1 homolog (HMG protein) {Arabidopsis thaliana}; contains Pfam profile PF00505: HMG (high mobility group) box; contains Pfam profile PF03531: Structure-specific recognition protein   chr3:10786126-10790386 FORWARD   Aliases: HIGH MOBILITY GROUP, T19N8.3	8.8	9.0	-0.3	-1.5	100.0%	-4.0
4105	AT4G02150.1   Symbol: ATIMPALPHA3/MOS6   Encodes IMPORTIN ALPHA 3. Mutant plants act as suppressors of snc1 response and salicylic acid accumulation. Located in the nucleus. Involved in protein import.   chr4:950649-953689 REVERSE   Aliases: ATIMPALPHA3, MOS6, T10M13.16, T10M13_16	8.0	9.0	-0.9	-1.5	100.0%	-3.8
4106	AT3G27210.1   expressed protein   chr3:10046423-10048580 REVERSE   Aliases: K17E12.3	4.4	3.9	0.5	1.5	100.0%	-3.8
4107	AT2G45880.1   glycosyl hydrolase family 14 protein, similar to beta-amylase GI:13560977 from (Castanea crenata)   chr2:18885593-18889649 REVERSE   Aliases: F4I18.14	4.1	3.7	0.4	1.5	100.0%	-4.2
4108	AT4G34240.2   Symbol: ALDH3I1   aldehyde dehydrogenase (ALDH3), similar to aldehyde dehydrogenase (Arabidopsis thaliana) gi:17065876:emb:CAC84903; contains Pfam profile PF00171: aldehyde dehydrogenase (NAD) family protein; identical to cDNA aldehyde dehydrogenase (ALDH3 gene) GI:17065875, aldehyde dehydrogenase (Arabidopsis thaliana) GI:17065876   chr4:16389782-16392086 FORWARD   Aliases: ALDH3, F10M10.10, F10M10_10	6.8	7.4	-0.6	-1.5	100.0%	-3.5
4109	AT1G52640.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:19612525-19614096 REVERSE   Aliases: F6D8.14, F6D8_14	2.7	2.9	-0.3	-1.5	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4110	AT5G16390.2   Symbol: BCCP1   biotin carboxyl carrier protein 1 (BCCP1), identical to biotin carboxyl carrier protein of acetyl-CoA carboxylase precursor (Arabidopsis thaliana) gi:9759121:dbj:BAB09606   chr5:5360844-5363126 REVERSE   Aliases: BCCP, BIOTIN CARBOXYL CARRIER, BIOTIN CARBOXYL CARRIER PROTEIN 1, CAC1A, MQK4.12, MQK4_12	6.3	6.8	-0.5	-1.5	100.0%	-3.7
4111	AT1G15220.2   cytochrome c biogenesis protein family, contains Pfam PF03918: Cytochrome C biogenesis protein; similar to Cytochrome c-type biogenesis protein cycl precursor.(SP:P45405) {Bradyrhizobium japonicum}   chr1:5240024-5241516 REVERSE   Aliases: F9L1.17, F9L1_17	3.6	3.3	0.3	1.5	100.0%	-3.9
4112	AT3G51420.1   strictosidine synthase family protein, similar to hemomucin (Drosophila melanogaster)(GI:1280434), strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088   chr3:19095014-19096837 FORWARD   Aliases: F26O13.60	2.7	2.4	0.3	1.5	100.0%	-4.3
4113	AT3G23920.1   beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative, similar to beta-amylase enzyme (Arabidopsis thaliana) GI:6065749, beta-amylase PCT-BMYI from (Solanum tuberosum); contains Pfam profile PF01373: Glycosyl hydrolase family 14   chr3:8641576-8644456 FORWARD   Aliases: F14O13.12	6.0	5.2	0.8	1.5	100.0%	-3.8
4114	AT5G45760.2   transducin family protein / WD-40 repeat family protein   chr5:18578338-18580422 FORWARD   Aliases: MRA19.19, MRA19_19	5.9	6.4	-0.5	-1.5	100.0%	-3.7
4115	AT4G03180.1   expressed protein   chr4:1403201-1405570 FORWARD   Aliases: F4C21.10, F4C21_10	6.5	6.9	-0.4	-1.5	100.0%	-3.9
4116	AT3G02180.2   Symbol: SP1L   expressed protein   chr3:404891-405656 FORWARD   Aliases: F1C9.3, SPIRAL 1 LIKE	9.9	10.3	-0.4	-1.5	100.0%	-3.9
4117	AT3G18270.1   Symbol: CYP77A5P   mandelate racemase/muconate lactonizing enzyme family protein, low similarity to cis,cis-muconate lactonizing enzyme (Burkholderia sp. TH2) GI:23491535; contains Pfam profile: PF01188 Mandelate racemase/muconate lactonizing enzyme, C-terminal domain, PF02746: Mandelate racemase/muconate lactonizing enzyme, N-terminal domain   chr3:6261917-6264315 FORWARD   Aliases: MIE15.6	4.4	4.0	0.3	1.5	100.0%	-3.9
4118	AT3G10210.1   expressed protein, similar to putative protein GB:CAA20045 (Arabidopsis thaliana)   chr3:3160244-3161599 REVERSE   Aliases: F14P13.19	5.0	4.6	0.5	1.5	100.0%	-3.8
4119	AT1G63670.1   expressed protein   chr1:23611085-23613666 REVERSE   Aliases: F24D7.14, F24D7_14	3.0	3.4	-0.3	-1.5	100.0%	-4.0
4120	AT3G51895.1   Symbol: SULTR3;1   sulfate transporter (ST1), identical to sulfate transporter (Arabidopsis thaliana) GI:2285885   chr3:19262274-19266738 REVERSE   Aliases: AST12, ATST1, SULFATE TRANSPORTER 1	4.6	4.1	0.5	1.5	100.0%	-3.6
4121	AT2G18250.1   cytidyltransferase domain-containing protein, similar to CoA synthase (Mus musculus) GI:21780289, bifunctional phosphopantetheine adenylyl transferase / dephospho CoA kinase (Sus scrofa) GI:20465246; contains Pfam profile PF01467: Cytidyltransferase   chr2:7947107-7948581 FORWARD   Aliases: T30D6.24, T30D6_24	8.8	7.8	1.1	1.5	100.0%	-3.6
4122	AT5G67070.1   Symbol: RALFL34   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr5:26785321-26786072 FORWARD   Aliases: K21H1.3, K21H1_3, RALF LIKE 34	4.5	5.1	-0.5	-1.5	100.0%	-3.6
4123	AT5G08430.1   SWIB complex BAF60b domain-containing protein / plus-3 domain-containing protein / GYF domain-containing protein, similar to CPRF interacting protein (Petroselinum crispum) GI:9588690; contains Pfam profiles PF02201: BAF60b domain of the SWIB complex, PF03126: Plus-3 domain, PF02213: GYF domain; contains non-consensus AT-AC splice sites at intron 5   chr5:2716701-2720213 FORWARD   Aliases: F8L15.160, F8L15_160	7.1	7.6	-0.5	-1.5	100.0%	-4.1
4124	AT3G53150.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:19708714-19710237 REVERSE   Aliases: T4D2.80	3.0	3.8	-0.8	-1.5	100.0%	-3.4
4125	AT5G62990.1   Symbol: EMB1692   expressed protein   chr5:25295054-25296538 FORWARD   Aliases: EMB1692, EMBRYO DEFECTIVE 1692, MJH22.4, MJH22_4	3.2	3.5	-0.3	-1.5	100.0%	-4.4
4126	AT2G23960.1   defense-related protein, putative, similar to defense-related protein (Brassica carinata) GI:14009290   chr2:10203139-10204690 FORWARD   Aliases: T29E15.16, T29E15_16	2.8	3.2	-0.4	-1.5	100.0%	-3.8
4127	AT1G66660.1   seven in absentia (SINA) protein, putative, similar to SIAH2 protein (Brassica napus var. napus) GI:7657878; contains Pfam profile PF03145: Seven in absentia protein family   chr1:24865539-24867031 REVERSE   Aliases: F4N21.20, F4N21_20	4.9	4.5	0.4	1.5	100.0%	-3.8
4128	AT1G43900.1   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase type 2C GI:4336436 from (Lotus japonicus)   chr1:16656485-16658885 FORWARD   Aliases: F9C16.6, F9C16_6	9.2	9.6	-0.4	-1.5	100.0%	-4.1
4129	AT2G35340.1   RNA helicase, putative, similar to ATP-dependent RNA helicase #3 (Homo sapiens) GI:3107913; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr2:14879807-14886694 FORWARD   Aliases: T32F12.28, T32F12_28	3.2	3.4	-0.2	-1.5	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4130	AT4G35950.1   Symbol: ARAC6   Rac-like GTP-binding protein (ARAC6), identical to rac-like GTP binding protein Arac6 GI:3406757 from (Arabidopsis thaliana)   chr4:17023840-17025866 REVERSE   Aliases: RAC2, T19K4.80	7.9	8.4	-0.4	-1.5	100.0%	-3.8
4131	AT4G02590.2   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g03040.1); similar to bHLH transcription factor PTF1-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD29274.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr4:1137508-1140490 REVERSE   Aliases: T10P11.13, T10P11_13	5.1	4.4	0.7	1.5	100.0%	-4.0
4132	AT1G64970.1   Symbol: G TMT   expressed protein   chr1:24137050-24139723 REVERSE   Aliases: F13O11.27, F13O11_27, GAMMA TOCOPHEROL METHYLTRANSFERASE, TMT1, VITAMIN E DEFICIENT 4, VTE4	4.3	3.9	0.4	1.5	100.0%	-3.7
4133	AT2G20930.1   expressed protein   chr2:9007700-9008818 REVERSE   Aliases: F5H14.10, F5H14_10	6.6	7.0	-0.5	-1.5	100.0%	-3.9
4134	AT1G22110.1   expressed protein   chr1:7801405-7802462 REVERSE   Aliases: F2E2.18, F2E2_18	3.8	3.5	0.3	1.5	100.0%	-4.0
4135	AT5G13090.1   expressed protein, predicted proteins - Arabidopsis thaliana   chr5:4153589-4154675 REVERSE   Aliases: T19L5.50, T19L5_50	5.7	5.3	0.4	1.5	100.0%	-3.8
4136	AT2G42770.1   peroxisomal membrane 22 kDa family protein, contains Mpv17 / PMP22 family domain, Pfam:PF04117   chr2:17805363-17807083 REVERSE   Aliases: F7D19.23, F7D19_23	7.7	7.0	0.7	1.5	100.0%	-3.3
4137	AT4G32900.2   expressed protein   chr4:15878751-15881044 REVERSE   Aliases: F26P21.20, F26P21_20	3.6	3.1	0.4	1.5	100.0%	-3.8
4138	AT1G33290.2   sporulation protein-related, isoform contains non-consensus AT-donor acceptor site at intron 6; similar to Stage III sporulation protein AA. (Swiss-Prot:Q01367) (Bacillus subtilis); similar to SpoIIIAA (GI:1303904) (Bacillus subtilis); similar to stage III sporulation protein AA (GI:18145497) (Clostridium perfringens str. 13)   chr1:12074090-12076081 FORWARD   Aliases: T16O9.17, T16O9_17	7.5	6.8	0.7	1.5	100.0%	-3.8
4139	AT2G25070.1   protein phosphatase 2C, putative / PP2C, putative   chr2:10670319-10673043 REVERSE   Aliases: F13D4.1	9.8	9.5	0.4	1.5	100.0%	-4.3
4140	AT1G19660.2   similar to wound-responsive protein-related [Arabidopsis thaliana] (TAIR:At1g75380.2); similar to wound-responsive protein-related [Arabidopsis thaliana] (TAIR:At1g75380.1); similar to wound-responsive protein-related [Arabidopsis thaliana] (TAIR:At1g75380.3); similar to putative wound inductive gene [Oryza sativa (japonica cultivar-group)] (GB:XP_481914.1)   chr1:6799972-6802643 REVERSE   Aliases: F14P1.1, F14P1_1	10.0	8.7	1.3	1.5	100.0%	-3.5
4141	AT1G75380.3   wound-responsive protein-related, similar to wound inductive gene GI:8096273 from (Nicotiana tabacum)   chr1:28285050-28287694 REVERSE   Aliases: F1B16.9, F1B16_9	10.0	8.7	1.3	1.5	100.0%	-3.5
4142	AT1G22240.1   pumilio/Puf RNA-binding domain-containing protein, contains Pfam profile: PF00806 pumilio-family RNA binding domain   chr1:7853073-7854952 FORWARD   Aliases: F16L1.3, F16L1_3	3.0	2.8	0.2	1.5	100.0%	-4.3
4143	AT4G33970.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	2.4	2.3	0.2	1.5	100.0%	-4.5
4144	AT5G65630.1   DNA-binding bromodomain-containing protein, similar to 5.9 kb fsh membrane protein (Drosophila melanogaster) GI:157455; contains Pfam profile PF00439: Bromodomain   chr5:26243058-26245675 REVERSE   Aliases: K21L13.15, K21L13_15	4.6	5.2	-0.6	-1.5	100.0%	-3.9
4145	AT5G17060.1   Gene encoding ADP-ribosylation factor and similar to ADP-ribosylation factor 1; ARF 1 (GP:385340) {Drosophila melanogaster}, other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding.   chr5:5610809-5613063 FORWARD   Aliases: F2K13.210, F2K13_210	6.9	6.3	0.6	1.5	100.0%	-4.0
4146	AT2G27010.1   Symbol: CYP705A9   cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798) {Glycine max};   chr2:11533246-11534932 REVERSE   Aliases: T20P8.6, T20P8_6	4.4	3.4	1.0	1.5	100.0%	-3.6
4147	AT5G09310.1   expressed protein   chr5:2887194-2888528 REVERSE   Aliases: T5E8.110, T5E8_110	7.9	7.1	0.8	1.5	100.0%	-3.7
4148	AT5G55220.1   trigger factor type chaperone family protein, contains Pfam profiles PF05697: Bacterial trigger factor protein (TF), PF05698: Bacterial trigger factor protein (TF) C-terminus, PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr5:22414842-22418062 FORWARD   Aliases: MCO15.17, MCO15_17	3.3	3.7	-0.4	-1.5	100.0%	-3.9
4149	AT5G60360.2   Symbol: AALP   similar to cysteine proteinase, putative [Arabidopsis thaliana] (TAIR:At3g45310.1); similar to cysteine protease [Nicotiana tabacum] (GB:BAA96501.1); contains InterPro domain Papain cysteine protease (C1) (InterPro:IPR000668); contains InterPro domain Eukaryotic thiol (cysteine) protease (InterPro:IPR000169)   chr5:24297123-24299623 FORWARD   Aliases: MUF9.4, MUF9_4	11.4	10.4	1.0	1.5	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4150	AT5G38830.1   tRNA synthetase class I (C) family protein, similar to SP:Q06752 Cysteinyl-tRNA synthetase (EC 6.1.1.16) (Cysteine--tRNA ligase) (CysRS) {Bacillus subtilis}; contains Pfam profile PF01406: tRNA synthetases class I (C)   chr5:15562994-15565382 REVERSE   Aliases: K15E6.3, K15E6_3	8.3	9.0	-0.7	-1.5	100.0%	-3.8
4151	AT4G11130.1   Symbol: RDR2   RNA-dependent RNA polymerase, putative, similar to RNA-directed RNA polymerase (Lycopersicon esculentum) gi:4038592:emb:CAA71421	4.4	4.7	-0.3	-1.5	100.0%	-4.2
4152	AT4G01940.1   Symbol: NFU1   nitrogen fixation NifU-like family protein, similar to apricot NifU homolog partial CDS, GenBank accession number U95179; contains Pfam profile: PF01106 NifU-like domain   chr4:841989-843459 REVERSE   Aliases: ATCNFU1, T7B11.20, T7B11_20	5.2	4.7	0.5	1.5	100.0%	-3.6
4153	AT4G00780.1   mepirin and TRAF homology domain-containing protein / MATH domain-containing protein, contains Pfam profile PF00917: MATH domain   chr4:334733-336310 FORWARD   Aliases: A_TM018A10.12, A_TM018A10_12, T18A10.3, T18A10_3	2.5	2.3	0.2	1.5	100.0%	-4.5
4154	AT2G25300.1   similar to galactosyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g32120.1); similar to beta 1,3-glycosyltransferase-like protein I [Lycopersicon esculentum] (GB:CAD30015.1); contains InterPro domain Glycosyl transferase, family 31 (InterPro:IPR002659)   chr2:10778773-10781373 REVERSE   Aliases: T22F11.11, T22F11_11	7.3	6.7	0.6	1.5	100.0%	-3.7
4155	AT1G68130.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:25535907-25538249 FORWARD   Aliases: T23K23.2, T23K23_2	4.0	3.4	0.6	1.5	100.0%	-3.8
4156	AT3G14900.1   expressed protein   chr3:5013299-5015284 REVERSE   Aliases: K15M2.4	4.5	5.5	-1.0	-1.5	100.0%	-3.6
4157	AT3G07000.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.6	4.2	0.4	1.5	100.0%	-3.8
4158	AT3G15610.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to serine/threonine kinase receptor associated protein GB:NP_035629 (SP:Q9Z1Z2) (Mus musculus); UNR-interacting protein GB:NP_009109 (Homo sapiens)	9.9	10.2	-0.3	-1.5	100.0%	-4.3
4159	AT5G49110.1   expressed protein, ; expression supported by MPSS   chr5:19917429-19923151 FORWARD   Aliases: K20J1.8, K20J1_8	3.5	3.8	-0.2	-1.5	100.0%	-4.4
4160	AT4G21960.1   Symbol: PRXR1   peroxidase 42 (PER42) (P42) (PRXR1), identical to SP:Q9SB81 Peroxidase 42 precursor (EC 1.11.1.7) (Atperox P42) (PRXR1) (ATP1a/ATP1b) {Arabidopsis thaliana}   chr4:11646186-11648373 REVERSE   Aliases: F1N20.3, PEROXIDASE PRXR1	13.0	12.3	0.7	1.5	100.0%	-4.6
4161	AT3G55140.2   pectate lyase family protein, similar to pollen allergen Amb a 1.3 SP:P27761 from (Ambrosia artemisiifolia)   chr3:20449760-20451404 FORWARD   Aliases: T26I12.20	7.2	7.7	-0.6	-1.5	100.0%	-3.6
4162	AT2G35650.1   Symbol: ATCSLA07   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535; identical to cDNA for partial mRNA for glycosyltransferase (csla07 gene) GI:28551963   chr2:14992567-14995436 FORWARD   Aliases: ATCSLA7, CELLULOSE SYNTHASE LIKE, CSLA07, CSLA7, T20F21.16, T20F21_16	5.6	5.9	-0.3	-1.5	100.0%	-4.1
4163	AT1G09140.2   Symbol: ATSRP30.1   similar to pre-mRNA splicing factor SF2 (SF2) / SR1 protein [Arabidopsis thaliana] (TAIR:At1g02840.1); similar to pre-mRNA splicing factor SF2 (SF2) / SR1 protein [Arabidopsis thaliana] (TAIR:At1g02840.3); similar to ASF/SF2-like pre-mRNA splicing factor SRP32 [Zea mays] (GB:AAU29328.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr1:2942566-2945961 REVERSE   Aliases: ATSRP30, T12M4.19, T12M4_19	6.3	5.7	0.6	1.5	100.0%	-3.8
4164	AT1G33820.1   hypothetical protein   chr1:12278418-12279431 REVERSE   Aliases: F14M2.4, F14M2_4	2.4	2.6	-0.2	-1.5	100.0%	-4.9
4165	AT5G56100.1   glycine-rich protein / oleosin, contains Pfam PF01277: Oleosin domain   chr5:22734341-22734977 FORWARD   Aliases: MDA7.16, MDA7_16	7.7	6.6	1.1	1.5	100.0%	-3.7
4166	AT5G54110.1   Symbol: ATMAMI	6.9	6.6	0.3	1.5	100.0%	-4.1
4167	AT2G35160.1   Symbol: SUVH5   SET domain-containing protein (SUVH5), identical to SUVH5 (Arabidopsis thaliana) GI:13517751; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH5 (SUVH5) GI:13517750	3.8	4.1	-0.3	-1.5	100.0%	-4.2
4168	AT1G49600.1   Symbol: ATRBP47A   RNA-binding protein 47 (RBP47), putative, similar to DNA binding protein ACBF GB:U90212 GI:1899187 from (Nicotiana tabacum)   chr1:18360554-18363818 REVERSE   Aliases: ATRBP47A, F14J22.16, F14J22_16	5.0	5.5	-0.5	-1.5	100.0%	-3.8
4169	AT2G07340.2   prefoldin-related KE2 family protein, contains similarity to Swiss-Prot:O60925 prefoldin subunit 1 (Homo sapiens); contains Pfam domain, PF01920: KE2 family protein   chr2:3045556-3046716 FORWARD   Aliases: T13E11.11, T13E11_11	9.6	10.0	-0.4	-1.5	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4170	AT5G08190.1   TATA-binding protein-associated phosphoprotein Dr1 protein, putative, similar to Dr1 protein homolog (SP:P49592) (Arabidopsis thaliana); similar to TATA-binding protein-associated phosphoprotein (Down-regulator of transcription 1) (DR1 protein) (SP:Q01658) (Homo sapiens); contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone   chr5:2635907-2637431 FORWARD   Aliases: T22D6.130, T22D6_130	5.5	5.0	0.5	1.5	100.0%	-3.8
4171	AT1G63300.1   expressed protein, similar to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae); similar to Myosin II heavy chain, non muscle (Swiss-Prot:P08799) (Dictyostelium discoideum)   chr1:23485858-23489885 FORWARD   Aliases: F9N12.8, F9N12_8	3.9	4.4	-0.5	-1.5	100.0%	-3.9
4172	AT3G58650.1   expressed protein   chr3:21707223-21709828 REVERSE   Aliases: F14P22.240	2.8	3.0	-0.2	-1.5	100.0%	-4.6
4173	AT4G18010.2   Symbol: IP5PII	5.6	4.9	0.6	1.5	100.0%	-3.8
4174	AT4G34340.1   expressed protein   chr4:16426643-16428014 REVERSE   Aliases: F10M10.110, F10M10_110	4.3	4.9	-0.7	-1.5	100.0%	-3.7
4175	AT1G63810.1   nucleolar RNA-associated family protein / Nrap family protein, contains Pfam profile PF03813: Nrap protein; similar to nucleolar RNA-associated protein alpha (GI:18539461) (Mus musculus)   chr1:23673215-23679223 REVERSE   Aliases: T12P18.17, T12P18_17	4.3	4.9	-0.6	-1.5	100.0%	-3.7
4176	AT5G27560.1   expressed protein, hypothetical protein slr1702 - Synechocystis sp., PIR:S75312   chr5:9731731-9733921 FORWARD   Aliases: F15A18.20, F15A18_20	8.4	7.9	0.5	1.5	100.0%	-3.6
4177	AT5G10260.1   Ras-related GTP-binding protein, putative, similar to Ras-related protein Rab-6A SP:P20340 from (Homo sapiens)   chr5:3220064-3221516 FORWARD   Aliases: F18D22.30, F18D22_30	3.6	4.0	-0.5	-1.5	100.0%	-3.8
4178	AT3G62790.1   NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 15 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-15 kDa) (CI-15 kDa) (Swiss-Prot:O43920) (Homo sapiens)   chr3:23234059-23235283 REVERSE   Aliases: F26K9.220	10.7	11.0	-0.3	-1.5	100.0%	-4.3
4179	AT5G22570.1   Symbol: WRKY38	2.6	2.3	0.2	1.5	100.0%	-4.6
4180	AT3G03950.3   similar to YT521-B-like family protein [Arabidopsis thaliana] (TAIR:At5g61020.2); similar to YT521-B-like family protein [Arabidopsis thaliana] (TAIR:At5g61020.1); similar to high-glucose-regulated protein 8-like [Oryza sativa (japonica cultivar-group)] (GB:XP_476753.1); contains InterPro domain YT521-B-like protein (InterPro:IPR007275)   chr3:1021267-1024016 FORWARD   Aliases: T11I18.6, T11I18_6	7.3	8.2	-0.9	-1.5	100.0%	-3.4
4181	AT2G21290.1   expressed protein   chr2:9119937-9120411 FORWARD   Aliases: F3K23.5, F3K23_5	11.0	10.6	0.4	1.5	100.0%	-4.4
4182	AT5G66960.1   prolyl oligopeptidase family protein, similar to OpdB (Treponema denticola) GI:13786054; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain   chr5:26753435-26756719 REVERSE   Aliases: K8A10.3, K8A10_3	3.3	3.5	-0.2	-1.5	100.0%	-4.6
4183	AT2G02180.1   Symbol: TOM3   tobamovirus multiplication protein 3 (TOM3), identical to tobamovirus multiplication protein (TOM3) GI:15425641 from (Arabidopsis thaliana)   chr2:560863-563232 FORWARD   Aliases: F5O4.5, F5O4_5	5.7	5.3	0.4	1.5	100.0%	-3.8
4184	AT4G10930.1   expressed protein   chr4:6705143-6708842 REVERSE   Aliases: F25I24.140, F25I24_140	4.8	5.3	-0.5	-1.5	100.0%	-4.1
4185	AT1G09420.1   Symbol: G6PD4   Encodes a protein similar to glucose-6-phosphate dehydrogenase but, based on amino acid differences in the active site and lack of activity, does not encode a functional G6PDH. The amino acid sequence for the consensus sequence of the G6PDH active site (DHYLGKE) differs in three places in this protein. gc exon splice site at 20574 is based on protein alignment, and is not confirmed experimentally.   chr1:3038464-3041806 REVERSE   Aliases: F14J9.8, F14J9_8, G6PD4, GLUCOSE 6 PHOSPHATE DEHYDROGENASE 4	5.2	4.9	0.4	1.5	100.0%	-3.8
4186	AT5G23130.1   peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	3.3	3.0	0.3	1.5	100.0%	-4.2
4187	AT5G62110.1   expressed protein   chr5:24960130-24963307 REVERSE   Aliases: MTG10.14, MTG10_14	2.3	2.4	-0.1	-1.5	100.0%	-5.1
4188	AT1G79780.1   integral membrane protein, putative, contains 1 transmembrane domain; contains plant integral membrane protein domain, TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)   chr1:30020823-30021749 FORWARD   Aliases: F20B17.26, F20B17_26	4.1	3.8	0.3	1.5	100.0%	-4.1
4189	AT5G15550.2   transducin family protein / WD-40 repeat family protein, similar to YTM1 - Homo sapiens, EMBL:AF242546; contains Pfam PF00400: WD domain, G-beta repeat (7 copies,1 weak);   chr5:5058839-5062090 REVERSE   Aliases: T20K14.160, T20K14_160	6.6	7.2	-0.6	-1.5	100.0%	-3.6
4190	AT1G14820.3   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, contains Pfam PF00650 : CRAL/TRIO domain; similar to phosphatidylinositol/phosphatidylcholine transfer protein SP:P24280 (Saccharomyces cerevisiae (Baker's yeast))   chr1:5105109-5106790 REVERSE   Aliases: F10B6.40, F10B6_40	7.2	7.7	-0.5	-1.5	100.0%	-3.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4191	AT4G14540.1   CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3 ) (AHAP3) family, contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to LEC1-like protein (GI:22536010) (Phaseolus coccineus)   chr4:8344612-8345214 FORWARD   Aliases: DL3310W, FCAALL.252	7.0	6.3	0.7	1.5	100.0%	-3.5
4192	AT2G16700.1   Symbol: ADF5   actin-depolymerizing factor 5 (ADF5), identical to SP:Q9ZNT3 Actin-depolymerizing factor 5 (ADF-5) (AtADF5) {Arabidopsis thaliana}   chr2:7251704-7252823 FORWARD   Aliases: ACTIN DEPOLYMERIZING FACTOR 5, T24I21.11, T24I21_11	7.5	7.1	0.4	1.5	100.0%	-3.8
4193	NA	12.2	12.4	-0.2	-1.5	100.0%	-4.7
4194	AT1G53430.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr1:19938835-19944756 FORWARD   Aliases: T3F20.25, T3F20_25	5.3	4.4	0.8	1.5	100.0%	-3.6
4195	AT3G53960.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:19989100-19991912 REVERSE   Aliases: F5K20.260	5.7	5.2	0.6	1.5	100.0%	-3.5
4196	AT2G42740.1   Symbol: RPL16A	8.3	8.7	-0.5	-1.5	100.0%	-3.7
4197	AT2G16750.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr2:7278094-7281775 FORWARD   Aliases: T24I21.16, T24I21_16	2.3	2.7	-0.4	-1.5	100.0%	-4.3
4198	AT1G48550.1   vacuolar protein sorting-associated protein 26 family protein / VPS26 family protein, contains Pfam profile PF03643: Vacuolar protein sorting-associated protein 26   chr1:17954247-17956361 REVERSE   Aliases: T1N15.17, T1N15_17	4.8	4.4	0.3	1.5	100.0%	-4.0
4199	AT5G58230.1   Symbol: MSI1   WD-40 repeat protein (MSI1), contains 6 WD-40 repeats (PF0400); identical to WD-40 repeat protein (SP:O22467) (Arabidopsis thaliana)   chr5:23573258-23575471 FORWARD   Aliases: MCK7.10, MCK7_10, MEDICIS, MULTICOPY SUPPRESSOR OF IRA1	6.7	7.4	-0.7	-1.5	100.0%	-3.8
4200	AT1G68820.1   membrane protein, putative, contains 7 transmembrane domains; similar to inhibitor of apoptosis-2 IAP-2 (GI:20043383) (Mamestra configurata nucleopolyhedrovirus)   chr1:25869337-25872648 FORWARD   Aliases: F14K14.7, F14K14_7	5.9	5.4	0.5	1.5	100.0%	-3.5
4201	AT5G58950.1   protein kinase family protein, concontains protein kinase domain, Pfam:PF00069   chr5:23818154-23820868 REVERSE   Aliases: K19M22.20, K19M22_20	8.5	8.1	0.5	1.5	100.0%	-3.9
4202	AT3G23210.1   basic helix-loop-helix (bHLH) family protein, similar to hypothetical protein GB:CAB10220 from (Arabidopsis thaliana)   chr3:8283097-8285087 REVERSE   Aliases: K14B15.12	6.1	5.8	0.3	1.5	100.0%	-4.0
4203	AT1G72390.1   expressed protein   chr1:27250615-27255238 FORWARD   Aliases: T10D10.14, T10D10_14	4.2	4.5	-0.3	-1.5	100.0%	-3.9
4204	AT3G54990.1   Symbol: SMZ   similar to AP2 domain-containing transcription factor, putative [Arabidopsis thaliana] (TAIR:At2g39250.1); similar to PHAP2B protein [Petunia x hybrida] (GB:AAD39440.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr3:20384695-20387499 REVERSE   Aliases: SCHLAFMUTZE, T15C9.6	4.9	4.2	0.7	1.5	100.0%	-3.6
4205	AT2G07240.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr2:3007099-3012136 REVERSE   Aliases: T13E11.1, T13E11_1	3.4	3.6	-0.2	-1.5	100.0%	-4.3
4206	AT2G07360.1   SH3 domain-containing protein, contains Pfam profile PF00018: SH3 domain	4.3	4.5	-0.3	-1.5	100.0%	-4.3
4207	AT4G24800.2   similar to MA3 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g63190.2); similar to MA3 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g48390.1); similar to MA3 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g63190.1); similar to OSJNBb0011N17.20 [Oryza sativa (japonica cultivar-group)] (GB:XP_472924.1); contains InterPro domain Initiation factor eIF-4 gamma, MA3 (InterPro:IPR003891)   chr4:12781772-12785207 FORWARD   Aliases: F6I7.10, F6I7_10	5.4	5.8	-0.4	-1.5	100.0%	-3.9
4208	AT5G05520.1   outer membrane OMP85 family protein, contains Pfam profile PF01103: outer membrane protein, OMP85 family	6.5	7.0	-0.5	-1.5	100.0%	-3.9
4209	AT1G02710.1   glycine-rich protein   chr1:589706-589996 REVERSE   Aliases: T14P4.26, T14P4_26	6.5	5.9	0.7	1.5	100.0%	-3.7
4210	AT1G06830.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.8	3.3	0.5	1.5	100.0%	-4.0
4211	AT2G13290.2   glycosyl transferase family 17 protein, low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus (SP:Q10470), Rattus norvegicus (SP:Q02527), Homo sapiens (SP:Q09327) ; contains Pfam profile PF04724 :Glycosyltransferase family 17   chr2:5518678-5520347 FORWARD   Aliases: F15O11.7, F15O11_7	3.9	3.5	0.3	1.5	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4212	AT3G43520.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)   chr3:15417012-15418896 FORWARD   Aliases: T18D12.90	10.3	9.6	0.7	1.5	100.0%	-4.0
4213	AT1G47870.1   Symbol: E2FC   E2F transcription factor-2 (E2F2) / transcription factor E2Fc (E2Fc), identical to transcription factor E2Fc (Arabidopsis thaliana) GI:19578311; contains Pfam profile PF02319: Transcription factor E2F/dimerisation partner; identical to cDNA E2F transcription factor-2 E2F2 GI:10443850   chr1:17637228-17640210 FORWARD   Aliases: ATE2F2, E2FC, E2FC TRANSCRIPTION FACTOR, T2E6.2, T2E6_2, TRANSCRIPTION FACTOR 2 E2F2	6.2	6.6	-0.4	-1.5	100.0%	-3.8
4214	ATMG00640.1   Symbol: ORF25   encodes a plant b subunit of mitochondrial ATP synthase based on structural similarity and the presence in the F(0) complex.   chrM:188084-188662 REVERSE   Aliases: ORF25	4.4	3.5	0.9	1.5	100.0%	-3.7
4215	AT2G21340.2   enhanced disease susceptibility protein, putative / salicylic acid induction deficient protein, putative, similar to enhanced disease susceptibility 5 (Arabidopsis thaliana) GI:16589070   chr2:9139638-9143524 FORWARD   Aliases: F3K23.10, F3K23_10	6.3	6.6	-0.3	-1.5	100.0%	-4.0
4216	AT3G59530.2   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324)   chr3:22004259-22006238 FORWARD   Aliases: T16L24.80	4.8	4.4	0.4	1.5	100.0%	-4.2
4217	AT1G06450.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)   chr1:1965839-1967239 FORWARD   Aliases: F12K11.20, F12K11_20	3.7	4.3	-0.6	-1.5	100.0%	-3.8
4218	AT3G05500.1   rubber elongation factor (REF) family protein, contains Pfam profile: PF05755 rubber elongation factor protein (REF)   chr3:1593440-1595021 FORWARD   Aliases: F22F7.5, F22F7_5	8.7	7.8	0.9	1.5	100.0%	-3.8
4219	AT3G55970.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to leucoanthocyanidin dioxygenase, Malus domestica, SP:P51091; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr3:20777718-20780303 REVERSE   Aliases: F27K19.150	3.4	3.8	-0.4	-1.5	100.0%	-3.7
4220	AT4G21300.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:11336489-11339062 FORWARD   Aliases: T6K22.30, T6K22_30	3.5	3.3	0.2	1.5	100.0%	-4.3
4221	AT4G13690.1   expressed protein   chr4:7953658-7955090 REVERSE   Aliases: F18A5.80, F18A5_80	3.7	4.3	-0.6	-1.5	100.0%	-3.7
4222	AT2G18440.1   Symbol: GUT15   expressed protein   chr2:8002811-8004000 REVERSE   Aliases: GENE WITH UNSTABLE TRANSCRIPT 15, GUT15, T30D6.5, T30D6_5	8.5	7.7	0.8	1.5	100.0%	-3.9
4223	AT3G07040.1   Symbol: RPM1   disease resistance protein RPM1 (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPM1 (gi:1361985)   chr3:2225958-2229030 REVERSE   Aliases: DISEASE RESISTANCE PROTEIN RPM1, F17A9.20, RESISTANCE TO P. SYRINGAE PV MACULICOLA 1, RESISTANCE TO PSEUDOMONAS SYRINGAE 3, RPS3	3.4	3.1	0.3	1.5	100.0%	-4.2
4224	AT1G63770.2   peptidase M1 family protein, similar to SP:P04825 Aminopeptidase N (EC 3.4.11.2) (Alpha-aminoacylpeptide hydrolase) {Escherichia coli}; contains Pfam profile PF01433: Peptidase family M1   chr1:23661169-23667906 REVERSE   Aliases: F24D7.4, F24D7_4	10.4	11.1	-0.7	-1.5	100.0%	-4.0
4225	AT5G53450.3   Symbol: ORG1   expressed protein, contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:21705999-21709677 FORWARD   Aliases: MYN8.6, MYN8_6	7.8	7.4	0.4	1.5	100.0%	-4.0
4226	AT1G51420.1   sucrose-phosphatase, putative, similar to sucrose-phosphatase (SPP1) (Arabidopsis thaliana) GI:11127757; contains Pfam profile PF05116: Sucrose-6F-phosphate phosphohydrolase   chr1:19068520-19070372 REVERSE   Aliases: F5D21.9, F5D21_9	4.0	4.8	-0.8	-1.5	100.0%	-3.7
4227	AT1G16020.2   expressed protein   chr1:5498159-5501352 FORWARD   Aliases: T24D18.12, T24D18_12	4.9	5.3	-0.4	-1.5	100.0%	-3.9
4228	AT2G44120.2   60S ribosomal protein L7 (RPL7C)	8.3	8.8	-0.6	-1.5	100.0%	-3.9
4229	AT4G17430.1   expressed protein, weak similarity to CigA protein (Mucor circinelloides) GI:9717020   chr4:9724852-9726840 REVERSE   Aliases: DL4750C, FCAALL.1	4.7	5.1	-0.4	-1.5	100.0%	-3.9
4230	AT3G51250.1   senescence/dehydration-associated protein-related, similar to senescence-associated protein 12 (Hemerocallis hybrid cultivar) gi:3551958;gb:AAC34857; similar to early-responsive to dehydration stress ERD7 protein (Arabidopsis thaliana) gi:15320412;dbj:BAB63916   chr3:19039182-19041655 FORWARD   Aliases: F24M12.290	7.1	6.5	0.6	1.5	100.0%	-3.6
4231	AT2G16060.1   Symbol: AHB1   non-symbiotic hemoglobin 1 (HB1) (GLB1), identical to SP:O24520 Non-symbiotic hemoglobin 1 (Hb1) (ARATH GLB1) {Arabidopsis thaliana}   chr2:6989703-6990713 REVERSE   Aliases: ARATH GLB1, F7H1.8, F7H1_8, GLB1, HEMOGLOBIN, NSHB1	10.6	10.1	0.5	1.5	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4232	AT3G15180.1   proteasome-related, similar to 26S proteasome non-ATPase regulatory subunit 5 (26S proteasome subunit S5B) (26S protease subunit S5 basic) (Swiss-Prot:Q16401) (Homo sapiens)   chr3:5111900-5115993 FORWARD   Aliases: F4B12.9	6.0	6.3	-0.2	-1.5	100.0%	-4.2
4233	AT3G60200.1   expressed protein, hypothetical proteins At2g44600 - Arabidopsis thaliana, EMBL:AAC27462	4.3	4.0	0.3	1.5	100.0%	-4.1
4234	AT5G02560.1   histone H2A, putative, similar to histone H2A from Pisum sativum SP:P25470, Zea mays SP:P40280, Petroselinum crispum SP:P19177; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	7.8	7.5	0.3	1.5	100.0%	-4.0
4235	AT1G09280.2   expressed protein, contains Pfam profile: PF03959 domain of unknown function (DUF341)   chr1:2997552-3001296 REVERSE   Aliases: T12M4.1, T12M4_1	7.1	7.4	-0.4	-1.5	100.0%	-4.3
4236	AT1G26170.1   importin beta-2 subunit family protein, similar to Importin9 isoform 1 (Mus musculus) GI:15186756; contains Pfam profile PF03810: Importin-beta N-terminal domain   chr1:9047526-9054425 REVERSE   Aliases: F28B23.15, F28B23_15	3.5	3.8	-0.3	-1.5	100.0%	-4.2
4237	AT2G35210.2   human Rev interacting-like family protein / hRIP family protein, similar to ARFGAP1 protein GI:7211442 from (Homo sapiens); contains InterPro accession IPR001164: Human Rev interacting-like protein (hRIP)   chr2:14843193-14845228 FORWARD   Aliases: T4C15.12, T4C15_12	3.2	2.9	0.3	1.5	100.0%	-4.4
4238	AT5G07020.1   proline-rich family protein   chr5:2180503-2182387 REVERSE   Aliases: MOJ9.19, MOJ9_19	7.2	6.5	0.7	1.5	100.0%	-3.5
4239	AT3G51510.1   expressed protein   chr3:19120041-19121030 FORWARD   Aliases: F26O13.150	7.2	6.4	0.8	1.5	100.0%	-3.3
4240	AT2G18950.1   Symbol: HPT1   homogentisate phytylprenyltransferase family protein (HPT1) / tocopherol phytyltransferase family protein (TPT1), identical to gi:17104828; contains Pfam profile PF01040: UbiA prenyltransferase family; identical to cDNA tocopherol polyprenyltransferase (TPT1) GI:17104827   chr2:8214424-8217456 FORWARD   Aliases: ATHPT, F19F24.15, F19F24_15, HOMOGENITISATE PHYTYLTRANSFERASE, HOMOGENITISATE PHYTYLTRANSFERASE 1, HPT, TOCOPHEROL PHYTYLTRANSFERASE, TOCOPHEROL POLYPRENYLTRANSFERASE, TPT1, VITAMIN E 2, VTE2	5.2	4.6	0.6	1.5	100.0%	-3.6
4241	AT2G37060.3   similar to CCAAT-box binding transcription factor, putative [Arabidopsis thaliana] (TAIR:At3g53340.1); similar to CAAT-box DNA binding protein subunit B (NF-YB) [Zea mays] (GB:CAA42234.1); contains InterPro domain Transcription factor CBF/NF-Y/archaeal histone (InterPro:IPR003958); contains InterPro domain Histone-like transcription factor/archaeal histone/topoisomerase (InterPro:IPR003957); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124); contains InterPro domain Histone-like transcription factor CBF/NF-Y/archaeal histone, subunit A (InterPro:IPR003956)   chr2:15583103-15584956 FORWARD   Aliases: T2N18.18, T2N18_18	3.5	4.1	-0.6	-1.5	100.0%	-3.6
4242	AT5G37780.1   Symbol: CAM1   calmodulin-1/4 (CAM1), identical to calmodulin 4 (Arabidopsis thaliana) GI:16223, SP:P25854 Calmodulin-1/4 {Arabidopsis thaliana}   chr5:15021763-15023435 REVERSE   Aliases: ACAM 1, CALMODULIN 1, CAM1, K22F20.20, K22F20_20, TCH1	12.2	11.5	0.7	1.5	100.0%	-4.3
4243	AT3G08990.1   yippee family protein, similar to qdgl-1 (Coturnix coturnix) GI:10441650, Yippee protein (Drosophila melanogaster) GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein   chr3:2743081-2744937 FORWARD   Aliases: T16O11.5	6.1	5.6	0.5	1.5	100.0%	-3.7
4244	AT1G30550.1   expressed protein, similar to PIMT (GI:15127914) (Mus musculus); similar to hypothetical protein GB:AAF19758 GI:6634778 from (Arabidopsis thaliana)   chr1:10820682-10823623 REVERSE   Aliases: F26G16.17, F26G16_17	4.4	3.9	0.5	1.5	100.0%	-4.0
4245	AT1G22380.1   similar to UDP-glucose glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:At1g78270.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22340.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22360.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22400.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22370.2); similar to glycosyltransferase NTGT5a [Nicotiana tabacum] (GB:BAD93689.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyl transferase (InterPro:IPR002213)   chr1:7900376-7902321 REVERSE   Aliases: F12K8.28	3.1	2.8	0.3	1.5	100.0%	-4.2
4246	AT1G26190.1   phosphoribulokinase/uridine kinase family protein, weak similarity to SP:Q59190 Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine monophosphokinase) {Borrelia burgdorferi}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family	3.2	3.5	-0.3	-1.5	100.0%	-4.1
4247	AT1G23760.1   Symbol: JP630   BURP domain-containing protein / polygalacturonase, putative, similar to polygalacturonase isoenzyme 1 beta subunit (Lycopersicon esculentum) GI:170480; contains Pfam profile PF03181: BURP domain   chr1:8402035-8404280 FORWARD   Aliases: F5O8.31, F5O8_31, JP630	3.7	4.6	-0.9	-1.5	100.0%	-3.5
4248	AT4G35840.1   zinc finger (C3HC4-type RING finger) family protein, contains a TG non-consensus donor splice site at exon 2; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:16980965-16982368 FORWARD   Aliases: F4B14.110, F4B14_110	9.0	8.2	0.8	1.5	100.0%	-3.8
4249	AT5G25470.2   expressed protein   chr5:8865732-8867688 REVERSE   Aliases: T14C9.20, T14C9_20	5.3	4.7	0.7	1.5	100.0%	-3.4
4250	AT4G27850.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:13870388-13873515 FORWARD   Aliases: T27E11.90, T27E11_90	3.3	3.1	0.2	1.5	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4251	AT1G78895.1   expressed protein   chr1:29663009-29664869 REVERSE   Aliases: None	6.2	5.2	1.0	1.5	100.0%	-3.6
4252	AT3G06170.1   TMS membrane family protein / tumour differentially expressed (TDE) family protein, contains Pfam domain, PF03348: TMS membrane protein/tumour differentially expressed protein (TDE)   chr3:1867518-1869944 FORWARD   Aliases: F28L1.11, F28L1_11	5.7	4.7	1.1	1.5	100.0%	-3.7
4253	AT3G05940.1   expressed protein, contains Pfam profile PF03619: Domain of unknown function   chr3:1777370-1779654 REVERSE   Aliases: F2O10.10	5.3	4.8	0.5	1.5	100.0%	-3.7
4254	AT3G23900.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28770.1); similar to B52-prov protein [Xenopus laevis] (GB:AAH44265.1); contains InterPro domain Filamin/ABP280 repeat (InterPro:IPR001298); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr3:8632698-8636052 REVERSE   Aliases: F14O13.8	4.3	5.3	-1.0	-1.5	100.0%	-3.4
4255	AT3G60680.1   expressed protein, contains Pfam profile PF04859: Plant protein of unknown function (DUF641)   chr3:22440935-22443017 FORWARD   Aliases: T4C21.90	4.3	3.9	0.4	1.5	100.0%	-3.9
4256	AT5G08310.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:2670135-2675255 REVERSE   Aliases: F8L15.40, F8L15_40	3.6	4.2	-0.6	-1.5	100.0%	-3.9
4257	AT5G52760.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:21404052-21404922 FORWARD   Aliases: F6N7.25, F6N7_25	2.4	2.6	-0.2	-1.5	100.0%	-4.6
4258	AT1G05040.1   expressed protein   chr1:1447757-1448447 REVERSE   Aliases: T7A14.9, T7A14_9	2.4	2.2	0.1	1.5	100.0%	-4.7
4259	AT3G16260.1   metallo-beta-lactamase family protein   chr3:5509418-5513210 FORWARD   Aliases: MYA6.7	5.8	6.5	-0.7	-1.5	100.0%	-3.7
4260	AT1G01240.3   expressed protein   chr1:99894-101834 FORWARD   Aliases: F633.5, F633_5, F6F3.27	7.0	6.5	0.5	1.5	100.0%	-4.0
4261	AT5G63110.1   Symbol: HDA6   histone deacetylase, putative, similar to SP:O22446 Histone deacetylase (HD) {Arabidopsis thaliana}; contains Pfam profile PF00850: Histone deacetylase family   chr5:25332863-25335573 REVERSE   Aliases: ATHDA6, AXE1, CAT1, CONSTITUTIVE EXPRESSION OF AUXIN RESPONSE TRANSGENES 1, HISTONE DEACETYLASE 6, MDC12.7, MDC12_7, RNA MEDIATED TRANSCRIPTIONAL SILENCING 1, RPD3B, RTS1	6.3	6.7	-0.4	-1.5	100.0%	-3.7
4262	AT1G77920.1   bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor   chr1:29303299-29305757 FORWARD   Aliases: F28K19.13, F28K19_13	7.9	7.5	0.4	1.5	100.0%	-3.8
4263	AT5G08360.1   expressed protein   chr5:2689714-2690973 FORWARD   Aliases: F8L15.90, F8L15_90	4.3	3.8	0.5	1.5	100.0%	-3.6
4264	AT4G25710.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr4:13098150-13099540 REVERSE   Aliases: L73G19.90, L73G19_90	6.3	5.8	0.4	1.5	100.0%	-3.8
4265	AT3G47990.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:17724129-17727293 REVERSE   Aliases: T17F15.140	6.8	5.9	0.9	1.5	100.0%	-3.8
4266	AT1G20910.1   ARID/BRIGHT DNA-binding domain-containing protein, low similarity to Chain A, Human Mrf-2 Domain (Homo sapiens) GI:14278238; contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain   chr1:7276932-7281127 REVERSE   Aliases: F9H16.11, F9H16_11	5.3	5.8	-0.5	-1.5	100.0%	-3.8
4267	AT3G26640.1   transducin family protein / WD-40 repeat family protein, contains 3 WD-40 repeats (PF00400); similar to ATAN11 (GI:2290528) (Arabidopsis thaliana) (Genes Dev. 11 (11), 1422-1434 (1997)); contains Pfam profile: PF00400 WD domain, G-beta repeat (3 copies)   chr3:9794459-9795694 FORWARD   Aliases: MLJ15.4	6.0	5.5	0.5	1.5	100.0%	-3.7
4268	AT2G35270.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr2:14864100-14864957 FORWARD   Aliases: T4C15.6, T4C15_6	4.8	3.9	0.9	1.5	100.0%	-3.6
4269	AT1G11780.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to alkB proteins from Homo sapiens (SP:Q13686), Caulobacter crescentus (GI:2055386); contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr1:3976838-3979194 REVERSE   Aliases: F25C20.6, F25C20_6	4.5	5.0	-0.5	-1.5	100.0%	-3.7
4270	AT1G43640.1   F-box family protein / tubby family protein, contains Pfam profile: PF01167: Tub family; contains Pfam PF00646: F-box domain; similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein Length(GI:6730158) (Mus musculus); similar to Tubby related protein 1 (Tubby-like protein 1) (Swiss-Prot:O00294) (Homo sapiens); similar to phosphodiesterase (GI:467578) (Mus musculus)   chr1:16441875-16444284 REVERSE   Aliases: T10P12.9, T10P12_9	3.0	2.8	0.3	1.5	100.0%	-4.3
4271	AT3G07190.1   expressed protein   chr3:2285811-2287161 REVERSE   Aliases: T1B9.14	6.1	5.6	0.5	1.5	100.0%	-3.6
4272	AT2G35610.1   expressed protein   chr2:14954444-14958326 REVERSE   Aliases: T20F21.19, T20F21_19	4.9	5.5	-0.6	-1.5	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4273	AT4G01210.1   glycosyltransferase family protein 1, contains Pfam profile: PF00534 Glycosyl transferases group 1   chr4:507738-512782 REVERSE   Aliases: F2N1.24, F2N1_24	7.5	8.3	-0.8	-1.5	100.0%	-4.0
4274	AT4G04330.1   expressed protein   chr4:2116551-2118592 REVERSE   Aliases: T19B17.5, T19B17_5	3.0	2.7	0.3	1.5	100.0%	-4.3
4275	AT1G32060.1   phosphoribulokinase (PRK) / phosphopentokinase, nearly identical to SP:P25697 Phosphoribulokinase, chloroplast precursor (EC 2.7.1.19) (Phosphopentokinase) (PRKASE) (PRK) {Arabidopsis thaliana}   chr1:11532530-11534619 FORWARD   Aliases: T12O21.4, T12O21_4	4.2	3.8	0.4	1.5	100.0%	-3.8
4276	AT3G07010.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa)   chr3:2212734-2216489 REVERSE   Aliases: F17A9.16	3.8	4.3	-0.5	-1.5	100.0%	-3.9
4277	AT4G30690.1   translation initiation factor 3 (IF-3) family protein, similar to SP:P33319 Translation initiation factor IF-3 {Proteus vulgaris}; contains Pfam profiles PF00707: Translation initiation factor IF-3, C-terminal domain, PF05198: Translation initiation factor IF-3, N-terminal domain	7.3	6.1	1.2	1.5	100.0%	-3.7
4278	AT1G04660.1   glycine-rich protein   chr1:1300485-1301772 REVERSE   Aliases: T1G11.8, T1G11_8	6.7	6.2	0.5	1.5	100.0%	-4.1
4279	AT4G16100.1   expressed protein   chr4:9105731-9108169 FORWARD   Aliases: DL4090W, FCAALL.70	5.6	5.1	0.4	1.5	100.0%	-4.0
4280	AT1G27150.1   expressed protein   chr1:9429044-9432235 FORWARD   Aliases: T7N9.21, T7N9_21	8.9	9.2	-0.3	-1.5	100.0%	-4.2
4281	AT5G35840.1   Symbol: PHYC   phytochrome C (PHYC), identical to SP:P14714 Phytochrome C {Arabidopsis thaliana}   chr5:14025056-14028994 FORWARD   Aliases: MIK22.15, MIK22_15, PHYTOCHROME C, PHYTOCHROME DEFECTIVE C	4.5	5.0	-0.5	-1.5	100.0%	-3.9
4282	AT1G60070.1   gamma-adaptin, putative, similar to gamma-adaptin GI:2765190 from (Homo sapiens); contains Pfam profiles PF01602: Adaptin N terminal region, PF02883: Adaptin C-terminal domain   chr1:22146347-22153116 REVERSE   Aliases: T2K10.12, T2K10_12	5.8	6.6	-0.8	-1.5	100.0%	-4.0
4283	AT5G24760.2   alcohol dehydrogenase, putative, similar to alcohol dehydrogenase from Solanum tuberosum (SP:p14673); contains Pfam zinc-binding dehydrogenase domain PF00107   chr5:8494795-8497303 REVERSE   Aliases: T4C12.30	8.6	9.2	-0.6	-1.5	100.0%	-3.8
4284	AT1G70650.1   zinc finger (Ran-binding) family protein, contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others   chr1:26641740-26643867 FORWARD   Aliases: F5A18.17, F5A18_17	3.5	3.9	-0.4	-1.5	100.0%	-4.2
4285	AT3G01720.1   expressed protein   chr3:262258-265912 REVERSE   Aliases: F4P13.27	7.3	7.9	-0.7	-1.5	100.0%	-3.7
4286	AT5G39740.1   60S ribosomal protein L5 (RPL5B), ribosomal protein L5, rice   chr5:15920551-15922688 FORWARD   Aliases: MKM21.30, MKM21_30	8.1	9.4	-1.2	-1.5	100.0%	-3.7
4287	AT5G52400.1   Symbol: CYP715A1   cytochrome P450 family protein, similar to Cytochrome P450 72A1 (SP:Q05047) (cytochrome P450 Ixxii hydroxylase) (ge10h) (Catharanthus roseus)   chr5:21290175-21292735 FORWARD   Aliases: K24M7.14, K24M7_14	3.5	3.1	0.3	1.5	100.0%	-4.2
4288	AT3G54940.3   cysteine proteinase, putative, contains similarity to cysteine proteinase GI:479060 from (Glycine max)   chr3:20365330-20367245 FORWARD   Aliases: F28P10.80	3.9	3.0	1.0	1.5	100.0%	-3.6
4289	AT1G14270.2   CAAX amino terminal protease family protein, contains Pfam profile PF02517: CAAX amino terminal protease family   chr1:4874870-4877221 REVERSE   Aliases: F14L17.3, F14L17_3	5.7	5.3	0.4	1.5	100.0%	-3.9
4290	AT3G15060.1   Ras-related GTP-binding family protein, similar to GTP-binding protein GI:303742 from (Pisum sativum); contains Pfam profile: PF00071 ras family	4.8	4.3	0.5	1.5	100.0%	-3.8
4291	AT4G27260.1   Symbol: GH3.5   encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro. Lines carrying insertions in this gene are hypersensitive to auxin.   chr4:13653624-13656210 FORWARD   Aliases: GH3.5, M4I22.70, M4I22_70	4.5	4.2	0.3	1.5	100.0%	-4.0
4292	AT5G64650.1   ribosomal protein L17 family protein, contains Pfam profile: PF01196 ribosomal protein L17   chr5:25856586-25858035 REVERSE   Aliases: MUB3.17, MUB3_17	7.2	7.8	-0.6	-1.5	100.0%	-3.6
4293	AT3G19470.2   similar to F-box family protein-related [Arabidopsis thaliana] (TAIR:At3g22770.1); similar to S2 self-incompatibility locus-linked putative F-box protein S2-A113 [Petunia integrifolia subsp. inflata] (GB:AAR15912.2); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain F-box protein interaction domain (InterPro:IPR006527)	3.8	4.3	-0.5	-1.5	100.0%	-3.7
4294	AT1G66530.1   arginyl-tRNA synthetase, putative / arginine--tRNA ligase, putative, similar to SP:P37880 Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ArgRS) {Cricetulus longicaudatus}; contains Pfam profiles PF00750: arginyl-tRNA synthetase, PF03485: arginyl-tRNA synthetase N-terminal domain   chr1:24822574-24826005 REVERSE   Aliases: F28G11.14, F28G11_14	8.8	9.7	-0.8	-1.5	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4295	AT4G16745.1   exostosin family protein, contains Pfam PF03016: Exostosin family   chr4:9411914-9414133 FORWARD   Aliases: None	3.6	3.1	0.5	1.5	100.0%	-3.8
4296	AT3G12860.1   nucleolar protein Nop56, putative, similar to XNop56 protein (Xenopus laevis) GI:14799394; contains Pfam profile PF01798: Putative snoRNA binding domain	6.1	6.7	-0.6	-1.5	100.0%	-3.8
4297	AT5G61020.2   YT521-B-like family protein, contains Pfam profile PF04146: YT521-B-like family   chr5:24574427-24577105 REVERSE   Aliases: MAF19.3, MAF19_3	6.9	7.8	-0.9	-1.5	100.0%	-3.4
4298	AT4G25480.1   Symbol: DREB1A	3.4	2.9	0.5	1.5	100.0%	-3.9
4299	AT5G14710.1   expressed protein   chr5:4746365-4747936 FORWARD   Aliases: T9L3.10, T9L3_10	7.2	6.5	0.7	1.5	100.0%	-3.7
4300	AT1G11170.2   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr1:3741129-3744675 FORWARD   Aliases: T28P6.16, T28P6_16	3.8	3.5	0.3	1.5	100.0%	-4.0
4301	AT1G73230.1   nascent polypeptide-associated complex (NAC) domain-containing protein, similar to SP:P20290 Transcription factor BTF3 (RNA polymerase B transcription factor 3) {Homo sapiens}; contains Pfam profile PF01849: NAC domain   chr1:27543969-27545603 REVERSE   Aliases: T18K17.10, T18K17_10	10.1	10.8	-0.7	-1.5	100.0%	-3.7
4302	AT4G35510.1   expressed protein   chr4:16860457-16862377 REVERSE   Aliases: F8D20.20, F8D20_20	5.9	6.5	-0.6	-1.5	100.0%	-3.6
4303	AT4G27510.1   expressed protein   chr4:13745615-13749037 REVERSE   Aliases: F27G19.110, F27G19_110	3.9	4.3	-0.4	-1.5	100.0%	-3.9
4304	AT1G03320.1   expressed protein   chr1:817027-817767 FORWARD   Aliases: F15K9.8, F15K9_8	2.7	2.5	0.2	1.5	100.0%	-4.4
4305	AT5G27050.1   MADS-box family protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr5:9520279-9520641 FORWARD   Aliases: F15P11.2, F15P11_2	3.9	3.7	0.3	1.5	100.0%	-4.3
4306	AT1G60590.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase PG1 (GI:5669846), PG2 (GI:5669848) from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:22317835-22320635 REVERSE   Aliases: F8A5.12, F8A5_12	2.5	2.7	-0.2	-1.5	100.0%	-4.6
4307	AT4G22820.2   zinc finger (AN1-like) family protein, contains Pfam domains, PF01428: AN1-like Zinc finger and PF01754: A20-like zinc finger   chr4:11987720-11988960 REVERSE   Aliases: F7H19.10	7.3	6.4	0.9	1.5	100.0%	-3.7
4308	AT1G10870.1   ARF GTPase-activating domain-containing protein   chr1:3616610-3623757 REVERSE   Aliases: T19D16.20, T19D16_20	5.7	6.3	-0.5	-1.5	100.0%	-3.6
4309	AT4G23640.1   Symbol: TRH1   potassium transporter / tiny root hair 1 protein (TRH1), identical to tiny root hair 1 protein (Arabidopsis thaliana) gi:11181958:emb:CAC16137; KUP/HAK/KT Transporter family member, PMID:11500563; identical to cDNA mRNA for tiny root hair 1 protein (trh1) GI:11181957   chr4:12320162-12324479 REVERSE   Aliases: ATKT3, F9D16.110, F9D16_110, KUP4, TINY ROOT HAIR 1	5.5	5.0	0.5	1.5	100.0%	-3.7
4310	AT4G15210.2   Symbol: ATBETA AMY   beta-amylase (BMY1) / 1,4-alpha-D-glucan maltohydrolase, identical to Beta-amylase (EC 3.2.1.2) (1,4-alpha-D-glucan maltohydrolase) SP:P25853 (Arabidopsis thaliana)   chr4:8666338-8669470 REVERSE   Aliases: AT BETA AMY, BETA AMYLASE, DL3650C, FCAALL.97, RAM1, REDUCED BETA AMYLASE	2.2	2.4	-0.2	-1.5	100.0%	-5.0
4311	AT5G18440.1   expressed protein   chr5:6113250-6115750 FORWARD   Aliases: F20L16.160, F20L16_160	5.3	5.6	-0.3	-1.5	100.0%	-4.1
4312	AT5G50375.1   Symbol: CPI1   cyclopropyl isomerase (CPI1)   chr5:20528893-20531468 FORWARD   Aliases: CYCLOEUCALENOL CYCLOISOMERASE, CYCLOPROPYL ISOMERASE	5.2	5.7	-0.5	-1.5	100.0%	-4.0
4313	AT1G07350.2   transformer serine/arginine-rich ribonucleoprotein, putative, similar to GB:Y09506 from (Nicotiana tabacum) (Plant Mol. Biol. 35 (3), 261-269 (1997))   chr1:2257499-2260087 REVERSE   Aliases: F22G5.31, F22G5_31	6.0	5.2	0.9	1.5	100.0%	-3.7
4314	AT5G59380.1   Symbol: MBD6   methyl-CpG-binding domain-containing protein, similar to testis specific methyl-CpG binding protein MBD2 (Homo sapiens) GI:3800801; contains Pfam profile PF01429: Methyl-CpG binding domain   chr5:23969487-23970933 FORWARD   Aliases: F2O15.4, F2O15_4	6.5	6.0	0.5	1.5	100.0%	-3.8
4315	AT3G01340.2   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At2g30050.1); similar to putative Sec13p [Oryza sativa (japonica cultivar-group)] (GB:XP_477253.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr3:127355-128973 REVERSE   Aliases: T22N4.3, T22N4_3	7.2	5.9	1.3	1.5	100.0%	-3.7
4316	AT1G16370.1   transporter-related, low similarity to organic cation transporter OCTN1 from (Homo sapiens) GI:2605501, (Mus musculus) GI:4126605, (Rattus norvegicus) GI:5679326; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:5596688-5598441 FORWARD   Aliases: F3O9.17, F3O9_17	5.0	4.7	0.4	1.5	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4317	AT1G73630.1   calcium-binding protein, putative, similar to calcium binding protein GI:14589311 from ( <i>Sesbania rostrata</i> ); contains Pfam profile: PF00036 EF hand (4 copies)   chr1:27688397-27689114 FORWARD   Aliases: F25P22.4, F25P22_4	2.8	2.5	0.3	1.5	100.0%	-3.9
4318	AT1G03380.1   expressed protein   chr1:835825-840891 FORWARD   Aliases: F21B7.1	5.2	4.7	0.5	1.5	100.0%	-3.8
4319	AT1G72890.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27433608-27435378 FORWARD   Aliases: F3N23.9, F3N23_9	5.1	4.6	0.5	1.5	100.0%	-3.7
4320	AT4G22270.1   expressed protein   chr4:11773340-11775984 FORWARD   Aliases: T10I14.100, T10I14_100	4.3	3.9	0.4	1.5	100.0%	-3.7
4321	AT5G11760.1   expressed protein   chr5:3789293-3790453 FORWARD   Aliases: T22P22.150, T22P22_150	7.9	7.1	0.8	1.5	100.0%	-3.7
4322	AT2G19790.1   clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	9.9	8.6	1.2	1.5	100.0%	-3.5
4323	NA	6.5	5.8	0.8	1.5	100.0%	-3.9
4324	AT1G26665.2   expressed protein   chr1:9214164-9215538 FORWARD   Aliases: None	8.8	8.3	0.5	1.5	100.0%	-3.7
4325	AT4G28085.2   expressed protein   chr4:13959976-13960578 FORWARD   Aliases: None	3.3	3.0	0.3	1.5	100.0%	-4.2
4326	AT3G53270.4   expressed protein, endopeptidase Clp ATP-binding chain C, <i>Chlamydia pneumoniae</i> , PIR:G72079   chr3:19761025-19764083 REVERSE   Aliases: T4D2.1	4.8	5.1	-0.3	-1.5	100.0%	-4.2
4327	AT5G18210.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain type dehydrogenase/reductase SP:Q08632 ( <i>Picea abies</i> )   chr5:6017867-6019995 FORWARD   Aliases: MRG7.17, MRG7_17	5.0	4.7	0.2	1.5	100.0%	-4.3
4328	AT1G56180.1   expressed protein   chr1:21029569-21031729 REVERSE   Aliases: F14G9.20	4.6	4.0	0.6	1.5	100.0%	-3.8
4329	AT1G18800.1   nucleosome assembly protein (NAP) family protein, similar to SP:Q01105:SET protein (HLA-DR associated protein II) (PHAPII) (Phosphatase 2A inhibitor I2PP2A) { <i>Homo sapiens</i> }; contains Pfam profile PF00956: Nucleosome assembly protein (NAP)   chr1:6481104-6483587 REVERSE   Aliases: F6A14.10, F6A14_10	3.4	3.9	-0.5	-1.5	100.0%	-4.0
4330	AT2G17130.2   Symbol: IDH2   isocitrate dehydrogenase subunit 2 / NAD+ isocitrate dehydrogenase subunit 2, nearly identical to NAD+ dependent isocitrate dehydrogenase subunit 2 ( <i>Arabidopsis thaliana</i> ) GI:1766048   chr2:7467896-7469636 REVERSE   Aliases: F6P23.14, F6P23_14, ISOCITRATE DEHYDROGENASE SUBUNIT 2, NAD+ DEPENDENT ISOCITRATE DEHYDROGENASE SUBUNIT 2	8.9	9.5	-0.6	-1.5	100.0%	-3.9
4331	AT5G43560.2   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, weak similarity to ubiquitin-specific protease 12 ( <i>Arabidopsis thaliana</i> ) GI:11993471; contains Pfam profile PF00917: MATH domain   chr5:17517656-17522873 FORWARD   Aliases: K9D7.6, K9D7_6	8.1	8.5	-0.4	-1.5	100.0%	-3.9
4332	AT1G12080.2   expressed protein   chr1:4084203-4085041 FORWARD   Aliases: F12F1.4, F12F1_4	4.6	3.4	1.2	1.5	100.0%	-3.4
4333	AT4G20280.1   transcription initiation factor IID (TFIID) 28 kDa subunit (TAFII-28) family protein, similar to SP:Q15544 Transcription initiation factor TFIID 28 kDa subunit (TAFII-28) (TAFII28) (TFIID subunit p30-beta) { <i>Homo sapiens</i> }; contains Pfam profile PF04719: hTAFII28-like protein conserved region   chr4:10953557-10954983 FORWARD   Aliases: F1C12.195, F1C12_195	7.6	7.2	0.4	1.5	100.0%	-3.8
4334	AT4G19650.1   similar to mitochondrial transcription termination factor-related / mTERF-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g45113.1); similar to unknown protein [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:NP_912680.1); contains InterPro domain Mitochondrial transcription termination factor-related (InterPro:IPR003690)   chr4:10691684-10695176 FORWARD   Aliases: T16H5.10, T16H5_10	2.4	2.2	0.2	1.5	100.0%	-4.7
4335	AT1G33270.2   patatin-related, contains Patatin domain PF01734	7.3	6.5	0.8	1.5	100.0%	-3.6
4336	AT3G28620.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 finger protein RHA2b ( <i>Arabidopsis thaliana</i> ) GI:3790571; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:10729063-10729698 FORWARD   Aliases: MZN14.9	2.9	2.7	0.3	1.5	100.0%	-4.5
4337	AT5G63650.1   serine/threonine protein kinase, putative, similar to serine/threonine-protein kinase ASK2( <i>Arabidopsis thaliana</i> ), SWISS-PROT:P43292; contains protein kinase domain, Pfam:PF00069   chr5:25498743-25500945 REVERSE   Aliases: MBK5.13, MBK5_13	5.7	5.1	0.6	1.5	100.0%	-3.8
4338	AT3G52760.1   integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain   chr3:19564657-19565790 REVERSE   Aliases: F3C22.160	6.0	5.7	0.3	1.5	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4339	AT3G08810.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr3:2675637-2676699 REVERSE   Aliases: F17O14.28	4.2	3.7	0.4	1.5	100.0%	-4.0
4340	AT5G55070.1   2-oxoacid dehydrogenase family protein, similar to SP:Q01205 Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) {Rattus norvegicus}; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme   chr5:22364490-22368043 FORWARD   Aliases: MCO15.2, MCO15_2	9.1	10.1	-1.0	-1.5	100.0%	-3.6
4341	AT4G10800.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr4:6643659-6644841 FORWARD   Aliases: F25I24.10, F25I24_10	3.7	4.0	-0.3	-1.5	100.0%	-4.4
4342	AT2G33810.1   Symbol: SPL3   squamosa promoter-binding protein-like 3 (SPL3), identical to squamosa-promoter binding protein like 3 (Arabidopsis thaliana) GI:2462081; contains Pfam profile PF03110: SBP domain   chr2:14312077-14313148 FORWARD   Aliases: SQUAMOSA PROMOTER BINDING PROTEIN LIKE 3, T1B8.11, T1B8_11	2.9	3.1	-0.2	-1.5	100.0%	-4.6
4343	AT1G53320.1   F-box family protein / tubby family protein (TULP7), similar to Tubby related protein 2 (Tubby-like protein 2) (P4-6 protein) (Fragment) (SP:P46686) (Mus musculus); similar to phosphodiesterase (GI:467578) (Mus musculus); similar to Tubby protein homolog 1. (Swiss-Prot:Q09306) (Caenorhabditis elegans) contains Pfam profile: PF01167: Tub family; contains Pfam PF00646: F-box domain   chr1:19894682-19897159 REVERSE   Aliases: F12M16.22, F12M16_22	11.1	10.8	0.3	1.5	100.0%	-4.5
4344	AT1G19330.1   expressed protein   chr1:6680558-6683498 REVERSE   Aliases: F18O14.5, F18O14_5	6.4	7.0	-0.6	-1.5	100.0%	-3.6
4345	AT5G46390.2   peptidase S41 family protein, similar to C-terminal peptidase of the D1 protein (Hordeum vulgare subsp vulgare) GI:1296805; contains Pfam profiles PF03572: Peptidase family S41B, PF00595: PDZ domain (Also known as DHR or GLGF)   chr5:18833831-18836574 FORWARD   Aliases: MPL12.19, MPL12_19	5.1	4.7	0.5	1.5	100.0%	-3.7
4346	AT2G41450.1   GCN5-related N-acetyltransferase (GNAT) family protein, low similarity to Swift (Xenopus laevis) GI:14164561; contains Pfam profiles PF00583: acetyltransferase, GNAT family, PF00533: BRCA1 C Terminus (BRCT) domain   chr2:17285268-17292165 FORWARD   Aliases: T26J13.4, T26J13_4	2.3	2.2	0.1	1.5	100.0%	-5.0
4347	AT2G19450.1   Symbol: TAG1   diacylglycerol O-acyltransferase / acyl CoA:diacylglycerol acyltransferase (DGAT), identical to gi:5050913, gi:6625553   chr2:8433288-8436818 FORWARD   Aliases: ABX45, AS11, ATDGAT, DGAT1, DIACYLGLYCEROL ACYLTRANSFERASE, F27F23.24, RDS1, REGULATION OF DESATURASES IN SEEDS 1, TRIACYLGLYCEROL BIOSYNTHESIS DEFECT 1	6.6	7.0	-0.5	-1.5	100.0%	-3.8
4348	AT4G36290.1   ATP-binding region, ATPase-like domain-containing protein, low similarity to microrchidia (Mus musculus) GI:5410255; contains Pfam profile PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein   chr4:17169467-17173208 REVERSE   Aliases: F23E13.180, F23E13_180	4.2	4.5	-0.3	-1.5	100.0%	-4.2
4349	AT5G22370.1   Symbol: EMB1705   ATP-binding family protein, contains Pfam domain, PF03029: Conserved hypothetical ATP binding protein	3.1	3.5	-0.4	-1.5	100.0%	-4.2
4350	AT1G20760.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:7209382-7214982 FORWARD   Aliases: F2D10.25, F2D10_25	5.7	4.9	0.8	1.5	100.0%	-3.7
4351	AT1G33970.3   similar to avirulence-responsive protein / avirulence induced gene (AIG1) [Arabidopsis thaliana] (TAIR:At1g33960.1); similar to putative NTGP4 [Oryza sativa (japonica cultivar-group)] (GB:XP_466219.1); contains InterPro domain AIG1 family (InterPro:IPR006703)   chr1:12349440-12351224 REVERSE   Aliases: F12G12.21, F12G12_21	7.0	6.5	0.5	1.5	100.0%	-3.9
4352	AT2G38650.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr2:16168886-16172804 REVERSE   Aliases: T6A23.15, T6A23_15	5.5	5.9	-0.3	-1.5	100.0%	-4.0
4353	AT5G65970.1   Symbol: MLO10   seven transmembrane MLO family protein / MLO-like protein 10 (MLO10), identical to membrane protein Mlo10 (Arabidopsis thaliana) gi:14091590:gb:AAK53803; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr5:26404654-26407678 REVERSE   Aliases: K2A18.3, K2A18_3	5.7	6.2	-0.5	-1.5	100.0%	-3.7
4354	AT3G59420.1   Symbol: ACR4   receptor protein kinase, putative (ACR4), identical to putative receptor protein kinase ACR4 (Arabidopsis thaliana) GI:20302590; contains protein kinase domain, Pfam:PF00069   chr3:21970624-21974018 REVERSE   Aliases: F25L23.280	3.3	3.7	-0.4	-1.5	100.0%	-4.1
4355	AT2G32300.1   Symbol: UCC1   uclacyanin I, identical to uclacyanin I GI:3399767 from (Arabidopsis thaliana); contains Pfam profile PF02298: Plastocyanin-like domain; identical to cDNA uclacyanin I GI:3399766   chr2:13729504-13730667 FORWARD   Aliases: UCLACYANIN 1	3.1	3.7	-0.6	-1.5	100.0%	-3.4
4356	AT3G03160.1   expressed protein   chr3:729775-730474 FORWARD   Aliases: T17B22.15, T17B22_15	10.0	9.7	0.3	1.5	100.0%	-4.4
4357	AT5G61540.3   similar to L-asparaginase, putative / L-asparagine amidohydrolase, putative [Arabidopsis thaliana] (TAIR:At3g16150.1); similar to hypothetical protein FG02189.1 [Gibberella zeae PH-1] (GB:EAA69124.1); contains InterPro domain Asparaginase 2 family (InterPro:IPR000246)   chr5:24762205-24764725 FORWARD   Aliases: K11J9.7, K11J9_7	4.0	3.7	0.3	1.5	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4358	AT1G75270.1   dehydroascorbate reductase, putative, similar to GI:6939839 from ( <i>Oryza sativa</i> )   chr1:28253736-28255010 REVERSE   Aliases: F22H5.1, F22H5_1	9.5	10.2	-0.6	-1.5	100.0%	-3.8
4359	AT2G34720.1   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr2:14656846-14658692 REVERSE   Aliases: T29F13.7, T29F13_7	4.9	4.5	0.4	1.5	100.0%	-3.8
4360	AT4G19210.1   Symbol: ATRLI2	7.6	8.9	-1.3	-1.5	100.0%	-3.8
4361	AT1G27030.1   expressed protein   chr1:9381790-9383970 FORWARD   Aliases: T7N9.9, T7N9_9	4.9	5.5	-0.5	-1.5	100.0%	-3.7
4362	AT1G34370.3   similar to zinc finger (C2H2 type) family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g22890.1); similar to putative zinc finger protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_470361.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087)   chr1:12550455-12552677 FORWARD   Aliases: F7P12.7, F7P12_7	8.9	8.4	0.5	1.5	100.0%	-3.9
4363	AT5G40750.1   expressed protein   chr5:16325584-16327047 FORWARD   Aliases: MNF13.30, MNF13_30	2.1	2.2	-0.1	-1.5	100.0%	-4.9
4364	AT4G36470.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:jasmonic acid carboxyl methyltransferase (JMT)(GI:13676829) and to SAM:salicylic acid carboxyl methyltransferase (SAMT)(GI:6002712)( <i>Clarkia breweri</i> )   chr4:17215131-17216478 REVERSE   Aliases: AP22.82, AP22_82	3.4	3.6	-0.2	-1.5	100.0%	-4.3
4365	AT2G33255.1   haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	6.1	6.9	-0.8	-1.5	100.0%	-3.8
4366	AT3G02530.1   chaperonin, putative, similar to SWISS-PROT:P80317- T-complex protein 1, zeta subunit (TCP-1-zeta) ( <i>Mus musculus</i> ); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr3:528581-532589 REVERSE   Aliases: F16B3.16, F16B3_16	7.9	8.9	-1.0	-1.5	100.0%	-3.8
4367	AT2G03390.1   uvrB/uvrC motif-containing protein, contains Pfam profile PF02151: UvrB/uvrC motif   chr2:1030399-1032619 REVERSE   Aliases: T4M8.18, T4M8_18	5.6	5.3	0.2	1.5	100.0%	-4.3
4368	AT1G15670.1   kelch repeat-containing F-box family protein, similar to SP:Q9ER30 Kelch-related protein 1 ( <i>Sarcosin</i> ) { <i>Rattus norvegicus</i> }; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:5389947-5391485 FORWARD   Aliases: F7H2.1, F7H2_1	4.0	3.3	0.7	1.5	100.0%	-3.5
4369	AT4G21380.1   Symbol: ARK3   S-locus protein kinase, putative (ARK3), identical to PIR:T05180:T05180 S-receptor kinase ARK3 precursor - ( <i>Arabidopsis thaliana</i> )   chr4:11388936-11393237 REVERSE   Aliases: T6K22.110, T6K22_110	3.0	3.2	-0.2	-1.5	100.0%	-4.4
4370	AT1G26390.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) ( <i>Eschscholzia californica</i> ); contains PF01565 FAD binding domain   chr1:9130004-9131766 REVERSE   Aliases: T1K7.23, T1K7_23	2.7	2.9	-0.2	-1.5	100.0%	-4.3
4371	AT4G30570.1   GDP-mannose pyrophosphorylase, putative, similar to GDP-mannose pyrophosphorylase ( <i>Arabidopsis thaliana</i> ) GI:3598958; contains Pfam profile PF00483: Nucleotidyl transferase   chr4:14930683-14931957 REVERSE   Aliases: F17I23.90, F17I23_90	4.4	4.0	0.4	1.5	100.0%	-4.2
4372	AT4G04610.1   Symbol: APR1   5'-adenylylsulfate reductase (APR1) / PAPS reductase homolog (PRH19), identical to 5'-adenylylsulfate reductase ( <i>Arabidopsis thaliana</i> ) GI:2738756; identical to cDNA PAPS reductase homolog (PRH19) GI:1710111   chr4:2325001-2327011 FORWARD   Aliases: 3' PHOSPHOADENOSINE 5' PHOSPHOSULFATE REDUCTASE, APR, APS REDUCTASE, ATAPR1, F4H6.13, F4H6_13, PAPS REDUCTASE HOMOLOG 19, PRH19	8.3	9.1	-0.8	-1.5	100.0%	-3.8
4373	AT1G65290.1   acyl carrier family protein / ACP family protein, similar to SP:P53665 Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (MtACP-1) { <i>Arabidopsis thaliana</i> }; contains InterPro accession IPR003881: Isochorismatase   chr1:24252515-24254065 REVERSE   Aliases: T8F5.6, T8F5_6	10.3	10.9	-0.6	-1.5	100.0%	-4.0
4374	AT4G26650.2   similar to RNA recognition motif (RRM)-containing protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g55550.3); similar to RNA recognition motif (RRM)-containing protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g55550.2); similar to RNA recognition motif (RRM)-containing protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g55550.1); similar to putative RNA-binding protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:AAP54226.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)	6.3	6.7	-0.4	-1.5	100.0%	-3.9
4375	AT3G08740.1   elongation factor P (EF-P) family protein, similar to SP:P33398 Elongation factor P (EF-P) { <i>Escherichia coli</i> O157:H7}; contains Pfam profile PF01132: Elongation factor P (EF-P)	7.9	8.7	-0.7	-1.5	100.0%	-3.4
4376	AT5G13460.1   calmodulin-binding family protein, low similarity to SF16 protein ( <i>Helianthus annuus</i> ) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr5:4315870-4318363 FORWARD   Aliases: T22N19.110, T22N19_110	5.1	5.5	-0.4	-1.5	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4377	AT1G19980.1   cytomatrix protein-related, contains weak similarity to CAST1 (Rattus norvegicus) gi:22138113:gb:AAL07517   chr1:6933022-6934993 FORWARD   Aliases: T20H2.28, T20H2_28	4.7	5.1	-0.3	-1.5	100.0%	-3.8
4378	AT1G01920.2   similar to ribulose-1,5 biphosphate carboxylase oxygenase large subunit N-methyltransferase, putative [Arabidopsis thaliana] (TAIR:At1g14030.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910361.1); contains InterPro domain Nuclear protein SET (InterPro:IPR001214)   chr1:316128-319637 FORWARD   Aliases: F22M8.5, F22M8_5	5.0	5.5	-0.5	-1.5	100.0%	-3.8
4379	AT1G35430.1   expressed protein   chr1:13030531-13031130 REVERSE   Aliases: F12A4.3, F12A4_3	6.0	5.4	0.6	1.5	100.0%	-3.9
4380	AT4G32870.1   expressed protein, hypothetical protein F17H15.20 Arabidopsis thaliana chromosome II BAC F17H15, PID:g3643606   chr4:15862147-15862745 FORWARD   Aliases: T16I18.80, T16I18_80	10.0	10.4	-0.4	-1.5	100.0%	-4.4
4381	AT3G53220.1   thioredoxin family protein, low similarity to SP:P29451 Thioredoxin (Rhesus macaque) {Macaca mulatta}; contains Pfam profile: PF00085 Thioredoxin   chr3:19732972-19733680 FORWARD   Aliases: T4D2.150	3.2	3.4	-0.2	-1.5	100.0%	-4.3
4382	AT2G17730.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam PF00097: Zinc finger, C3HC4 type (RING finger) domain; similar to RING-H2 finger protein RHA3a (GI:3790573) (Arabidopsis thaliana); similar to ReMemBR-H2 protein JR700 (GI:6942147) (Arabidopsis thaliana)   chr2:7710938-7712832 FORWARD   Aliases: T17A5.9, T17A5_9	6.2	5.6	0.5	1.5	100.0%	-3.7
4383	AT2G29690.1   Symbol: ASA2   anthranilate synthase, alpha subunit, component I-2 (ASA2), identical to SP:P32069   chr2:12700948-12704042 FORWARD   Aliases: ATHANSYNAB, T27A16.21, T27A16_21	7.7	8.2	-0.6	-1.5	100.0%	-3.6
4384	AT4G12430.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) (Arabidopsis thaliana) GI:2944180; contains Pfam profile PF02358: Trehalose-phosphatase   chr4:7365330-7368727 REVERSE   Aliases: T1P17.20, T1P17_20	3.7	4.1	-0.4	-1.5	100.0%	-3.9
4385	AT1G79490.1   Symbol: EMB2217   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr1:29905352-29908082 FORWARD   Aliases: EMB2217, EMBRYO DEFECTIVE 2217, T8K14.9, T8K14_9	4.9	5.3	-0.5	-1.5	100.0%	-3.8
4386	AT3G63200.1   patatin-related, low similarity to patatin-like latex protein allergen Hev b 7 - Hevea brasiliensis, EMBL:AF113546; contains patatin domain PF01734   chr3:23356877-23358539 FORWARD   Aliases: F16M2.50	5.1	5.8	-0.7	-1.5	100.0%	-3.6
4387	AT5G17400.1   ADP, ATP carrier protein, mitochondrial, putative / ADP/ATP translocase, putative / adenine nucleotide translocator, putative, similar to SWISS-PROT:Q09188 ADP,ATP carrier protein (ADP/ATP translocase) (Schizosaccharomyces pombe); contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:5728793-5730378 REVERSE   Aliases: T10B6.60, T10B6_60	5.8	5.4	0.3	1.5	100.0%	-4.2
4388	AT1G03055.2   expressed protein   chr1:710063-711803 REVERSE   Aliases: None	2.9	2.7	0.2	1.5	100.0%	-4.4
4389	AT5G59980.1   RNase P subunit p30 family protein, contains Pfam PF01876: RNase P subunit p30   chr5:24164433-24166953 FORWARD   Aliases: MMN10.23, MMN10_23	3.2	3.5	-0.3	-1.5	100.0%	-3.9
4390	AT1G02720.2   glycosyl transferase family 8 protein, low similarity to putative glycosyl transferase from Neisseria gonorrhoeae (GI:595812); contains Pfam glycosyl transferase family 8 domain PF01501   chr1:591826-593289 FORWARD   Aliases: T14P4.1, T14P4_1	4.0	4.3	-0.3	-1.5	100.0%	-4.3
4391	AT3G03980.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain type dehydrogenase/reductase SP:Q08632 (Picea abies)   chr3:1031749-1033214 FORWARD   Aliases: T11I18.9, T11I18_9	8.8	9.8	-0.9	-1.5	100.0%	-3.4
4392	AT3G17710.1   F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.5	0.3	1.5	100.0%	-4.1
4393	AT5G46110.3   Symbol: APE2   similar to glucose-6-phosphate/phosphate translocator, putative [Arabidopsis thaliana] (TAIR:At5g54800.1); similar to triose phosphate/phosphate translocator precursor [Mesembryanthemum crystallinum] (GB:AAF86906.1); contains InterPro domain Tpt phosphate/phosphoenolpyruvate translocator (InterPro:IPR004696)   chr5:18714477-18717883 FORWARD   Aliases: ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT, MCL19.16, MCL19_16, TPT	6.5	5.5	1.0	1.5	100.0%	-3.6
4394	AT1G18170.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, similar to (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (SP:Q26486) (Spodoptera frugiperda); contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases   chr1:6254222-6255683 FORWARD   Aliases: T10F20.17	4.7	4.1	0.6	1.5	100.0%	-3.8
4395	AT4G05450.1   adrenodoxin-like ferredoxin 2, similar to SP:P46656 Adrenodoxin, mitochondrial precursor (Adrenal ferredoxin) from Mus musculus, SP:P10109 Adrenodoxin, mitochondrial precursor (Hepatoredoxin) from Homo sapiens, SP:P29330 Adrenodoxin from Ovis aries; contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domains; identical to cDNA GI: 28192430   chr4:2758653-2760895 FORWARD   Aliases: C6L9.130, C6L9_130	5.2	5.6	-0.4	-1.5	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4396	AT1G17720.2   Symbol: ATB BETA   serine/threonine protein phosphatase 2A (PP2A) 55 kDa regulatory subunit B, identical to type 2A protein serine/threonine phosphatase 55 kDa B regulatory subunit (GI:1408460) (Arabidopsis thaliana); similar to 55 kDa B regulatory subunit of phosphatase 2A GI:710330; contains Pfam PF00400: WD domain, G-beta repeat (5 copies, 3 weak)   chr1:6093201-6098326 REVERSE   Aliases: F11A6.6, F11A6_6	3.0	2.6	0.4	1.5	100.0%	-4.3
4397	AT3G44100.1   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain   chr3:15877028-15878291 REVERSE   Aliases: F26G5.50	8.8	9.2	-0.4	-1.5	100.0%	-4.3
4398	AT3G16340.1   ABC transporter family protein, similar to PDR5-like ABC transporter GI:1514643 from (Spirodela polyrhiza); contains Pfam profile: PF00005 ABC transporter   chr3:5539903-5546410 FORWARD   Aliases: MYA6.19	5.1	5.7	-0.6	-1.5	100.0%	-3.8
4399	AT5G14170.1   SWIB complex BAF60b domain-containing protein, similar to brahma associated protein 60 kDa (Drosophila melanogaster) GI:3378134, SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin D1 (Homo sapiens) GI:4566530; contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr5:4568549-4570943 REVERSE   Aliases: MUA22.17, MUA22_17	6.4	6.7	-0.3	-1.5	100.0%	-4.0
4400	AT3G43430.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:15365547-15366275 REVERSE   Aliases: T5C2.130	4.7	4.1	0.6	1.5	100.0%	-3.6
4401	AT1G31120.1   Symbol: KUP10   potassium transporter family protein, similar to HAK2 (Hordeum vulgare) GI:7108599, potassium transporter (Arabidopsis thaliana) gi:2654088:gb:AAB87687; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter   chr1:11104282-11108012 REVERSE   Aliases: F28K20.5, F28K20_5	4.4	4.9	-0.5	-1.5	100.0%	-3.9
4402	AT1G03000.1   Symbol: PEX6   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family ('A'ATPases 'A'associated with diverse cellular 'A'activities)   chr1:687908-692476 REVERSE   Aliases: F10O3.18, F10O3_18, PEROXIN6	5.4	5.8	-0.4	-1.5	100.0%	-4.0
4403	AT1G09910.1   expressed protein   chr1:3220037-3224543 REVERSE   Aliases: F21M12.30, F21M12_30	6.9	7.4	-0.4	-1.5	100.0%	-3.8
4404	AT5G16970.1   NADP-dependent oxidoreductase, putative (P1), identical to probable NADP-dependent oxidoreductase P1, zeta-crystallin homolog (SP:Q39172)(gi:886428), Arabidopsis thaliana; similar to allyl alcohol dehydrogenase (Nicotiana tabacum) GI:6692816; contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family   chr5:5576171-5578049 REVERSE   Aliases: F2K13.120, F2K13_120	9.4	9.0	0.4	1.5	100.0%	-4.1
4405	AT3G13280.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537; expression supported by MPSS   chr3:4295334-4297007 REVERSE   Aliases: MDC11.11	3.6	3.4	0.2	1.5	100.0%	-4.5
4406	AT1G71760.1   expressed protein   chr1:26993076-26994161 FORWARD   Aliases: F14O23.14, F14O23_14	3.1	3.5	-0.4	-1.5	100.0%	-3.9
4407	AT1G62530.1   expressed protein   chr1:23149997-23150961 REVERSE   Aliases: T3P18.9, T3P18_9	2.6	2.5	0.2	1.5	100.0%	-4.6
4408	AT5G24380.1   Symbol: YSL2   similar to transporter, putative [Arabidopsis thaliana] (TAIR:At5g53550.1); similar to oligopeptide transporter OPT family protein [Arabidopsis thaliana] (TAIR:At5g41000.1); similar to oligopeptide transporter OPT family protein [Arabidopsis thaliana] (TAIR:At1g65730.1); similar to oligopeptide transporter OPT family protein [Arabidopsis thaliana] (TAIR:At3g17650.1); similar to transporter, putative [Arabidopsis thaliana] (TAIR:At4g24120.1); similar to OSJNBb0103108.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_473374.1); similar to putative iron-phytosiderophore transporter protein yellow stripe 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_467066.1); similar to iron transport protein 1 [Oryza sativa] (GB:AAS49493.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD90812.1); similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] (GB:AAG17016.2); contains InterPro domain Oligopeptide transporter OPT superfamily (InterPro:IPR004813)   chr5:8323898-8326708 FORWARD   Aliases: ATYSL2, K16H17.9, K16H17_9, YELLOW STRIPE LIKE 2	7.1	6.5	0.6	1.5	100.0%	-3.8
4409	AT3G28740.1   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr3:10789935-10791790 REVERSE   Aliases: T19N8.17	6.5	6.0	0.5	1.5	100.0%	-4.0
4410	AT3G07700.2   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr3:2459497-2463648 REVERSE   Aliases: MLP3.15	4.3	3.9	0.4	1.5	100.0%	-4.0
4411	AT4G38380.1   MATE efflux protein-related, T19C21.18 Arabidopsis thaliana chromosome II BAC T19C21 genomic sequence, PID:g3395439   chr4:17972122-17974781 REVERSE   Aliases: F22I13.150, F22I13_150	4.5	4.2	0.3	1.5	100.0%	-4.0
4412	AT5G09960.1   expressed protein, similar to unknown protein (emb:CAB61744.1)   chr5:3106321-3107830 FORWARD   Aliases: MYH9.17, MYH9_17	8.7	7.8	0.9	1.5	100.0%	-3.6
4413	AT3G25920.1   Symbol: RPL15   50S ribosomal protein L15, chloroplast (CL15), identical to GB:P25873 from (Arabidopsis thaliana)   chr3:9491321-9493855 REVERSE   Aliases: MPE11.32, RIBOSOMAL PROTEIN CL15	8.8	9.4	-0.5	-1.5	100.0%	-3.6
4414	AT5G44390.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr5:17899423-17902231 REVERSE   Aliases: K9L2.19, K9L2_19	2.5	2.7	-0.3	-1.5	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4415	AT2G39700.1   Symbol: ATEXPA4   expansin, putative (EXP4), similar to alpha-expansin 6 precursor GI:16923359 from (Cucumis sativus); alpha-expansin gene family, PMID:11641069   chr2:16550910-16552662 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A4, ATEXP4, ATHEXP ALPHA 1.6, F17A14.7, F17A14_7	7.6	5.5	2.1	1.5	100.0%	-3.4
4416	AT1G77360.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:29076877-29078322 REVERSE   Aliases: F2P24.7, F2P24_7	4.1	4.5	-0.4	-1.5	100.0%	-4.0
4417	AT5G12330.3   Symbol: LRP1   lateral root primordium 1 (LRP1), identical to lateral root primordium 1 (LRP1) (Arabidopsis thaliana) GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702)   chr5:3988194-3989648 REVERSE   Aliases: LATERAL ROOT PRIMORDIUM 1	5.6	6.0	-0.5	-1.5	100.0%	-3.9
4418	AT5G26720.1   expressed protein   chr5:9304028-9304746 FORWARD   Aliases: None	6.1	5.6	0.5	1.5	100.0%	-4.1
4419	AT2G20280.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:8746992-8749430 REVERSE   Aliases: F11A3.17, F11A3_17	6.8	7.5	-0.7	-1.5	100.0%	-4.1
4420	AT1G63050.1   membrane bound O-acyl transferase (MBOAT) family protein, low similarity to porcupine from (Xenopus laevis) GI:6714514, GI:6714520, GI:6714518, GI:6714516; contains Pfam profile PF03062: MBOAT family   chr1:23379549-23381927 REVERSE   Aliases: F16M19.14, F16M19_14	7.0	7.7	-0.6	-1.5	100.0%	-3.9
4421	AT5G47750.1   protein kinase, putative, similar to protein kinase G11A (Oryza sativa) SWISS-PROT:P47997   chr5:19356929-19359582 REVERSE   Aliases: MCA23.7, MCA23_7	5.5	5.2	0.3	1.5	100.0%	-4.2
4422	AT1G16970.1   Symbol: KU70   Ku70-like protein, identical to Ku70-like protein GI:12006424 from (Arabidopsis thaliana); contains Pfam profiles PF03731: Ku70/Ku80 N-terminal alpha/beta domain, PF02735: Ku70/Ku80 beta-barrel domain, PF03730: Ku70/Ku80 C-terminal arm, and PF02037: SAP domain; contains TIGRfam profile TIGR00578: ATP-dependent DNA helicase ii, 70 kDa subunit   chr1:5800904-5805767 REVERSE   Aliases: F6I1.2, F6I1_2, KU70 LIKE PROTEIN	4.4	4.7	-0.4	-1.5	100.0%	-3.9
4423	AT5G49930.1   Symbol: EMB1441   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr5:20325261-20330034 REVERSE   Aliases: EMB1441, EMBRYO DEFECTIVE 1441, K9P8.7, K9P8_7	8.0	8.4	-0.4	-1.5	100.0%	-4.1
4424	AT5G45590.1   expressed protein   chr5:18501734-18503505 REVERSE   Aliases: K2N11.6, K2N11_6	4.5	5.2	-0.8	-1.5	100.0%	-3.5
4425	AT3G15360.1   Symbol: ATHM4   thioredoxin M-type 4, chloroplast (TRX-M4), nearly identical to SP:Q9SEU6 Thioredoxin M-type 4, chloroplast precursor (TRX-M4) {Arabidopsis thaliana}   chr3:5188395-5189704 FORWARD   Aliases: MJK13.20	8.6	8.0	0.7	1.5	100.0%	-3.9
4426	AT2G22240.2   inositol-3-phosphate synthase isozyme 2 / myo-inositol-1-phosphate synthase 2 / MI-1-P synthase 2 / IPS 2, identical to SP:Q38862 Myo-inositol-1-phosphate synthase isozyme 2 (EC 5.5.1.4) (MI-1-P synthase 2) (IPS 2) {Arabidopsis thaliana}   chr2:9458255-9461159 REVERSE   Aliases: T26C19.10, T26C19_10	5.0	5.7	-0.6	-1.5	100.0%	-3.6
4427	AT5G55120.1   expressed protein, strong similarity to unknown protein (pir::T04808)   chr5:22386321-22389093 FORWARD   Aliases: MCO15.7, MCO15_7	4.8	5.2	-0.3	-1.5	100.0%	-4.1
4428	AT1G05560.1   Symbol: UGT1   UDP-glucose transferase (UGT75B2), similar to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase GI:2149127 from (Arabidopsis thaliana); identical to cDNA UDP-glucosyltransferase (UGT75B2) GI:13661274   chr1:1645497-1647146 REVERSE   Aliases: T25N20.21, UDP GLUCOSYLTRANSFERASE, UGT75B2	4.8	4.2	0.7	1.5	100.0%	-3.8
4429	AT1G54450.1   calcium-binding EF-hand family protein, contains Pfam profile: PF00036 EF hand   chr1:20340222-20343202 REVERSE   Aliases: F20D21.27, F20D21_27	4.1	4.4	-0.3	-1.5	100.0%	-4.3
4430	AT3G09890.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr3:3032564-3034448 FORWARD   Aliases: F8A24.6	5.0	4.5	0.5	1.5	100.0%	-3.7
4431	AT3G01370.1   expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578)   chr3:139018-143699 FORWARD   Aliases: T13O15.1, T13O15_1	5.3	5.8	-0.5	-1.5	100.0%	-3.8
4432	AT1G64580.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr1:23988741-23992412 REVERSE   Aliases: F1N19.15, F1N19_15	3.9	4.1	-0.2	-1.5	100.0%	-4.3
4433	AT1G22710.1   Symbol: SUC2   sucrose transporter / sucrose-proton symporter (SUC2), nearly identical to sucrose-proton symporter SUC2 (Arabidopsis thaliana) GI:407092   chr1:8030630-8033106 REVERSE   Aliases: ATSUC2, SUCROSE H+ SYMPORTER, SUT1, T22J18.12, T22J18_12	4.7	4.1	0.6	1.5	100.0%	-4.0
4434	AT4G29270.1   acid phosphatase class B family protein, similar to acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr4:14423671-14424888 REVERSE   Aliases: F17A13.90, F17A13_90	3.4	3.8	-0.5	-1.5	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4435	AT1G70310.1   Symbol: SPDS2   spermidine synthase 2 (SPDSYN2) / putrescine aminopropyltransferase 2, identical to SP:O48661 Spermidine synthase 2 (EC 2.5.1.16) (Putrescine aminopropyltransferase 2) (SPDSY 2) {Arabidopsis thaliana}   chr1:26488969-26491076 REVERSE   Aliases: F1707.16, F1707_16, SPERMIDINE SYNTHASE 2	11.5	12.0	-0.5	-1.5	100.0%	-4.2
4436	AT2G25210.1   60S ribosomal protein L39 (RPL39A)   chr2:10746934-10747631 FORWARD   Aliases: T22F11.20, T22F11_20	10.3	11.0	-0.6	-1.5	100.0%	-3.6
4437	AT5G28060.1   40S ribosomal protein S24 (RPS24B), 40S ribosomal protein S19, Cyanophora paradoxa, EMBL:CPA245654   chr5:10069553-10070897 REVERSE   Aliases: F15F15.130, F15F15_130	8.8	9.6	-0.8	-1.5	100.0%	-3.6
4438	AT1G08190.1   vacuolar assembly protein, putative (VPS41), 99.8% identical to Vacuolar assembly protein VPS41 homolog (SP:P93043) (Arabidopsis thaliana); similar to vacuolar assembly protein vps41 GI:1835787 from (Lycopersicon esculentum)	5.2	5.7	-0.5	-1.5	100.0%	-3.7
4439	AT4G20030.1   RNA recognition motif (RRM)-containing protein, low similarity to heterogeneous nuclear ribonucleoprotein G (Mus musculus) GI:5579009; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	4.9	4.5	0.5	1.5	100.0%	-3.8
4440	AT2G03240.1   EXS family protein / ERD1/XPR1/SYG1 family protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family	4.8	4.1	0.7	1.5	100.0%	-3.8
4441	AT3G07360.3   similar to armadillo/beta-catenin repeat family protein / U-box domain-containing protein [Arabidopsis thaliana] (TAIR:At5g18320.1); similar to OSJNBa0020102.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_472015.1); contains InterPro domain Armadillo repeat (InterPro:IPR000225)   chr3:2354725-2356845 FORWARD   Aliases: F21O3.7	5.2	4.8	0.4	1.5	100.0%	-4.2
4442	AT2G41870.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr2:17477944-17480014 REVERSE   Aliases: T11A7.3, T11A7_3	5.7	5.2	0.4	1.5	100.0%	-4.2
4443	AT3G14230.3   Symbol: RAP2.2	5.6	4.7	0.9	1.5	100.0%	-3.8
4444	AT3G57090.1   expressed protein   chr3:21139509-21141167 FORWARD   Aliases: F24I3.170	9.3	8.6	0.7	1.5	100.0%	-3.9
4445	AT1G78120.1   tetratricopeptide repeat (TPR)-containing protein, low similarity to SP:Q99615 DnaJ homolog subfamily C member 7 (Tetratricopeptide repeat protein 2) {Homo sapiens}; contains Pfam profile PF00515: TPR Domain   chr1:29398914-29400896 REVERSE   Aliases: T11I11.6, T11I11_6	5.6	5.2	0.4	1.5	100.0%	-3.8
4446	AT2G43780.1   expressed protein   chr2:18143521-18143724 REVERSE   Aliases: F18O19.11	10.7	11.0	-0.3	-1.5	100.0%	-4.3
4447	AT5G57590.1   Symbol: BIO1   aminotransferase class III family protein, low similarity to 7,8-diaminopelargonic acid aminotransferase BioA (Mesorhizobium loti) GI:12044306; contains Pfam profile PF00202: aminotransferase, class III   chr5:23335734-23338765 REVERSE   Aliases: BIOTIN AUXOTROPH 1, MUA2.17, MUA2_17	5.8	6.5	-0.6	-1.5	100.0%	-3.8
4448	AT3G16990.1   TENA/THI-4 family protein, contains Pfam profile: PF03070 TENA/THI-4 family   chr3:5795845-5796811 REVERSE   Aliases: K14A17.22	7.8	7.5	0.3	1.5	100.0%	-4.4
4449	AT2G06990.1   Symbol: HEN2   HUA enhancer 2 (HEN2) / DEXH-box RNA helicase, putative, nearly identical to HUA enhancer 2 (Arabidopsis thaliana) GI:16024936   chr2:2894937-2901075 FORWARD   Aliases: HUA ENHANCER 2, T4E14.10, T4E14_10	5.0	5.4	-0.3	-1.5	100.0%	-4.2
4450	AT5G42450.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:16994871-16996244 FORWARD   Aliases: MDH9.15, MDH9_15	3.3	3.7	-0.4	-1.5	100.0%	-4.1
4451	AT2G24450.1   fasciclin-like arabinogalactan family protein, similar to fasciclin-like arabinogalactan-protein 1 (Arabidopsis thaliana) gi:13377776:gb:AAK20857   chr2:10399871-10401003 REVERSE   Aliases: T28I24.18, T28I24_18	2.6	2.8	-0.2	-1.5	100.0%	-4.6
4452	AT5G59770.1   similar to protein tyrosine phosphatase-like protein, putative (PAS2) [Arabidopsis thaliana] (TAIR:At5g10480.1); similar to Protein tyrosine phosphatase-like (proline instead of catalytic arginine), member b [Homo sapiens] (GB:AAH49369.1); similar to hypothetical protein [Pongo pygmaeus] (GB:CAH90857.1); similar to Similar to RIKEN cDNA 6330408J20 gene [Danio rerio] (GB:AAH44396.1); contains InterPro domain Protein tyrosine phosphatase-like protein, PTPLA (InterPro:IPR007482)	5.4	4.9	0.5	1.5	100.0%	-3.7
4453	AT4G21980.1   Symbol: APG8A   autophagy 8a (APG8a), identical to autophagy 8a (Arabidopsis thaliana) GI:19912151; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3   chr4:11655742-11656980 FORWARD   Aliases: ATG8A, F1N20.80, F1N20_80	7.4	6.8	0.6	1.5	100.0%	-3.7
4454	AT3G51960.2   bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor   chr3:19293579-19295124 REVERSE   Aliases: F4F15.70	3.4	3.2	0.2	1.5	100.0%	-4.4
4455	AT4G22160.2   expressed protein   chr4:11733135-11734039 FORWARD   Aliases: T10I14.8	6.2	5.7	0.5	1.5	100.0%	-3.7
4456	AT2G42700.1   expressed protein   chr2:17785429-17789167 FORWARD   Aliases: F14N22.4	6.0	6.5	-0.5	-1.5	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4457	AT4G02550.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g02210.1); similar to putative transposase [Oryza sativa (japonica cultivar-group)] (GB:AAP51979.1); similar to putative polyprotein [Oryza sativa (japonica cultivar-group)] (GB:AAV43964.1)   chr4:1120421-1121725 REVERSE   Aliases: T10P11.16, T10P11_16	3.9	3.5	0.4	1.5	100.0%	-4.1
4458	AT5G27620.1   Symbol: CYCH;1	4.3	4.9	-0.5	-1.5	100.0%	-3.9
4459	AT3G08590.2   2,3-biphosphoglycerate-independent phosphoglycerate mutase, putative / phosphoglyceromutase, putative, strong similarity to SP:Q42908 2,3-bisphosphoglycerate-independent phosphoglycerate mutase (EC 5.4.2.1) (Phosphoglyceromutase) {Mesembryanthemum crystallinum}; contains Pfam profile PF01676: Metalloenzyme superfamily   chr3:2608483-2611333 REVERSE   Aliases: F17O14.6	10.9	11.6	-0.7	-1.5	100.0%	-4.2
4460	AT5G48640.1   cyclin family protein, similar to SP:P55168 Cyclin C {Gallus gallus}; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr5:19740759-19742915 REVERSE   Aliases: K15N18.11, K15N18_11	6.2	6.7	-0.5	-1.5	100.0%	-3.9
4461	AT1G04160.1   Symbol: XIB   myosin family protein, contains Pfam profiles: PF02736 myosin N-terminal SH3-like domain, PF00063 myosin head (motor domain), PF00612 IQ calmodulin-binding motif, PF01843: DIL domain   chr1:1086494-1096145 FORWARD   Aliases: ATXIB, F20D22.7, F20D22_7	3.9	4.2	-0.4	-1.5	100.0%	-4.0
4462	AT4G19110.2   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr4:10454540-10459309 REVERSE   Aliases: T18B16.80, T18B16_80	6.5	5.5	1.0	1.4	100.0%	-3.6
4463	AT2G16780.1   Symbol: MSI2   WD-40 repeat protein (MSI2), contains 5 WD-40 repeats (PF0400); identical to WD-40 repeat protein MSI2 (SP:O22468) (Arabidopsis thaliana) WD-40 repeats (PF0400);   chr2:7288544-7290715 REVERSE   Aliases: MSI02, MSI2, NFC02, NFC2, T24I21.19, T24I21_19	6.9	7.6	-0.7	-1.4	100.0%	-3.5
4464	AT2G36320.1   zinc finger (AN1-like) family protein, contains Pfam domain, PF01428: AN1-like Zinc finger   chr2:15235867-15237575 FORWARD   Aliases: F2H17.7, F2H17_7	7.3	6.6	0.8	1.4	100.0%	-3.6
4465	AT5G24580.2   copper-binding family protein, similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:8410261-8412268 REVERSE   Aliases: K18P6.11, K18P6_11	6.3	5.7	0.7	1.4	100.0%	-3.4
4466	AT4G21170.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:11286766-11288641 REVERSE   Aliases: F7J7.110, F7J7_110	4.8	5.3	-0.5	-1.4	100.0%	-4.0
4467	AT5G42050.1   expressed protein, similar to gda-1 (Pisum sativum) GI:2765418   chr5:16832717-16834521 FORWARD   Aliases: MJC20.15, MJC20_15	7.9	6.9	0.9	1.4	100.0%	-3.9
4468	AT3G06840.1   expressed protein   chr3:2156868-2157856 FORWARD   Aliases: F3E22.2	2.4	2.6	-0.2	-1.4	100.0%	-4.5
4469	AT2G14835.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:6373993-6378116 FORWARD   Aliases: None	4.7	4.4	0.4	1.4	100.0%	-4.1
4470	AT2G34070.1   expressed protein   chr2:14394505-14397309 REVERSE   Aliases: T14G11.19, T14G11_19	4.9	5.3	-0.4	-1.4	100.0%	-3.8
4471	AT4G16160.2   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr4:9157530-9158948 FORWARD   Aliases: DL4120W, FCAALL.207	2.7	2.6	0.2	1.4	100.0%	-4.6
4472	AT1G32790.2   Symbol: CID11   similar to RNA-binding protein, putative [Arabidopsis thaliana] (TAIR:At4g10610.1); similar to putative RNA-binding protein RBP37 [Oryza sativa (japonica cultivar-group)] (GB:XP_479783.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr1:11874684-11877367 REVERSE   Aliases: CID11, F6N18.17, F6N18_17	9.6	8.6	0.9	1.4	100.0%	-3.8
4473	AT1G53980.1   polyubiquitin-related, contains similarity to polyubiquitin GI:166336 from (Aglaothamnion neglectum)   chr1:20153002-20153277 REVERSE   Aliases: T18A20.18	3.5	3.2	0.3	1.4	100.0%	-4.4
4474	AT1G12160.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase FMO2 from Homo sapiens (SP:Q99518); contains Pfam profile PF00743 Flavin-binding monooxygenase-like   chr1:4126064-4128308 FORWARD   Aliases: T28K15.10, T28K15_10	8.1	8.6	-0.5	-1.4	100.0%	-3.7
4475	AT3G17820.1   Symbol: ATGSKB6   glutamine synthetase (GS1), identical to glutamine synthetase, cytosolic isozyme (glutamate-- ammonia ligase, GS1) (Arabidopsis thaliana) SWISS-PROT:Q9LVI8   chr3:6097420-6099601 FORWARD   Aliases: GLN1;3, MEB5.4	11.5	12.0	-0.6	-1.4	100.0%	-3.6
4476	AT2G05210.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g06310.1)   chr2:1891769-1894359 FORWARD   Aliases: F5G3.11, F5G3_11	3.3	3.8	-0.4	-1.4	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4477	AT4G23890.1   expressed protein, hypothetical protein, Synechocystis sp., PIR:S76577   chr4:12420424-12421474 REVERSE   Aliases: T32A16.60, T32A16_60	5.5	4.9	0.6	1.4	100.0%	-3.7
4478	AT2G32100.1   ovate protein-related, contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568   chr2:13654929-13655862 FORWARD   Aliases: F22D22.15, F22D22_15	2.3	2.5	-0.2	-1.4	100.0%	-4.4
4479	AT1G66220.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa); contains Pfam profiles: PF00082 Subtilase family (3 copies)   chr1:24674199-24677324 FORWARD   Aliases: T6J19.4, T6J19_4	2.7	2.5	0.2	1.4	100.0%	-4.3
4480	AT5G58090.1   glycosyl hydrolase family 17 protein, similar to 3-glucanase GI:18483232 from (Sorghum bicolor)   chr5:23522592-23524514 REVERSE   Aliases: K21L19.12, K21L19_12	8.0	7.1	0.9	1.4	100.0%	-3.8
4481	AT4G18593.1   dual specificity protein phosphatase-related, contains weak similarity to Dual specificity protein phosphatase 12 (EC 3.1.3.48) (EC 3.1.3.16) (Dual-specificity tyrosine phosphatase YVH1) (Swiss-Prot:Q9UNI6) (Homo sapiens)   chr4:10237583-10238847 FORWARD   Aliases: None	8.8	8.4	0.4	1.4	100.0%	-3.8
4482	AT5G47890.1   NADH-ubiquinone oxidoreductase B8 subunit, putative, similar to SP:O43678 NADH-ubiquinone oxidoreductase B8 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B8) (CI-B8) {Homo sapiens}; contains Pfam profile PF05047: Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain   chr5:19405963-19407852 FORWARD   Aliases: MCA23.23, MCA23_23	10.5	10.9	-0.4	-1.4	100.0%	-4.3
4483	AT4G11370.1   Symbol: RHA1A   zinc finger (C3HC4-type RING finger) family protein, strong similarity to RING-H2 finger protein RHA1a (Arabidopsis thaliana) GI:3790554; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:6907669-6908378 FORWARD   Aliases: F8L21.160, F8L21_160, RING H2 FINGER PROTEIN RHA1A	3.0	3.2	-0.2	-1.4	100.0%	-4.5
4484	AT5G09860.1   nuclear matrix protein-related, low similarity to nuclear matrix protein p84 (Homo sapiens) GI:550058   chr5:3066641-3070934 FORWARD   Aliases: MYH9.7, MYH9_7	5.9	6.3	-0.4	-1.4	100.0%	-3.8
4485	AT5G10430.1   Symbol: AGP4   arabinogalactan-protein (AGP4), identical to gi_3883126_gb_AAC77826   chr5:3277533-3278314 REVERSE   Aliases: ARABINOGALACTAN PROTEIN 4, ATAGP4, F12B17.220, F12B17_220	4.4	3.7	0.6	1.4	100.0%	-3.6
4486	AT4G32140.1   expressed protein   chr4:15522905-15525433 REVERSE   Aliases: F10N7.50, F10N7_50	5.8	5.3	0.5	1.4	100.0%	-3.8
4487	AT5G16540.3   Symbol: ZFN3   zinc finger (CCCH-type) family protein, identical to zinc finger protein 3 (Arabidopsis thaliana) gi:4689376:gb:AAD27875; contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)	5.4	4.9	0.5	1.4	100.0%	-3.9
4488	AT5G12310.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:3980227-3982443 REVERSE   Aliases: None	8.4	7.9	0.4	1.4	100.0%	-4.0
4489	AT4G30760.2   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr4:14982528-14983425 FORWARD   Aliases: T10C21.110, T10C21_110	8.9	9.1	-0.1	-1.4	100.0%	-4.8
4490	AT1G48750.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to TED4 (Zinnia elegans) GI:493721; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	12.3	11.8	0.5	1.4	100.0%	-4.5
4491	AT3G61310.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr3:22701167-22703797 REVERSE   Aliases: T20K12.210	5.3	4.8	0.5	1.4	100.0%	-3.6
4492	AT5G02030.1   Symbol: LSN   homeodomain protein (BELLRINGER), several homeodomain proteins;   chr5:395631-399038 FORWARD   Aliases: BELLRINGER, BLR, HB 6, LARSON, PENNYWISE, PNY, REPLUMLESS, RPL, T7H20.80, T7H20_80	6.4	5.7	0.7	1.4	100.0%	-3.5
4493	AT3G42130.1   glycine-rich protein   chr3:14309227-14309869 REVERSE   Aliases: F4M19.90	7.0	6.3	0.8	1.4	100.0%	-3.6
4494	AT3G49990.1   expressed protein   chr3:18543308-18545257 REVERSE   Aliases: F3A4.70	5.9	6.6	-0.7	-1.4	100.0%	-3.9
4495	AT4G16440.1   iron hydrogenase family protein, contains Pfam profiles: PF02906 Iron only hydrogenase large subunit, C-terminal domain, PF02256 Iron hydrogenase small subunit   chr4:9269286-9271532 REVERSE   Aliases: DL4245C, FCAALL.367	6.7	7.3	-0.6	-1.4	100.0%	-3.9
4496	AT5G23430.2   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); katanin p80 subunit (GI:3005601) (Strongylocentrotus purpuratus)   chr5:7893674-7900390 REVERSE   Aliases: K19M13.6, K19M13_6	4.2	4.6	-0.4	-1.4	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4497	AT5G03030.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain; DNAJ domain-containing protein, Homo sapiens, EMBL:AF126743   chr5:708341-709701 REVERSE   Aliases: F15A17.60, F15A17_60	8.2	7.8	0.4	1.4	100.0%	-4.0
4498	AT1G31280.1   Symbol: AGO2   PAZ domain-containing protein / piwi domain-containing protein, similar to SP:O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}, SP:Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain   chr1:11181758-11185093 FORWARD   Aliases: T19E23.7, T19E23_7	3.0	3.4	-0.4	-1.4	100.0%	-4.0
4499	AT1G28090.2   polynucleotide adenylyltransferase family protein, low similarity to SP:P13685 Poly(A) polymerase (EC 2.7.7.19) {Escherichia coli O157:H7}; contains Pfam profile PF01743: polyA polymerase family protein   chr1:9795774-9799008 FORWARD   Aliases: F13K9.19, F13K9_19	2.5	2.6	-0.2	-1.4	100.0%	-4.6
4500	AT5G44210.1   Symbol: ATERF 9/ATERF9/ERF9   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ATERF-9). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.   chr5:17823699-17824760 FORWARD   Aliases: ATERF 9, ATERF9, ERF9, MLN1.14, MLN1_14	3.0	3.7	-0.7	-1.4	100.0%	-3.6
4501	AT1G33560.1   Symbol: ADR1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.4	3.8	-0.4	-1.4	100.0%	-3.7
4502	AT4G13200.1   expressed protein, hypothetical protein sll1769 - Synechocystis sp,PID:d1018406   chr4:7668146-7669197 REVERSE   Aliases: F17N18.90, F17N18_90	6.5	6.2	0.3	1.4	100.0%	-4.1
4503	AT2G20780.1   mannitol transporter, putative, similar to mannitol transporter (Apium graveolens var. dulce) GI:12004316; contains Pfam profile PF00083: major facilitator superfamily protein	5.2	4.9	0.3	1.4	100.0%	-4.0
4504	AT5G15740.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;   chr5:5134530-5137629 REVERSE   Aliases: F14F8.120, F14F8_120	4.1	4.5	-0.5	-1.4	100.0%	-4.0
4505	AT2G19080.1   metaxin-related, contains 1 transmembrane domain; similar to Metaxin 1 (component of a preprotein import complex) (Swiss-Prot:P47802) (Mus musculus);   chr2:8269839-8272046 FORWARD   Aliases: METAXIN, T20K24.9, T20K24_9	5.5	6.0	-0.5	-1.4	100.0%	-3.9
4506	AT4G11210.1   disease resistance-responsive family protein / dirigent family protein, similar to dirigent protein (Thuja plicata) gi:6694699:gb:AAF25360; similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669   chr4:6832687-6833241 FORWARD   Aliases: F8L21.1	3.9	3.4	0.5	1.4	100.0%	-3.7
4507	AT1G30540.1   ATPase, BadF/BadG/BcrA/BcrD-type family, contains Pfam PF01869: BadF/BadG/BcrA/BcrD ATPase family; similar to Transcriptional regulators of NagC/XylR (ROK) family, sugar kinase (GI:15023013) (Clostridium acetobutylicum); similar to N-acetylglucosamine kinase (EC 2.7.1.59) (GlcNAc kinase) (Swiss-Prot:Q9UJ70) (Homo sapiens)   chr1:10816756-10819309 REVERSE   Aliases: F26G16.16, F26G16_16	5.2	4.7	0.5	1.4	100.0%	-3.8
4508	AT3G32940.1   expressed protein   chr3:13494664-13497497 REVERSE   Aliases: T13O13.2	4.9	5.8	-0.8	-1.4	100.0%	-3.8
4509	AT3G54290.1   expressed protein, contains Pfam PF03794: Domain of Unknown function   chr3:20115377-20117022 REVERSE   Aliases: F24B22.250	7.7	7.4	0.4	1.4	100.0%	-4.2
4510	AT3G13980.1   expressed protein   chr3:4619045-4620269 REVERSE   Aliases: MDC16.10	4.0	4.4	-0.3	-1.4	100.0%	-4.0
4511	AT3G50930.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr3:18940507-18942820 FORWARD   Aliases: F18B3.210	3.2	3.4	-0.2	-1.4	100.0%	-4.7
4512	AT5G06210.1   RNA-binding protein, putative, contains similarity to RNA-binding protein from (Nicotiana tabacum) GI:15822703, (Nicotiana glauca) GI:624925, (Solanum tuberosum) GI:15822705; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:1878472-1879741 FORWARD   Aliases: MBL20.9, MBL20_9	9.9	9.5	0.4	1.4	100.0%	-3.8
4513	AT3G60810.2   expressed protein   chr3:22481494-22483079 FORWARD   Aliases: T4C21.220	6.8	7.1	-0.4	-1.4	100.0%	-3.8
4514	AT2G24140.1   expressed protein, contains Pfam PF04576: Protein of unknown function, DUF593   chr2:10269634-10271113 REVERSE   Aliases: F27D4.5, F27D4_5	3.7	4.0	-0.3	-1.4	100.0%	-4.6
4515	AT2G42120.2   DNA polymerase delta small subunit-related, similar to DNA polymerase delta small subunit SP:Q9LRE5 from (Oryza sativa)   chr2:17570254-17573110 REVERSE   Aliases: T24P15.3, T24P15_3	4.7	5.2	-0.5	-1.4	100.0%	-3.8
4516	AT5G10980.1   histone H3, identical to HISTONE H3.2, MINOR, Medicago sativa, SWISSPROT:P11105, histone H3 variant H3.3 Lycopersicon esculentum GI:1435157; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:3472429-3473442 REVERSE   Aliases: T30N20.250, T30N20_250	11.6	12.0	-0.3	-1.4	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4517	AT5G65430.2   Symbol: GRF8   14-3-3 protein GF14 kappa (GRF8), identical to 14-3-3 protein GF14 kappa GI:5802794, SP:P48348 from (Arabidopsis thaliana)   chr5:26165427-26167568 REVERSE   Aliases: GF14 KAPPA, GF14 KAPPA ISOFORM, MNA5.16, MNA5_16	10.3	9.4	0.9	1.4	100.0%	-3.9
4518	AT1G09810.1   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr1:3180964-3182832 REVERSE   Aliases: F21M12.20, F21M12_20	4.4	4.9	-0.5	-1.4	100.0%	-3.8
4519	AT4G39830.1   L-ascorbate oxidase, putative, similar to SP:P14133 L-ascorbate oxidase precursor (EC 1.10.3.3) (Ascorbase) {Cucumis sativus}; contains Pfam profile PF00394: Multicopper oxidase   chr4:18478923-18481337 FORWARD   Aliases: T5J17.9	4.0	4.3	-0.3	-1.4	100.0%	-4.0
4520	AT1G74050.1   60S ribosomal protein L6 (RPL6C), similar to 60S ribosomal protein L6 (YL 16 like) GB:CAB57309 from (Cyanophora paradoxa)   chr1:27850710-27852467 REVERSE   Aliases: F2P9.8, F2P9_8	11.9	12.1	-0.2	-1.4	100.0%	-4.7
4521	AT1G74060.1   60S ribosomal protein L6 (RPL6B), similar to 60S ribosomal protein L6 (YL 16 like) GB:CAB57309 from (Cyanophora paradoxa)   chr1:27853497-27855028 REVERSE   Aliases: F2P9.7, F2P9_7	11.9	12.1	-0.2	-1.4	100.0%	-4.7
4522	AT1G53440.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr1:19949627-19955230 FORWARD   Aliases: T3F20.24, T3F20_24	5.1	5.5	-0.3	-1.4	100.0%	-4.0
4523	AT1G63020.1   Symbol: NRPD1a	5.6	6.3	-0.7	-1.4	100.0%	-3.5
4524	AT1G12620.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr1:4294592-4297082 REVERSE   Aliases: T12C24.15, T12C24_15	4.7	5.3	-0.6	-1.4	100.0%	-3.8
4525	AT1G29820.1   expressed protein   chr1:10437646-10440770 FORWARD   Aliases: F1N18.14, F1N18_14	6.9	7.3	-0.4	-1.4	100.0%	-4.0
4526	AT1G13170.1   oxysterol-binding family protein, similar to SP:P16258 Oxysterol-binding protein 1 {Oryctolagus cuniculus}; contains Pfam profiles PF00169: PH domain, PF01237: Oxysterol-binding protein   chr1:4488622-4492578 REVERSE   Aliases: F3F19.19, F3F19_19	4.2	4.8	-0.6	-1.4	100.0%	-4.0
4527	AT1G01070.2   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr1:38753-40927 REVERSE   Aliases: T25K16.7, T25K16_7	9.6	8.9	0.7	1.4	100.0%	-3.6
4528	AT2G38820.2   expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506)   chr2:16228914-16230740 FORWARD   Aliases: F13I13.5, F13I13_5	5.2	5.5	-0.3	-1.4	100.0%	-4.2
4529	AT4G17660.1   protein kinase, putative, similar to protein kinase (Lophopyrum elongatum) gi:13022177:gb:AAK11674   chr4:9831372-9833019 FORWARD   Aliases: DL4865W, FCAALL.77	2.7	2.9	-0.2	-1.4	100.0%	-4.4
4530	AT1G27480.1   lecithin:cholesterol acyltransferase family protein / LACT family protein, similar to LCAT-like lysophospholipase (LLPL) (Homo sapiens) GI:4589720; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)   chr1:9544501-9546272 FORWARD   Aliases: F17L21.27, F17L21_27	4.9	4.4	0.5	1.4	100.0%	-3.5
4531	AT4G13850.2   Symbol: ATGRP2	8.1	7.1	1.0	1.4	100.0%	-3.6
4532	AT4G39100.1   Symbol: SHL1   PHD finger family protein / bromo-adjacent homology (BAH) domain-containing protein, contains Pfam domain, PF00628: PHD-finger and PF01426: BAH domain   chr4:18217933-18220276 REVERSE   Aliases: SHORT LIFE, T22F8.2	6.6	6.1	0.4	1.4	100.0%	-4.2
4533	AT5G56590.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr5:22924549-22926715 FORWARD   Aliases: MIK19.3, MIK19_3	6.9	7.3	-0.5	-1.4	100.0%	-3.9
4534	AT3G28850.1   glutaredoxin family protein   chr3:10849906-10851359 FORWARD   Aliases: T19N8.15	6.6	6.2	0.5	1.4	100.0%	-4.0
4535	AT4G14660.1   RNA polymerase Rpb7 N-terminal domain-containing protein, similar to SP:P52433 DNA-directed RNA polymerase II 19 kDa polypeptide (EC 2.7.7.6) (RPB7) {Rattus norvegicus}; contains Pfam profile PF03876: RNA polymerase Rpb7, N-terminal domain   chr4:8406330-8407042 REVERSE   Aliases: DL3370C, FCAALL.283	4.9	5.2	-0.3	-1.4	100.0%	-4.2
4536	AT1G21410.1   F-box family protein, similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	7.7	7.2	0.5	1.4	100.0%	-3.9
4537	AT4G29410.1   60S ribosomal protein L28 (RPL28C), unknown protein chromosome II BAC F6F22 - Arabidopsis thaliana,PID:g3687251   chr4:14468250-14470173 REVERSE   Aliases: F17A13.230, F17A13_230	11.0	11.4	-0.5	-1.4	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4538	AT2G40910.2   F-box protein-related, similar to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana); similar to F-box protein family, AtFBX8 (GI:20197464) (Arabidopsis thaliana)   chr2:17076946-17078735 REVERSE   Aliases: T20B5.11, T20B5_11	3.8	3.4	0.4	1.4	100.0%	-4.1
4539	AT5G48170.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to unknown protein (pir::T09884);   chr5:19549763-19550428 REVERSE   Aliases: MIF21.6, MIF21_6	2.7	2.6	0.2	1.4	100.0%	-4.7
4540	AT3G01650.1   copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens}   chr3:242018-245275 FORWARD   Aliases: F4P13.19, F4P13_19	5.6	5.2	0.3	1.4	100.0%	-3.9
4541	AT5G39940.1   expressed protein   chr5:16004781-16007929 FORWARD   Aliases: MYH19.13, MYH19_13	4.0	4.2	-0.3	-1.4	100.0%	-4.2
4542	AT3G49880.1   glycosyl hydrolase family protein 43, contains similarity to xylanase GI:2645416 from (Caldicellulosiruptor saccharolyticus)   chr3:18507234-18509698 FORWARD   Aliases: T16K5.230	4.5	4.2	0.4	1.4	100.0%	-3.9
4543	AT1G22840.1   cytochrome c, putative, similar to cytochrome c (Pumpkin, Winter squash) SWISS-PROT:P00051   chr1:8079279-8080563 FORWARD   Aliases: F19G10.20, F19G10_20	11.9	12.3	-0.3	-1.4	100.0%	-4.3
4544	AT3G19660.1   expressed protein   chr3:6825527-6826012 REVERSE   Aliases: MMB12.13	5.9	5.4	0.5	1.4	100.0%	-3.7
4545	AT1G62150.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr1:22973694-22975429 REVERSE   Aliases: F19K23.9, F19K23_9	5.4	5.8	-0.5	-1.4	100.0%	-3.7
4546	AT1G49740.1   expressed protein, similar to MAP3K-like protein kinase GB:CAB16796 GI:4006878 from (Arabidopsis thaliana)   chr1:18411247-18413690 FORWARD   Aliases: F14J22.5, F14J22_5	6.8	7.3	-0.5	-1.4	100.0%	-3.8
4547	AT5G24120.1   Symbol: SIGE   RNA polymerase sigma subunit SigE (sigE) / sigma-like factor (SIG5), identical to RNA polymerase sigma subunit SigE (Arabidopsis thaliana) GI:4972299, sigma-like factor (Arabidopsis thaliana) GI:4033838; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2   chr5:8157554-8160231 REVERSE   Aliases: MLE8.4, MLE8_4, SIG5, SIGMA FACTOR	6.2	5.7	0.5	1.4	100.0%	-3.9
4548	AT5G55060.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g58510.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAF94658.1)   chr5:22359183-22363803 FORWARD   Aliases: MCO15.1, MCO15_1	5.2	5.9	-0.7	-1.4	100.0%	-4.0
4549	AT1G15880.1   Symbol: GOS11   Golgi SNARE 11 protein, identical to Golgi SNARE 11 protein (GI:13898893) {Arabidopsis thaliana}; similar to putative cis-Golgi SNARE protein GI:2583133 from (Arabidopsis thaliana); similar to SP:O95249: 28 kDa Golgi SNARE protein (28 kDa cis-Golgi SNARE p28) (GOS-28). (Homo sapiens); similar to Golgi SNARE protein (Golgi SNAP receptor complex member 1) (28 kDa cis-Golgi SNARE p28) (GOS-28) (SP:Q62931) {Rattus norvegicus}	8.5	7.9	0.5	1.4	100.0%	-4.0
4550	AT1G47250.1   Symbol: PAF2   20S proteasome alpha subunit F2 (PAF2) (PRC2B) (PRS1), identical to GB:AAC32063 from (Arabidopsis thaliana) (Genetics 149 (2), 677-692 (1998)); identical to cDNA proteasome subunit prc2b GI:2511585   chr1:17321617-17324100 FORWARD   Aliases: 20S PROTEASOME SUBUNIT PAF2, F8G22.3, F8G22_3	9.1	10.0	-0.9	-1.4	100.0%	-3.6
4551	AT3G27960.1   kinesin light chain-related, low similarity to kinesin light chain (Plectonema boryanum) GI:2645229; contains Pfam profile PF00515: TPR Domain   chr3:10381617-10383830 REVERSE   Aliases: K24A2.5	6.1	5.1	0.9	1.4	100.0%	-3.7
4552	AT1G17470.1   Symbol: ATDRG1	9.4	9.9	-0.5	-1.4	100.0%	-3.9
4553	AT3G49920.1   porin, putative, similar to SP:P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin   chr3:18516821-18518684 REVERSE   Aliases: F3A4.1	4.9	4.5	0.5	1.4	100.0%	-4.0
4554	AT4G26520.1   fructose-bisphosphate aldolase, cytoplasmic, identical to SP:P22197 Fructose-bisphosphate aldolase, cytoplasmic isozyme (EC 4.1.2.13) {Arabidopsis thaliana}   chr4:13388683-13390381 FORWARD   Aliases: M3E9.50, M3E9_50	2.7	2.9	-0.2	-1.4	100.0%	-4.3
4555	AT2G24350.1   RNA recognition motif (RRM)-containing protein, low similarity to poly(A) binding protein II from (Xenopus laevis) GI:11527140, (Mus musculus) GI:2351846, (Bos taurus) GI:1051125; contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain   chr2:10368206-10371434 FORWARD   Aliases: T28I24.8, T28I24_8	2.6	2.9	-0.3	-1.4	100.0%	-4.3
4556	AT3G44280.1   expressed protein   chr3:15979580-15982083 REVERSE   Aliases: T10D17.70	6.5	7.2	-0.7	-1.4	100.0%	-3.8
4557	AT3G13070.1   CBS domain-containing protein / transporter associated domain-containing protein, similar to SP:Q54318 Hemolysin C (Serpulina hyodysenteriae) {Treponema hyodysenteriae}; contains Pfam profiles PF00571: CBS domain, PF03471: Transporter associated domain, PF01595: Domain of unknown function   chr3:4191518-4195119 REVERSE   Aliases: MJG19.2	9.8	10.3	-0.5	-1.4	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4558	AT1G28110.2   Symbol: SCPL45	9.4	10.0	-0.5	-1.4	100.0%	-3.8
4559	AT3G17880.1   Symbol: ATTDX   tetratricoredoxin (TDX), identical to tetratricoredoxin (Arabidopsis thaliana) GI:18041544; similar to SP:Q42443 Thioredoxin H-type (TRX-H) (Phloem sap 13 kDa protein-1) {Oryza sativa}; contains Pfam profile: PF00085 Thioredoxin   chr3:6123452-6126276 FORWARD   Aliases: AT3G17870, MEB5.24, TETRATICOPEPTIDE DOMAIN CONTAINING THIOREDOXIN, TETRATRICOREDOXIN	7.1	6.6	0.5	1.4	100.0%	-4.2
4560	AT5G04540.1   expressed protein   chr5:1296443-1302429 REVERSE   Aliases: T32M21.150, T32M21_150	7.1	6.5	0.5	1.4	100.0%	-3.8
4561	AT3G12390.1   nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative, similar to alpha-NAC, non-muscle form (Mus musculus) GI:1666690; contains Pfam profiles PF01849: NAC domain, PF00627: UBA/TS-N domain   chr3:3942266-3943789 FORWARD   Aliases: T2E22.29	10.7	11.0	-0.3	-1.4	100.0%	-4.1
4562	AT3G23430.1   Symbol: PHO1   phosphate transporter, putative (PHO1), identical to PHO1 protein (Arabidopsis thaliana) GI:20069032; supporting cDNA gi:20069031:gb:AF474076.1.; contains Pfam profiles PF03124: EXS family and PF03105: SPX domain   chr3:8387521-8393303 REVERSE   Aliases: MLM24.26, PHOSPHATE 1	7.3	6.6	0.7	1.4	100.0%	-3.9
4563	AT3G51750.2   expressed protein   chr3:19207482-19208313 REVERSE   Aliases: T18N14.130	4.7	4.0	0.6	1.4	100.0%	-3.9
4564	AT1G23020.1   ferric-chelate reductase, putative, similar to ferric-chelate reductase (FRO1) (Pisum sativum) GI:15341529; contains Pfam profile PF01794: Ferric reductase like transmembrane component	6.0	6.6	-0.6	-1.4	100.0%	-3.6
4565	AT4G01790.1   ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein / ribonuclease P-related, similar to human RNaseP-associate protein P38, GenBank accession number U77664   chr4:769868-770728 FORWARD   Aliases: T7B11.5	3.2	3.0	0.2	1.4	100.0%	-4.4
4566	AT3G60850.1   expressed protein   chr3:22492869-22495077 FORWARD   Aliases: T4C21.260	5.0	4.6	0.4	1.4	100.0%	-3.9
4567	AT3G19080.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr3:6596088-6598673 FORWARD   Aliases: K13E13.21	3.0	3.4	-0.4	-1.4	100.0%	-4.2
4568	AT5G42220.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr5:16889582-16894894 FORWARD   Aliases: K5J14.2, K5J14_2	7.0	7.5	-0.4	-1.4	100.0%	-4.0
4569	AT2G31870.1   Symbol: TEJ   poly (ADP-ribose) glycohydrolase (PARG) family protein, similar to poly(ADP-ribose) glycohydrolase (Bos taurus) GI:2062407; contains Pfam domain, PF05028: poly (ADP-ribose) glycohydrolase (PARG)   chr2:13557076-13560833 REVERSE   Aliases: F20M17.9, F20M17_9	4.6	4.2	0.3	1.4	100.0%	-4.0
4570	AT5G48220.1   indole-3-glycerol phosphate synthase, putative, similar to SP:P49572   chr5:19567071-19569460 FORWARD   Aliases: MIF21.11, MIF21_11	8.3	7.8	0.4	1.4	100.0%	-3.8
4571	AT3G47960.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:17708927-17711754 REVERSE   Aliases: T17F15.170	4.0	3.6	0.4	1.4	100.0%	-3.9
4572	AT1G34410.1   Symbol: ARF21   transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related, contains Pfam profile: PF02309 AUX/IAA family   chr1:12577700-12580802 FORWARD   Aliases: ARF21, AUXIN RESPONSE FACTOR 21, F12K21.26, F12K21_26	2.3	2.1	0.2	1.4	100.0%	-4.4
4573	AT3G55600.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr3:20631661-20633449 FORWARD   Aliases: F1I16.10	5.6	5.3	0.4	1.4	100.0%	-4.0
4574	AT3G29110.1   terpene synthase/cyclase family protein, contains Pfam profile: PF01397 terpene synthase family; similar to epidermal germacrene C synthase GB:AAC39431 (Lycopersicon esculentum), (+)-delta-cadinene synthase GB:P93665 (Gossypium hirsutum)   chr3:11083389-11087128 REVERSE   Aliases: MXE2.1	3.7	3.4	0.3	1.4	100.0%	-4.4
4575	AT2G42070.1   MutT/nudix family protein, similar to SP:Q58549 ADP-ribose pyrophosphatase (EC 3.6.1.13) {Methanococcus jannaschii}; contains Pfam profile PF00293: NUDIX domain	4.7	4.4	0.3	1.4	100.0%	-4.1
4576	AT1G59990.1   DEAD/DEAH box helicase, putative (RH22), similar to RNA helicase GI:3776015 from (Arabidopsis thaliana); contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00270: DEAD/DEAH box helicase; matches EST OAO811-2   chr1:22093904-22096667 REVERSE   Aliases: T2K10.4, T2K10_4	7.5	8.2	-0.7	-1.4	100.0%	-3.7
4577	AT4G36690.3   Symbol: ATU2AF65A   U2 snRNP auxiliary factor large subunit, putative, similar to U2 snRNP auxiliary factor, large subunit (Nicotiana plumbaginifolia) GI:3850823   chr4:17294019-17297725 REVERSE   Aliases: AP22.29, AP22_29, ATU2AF65A	7.9	7.4	0.5	1.4	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4578	AT3G25990.1   DNA-binding protein GT-1-related, similar to GT-1 GI:598073 from (Arabidopsis thaliana)   chr3:9505922-9507940 REVERSE   Aliases: MPE11.20	3.4	3.7	-0.3	-1.4	100.0%	-4.0
4579	AT4G30560.1   Symbol: ATCNGC9   cyclic nucleotide-regulated ion channel, putative, similar to cyclic nucleotide and calmodulin-regulated ion channel cngc6 GI:4581207 from (Arabidopsis thaliana)   chr4:14926980-14929687 REVERSE   Aliases: CNGC9, CYCLIC NUCLEOTIDE GATED CHANNEL 9, F17I23.100, F17I23_100	4.5	4.9	-0.4	-1.4	100.0%	-4.0
4580	AT5G54200.1   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP:Q9UGP9) (Homo sapiens)   chr5:22010575-22014302 REVERSE   Aliases: K18G13.8, K18G13_8	3.6	3.9	-0.3	-1.4	100.0%	-4.3
4581	AT4G03190.1   Symbol: GRH1   F-box family protein (FBL18), almost identical to GRR1-like protein 1 GI:12658970 from (Arabidopsis thaliana); similar to leucine-rich repeats containing F-box protein FBL3 (GI:5919219) (Homo sapiens); similar to F-box protein FBL2 (GI:6063090) (Homo sapiens)   chr4:1404445-1407139 REVERSE   Aliases: ATFBL18, ATGER1, ATGRH1, F4C21.11, F4C21_11, GRR1 LIKE PROTEIN 1	3.5	3.8	-0.3	-1.4	100.0%	-4.4
4582	AT3G58710.2   Symbol: WRKY69	6.1	5.5	0.7	1.4	100.0%	-3.8
4583	AT4G37430.1   Symbol: CYP91A2   cytochrome P450 81F1 (CYP81F1) (CYP91A2), identical to cytochrome P450 81F1 (91A2) (SP:O65790) (Arabidopsis thaliana)	5.1	5.4	-0.3	-1.4	100.0%	-4.1
4584	AT3G61890.1   Symbol: ATHB 12   homeobox-leucine zipper protein 12 (HB-12) / HD-ZIP transcription factor 12, identical to homeobox-leucine zipper protein ATHB-12 (GI:6899887) (Arabidopsis thaliana)	4.3	3.7	0.6	1.4	100.0%	-4.0
4585	AT1G64400.1   long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase, putative, similar to GI:1617270 (MF7P) from (Brassica napus)   chr1:23919261-23923446 REVERSE   Aliases: F15H21.7, F15H21_7	2.7	3.3	-0.6	-1.4	100.0%	-3.5
4586	AT5G06180.2   expressed protein, similar to unknown protein (sp:Q9ZE28)   chr5:1873166-1876045 FORWARD   Aliases: MBL20.6, MBL20_6	4.6	4.9	-0.3	-1.4	100.0%	-4.1
4587	AT1G63990.1   DNA topoisomerase VIA, putative (SPO11-2), similar to topoisomerase 6 subunit A (spo11) (Arabidopsis thaliana) GI:12331186; contains Pfam profile PF04406: Type IIB DNA topoisomerase; identical to cDNA putative topoisomerase VIA (SPO11 gene 2) GI:7270976   chr1:23746505-23749037 REVERSE   Aliases: F22C12.24, F22C12_24	2.2	2.3	-0.1	-1.4	100.0%	-4.9
4588	AT3G53570.4   Symbol: AFC1   similar to protein kinase (AFC2) [Arabidopsis thaliana] (TAIR:At4g24740.1); similar to putative protein kinase (AME2/AFC1) [Oryza sativa (japonica cultivar-group)] (GB:BAD81689.1); similar to putative protein kinase AFC1 [Oryza sativa (japonica cultivar-group)] (GB:NP_915397.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr3:19872157-19875566 REVERSE   Aliases: AME2, ARABIDOPSIS FUS3 COMPLEMENTING GENE 1, CLK/STY (LAMMER TYPE) PROTEIN KINASE, F4P12.270	7.0	6.3	0.7	1.4	100.0%	-3.9
4589	AT3G50590.1   transducin family protein / WD-40 repeat family protein, contains 3 WD-40 repeats (PF00400); some similarity to s-tomosyn isoform (GI:4689231)(Rattus norvegicus); contains non-consensus AT-AC splice sites at intron 18   chr3:18782000-18790483 FORWARD   Aliases: AT3G50600, T20E23.190	4.3	4.6	-0.3	-1.4	100.0%	-4.3
4590	AT4G37890.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF00092: von Willebrand factor type A domain	4.9	5.3	-0.5	-1.4	100.0%	-3.9
4591	AT2G01540.1   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr2:242122-243408 REVERSE   Aliases: F2I9.16, F2I9_16	6.2	5.8	0.4	1.4	100.0%	-4.2
4592	AT5G03650.1   Symbol: SBE2.2	9.0	8.2	0.9	1.4	100.0%	-3.7
4593	AT2G23040.1   expressed protein, ; expression supported by MPSS   chr2:9814973-9816289 REVERSE   Aliases: F21P24.10, F21P24_10	2.8	3.1	-0.3	-1.4	100.0%	-4.3
4594	AT5G05220.1   expressed protein   chr5:1550268-1550929 FORWARD   Aliases: K18I23.2, K18I23_2	3.7	3.5	0.2	1.4	100.0%	-4.7
4595	AT4G38950.1   kinesin motor family protein, similar to AtNACK1 kinesin-like protein (GI:19979627) (Arabidopsis thaliana); similar to kinesin-like protein NACK1 (GI:19570247) (Nicotiana tabacum)   chr4:18154466-18158455 REVERSE   Aliases: F19H22.50, F19H22_50	3.6	4.2	-0.6	-1.4	100.0%	-3.9
4596	AT1G09530.2   Symbol: PIF3   phytochrome interacting factor 3 (PIF3), identical to phytochrome interacting factor 3 (PIF3) GI:3929585 from (Arabidopsis thaliana)   chr1:3076604-3079541 FORWARD   Aliases: F14J9.19, F14J9_19, PAP3, PHOTOCURRENT 1, PHYTOCHROME INTERACTING FACTOR 3, PHYTOCHROME ASSOCIATED PROTEIN 3, POC1	4.1	4.5	-0.4	-1.4	100.0%	-4.0
4597	AT2G02360.1   Symbol: ATPP2 B10   F-box family protein / SKP1 interacting partner 3-related, contains similarity to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)   chr2:619407-620743 REVERSE   Aliases: ATPP2 B10, T16F16.15, T16F16_15	4.1	3.7	0.5	1.4	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4598	AT1G16720.1   expressed protein   chr1:5723081-5726471 FORWARD   Aliases: F19K19.14	8.4	7.9	0.4	1.4	100.0%	-4.0
4599	AT1G72180.1   leucine-rich repeat transmembrane protein kinase, putative, similar to Gl:3641252 from (Malus x domestica) (Plant Mol. Biol. 40 (6), 945-957 (1999))   chr1:27166482-27171092 FORWARD   Aliases: T9N14.3, T9N14_3	4.6	4.2	0.4	1.4	100.0%	-4.0
4600	AT5G49950.1   embryogenesis-associated protein-related, contains weak similarity to Embryogenesis-associated protein EMB8 (Swiss-Prot:Q40863) (Picea glauca)   chr5:20336442-20340842 REVERSE   Aliases: K9P8.9, K9P8_9	7.1	7.4	-0.3	-1.4	100.0%	-4.1
4601	AT1G55020.1   Symbol: LOX1   lipoxygenase (LOX1), identical to SP:Q06327   chr1:20529375-20533940 FORWARD   Aliases: LIPOXYGENASE	4.7	5.4	-0.7	-1.4	100.0%	-3.7
4602	AT3G62600.1   DNAJ heat shock family protein, similar to DnaJ homolog subfamily B member 11 precursor (SP:Q99KV1){Mus musculus}; contains Pfam PF00226: DnaJ domain; contains PfaPF01556: DnaJ C terminal regionm   chr3:23161766-23164486 REVERSE   Aliases: F26K9.30	9.5	10.2	-0.6	-1.4	100.0%	-4.1
4603	AT5G21160.1   La domain-containing protein / proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965, PF05383: La domain   chr5:7198744-7204093 REVERSE   Aliases: T10F18.190, T10F18_190	4.7	5.1	-0.4	-1.4	100.0%	-4.4
4604	AT2G40760.1   rhodanese-like domain-containing protein, contains rhodanese-like domain PF00581	7.6	8.0	-0.4	-1.4	100.0%	-3.9
4605	AT5G13930.1   Symbol: CHS   chalcone synthase / naringenin-chalcone synthase, identical to SP:P13114   chr5:4488692-4490266 FORWARD   Aliases: ATCHS, CHALCONE SYNTHASE, CHALCONE/STILBENE SYNTHASE, MAC12.28, MAC12_28, NARINGENIN CHALCONE SYNTHASE, TESTA 4 PROTEIN, TRANSPARENT TESTA 4, TT4	5.7	6.4	-0.7	-1.4	100.0%	-3.7
4606	AT4G36960.1   RNA recognition motif (RRM)-containing protein, similar to SP:P48809 Heterogeneous nuclear ribonucleoprotein 27C (hnRNP 48) {Drosophila melanogaster}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); non-consensus TA donor splice site at exon 6   chr4:17426927-17429757 FORWARD   Aliases: AP22.66, AP22_66	6.2	5.8	0.4	1.4	100.0%	-3.9
4607	AT2G33860.1   Symbol: ETT   auxin-responsive factor (ARF3) / ETTIN protein (ETT), identical to ETTIN GB:AF007788 from (Arabidopsis thaliana)   chr2:14332345-14335847 REVERSE   Aliases: ARF3, AUXIN RESPONSE TRANSCRIPTION FACTOR 3, ETTIN, T1B8.30, T1B8_30	6.3	6.8	-0.4	-1.4	100.0%	-3.8
4608	AT1G01500.1   expressed protein, identical to cDNA unknown protein Gl:1922247 embY10087.1   chr1:185133-186923 FORWARD   Aliases: F22L4.17, F22L4_17	6.7	6.5	0.3	1.4	100.0%	-4.2
4609	AT3G55410.1   2-oxoglutarate dehydrogenase E1 component, putative / oxoglutarate decarboxylase, putative / alpha-ketoglutaric dehydrogenase, putative, similar to SP:P20967 2-oxoglutarate dehydrogenase E1 component, mitochondrial precursor (EC 1.2.4.2) (Alpha-ketoglutarate dehydrogenase) {Saccharomyces cerevisiae}; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF00676: Dehydrogenase E1 component   chr3:20552412-20557011 FORWARD   Aliases: T22E16.70	6.8	7.5	-0.7	-1.4	100.0%	-4.1
4610	AT5G55280.1   Symbol: FTSZ1 1   cell division protein FtsZ, chloroplast, putative (FTSZ), identical to SP:Q42545 Cell division protein ftsZ homolog, chloroplast precursor {Arabidopsis thaliana}; similar to FtsZ1 (Tagetes erecta) Gl:8896066; contains Pfam profiles PF00091: Tubulin/FtsZ family, GTPase domain, PF03953: Tubulin/FtsZ family, C-terminal domain   chr5:22437882-22439838 REVERSE   Aliases: ATFTSZ1 1, CPFTSZ, MCO15.23, MCO15_23	8.5	9.1	-0.6	-1.4	100.0%	-3.6
4611	AT1G03610.1   expressed protein   chr1:900886-903002 FORWARD   Aliases: F21B7.22	5.2	4.7	0.4	1.4	100.0%	-3.9
4612	AT3G15350.2   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr3:5166249-5169527 FORWARD   Aliases: K7L4.15	4.0	4.2	-0.3	-1.4	100.0%	-4.1
4613	AT1G71950.1   expressed protein, similar to Pi starvation-induced protein GB:BAA06151 from (Nicotiana tabacum)	8.7	8.2	0.5	1.4	100.0%	-4.0
4614	AT5G63960.1   DNA-directed DNA polymerase delta catalytic subunit, putative (POLD1), similar to DNA polymerase delta (Glycine max) Gl:2895198, OsPol delta large subunit (Oryza sativa (japonica cultivar-group) Gl:9188570; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain	4.2	4.6	-0.4	-1.4	100.0%	-3.8
4615	AT3G27690.1   Symbol: LHCB2:4   chlorophyll A-B binding protein (LHCB2:4), nearly identical to Lhcb2 protein (Arabidopsis thaliana) Gl:4741950; similar to chlorophyll A-B binding protein 151 precursor (LHCP) GB:P27518 from (Gossypium hirsutum); contains Pfam PF00504: Chlorophyll A-B binding protein   chr3:10257184-10258248 FORWARD   Aliases: LHCB2.3, MGF10.10	7.4	6.6	0.7	1.4	100.0%	-3.5
4616	AT1G74590.1   Symbol: ATGSTU10   glutathione S-transferase, putative, similar to putative glutathione S-transferase GB:CAA10060 (Arabidopsis thaliana); contains Pfam profile: PF00043 Glutathione S-transferases   chr1:28027288-28028387 REVERSE   Aliases: F1M20.27, F1M20_27	3.1	3.9	-0.8	-1.4	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4617	AT4G09570.1   Symbol: CPK4   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Arabidopsis thaliana) gi:604881:dbj:BAA04830; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr4:6049518-6052332 FORWARD   Aliases: T25P22.10, T25P22_10	9.0	9.4	-0.5	-1.4	100.0%	-4.2
4618	AT3G46960.1   similar to HUA enhancer 2 (HEN2) / DExH-box RNA helicase, putative [Arabidopsis thaliana] (TAIR:At2g06990.1); similar to superkiller viralicidic activity 2-like (S. cerevisiae) [Homo sapiens] (GB:CAI41730.1); similar to superkiller viralicidic activity 2-like (S. cerevisiae) [Homo sapiens] (GB:CAI41863.1); similar to similar to putative DEAD/DEAH box helicase [Schizosaccharomyces pombe] [Dictyostelium discoideum] (GB:AAO51181.1); similar to superkiller viralicidic activity 2-like [Rattus norvegicus] (GB:NP_998724.1); similar to superkiller viralicidic activity 2-like [Mus musculus] (GB:NP_067312.1); contains InterPro domain Helicase, C-terminal (InterPro:IPR001650); contains InterPro domain DEAD/DEAH box helicase (InterPro:IPR001410)   chr3:17301878-17309052 REVERSE   Aliases: F13I12.10	7.1	7.3	-0.2	-1.4	100.0%	-4.3
4619	AT1G24090.1   RNase H domain-containing protein, very low similarity to GAG-POL precursor (Oryza sativa (japonica cultivar-group)) GI:5902445; contains Pfam profiles PF00075: RNase H, PF04134: Protein of unknown function, DUF393   chr1:8520823-8524679 FORWARD   Aliases: T23E23.25	3.0	3.2	-0.2	-1.4	100.0%	-4.7
4620	AT4G22330.1   Symbol: ATCES1	5.7	5.0	0.7	1.4	100.0%	-4.0
4621	AT1G10670.2   Symbol: ACLA 1	11.0	11.5	-0.5	-1.4	100.0%	-4.3
4622	AT4G23050.2   protein kinase, putative, similar to MAP3K delta-1 protein kinase (Arabidopsis thaliana) gi:2253010:emb:CAA74591; contains Pfam PF00069 Protein kinase domain and PF00989 PAS domain   chr4:12080071-12084267 FORWARD   Aliases: F7H19.240, F7H19_240	7.3	6.9	0.4	1.4	100.0%	-3.9
4623	AT4G25700.2   Symbol: BETA OHASE 1   similar to beta-carotene hydroxylase, putative [Arabidopsis thaliana] (TAIR:At5g52570.1); similar to beta-carotene hydroxylase [Citrus unshiu] (GB:AAG10793.1); contains InterPro domain Carotene hydroxylase (InterPro:IPR005596); contains InterPro domain SUR2-type hydroxylase/desaturase, catalytic domain (InterPro:IPR006087)   chr4:13094782-13095944 REVERSE   Aliases: BETA HYDROXYLASE 1, L73G19.80, L73G19_80	8.2	7.7	0.5	1.4	100.0%	-3.8
4624	AT5G23740.1   Symbol: RPS11 BETA   40S ribosomal protein S11 (RPS11C)	11.3	11.7	-0.4	-1.4	100.0%	-4.0
4625	AT5G13800.2   hydrolase, alpha/beta fold family protein, low similarity to hydrolase (Terrabacter sp. DBF63) GI:14196240; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:4451840-4454559 REVERSE   Aliases: MAC12.25, MAC12_25	6.5	6.1	0.4	1.4	100.0%	-4.0
4626	AT5G62210.1   embryo-specific protein-related, contains weak similarity to embryo-specific protein 3 (GI:3335171) (Arabidopsis thaliana)   chr5:25003553-25004715 REVERSE   Aliases: MMI9.4, MMI9_4	4.1	4.5	-0.4	-1.4	100.0%	-4.0
4627	AT2G40430.1   expressed protein, identical to Protein At2g40430 (Swiss-Prot:O22892) (Arabidopsis thaliana); similar to Glioma tumor suppressor candidate region gene 2 protein (p60) (Swiss-Prot:Q9NZM5) (Homo sapiens)   chr2:16886297-16889505 REVERSE   Aliases: T2P4.22	9.4	9.8	-0.4	-1.4	100.0%	-3.9
4628	AT1G51390.2   Symbol: NFU5   similar to nitrogen fixation NifU-like family protein [Arabidopsis thaliana] (TAIR:At3g20970.1); similar to hypothetical protein UM04972.1 [Ustilago maydis 521] (GB:EAK85802.1); contains InterPro domain Nitrogen-fixing NifU, C-terminal (InterPro:IPR001075)	4.4	4.7	-0.3	-1.4	100.0%	-4.2
4629	AT5G25110.1   Symbol: CIPK25	6.0	5.0	1.0	1.4	100.0%	-3.6
4630	AT5G61640.1   Symbol: PMSR1   peptide methionine sulfoxide reductase, putative, similar to peptide methionine sulfoxide reductase (msr) (Arabidopsis thaliana) GI:4884033; contains Pfam profile PF01625: Peptide methionine sulfoxide reductase   chr5:24792261-24793616 FORWARD   Aliases: K11J9.18, K11J9_18, PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 1	5.3	4.6	0.7	1.4	100.0%	-3.8
4631	AT2G27150.1   Symbol: AAO3   aldehyde oxidase 3 (AAO3), identical to GP:3172044:gnl:PID:d1029570:AB010080   chr2:11608832-11614239 FORWARD   Aliases: ALDEHYDE OXIDASE 3, F20F1.2, F20F1_2	7.0	7.4	-0.4	-1.4	100.0%	-4.0
4632	AT5G50120.1   transducin family protein / WD-40 repeat family protein, Similar to En/Spm-like transposon protein (gi:2739374)(Arabidopsis thaliana); similar to GTP-binding regulatory protein and WD-repeat protein; contains 7 WD-40 repeats	5.1	4.6	0.6	1.4	100.0%	-3.8
4633	AT2G34820.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.3	-0.1	-1.4	100.0%	-4.9
4634	AT2G27790.1   expressed protein   chr2:11854412-11856362 REVERSE   Aliases: F15K20.11, F15K20_11	3.5	3.3	0.2	1.4	100.0%	-4.3
4635	AT1G31770.1   ABC transporter family protein, contains Pfam profile: PF00005: ABC transporter   chr1:11374874-11377775 REVERSE   Aliases: F5M6.22	6.1	6.8	-0.8	-1.4	100.0%	-3.8
4636	AT2G41000.1   Symbol: LCR51   DNAJ heat shock N-terminal domain-containing protein, similar to SP:O75190 DnaJ homolog subfamily B member 6 (Heat shock protein J2) Homo sapiens; contains Pfam profile PF00226 DnaJ domain   chr2:17117906-17120673 FORWARD   Aliases: LCR51, Low molecular weight cysteine rich 51, T3K9.23, T3K9_23	4.9	4.5	0.4	1.4	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4637	AT4G27370.1   Symbol: VIIIIB   myosin family protein, contains Pfam profiles: PF00063 myosin head (motor domain), PF00612 IQ calmodulin-binding motif   chr4:13694887-13700786 REVERSE   Aliases: F27G19.14, TVIIIIB	4.0	4.3	-0.3	-1.4	100.0%	-4.2
4638	AT4G36880.1   cysteine proteinase, putative, strong similarity to cysteine proteinase COT44 precursor SP:P25251 from (Brassica napus) (Rape)   chr4:17374459-17376220 REVERSE   Aliases: AP22.67, AP22_67	5.0	4.5	0.5	1.4	100.0%	-3.8
4639	AT5G19440.1   similar to Eucalyptus gunnii alcohol dehydrogenase of unknown physiological function (GI:1143445), apple tree, PIR:T16995; NOT a cinnamyl-alcohol dehydrogenase   chr5:6556422-6558344 FORWARD   Aliases: F7K24.190, F7K24_190	10.3	11.2	-0.9	-1.4	100.0%	-3.9
4640	AT1G73510.1   expressed protein   chr1:27646312-27646779 REVERSE   Aliases: T9L24.31, T9L24_31	2.5	2.4	0.2	1.4	100.0%	-4.7
4641	AT5G13530.1   protein kinase family protein / ankyrin repeat family protein, contains similarity to ankyrin-related gene UNC-44 gi:790608:gb:AAA85854; contains Pfam domains PF00023: Ankyrin repeat and PF00069: Protein kinase domain   chr5:4345621-4351150 FORWARD   Aliases: T6I14.60, T6I14_60	2.6	2.4	0.2	1.4	100.0%	-4.9
4642	AT5G18690.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; Common family member: At3g06360 (Arabidopsis thaliana)   chr5:6233521-6234128 REVERSE   Aliases: T1A4.70, T1A4_70	2.8	3.6	-0.7	-1.4	100.0%	-4.0
4643	AT2G17800.1   Symbol: ARAC1   Rac-like GTP-binding protein (ARAC1) (ATGP2), identical to Rac-like GTP-binding protein (ARAC1) SP:Q38902 from (Arabidopsis thaliana)   chr2:7746954-7749237 FORWARD   Aliases: ATGP2, T17A5.14, T17A5_14	7.1	7.6	-0.5	-1.4	100.0%	-3.9
4644	AT5G09510.1   40S ribosomal protein S15 (RPS15D), ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161   chr5:2955114-2956674 REVERSE   Aliases: T5E8.310, T5E8_310	7.9	8.6	-0.6	-1.4	100.0%	-3.9
4645	AT1G47230.2   Symbol: CYCA3;4   cyclin, putative, similar to cyclin A-like protein (Nicotiana tabacum) GI:1064931, A-type cyclin (Catharanthus roseus) GI:2190259; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:17309017-17311674 FORWARD   Aliases: CYCA3;4, Cyclin A3;4, F8G22.5, F8G22_5	4.5	4.9	-0.4	-1.4	100.0%	-4.0
4646	AT5G24400.1   Symbol: EMB2024   glucosamine/galactosamine-6-phosphate isomerase family protein, low similarity to SP:O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) {Homo sapiens}; contains Pfam profile PF01182: Glucosamine-6-phosphate isomerase/6-phosphogluconolactonase	8.0	8.6	-0.7	-1.4	100.0%	-3.9
4647	AT5G45160.1   root hair defective 3 GTP-binding (RHD3) family protein, contains Pfam profile: PF05879 root hair defective 3 GTP-binding protein (RHD3) family   chr5:18282218-18287510 FORWARD   Aliases: K18C1.4, K18C1_4	6.6	5.9	0.6	1.4	100.0%	-4.0
4648	AT5G37670.1   15.7 kDa class I-related small heat shock protein-like (HSP15.7-CI), contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.	7.3	6.7	0.6	1.4	100.0%	-3.9
4649	AT5G02540.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr5:568524-570918 FORWARD   Aliases: T22P11.130, T22P11_130	2.2	2.4	-0.2	-1.4	100.0%	-4.7
4650	AT1G05805.1   basic helix-loop-helix (bHLH) family protein   chr1:1744773-1747692 FORWARD   Aliases: None	4.4	4.0	0.4	1.4	100.0%	-3.9
4651	AT2G37430.1   zinc finger (C2H2 type) family protein (ZAT11), contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:15713440-15714303 FORWARD   Aliases: F3G5.22, F3G5_22	2.4	2.6	-0.2	-1.4	100.0%	-4.5
4652	AT1G69840.4   band 7 family protein, strong similarity to hypersensitive-induced response protein (Zea mays) GI:7716466; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr1:26297331-26299298 REVERSE   Aliases: T17F3.13, T17F3_13	8.1	6.9	1.1	1.4	100.0%	-3.6
4653	AT1G18060.1   expressed protein   chr1:6211867-6213358 REVERSE   Aliases: T10F20.7	7.1	6.7	0.4	1.4	100.0%	-3.9
4654	AT3G56820.1   expressed protein   chr3:21050790-21052724 REVERSE   Aliases: T8M16.150	7.1	6.8	0.3	1.4	100.0%	-4.1
4655	AT2G34620.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr2:14584275-14585367 FORWARD   Aliases: T31E10.4, T31E10_4	2.7	2.9	-0.2	-1.4	100.0%	-4.5
4656	AT3G59780.1   expressed protein   chr3:22097904-22101421 FORWARD   Aliases: F24G16.50	7.7	8.4	-0.6	-1.4	100.0%	-3.5
4657	AT3G10690.1   DNA gyrase subunit A family protein, similar to SP:P94605 DNA gyrase subunit A (EC 5.99.1.3). {Clostridium acetobutylicum}; contains Pfam profiles PF00521: DNA gyrase/topoisomerase IV A subunit, PF03989: DNA gyrase C-terminal domain beta-propeller   chr3:3339397-3346345 REVERSE   Aliases: T7M13.23	4.4	5.3	-0.9	-1.4	100.0%	-3.8
4658	AT5G41960.1   expressed protein   chr5:16806942-16808270 FORWARD   Aliases: MJC20.6, MJC20_6	7.8	7.4	0.4	1.4	100.0%	-4.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4659	AT1G52260.1   Symbol: ATPDIL1 5   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	5.8	6.3	-0.5	-1.4	100.0%	-3.9
4660	AT1G47128.1   cysteine proteinase (RD21A) / thiol protease, identical to SP:P43297 Cysteine proteinase RD21A precursor (EC 3.4.22.-) {Arabidopsis thaliana}, thiol protease RD21A SP:P43297 from (Arabidopsis thaliana)   chr1:17285265-17288110 REVERSE   Aliases: F2G19.31, F2G19_31	9.5	8.8	0.7	1.4	100.0%	-4.2
4661	AT3G27820.1   monodehydroascorbate reductase, putative, similar to cytosolic monodehydroascorbate reductase GB:BAA77214 (Oryza sativa)	7.6	8.0	-0.4	-1.4	100.0%	-4.1
4662	AT4G11670.1   expressed protein, contains Pfam PF05664: Protein of unknown function (DUF810)   chr4:7044395-7053085 REVERSE   Aliases: T5C23.100, T5C23_100	4.9	5.4	-0.5	-1.4	100.0%	-3.8
4663	AT5G49800.1   expressed protein   chr5:20251868-20253410 REVERSE   Aliases: K21G20.1, K21G20_1	3.2	3.5	-0.3	-1.4	100.0%	-4.3
4664	AT5G49670.1   expressed protein   chr5:20193611-20198897 FORWARD   Aliases: K2I5.3, K2I5_3	3.2	2.9	0.3	1.4	100.0%	-4.4
4665	AT5G58520.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:23672476-23675388 FORWARD   Aliases: MQJ2.14, MQJ2_14	5.7	6.2	-0.4	-1.4	100.0%	-3.8
4666	AT1G65650.1   ubiquitin carboxyl-terminal hydrolase family 1 protein, similar to 26S proteasome regulatory complex subunit p37A (Drosophila melanogaster) GI:6434962; contains Pfam profile PF01088: Ubiquitin carboxyl-terminal hydrolase, family 1   chr1:24418678-24421372 REVERSE   Aliases: F1E22.3	7.8	8.6	-0.8	-1.4	100.0%	-3.9
4667	AT5G02840.3   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At3g09600.1); similar to myb family transcription factor-like [Oryza sativa (japonica cultivar-group)] (GB:BAD29385.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005); contains InterPro domain Myb-like DNA-binding domain, SHAQKYF class (InterPro:IPR006447)   chr5:648702-651956 FORWARD   Aliases: F9G14.150, F9G14_150	6.2	5.2	0.9	1.4	100.0%	-3.8
4668	AT3G30260.1   MADS-box protein (AGL79), similar to GB:Q38876 from (Arabidopsis thaliana) (Plant Cell 7 (11), 1763-1771 (1995)); contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr3:11911598-11915359 FORWARD   Aliases: T6J22.1	3.2	3.0	0.2	1.4	100.0%	-4.9
4669	AT3G47640.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	4.0	3.7	0.3	1.4	100.0%	-4.0
4670	AT1G71260.1   expressed protein   chr1:26865327-26867080 REVERSE   Aliases: F3I17.9, F3I17_9	7.4	8.2	-0.8	-1.4	100.0%	-3.7
4671	AT5G24870.2   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:8544788-8547116 REVERSE   Aliases: F6A4.80, F6A4_80	4.9	4.3	0.6	1.4	100.0%	-3.6
4672	AT3G12830.1   auxin-responsive family protein, similar to auxin-induced protein (SP:P33082) (Glycine max)   chr3:4078658-4079615 REVERSE   Aliases: MBK21.19	4.5	3.9	0.6	1.4	100.0%	-4.0
4673	AT2G45600.1   expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873   chr2:18796662-18798026 FORWARD   Aliases: F17K2.13	3.8	4.3	-0.5	-1.4	100.0%	-3.8
4674	AT1G17550.1   Symbol: HAB2   protein phosphatase 2C-related / PP2C-related, similar to protein phosphatase 2C GI:3242077 from (Arabidopsis thaliana)   chr1:6034355-6037282 FORWARD   Aliases: F1L3.38	6.4	6.1	0.3	1.4	100.0%	-4.3
4675	AT4G25820.1   Symbol: XTR9   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR9), identical to xyloglucan endotransglycosylase GI:4218963 from (Arabidopsis thaliana)   chr4:13130306-13131797 FORWARD   Aliases: F14M19.100, F14M19_100, XYLOGLUCAN ENDOTRANSGLYCOSYLASE 9	4.4	3.9	0.5	1.4	100.0%	-3.8
4676	AT2G36720.1   PHD finger transcription factor, putative   chr2:15400150-15406497 FORWARD   Aliases: F13K3.12, F13K3_12	5.2	5.7	-0.5	-1.4	100.0%	-4.0
4677	AT5G63870.3   Symbol: PP7   serine/threonine protein phosphatase (PP7), identical to PP7 (Arabidopsis thaliana) GI:2791900   chr5:25578398-25580500 REVERSE   Aliases: MGI19.12, MGI19_12	4.2	4.6	-0.4	-1.4	100.0%	-3.9
4678	AT5G63040.2   expressed protein, similar to unknown protein (emb:CAB81845.1)   chr5:25305372-25307638 FORWARD   Aliases: MJH22.10, MJH22_10	3.8	4.1	-0.3	-1.4	100.0%	-4.1
4679	AT1G16840.4   expressed protein   chr1:5762706-5764027 REVERSE   Aliases: F17F16.27	7.7	7.0	0.8	1.4	100.0%	-3.8
4680	AT2G26120.1   glycine-rich protein   chr2:11130508-11130895 FORWARD   Aliases: T19L18.7, T19L18_7	5.1	4.5	0.6	1.4	100.0%	-3.8
4681	AT5G04870.1   Symbol: CPK1   calcium-dependent protein kinase isoform AK1 (AK1), identical to calcium-dependent protein kinase, isoform AK1 (CDPK) (Arabidopsis thaliana) SWISS-PROT:Q06850; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr5:1416784-1420339 REVERSE   Aliases: AK1, ATCPK1, CALCIUM DEPENDENT PROTEIN KINASE, MUK11.19, MUK11_19	8.5	8.9	-0.4	-1.4	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4682	AT5G66280.1   Symbol: GMD1   GDP-D-mannose 4,6-dehydratase, putative, strong similarity to GDP-D-mannose-4,6-dehydratase (Arabidopsis thaliana) GI:1764100   chr5:26493392-26495344 FORWARD   Aliases: GDP D MANNOSE 4,6 DEHYDRATASE 1, K1L20.6, K1L20_6	3.9	4.3	-0.4	-1.4	100.0%	-4.0
4683	AT1G26260.3   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g68920.2); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910691.1); similar to putative TA1 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD68029.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr1:9087201-9089365 FORWARD   Aliases: F28B23.8, F28B23_8	2.7	3.0	-0.2	-1.4	100.0%	-4.4
4684	AT1G73690.1   Symbol: CDKD1;1   cell division protein kinase, putative, similar to cell division protein kinase 7 (Homo sapiens) SWISS-PROT:P50613   chr1:27718609-27720942 FORWARD   Aliases: CDKD1;1, Cyclin dependent kinase D1;1, F25P22.11, F25P22_11	3.3	3.9	-0.6	-1.4	100.0%	-4.2
4685	AT3G04590.2   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr3:1238859-1241646 REVERSE   Aliases: F7O18.6, F7O18_6	5.4	5.0	0.4	1.4	100.0%	-3.8
4686	AT1G05350.1   thiF family protein, low similarity to SP:P30138 Adenylyltransferase thiF (EC 2.7.7.-) {Escherichia coli}; contains Pfam profile PF00899: ThiF family   chr1:1560890-1564004 REVERSE   Aliases: YUP8H12.3, YUP8H12_3	7.8	8.4	-0.6	-1.4	100.0%	-3.7
4687	AT2G46060.2   transmembrane protein-related, contains weak similarity to Swiss-Prot:Q9HCN3 transmembrane protein 8 precursor (M83 protein) (Homo sapiens)   chr2:18948172-18952129 REVERSE   Aliases: T3F17.29	5.7	5.3	0.5	1.4	100.0%	-4.0
4688	AT5G09390.2   similar to SMC2orf [Podocoryne carnea] (GB:CAA08790.1)   chr5:2913535-2915924 FORWARD   Aliases: T5E8.190, T5E8_190	7.8	7.5	0.3	1.4	100.0%	-4.1
4689	AT3G55000.1   Symbol: TON1A   tonneau family protein, similar to tonneau 1b (GI:11494367) (Arabidopsis thaliana)   chr3:20392485-20394764 FORWARD   Aliases: T15C9.7, TON1, TONNEAU 1	4.8	5.3	-0.5	-1.4	100.0%	-4.1
4690	AT5G27720.1   Symbol: EMB1644   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to SWISS-PROT:Q9QXA5 U6 snRNA-associated Sm-like protein LSm4 (Mus musculus)   chr5:9815579-9817576 FORWARD   Aliases: EMB1644, EMBRYO DEFECTIVE 1644, T1G16.50, T1G16_50	8.2	7.7	0.5	1.4	100.0%	-3.9
4691	AT1G22020.1   glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, similar to serine hydroxymethyltransferase (Chlamydomonas reinhardtii) GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase	4.6	4.2	0.4	1.4	100.0%	-4.0
4692	AT3G16190.1   isochorismatase hydrolase family protein, low similarity to SP:P32400 N-carbamoylsarcosine amidase (EC 3.5.1.59) (N-carbamoylsarcosine amidohydrolase) {Arthrobacter sp}; contains Pfam profile PF00857: isochorismatase family protein   chr3:5489707-5491254 REVERSE   Aliases: MYA6.5	8.0	7.6	0.5	1.4	100.0%	-3.8
4693	AT5G24150.2   Symbol: SQP1   similar to squalene monooxygenase 1,2 / squalene epoxidase 1,2 (SQP1,2) [Arabidopsis thaliana] (TAIR:At5g24160.1); similar to squalene monooxygenase 2 / squalene epoxidase 2 (SQP2) [Arabidopsis thaliana] (TAIR:At5g24140.1); similar to squalene epoxidase homologue [Brassica napus] (GB:CAA06770.1); contains InterPro domain Flavoprotein monooxygenase (InterPro:IPR000733); contains InterPro domain NAD-binding site (InterPro:IPR000205); contains InterPro domain Aromatic-ring hydroxylase (InterPro:IPR003042)   chr5:8172319-8175434 REVERSE   Aliases: K12G2.2, K12G2_2	3.7	3.5	0.3	1.4	100.0%	-4.3
4694	AT4G15980.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:9057478-9059995 REVERSE   Aliases: DL4030C, FCAALL.248	2.0	2.1	-0.2	-1.4	100.0%	-4.8
4695	AT1G49540.1   transducin family protein / WD-40 repeat family protein, similar to signal transducer and activator of transcription interacting protein 1 (GI:15929722) {Mus musculus}; similar to hypothetical protein GB:AAD43147 GI:5430747 from (Arabidopsis thaliana); contains Pfam PF00400: WD domain, G-beta repeat (11 copies, 2 weak)	4.5	4.8	-0.3	-1.4	100.0%	-4.2
4696	AT1G51915.1   cryptdin protein-related, contains weak similarity to Swiss-Prot:P17533 cryptdin-related protein 1C precursor (CRS1C) (Mus musculus)   chr1:19297147-19297638 FORWARD   Aliases: None	2.0	2.0	0.1	1.4	100.0%	-5.4
4697	AT1G14370.1   Symbol: APK2A   protein kinase (APK2a), identical to protein kinase APK2a GI:2852447 from (Arabidopsis thaliana)   chr1:4915662-4918303 FORWARD   Aliases: F14L17.14, F14L17_14, PROTEIN KINASE 2A	5.2	4.8	0.5	1.4	100.0%	-3.8
4698	AT2G31320.1   poly (ADP-ribose) polymerase, putative / NAD(+) ADP-ribosyltransferase, putative / poly(ADP-ribose) synthetase, putative, similar to poly(ADP-ribose) polymerase (Zea mays) GI:3928871 ; contains Pfam profiles PF00644: Poly(ADP-ribose) polymerase catalytic domain, PF00645: Poly(ADP-ribose) polymerase and DNA-Ligase Zn-finger region, PF02877: Poly(ADP-ribose) polymerase, regulatory domain, PF00533: BRCA1 C Terminus (BRCT) domain   chr2:13360898-13366805 REVERSE   Aliases: F16D14.16, F16D14_16	5.1	5.6	-0.4	-1.4	100.0%	-3.8
4699	AT4G34110.1   Symbol: PAB2   polyadenylate-binding protein 2 (PABP2), non-consensus TA donor splice site at exon 2, polyadenylate-binding protein - Triticum aestivum (common wheat),PIR:T06979   chr4:16336392-16340102 FORWARD   Aliases: F28A23.130, F28A23_130, POLY(A) BINDING PROTEIN 2	10.9	10.2	0.8	1.4	100.0%	-3.9
4700	AT2G22600.1   KH domain-containing protein   chr2:9603697-9606130 FORWARD   Aliases: T9I22.4, T9I22_4	4.8	5.2	-0.4	-1.4	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4701	AT1G08250.1   prephenate dehydratase family protein, contains similarity to prephenate dehydratase GI:1008717 from ( <i>Amycolatopsis methanolica</i> )	6.1	6.4	-0.4	-1.4	100.0%	-4.0
4702	AT3G25220.1   Symbol: FKBP15 1   FK506-binding protein 2-1 (FKBP15-1) / immunophilin / peptidyl-prolyl cis-trans isomerase / rotamase, identical to SP:Q38935 FK506-binding protein 2-1 precursor (EC 5.2.1.8) (Peptidyl-prolyl cis- trans isomerase) (PPIase) (Rotamase) (15 kDa FKBP) (FKBP-15-1) { <i>Arabidopsis thaliana</i> }, immunophilin (FKBP15-1) GB:U52046 ( <i>Arabidopsis thaliana</i> ) (Proc. Natl. Acad. Sci. U.S.A. 93 (14), 6964-6969 (1996))   chr3:9183855-9185849 FORWARD   Aliases: MJL12.19	9.8	10.1	-0.3	-1.4	100.0%	-4.2
4703	AT2G10870.1   expressed protein   chr2:4290762-4291013 FORWARD   Aliases: F16G22.7, F16G22_7	4.0	3.7	0.3	1.4	100.0%	-4.3
4704	AT2G30920.1   Symbol: ATCOQ3	6.7	6.2	0.5	1.4	100.0%	-3.8
4705	AT5G16010.1   3-oxo-5-alpha-steroid 4-dehydrogenase family protein / steroid 5-alpha-reductase family protein, similar to steroid 5alpha-reductase - <i>Rattus norvegicus</i> , PIR:A34239 (SP:24008); contains Pfam 3-oxo-5-alpha-steroid 4-dehydrogenase domain PF02544   chr5:5227927-5229119 FORWARD   Aliases: F1N13.150, F1N13_150	9.1	8.2	0.9	1.4	100.0%	-3.7
4706	AT1G70850.3   similar to Bet v I allergen family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g70830.1); similar to Bet v I allergen family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g70830.2); similar to Csf-2 [ <i>Cucumis sativus</i> ] (GB:BAA83470.1); contains InterPro domain Bet v I allergen (InterPro:IPR000916)   chr1:26718528-26720445 REVERSE   Aliases: F15H11.10, F15H11_10	4.5	5.0	-0.5	-1.4	100.0%	-3.9
4707	AT4G29750.1   expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578)   chr4:14569734-14572810 FORWARD   Aliases: T16L4.260, T16L4_260	5.0	5.5	-0.5	-1.4	100.0%	-3.9
4708	AT5G65390.1   Symbol: AGP7   arabinogalactan-protein (AGP7)   chr5:26145810-26146564 REVERSE   Aliases: MNA5.12, MNA5_12	7.1	6.6	0.5	1.4	100.0%	-3.9
4709	AT1G03905.1   ABC transporter family protein, similar to NBD-like protein GB:AAD20643   chr1:993477-995593 FORWARD   Aliases: None	6.5	7.1	-0.6	-1.4	100.0%	-3.8
4710	AT5G14120.1   nodulin family protein, similar to nodulin-like protein ( <i>Arabidopsis thaliana</i> ) GI:3329368, nodule-specific protein Nlj70 ( <i>Lotus japonicus</i> ) GI:3329366   chr5:4555984-4559116 FORWARD   Aliases: MUA22.12, MUA22_12	7.1	6.6	0.5	1.4	100.0%	-3.8
4711	AT1G48450.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g17800.1); similar to unknown [ <i>Brassica napus</i> ] (GB:AAK30572.1); contains InterPro domain Protein of unknown function DUF760 (InterPro:IPR008479)   chr1:17912171-17914113 REVERSE   Aliases: T1N15.6, T1N15_6	9.5	9.1	0.4	1.4	100.0%	-4.1
4712	AT3G49710.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:18448830-18450995 FORWARD   Aliases: T16K5.60	5.1	5.9	-0.8	-1.4	100.0%	-4.0
4713	AT2G01980.1   Symbol: SOS1   sodium proton exchanger, putative (NHX7) (SOS1), identical to putative Na <sup>+</sup> /H <sup>+</sup> antiporter SOS1 ( <i>Arabidopsis thaliana</i> ) gi:8515714;gb:AAF76139; Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563   chr2:457009-463325 FORWARD   Aliases: ATSOS1, F14H20.5, F14H20_5, SALT OVERLY SENSITIVE 1	5.4	5.8	-0.4	-1.4	100.0%	-3.9
4714	AT1G76420.1   Symbol: CUC3   no apical meristem (NAM) family protein, N-term similar to N-term of NAM GB:CAA63101 ( <i>Petunia x hybrida</i> ) (apical meristem formation), CUC2 GB:BAA19529 ( <i>Arabidopsis thaliana</i> ), GRAB2 protein GB:CAA09372 ( <i>Triticum sp.</i> )	2.1	2.0	0.1	1.4	100.0%	-5.1
4715	AT3G03840.1   auxin-responsive protein, putative, similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) ( <i>Raphanus sativus</i> )   chr3:981079-981805 FORWARD   Aliases: F20H23.14, F20H23_14	2.1	2.0	0.1	1.4	100.0%	-5.3
4716	AT1G73400.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:27602073-27603473 FORWARD   Aliases: T9L24.39, T9L24_39	3.3	3.7	-0.3	-1.4	100.0%	-4.2
4717	AT2G20690.1   lumazine-binding family protein, SP:P50854 Riboflavin synthase alpha chain (EC 2.5.1.9) { <i>Actinobacillus pleuropneumoniae</i> }; contains Pfam profile PF00677: Lumazine binding domain   chr2:8930386-8932052 FORWARD   Aliases: F5H14.34, F5H14_34	5.3	4.9	0.4	1.4	100.0%	-4.2
4718	AT1G76280.2   similar to pentatricopeptide (PPR) repeat-containing protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g18940.1); similar to P0529E05.10 [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:NP_915531.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr1:28623258-28627625 REVERSE   Aliases: F15M4.22	3.4	3.7	-0.3	-1.4	100.0%	-4.4
4719	AT5G17270.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr5:5679997-5685599 FORWARD   Aliases: MKP11.12, MKP11_12	4.4	4.9	-0.5	-1.4	100.0%	-3.8
4720	AT5G27660.1   DegP protease, putative, similar to Serine protease HTRA2, mitochondrial precursor (High temperature requirement protein A2) (HtrA2) (Omi stress-regulated endoprotease) (Serine proteinase OMI) (SP:O43464) { <i>Homo sapiens</i> }   chr5:9789902-9792427 REVERSE   Aliases: T1G16.1	4.4	4.8	-0.4	-1.4	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4721	AT3G17170.1   Symbol: RFC3   ribosomal protein S6 family protein (RFC3), annotation temporarily based on supporting cDNA gi:15620809:dbj:AB057424.1.; contains TIGRfam TIGR00166 and Pfam PF01250 profiles ribosomal protein S6.   chr3:5852646-5854912 REVERSE   Aliases: K14A17.25, REGULATOR OF FATTY ACID COMPOSITION 3	5.5	6.6	-1.1	-1.4	100.0%	-3.7
4722	AT3G49870.1   Symbol: ATARLA1C   ADP-ribosylation factor, putative, similar to ADP-ribosylation factor-like protein 1 (SP:P40616) (Homo sapiens); ARF3 ADP-RIBOSYLATION FACTOR,GP:453191 Arabidopsis thaliana; contains domain PF00025: ADP-ribosylation factor family   chr3:18503435-18505124 REVERSE   Aliases: ATARLA1C, T16K5.220	9.2	8.8	0.4	1.4	100.0%	-3.9
4723	AT1G21840.1   expressed protein, weak similarity to SP:Q07402 Urease accessory protein ureF (strain TB-90) {Bacillus sp.}   chr1:7666489-7667657 FORWARD   Aliases: T26F17.5	5.5	5.1	0.5	1.4	100.0%	-4.0
4724	AT2G29410.1   Symbol: MTPB1   zinc transporter, putative, similar to zinc transporter ZAT (Arabidopsis thaliana) gi:4206640:gb:AAD11757; similar to zinc transporter ZnT-2 (Rattus norvegicus) gi:1256378:gb:AAB02775; member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr2:12623652-12625064 FORWARD   Aliases: ATMTPB1, F16P2.21, F16P2_21	2.7	3.1	-0.4	-1.4	100.0%	-4.0
4725	AT5G04000.1   expressed protein   chr5:1079102-1079839 REVERSE   Aliases: F8F6.210, F8F6_210	5.6	4.8	0.8	1.4	100.0%	-3.6
4726	AT5G22830.1   Symbol: GMN10   magnesium transporter CorA-like family protein, weak similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg2+ transporter protein; supporting cDNA gi:12007446:gb:AF322255.1:AF322255   chr5:7627653-7631371 FORWARD   Aliases: GMN10, MRN17.6, MRN17_6	6.9	6.6	0.3	1.4	100.0%	-4.1
4727	AT1G13020.1   eukaryotic translation initiation factor, putative (EIF4B5), eukaryotic initiation factor 4B (GI:6739522) {Arabidopsis thaliana}; EST gb:T22808 comes from this gene   chr1:4440542-4443682 REVERSE   Aliases: F3F19.4, F3F19_4	5.5	6.0	-0.5	-1.4	100.0%	-3.9
4728	AT2G31730.1   ethylene-responsive protein, putative, similar to ethylene-inducible ER33 protein (Lycopersicon esculentum) gi:5669656:gb:AAD46413   chr2:13494769-13495670 REVERSE   Aliases: T9H9.27	3.8	4.3	-0.5	-1.4	100.0%	-3.8
4729	AT3G62620.1   sucrose-phosphatase-related, contains weak similarity to sucrose-phosphatase (Arabidopsis thaliana) gi:11127757:gb:AAG31075   chr3:23170779-23172830 FORWARD   Aliases: F26K9.50	3.8	4.1	-0.3	-1.4	100.0%	-4.1
4730	AT5G44785.2   expressed protein, contains Pfam PF05329: Protein of unknown function (DUF731)   chr5:18087918-18090356 REVERSE   Aliases: None	6.2	6.7	-0.5	-1.4	100.0%	-3.9
4731	AT5G57440.1   Symbol: GS1   haloacid dehalogenase-like hydrolase family protein, similar to SP:Q08623 GS1 protein {Homo sapiens}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	4.7	5.5	-0.8	-1.4	100.0%	-3.6
4732	AT2G16570.1   Symbol: ATASE   amidophosphoribosyltransferase / glutamine phosphoribosylpyrophosphate amidotransferase / phosphoribosyldiphosphate 5-amidotransferase, identical to amidophosphoribosyltransferase (Arabidopsis thaliana) GI:469193; identical to cDNA amidophosphoribosyltransferase GI:469192   chr2:7187227-7189275 REVERSE   Aliases: ATASE1, F1P15.5, F1P15_5, GLN PHOSPHORIBOSYL PYROPHOSPHATE AMIDOTRANSFERASE 1	7.7	8.3	-0.6	-1.4	100.0%	-3.8
4733	AT1G26570.1   UDP-glucose 6-dehydrogenase, putative, strong similarity to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profiles PF03721: UDP-glucose/GDP-mannose dehydrogenase family NAD binding domain, PF00984: UDP-glucose/GDP-mannose dehydrogenase family central domain, PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain   chr1:9182191-9184380 FORWARD   Aliases: T1K7.6, T1K7_6	4.8	5.2	-0.4	-1.4	100.0%	-3.9
4734	AT4G13360.1   similar to enoyl-CoA hydratase/isomerase family protein [Arabidopsis thaliana] (TAIR:At3g24360.1); similar to ENSANGP00000024573 [Anopheles gambiae str. PEST] (GB:XP_312972.2); contains InterPro domain Enoyl-CoA hydratase/isomerase (InterPro:IPR001753)   chr4:7775124-7778223 FORWARD   Aliases: T9E8.100, T9E8_100	7.2	8.7	-1.4	-1.4	100.0%	-3.9
4735	AT2G17845.1   short-chain dehydrogenase/reductase (SDR) family protein, contains similarity to 3-oxoacyl-(acyl-carrier protein) reductase SP:P51831 from (Bacillus subtilis)   chr2:7765928-7766963 FORWARD   Aliases: None	3.3	3.0	0.2	1.4	100.0%	-4.5
4736	AT5G07440.1   Symbol: GDH2   glutamate dehydrogenase 2 (GDH2), identical to glutamate dehydrogenase 2 (GDH 2) (Arabidopsis thaliana) SWISS-PROT:Q38946   chr5:2355938-2358195 FORWARD   Aliases: GLUTAMATE DEHYDROGENASE 2, T2I1.150, T2I1_150	8.7	9.2	-0.5	-1.4	100.0%	-4.2
4737	AT4G20070.1   peptidase M20/M25/M40 family protein, contains similarity to hydantoin utilization protein C (Pseudomonas sp.) SWISS-PROT:Q01264; contains Pfam profile PF01546: Peptidase family M20/M25/M40   chr4:10861465-10864705 FORWARD   Aliases: F18F4.170, F18F4_170	5.5	5.2	0.3	1.4	100.0%	-4.3
4738	AT2G30730.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 (serine/threonine protein kinase) (Lycopersicon esculentum) gi:3668069:gb:AAC61805; contains protein kinase domain, Pfam:PF00069   chr2:13100222-13101754 FORWARD   Aliases: T11J7.12, T11J7_12	2.3	2.1	0.1	1.4	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4739	AT3G59980.1   tRNA-binding region domain-containing protein, similar to SP:O54873 Multisynthetase complex auxiliary component p43 (Contains: Endothelial-monocyte activating polypeptide II (EMAP-II) (Small inducible cytokine subfamily E member 1)) {Cricetulus griseus}; contains Pfam profile PF01588: Putative tRNA binding domain   chr3:22165221-22166618 REVERSE   Aliases: F24G16.250	7.6	8.1	-0.4	-1.4	100.0%	-3.8
4740	AT3G47120.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:17362126-17363807 REVERSE   Aliases: F13I12.170	6.9	6.3	0.6	1.4	100.0%	-3.9
4741	AT1G22440.1   alcohol dehydrogenase, putative, similar to alcohol dehydrogenase ADH GI:7705214 from (Lycopersicon esculentum); contains Pfam zinc-binding dehydrogenase domain PF00107	6.5	7.1	-0.6	-1.4	100.0%	-4.0
4742	AT1G04080.1   hydroxyproline-rich glycoprotein family protein, Contains similarity to pre-mRNA processing protein PRP39 gb L29224 from S. cerevisiae. ESTs gb:R64908 and gb:T88158, gb:N38703 and gb:AA651043 come from this gene   chr1:1051375-1056750 FORWARD   Aliases: F20D22.14	8.1	8.6	-0.5	-1.4	100.0%	-4.3
4743	AT5G29000.2   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:11022087-11024279 REVERSE   Aliases: F3F24.100, F3F24_100	5.3	4.8	0.4	1.4	100.0%	-3.9
4744	AT3G02560.2   40S ribosomal protein S7 (RPS7B), similar to ribosomal protein S7 GB:AAD26256 from (Secale cereale)   chr3:541807-543341 FORWARD   Aliases: F16B3.19, F16B3_19	10.1	10.7	-0.6	-1.4	100.0%	-4.2
4745	AT3G04810.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g54510.1); similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At5g28290.1); similar to putative LSTK-1-like kinase [Oryza sativa (japonica cultivar-group)] (GB:AAR01739.1); similar to LSTK-1-like kinase [Lycopersicon esculentum] (GB:AAL04423.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:1317266-1321300 FORWARD   Aliases: T9J14.24, T9J14_24	3.9	4.7	-0.8	-1.4	100.0%	-3.6
4746	AT1G70480.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g23560.1); contains InterPro domain Protein of unknown function DUF220 (InterPro:IPR003863)   chr1:26565722-26567472 FORWARD   Aliases: F24J13.5, F24J13_5	9.6	8.8	0.8	1.4	100.0%	-3.9
4747	AT4G35180.1   amino acid transporter family protein, similar to amino acid permease 1 GI:976402 from (Nicotiana glauca); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr4:16738344-16740371 REVERSE   Aliases: T12J5.50, T12J5_50	3.7	3.4	0.2	1.4	100.0%	-4.6
4748	AT3G17020.1   universal stress protein (USP) family protein, similar to early nodulin ENOD18 (Vicia faba) GI:11602747; contains Pfam profile PF00582: universal stress protein family   chr3:5802555-5804130 REVERSE   Aliases: K14A17.9	9.9	8.8	1.1	1.4	100.0%	-4.2
4749	AT5G65470.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;   chr5:26189358-26192259 FORWARD   Aliases: MNA5.21, MNA5_21	8.4	7.9	0.4	1.4	100.0%	-4.1
4750	AT5G10690.1   pentatricopeptide (PPR) repeat-containing protein / CBS domain-containing protein, contains CBS and PPR domain repeats   chr5:3374394-3377431 REVERSE   Aliases: MAJ23.50, MAJ23_50	6.1	6.5	-0.5	-1.4	100.0%	-3.7
4751	AT5G23250.1   succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative, similar to SP:P36967 Succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, alpha chain) (SCS-alpha) {Dictyostelium discoideum}; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain   chr5:7830392-7832846 FORWARD   Aliases: MKD15.11, MKD15_11	10.5	11.1	-0.6	-1.4	100.0%	-3.9
4752	AT2G27230.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g64625.1); similar to transcription factor-like [Oryza sativa (japonica cultivar-group)] (GB:BAD29456.1)   chr2:11657437-11661221 FORWARD   Aliases: F12K2.19, F12K2_19	7.2	7.7	-0.5	-1.4	100.0%	-3.9
4753	AT1G13610.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g30380.1); similar to putative Cgi67 serine protease [Oryza sativa (japonica cultivar-group)] (GB:XP_464411.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr1:4663832-4666028 REVERSE   Aliases: F21F23.4	5.8	5.2	0.6	1.4	100.0%	-3.8
4754	AT4G32830.1   Encodes a member of a family of Ser/Thr kinases whose activities peak during cell division. Transcripts are abundant in tissues rich in dividing cells like roots and flowers but are low or absent in fully expanded leaves and stems.	5.8	5.3	0.5	1.4	100.0%	-4.0
4755	AT1G72240.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g22470.1); contains domain SER_RICH (PS50324)   chr1:27193841-27194411 FORWARD   Aliases: T9N14.5, T9N14_5	4.8	3.9	0.9	1.4	100.0%	-3.7
4756	AT4G03140.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to stem secoisolariciresinol dehydrogenase GI:13752458 from {Forsythia x intermedia}; similar to sex determination protein tasselseed 2 SP:P50160 from (Zea mays)   chr4:1392601-1393662 FORWARD   Aliases: F4C21.6, F4C21_6	2.8	3.3	-0.5	-1.4	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4757	AT2G21130.1   peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP2) / rotamase, identical to cyclophilin (Arabidopsis thaliana) gi:2443757:gb:AAB71402; similar to peptidyl-prolyl cis-trans isomerase, PPIase (cyclophilin, cyclosporin A-binding protein) (Arabidopsis thaliana) SWISS-PROT:P34790   chr2:9062479-9063313 REVERSE   Aliases: F26H11.11, F26H11_11	11.4	10.5	0.9	1.4	100.0%	-3.5
4758	AT1G21880.2   peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	5.5	6.4	-0.9	-1.4	100.0%	-3.9
4759	AT2G02950.1   Symbol: PKS1   phytochrome kinase substrate 1 (PKS1), identical to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 (Arabidopsis thaliana)   chr2:854946-856537 REVERSE   Aliases: PHYTOCHROME KINASE SUBSTRATE 1, T17M13.12, T17M13_12	2.5	2.3	0.2	1.4	100.0%	-4.9
4760	AT1G52560.1   26.5 kDa class I small heat shock protein-like (HSP26.5-P), contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.   chr1:19578429-19579435 REVERSE   Aliases: F6D8.22, F6D8_22	3.2	3.5	-0.3	-1.4	100.0%	-4.2
4761	AT3G04940.1   Symbol: ATCYSD1   cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to O-acetylserine(thiol) lyase (EC 4.2.99.8) (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme	6.5	6.9	-0.4	-1.4	100.0%	-3.9
4762	AT3G27260.1   Symbol: GTE8   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr3:10068875-10073898 FORWARD   Aliases: GLOBAL TRANSCRIPTION FACTOR GROUP E, K17E12.8	6.4	5.7	0.6	1.4	100.0%	-3.7
4763	AT5G13450.2   similar to F1-ATP synthase delta subunit [Ipomoea batatas] (GB:BAA77508.1); similar to oligomycin sensitivity conferring protein [Silene latifolia] (GB:AAN38066.1); contains InterPro domain H+-transporting two-sector ATPase, delta (OSCP) subunit (InterPro:IPR000711)   chr5:4310317-4312015 REVERSE   Aliases: T22N19.100, T22N19_100	10.6	11.4	-0.8	-1.4	100.0%	-3.9
4764	AT1G48880.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g06080.2); similar to leaf senescence related protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD81676.1); contains InterPro domain Protein of unknown function DUF231 (InterPro:IPR004253)   chr1:18084701-18086593 FORWARD   Aliases: F27K7.9, F27K7_9	4.5	4.8	-0.3	-1.4	100.0%	-4.2
4765	AT1G63710.1   Symbol: CYP86A7   cytochrome P450, putative, similar to cytochrome P450 GB:O23066 (Arabidopsis thaliana)   chr1:23635841-23637605 REVERSE   Aliases: F24D7.10, F24D7_10	2.6	2.5	0.2	1.4	100.0%	-4.7
4766	AT5G06670.1   kinesin motor protein-related   chr5:2048244-2055020 REVERSE   Aliases: F15M7.20, F15M7_20	6.3	5.9	0.3	1.4	100.0%	-4.0
4767	AT5G26210.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr5:9157982-9160357 REVERSE   Aliases: T19G15.60, T19G15_60	5.6	5.3	0.4	1.4	100.0%	-4.0
4768	AT1G15840.1   expressed protein   chr1:5451427-5452369 FORWARD   Aliases: F7H2.17, F7H2_17	7.3	6.6	0.7	1.4	100.0%	-3.9
4769	AT5G47400.1   expressed protein   chr5:19246389-19248749 FORWARD   Aliases: MQL5.26, MQL5_26	3.0	2.7	0.3	1.4	100.0%	-4.3
4770	AT5G11230.1   phosphate translocator-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}   chr5:3580563-3581618 FORWARD   Aliases: F2I11.120, F2I11_120	4.5	4.8	-0.3	-1.4	100.0%	-4.2
4771	AT4G27460.1   CBS domain-containing protein   chr4:13732916-13734310 FORWARD   Aliases: F27G19.60, F27G19_60	3.7	3.3	0.4	1.4	100.0%	-4.0
4772	AT3G48070.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g62910.1); similar to OSJNBa0060P14.3 [Oryza sativa (japonica cultivar-group)] (GB:CAD41040.2); contains domain SER_RICH (PS50324)   chr3:17761697-17763746 FORWARD   Aliases: T17F15.60	5.8	5.1	0.7	1.4	100.0%	-3.7
4773	AT5G15830.1   bZIP transcription factor family protein, similar to common plant regulatory factor 7 GI:9650828 from (Petroselinum crispum); contains Pfam profile: PF00170 bZIP transcription factor   chr5:5168546-5169364 FORWARD   Aliases: F14F8.210, F14F8_210	4.1	3.5	0.6	1.4	100.0%	-3.7
4774	AT2G41550.1   expressed protein   chr2:17335617-17338211 REVERSE   Aliases: T32G6.7, T32G6_7	5.0	5.5	-0.4	-1.4	100.0%	-3.9
4775	AT5G19970.1   expressed protein, ; expression supported by MPSS   chr5:6747552-6748643 FORWARD   Aliases: F28I16.120, F28I16_120	3.5	3.0	0.5	1.4	100.0%	-3.7
4776	AT5G64700.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula); contains Pfam profile PF00892: Integral membrane protein	3.5	3.2	0.3	1.4	100.0%	-4.2
4777	AT1G79190.1   expressed protein   chr1:29793532-29799063 FORWARD   Aliases: YUP8H12R.20, YUP8H12R_20	4.8	5.2	-0.4	-1.4	100.0%	-4.3
4778	AT3G49050.1   lipase class 3 family protein / calmodulin-binding heat-shock protein, putative, calmodulin-binding heat-shock protein, Nicotiana tabacum, PIR:T04107   chr3:18191953-18194737 FORWARD   Aliases: T2J13.110	4.5	5.1	-0.6	-1.4	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4779	AT4G16840.1   expressed protein   chr4:9474904-9475542 FORWARD   Aliases: DL4445W, FCAALL.92	4.2	3.8	0.3	1.4	100.0%	-4.0
4780	AT1G32200.2   Symbol: ATS1   glycerol-3-phosphate acyltransferase, chloroplast (ATS1), identical to SP:Q43307:PLSB_ARATH Glycerol-3-phosphate acyltransferase, chloroplast precursor (EC 2.3.1.15) (GPAT) (ATS1) {Arabidopsis thaliana}; contains Pfam profile PF01553: Acyltransferase   chr1:11602064-11605040 REVERSE   Aliases: ACT1, ACYLTRANSFERASE 1, F3C3.13, F3C3_13, GLYCEROL 3 PHOSPHATE ACYLTRANSFERASE	6.5	7.0	-0.5	-1.4	100.0%	-3.8
4781	AT3G58770.1   expressed protein, ; expression supported by MPSS   chr3:21743497-21746160 FORWARD   Aliases: T20N10.120	2.7	2.9	-0.2	-1.4	100.0%	-4.6
4782	AT2G45710.1   40S ribosomal protein S27 (RPS27A)   chr2:18838235-18839281 FORWARD   Aliases: F4I18.31	8.9	9.4	-0.6	-1.4	100.0%	-3.8
4783	AT2G32730.1   26S proteasome regulatory subunit, putative, contains similarity to 26S proteasome regulatory subunit S1 SP:O88761, GI:3288594 from (Rattus norvegicus)   chr2:13887137-13892813 FORWARD   Aliases: F24L7.13, F24L7_13	5.5	6.4	-0.9	-1.4	100.0%	-3.8
4784	AT5G38220.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g66900.1); similar to Cgi67 serine protease-like [Oryza sativa (japonica cultivar-group)] (GB:BAD82560.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr5:15286057-15288616 FORWARD   Aliases: MXA21.9, MXA21_9	5.2	4.7	0.5	1.4	100.0%	-3.8
4785	AT4G14030.1   selenium-binding protein, putative, contains Pfam profile PF05694: 56kDa selenium binding protein (SBP56); identical to Putative selenium-binding protein (Swiss-Prot:O23264) (Arabidopsis thaliana); similar to selenium binding protein (GI:15485232) (Arabidopsis thaliana); identical to cDNA from partial mRNA for selenium binding protein (sbp gene) GI:15485231	6.4	7.5	-1.1	-1.4	100.0%	-4.1
4786	AT4G14040.1   selenium-binding protein, putative, contains Pfam profile PF05694: 56kDa selenium binding protein (SBP56); similar to Putative selenium-binding protein (Swiss-Prot:O23264) (Arabidopsis thaliana); similar to selenium binding protein (GI:15485232) (Arabidopsis thaliana)   chr4:8100344-8102870 REVERSE   Aliases: DL3061C, FCAALL.29	6.4	7.5	-1.1	-1.4	100.0%	-4.1
4787	AT4G11870.1   expressed protein   chr4:7140489-7140713 REVERSE   Aliases: T26M18.80, T26M18_80	3.7	4.4	-0.7	-1.4	100.0%	-4.1
4788	AT4G03330.1   Symbol: SYP123	3.4	4.0	-0.6	-1.4	100.0%	-3.6
4789	AT1G01370.2   Symbol: HTR12   similar to histone H3.2 [Arabidopsis thaliana] (TAIR:At4g40030.1); similar to histone H3, putative [Arabidopsis thaliana] (TAIR:At1g19890.1); similar to histone H3.2 [Arabidopsis thaliana] (TAIR:At4g40040.1); similar to histone H3 [Arabidopsis thaliana] (TAIR:At5g10980.1); similar to histone H3 like protein [Arabis gemmifera] (GB:BAC79431.1); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124); contains InterPro domain Histone H3 (InterPro:IPR000164); contains InterPro domain Histone core (InterPro:IPR007125)   chr1:143717-145684 FORWARD   Aliases: F6F3.17, F6F3_17	2.7	3.0	-0.3	-1.4	100.0%	-4.3
4790	AT3G51730.1   saposin B domain-containing protein, contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1   chr3:19197645-19199670 FORWARD   Aliases: T18N14.110	8.3	7.1	1.2	1.4	100.0%	-3.8
4791	AT5G40550.1   expressed protein   chr5:16258333-16260609 FORWARD   Aliases: MNF13.7, MNF13_7	3.6	4.0	-0.4	-1.4	100.0%	-4.2
4792	AT3G12130.1   KH domain-containing protein / zinc finger (CCCH type) family protein   chr3:3864158-3866596 REVERSE   Aliases: T21B14.5	5.6	5.3	0.3	1.4	100.0%	-4.0
4793	AT2G44510.1   p21Cip1-binding protein-related, similar to p21Cip1-binding protein TOK-1beta (GI:7339688) (Homo sapiens); similar to BRCA2 and Cip1/p21 interacting protein (GI:25989375) (Homo sapiens)   chr2:18384147-18386255 FORWARD   Aliases: F4I1.32	4.2	4.5	-0.3	-1.4	100.0%	-4.1
4794	AT5G02680.1   expressed protein   chr5:605710-606763 FORWARD   Aliases: F9G14.1	4.1	3.5	0.5	1.4	100.0%	-3.8
4795	AT1G34470.1   permease-related, low similarity to purine permease (Arabidopsis thaliana) GI:7620007   chr1:12604278-12607011 FORWARD   Aliases: F12K21.21, F12K21_21	6.0	5.7	0.3	1.4	100.0%	-4.1
4796	AT3G09010.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:2749958-2752281 FORWARD   Aliases: T16O11.3	3.9	3.6	0.3	1.4	100.0%	-4.0
4797	AT1G32370.4   Symbol: TOM2B   expressed protein   chr1:11676941-11678427 FORWARD   Aliases: F5D14.14, F5D14_14, TTM1	5.0	4.6	0.4	1.4	100.0%	-4.0
4798	AT5G57815.1   cytochrome c oxidase subunit 6b, putative, similar to subunit 6b of cytochrome c oxidase (Arabidopsis thaliana) gi:6518353:dbj:BAA87883   chr5:23443903-23445077 FORWARD   Aliases: None	7.4	6.5	0.9	1.4	100.0%	-3.7
4799	AT2G21860.1   violaxanthin de-epoxidase-related, contains weak similarity to violaxanthin de-epoxidase precursor gi:1438875:gb:AAC49373   chr2:9325338-9327082 REVERSE   Aliases: F7D8.18, F7D8_18	7.0	6.4	0.6	1.4	100.0%	-3.6
4800	AT1G19970.1   ER lumen protein retaining receptor family protein, similar to SP:P33946 ER lumen protein retaining receptor 1 (KDEL receptor 1) {Bos taurus}; contains Pfam profile PF00810: ER lumen protein retaining receptor   chr1:6931009-6932680 REVERSE   Aliases: T20H2.24, T20H2_24	4.4	4.7	-0.3	-1.4	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4801	AT1G60780.1   clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	7.5	8.3	-0.9	-1.4	100.0%	-4.0
4802	AT1G22080.1   expressed protein   chr1:7792473-7794580 REVERSE   Aliases: F2E2.15, F2E2_15	3.3	3.1	0.2	1.4	100.0%	-4.5
4803	AT2G32400.1   Symbol: GLR5   glutamate receptor family protein (GLR3.7) (GLR5), identical to Glr5 (Arabidopsis thaliana) gi:6644388:gb:AAF21042; plant glutamate receptor family, PMID:11379626   chr2:13759742-13763930 REVERSE   Aliases: ATGLR3.7, GLR3.7, GLR5, T32F6.8, T32F6_8	4.0	4.2	-0.2	-1.4	100.0%	-4.4
4804	AT5G47920.1   expressed protein, similar to unknown protein (emb:CAB67623.1)   chr5:19420399-19421314 REVERSE   Aliases: MCA23.26, MCA23_26	3.3	3.1	0.2	1.4	100.0%	-4.3
4805	AT3G49240.1   Symbol: EMB1796   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:18266964-18269085 FORWARD   Aliases: EMB1796, EMBRYO DEFECTIVE 1796, F2K15.100	5.3	6.0	-0.7	-1.4	100.0%	-3.9
4806	AT3G04780.1   Encodes a protein with little sequence identity with any other protein of known structure or function. Part of this protein shows a 42% sequence identity with the C-terminal domain of the 32-kD human thioredoxin-like protein.   chr3:1311253-1313096 REVERSE   Aliases: F7O18.27, F7O18_27	6.5	7.2	-0.7	-1.4	100.0%	-3.8
4807	AT1G79200.1   expressed protein   chr1:29799281-29800933 FORWARD   Aliases: YUP8H12R.41, YUP8H12R_41	4.7	5.1	-0.4	-1.4	100.0%	-3.9
4808	AT1G07720.1   beta-ketoacyl-CoA synthase family protein, similar to GB:AAC99312 from (Arabidopsis thaliana) (Plant J. (1999) In press)	2.2	2.1	0.1	1.4	100.0%	-4.9
4809	AT5G43600.1   N-carbamyl-L-amino acid hydrolase, putative, similar to N-carbamoyl-L-amino acid hydrolase (Bacillus stearothermophilus) SWISS-PROT:Q53389   chr5:17529703-17532722 FORWARD   Aliases: K9D7.10, K9D7_10	7.3	6.7	0.7	1.4	100.0%	-3.9
4810	AT2G19720.1   Symbol: RPS15AB   40S ribosomal protein S15A (RPS15aB)   chr2:8516562-8518399 REVERSE   Aliases: F6F22.25, F6F22_25, RPS15AB	6.4	7.2	-0.7	-1.4	100.0%	-3.6
4811	ATCG00560.1   Symbol: PSBL   PSII L protein   chrC:63804-63920 REVERSE   Aliases: PSBL	6.9	8.2	-1.2	-1.4	100.0%	-3.8
4812	AT4G12880.1   plastocyanin-like domain-containing protein   chr4:7544379-7545301 REVERSE   Aliases: T20K18.230, T20K18_230	6.2	7.3	-1.1	-1.4	100.0%	-4.0
4813	AT2G35155.1   expressed protein   chr2:14826073-14829044 REVERSE   Aliases: None	5.3	5.9	-0.6	-1.4	100.0%	-3.7
4814	AT5G52050.1   MATE efflux protein-related, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr5:21156088-21157869 FORWARD   Aliases: MSG15.13, MSG15_13	7.1	6.2	0.9	1.4	100.0%	-3.4
4815	AT2G34060.1   peroxidase, putative, similar to peroxidase ATP20a {Arabidopsis thaliana} GP:9757794:dbj:BAB08292   chr2:14391993-14393748 FORWARD   Aliases: T14G11.18, T14G11_18	3.1	3.4	-0.3	-1.4	100.0%	-4.3
4816	AT5G16070.1   chaperonin, putative, similar to SWISS-PROT:P80317 T-complex protein 1, zeta subunit (TCP-1-zeta) (Mus musculus); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr5:5247357-5251182 REVERSE   Aliases: F1N13.210, F1N13_210	8.7	9.6	-0.9	-1.4	100.0%	-3.7
4817	AT3G09920.2   similar to phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] (TAIR:At1g60890.1); similar to phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] (TAIR:At1g10900.1); similar to phosphatidylinositol-4-phosphate 5-kinase [Oryza sativa (japonica cultivar-group)] (GB:CAD27794.1); similar to Putative Phosphatidylinositol-4-phosphate 5-Kinase [Oryza sativa (japonica cultivar-group)] (GB:AAX95508.1); contains InterPro domain Phosphatidylinositol-4-phosphate 5-kinase (InterPro:IPR002498); contains InterPro domain MORN motif (InterPro:IPR003409)   chr3:3040308-3044772 REVERSE   Aliases: F8A24.2	4.8	5.4	-0.5	-1.4	100.0%	-3.9
4818	AT5G17510.1   expressed protein   chr5:5769975-5772397 REVERSE   Aliases: K3M16.80, K3M16_80	3.1	2.8	0.3	1.4	100.0%	-4.2
4819	AT1G15980.1   expressed protein   chr1:5489292-5491303 FORWARD   Aliases: T24D18.8, T24D18_8	7.4	6.7	0.7	1.4	100.0%	-3.5
4820	AT5G23690.1   polynucleotide adenyltransferase family protein, low similarity to SP:P13685 Poly(A) polymerase (EC 2.7.7.19) {Escherichia coli O157:H7}; contains Pfam profile PF01743: polyA polymerase family protein   chr5:7987543-7990550 FORWARD   Aliases: MQM1.4, MQM1_4	4.3	4.6	-0.3	-1.4	100.0%	-4.3
4821	AT5G13690.1   alpha-N-acetylglucosaminidase family / NAGLU family, contains Pfam profile: PF05089 alpha-N-acetylglucosaminidase (NAGLU)   chr5:4415757-4420374 FORWARD   Aliases: MSH12.16, MSH12_16	4.3	4.7	-0.5	-1.4	100.0%	-4.0
4822	AT3G20280.2   PHD finger family protein, contains Pfam profile: PF00628 PHD-finger   chr3:7071199-7074647 FORWARD   Aliases: MQC12.7	2.3	2.5	-0.1	-1.4	100.0%	-4.9
4823	AT1G33500.1   hypothetical protein   chr1:12152754-12154665 FORWARD   Aliases: F10C21.15, F10C21_15	2.7	3.0	-0.2	-1.4	100.0%	-4.8
4824	AT5G14100.1   Symbol: ATNAP14   ABC transporter family protein, contains similarity to ABC transporter, ATP-binding protein   chr5:4549440-4551845 REVERSE   Aliases: MUA22.10, MUA22_10	3.6	3.3	0.3	1.4	100.0%	-4.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4825	AT3G62260.2   protein phosphatase 2C, putative / PP2C, putative, phosphoprotein phosphatase (EC 3.1.3.16) 1A-alpha - Homo sapiens, PIR:S22423   chr3:23049265-23051545 REVERSE   Aliases: T17J13.220	6.4	5.9	0.5	1.4	100.0%	-4.2
4826	AT3G26900.1   shikimate kinase family protein, similar to shikimate kinase precursor GB:CAA45121 (Lycopersicon esculentum); contains Pfam shikimate kinase domain PF01202   chr3:9913449-9915715 REVERSE   Aliases: MDJ14.24	7.2	6.7	0.5	1.4	100.0%	-3.8
4827	AT2G31800.1   ankyrin protein kinase, putative, similar to ankyrin-kinase (Medicago truncatula) gi:18700701:gb:AAL78674; contains Pfam profile PF00023: Ankyrin repeat; identical to cDNA calcineurin B-like protein 10 (CBL10) GI:29150247; blastp match of 67% identity and 1.9e-200 P-value to GP:18700701:gb:AAL78674.1:AF458699_1:AF458699 ankyrin-kinase {Medicago truncatula}   chr2:13526787-13530775 REVERSE   Aliases: F20M17.16, F20M17_16	5.9	5.5	0.5	1.4	100.0%	-3.8
4828	AT3G14950.1   tetratricopeptide repeat (TPR)-containing protein, low similarity to SP:Q99615 DnaJ homolog subfamily C member 7 (Tetratricopeptide repeat protein 2) {Homo sapiens}; contains Pfam profile PF00515: TPR Domain   chr3:5030223-5032899 REVERSE   Aliases: K15M2.9	2.5	2.7	-0.2	-1.4	100.0%	-4.6
4829	AT5G61460.1   Symbol: MIM   structural maintenance of chromosomes (SMC) family protein, very strong similarity to SMC-like protein (MIM) (Arabidopsis thaliana) GI:5880614; contains Pfam profile PF02463: RecF/RecN/SMC N terminal domain   chr5:24731302-24739166 REVERSE   Aliases: MCI2.2, MCI2_2	3.5	3.8	-0.3	-1.4	100.0%	-4.1
4830	AT2G14120.2   dynamin-like protein 2b (ADL2b), identical to dynamin like protein 2b (ADL2b) (Arabidopsis thaliana) GI:19032339	7.5	8.1	-0.6	-1.4	100.0%	-4.0
4831	AT5G35200.1   epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein short form, Rattus norvegicus, EMBL:AF041373; similar to Chain A, Calm-N N-Terminal Domain Of Clathrin Assembly Lymphoid Myeloid Leukaemia Protein, Pi(4,5)p2 Complex (GP:13399999) {Homo sapiens}   chr5:13479392-13483281 REVERSE   Aliases: T25C13.80, T25C13_80	6.5	5.9	0.6	1.4	100.0%	-4.1
4832	AT5G47110.1   lil3 protein, putative, similar to Lil3 protein (Arabidopsis thaliana) gi:4741966:gb:AAD28780   chr5:19151215-19152544 REVERSE   Aliases: K14A3.6, K14A3_6	9.0	8.4	0.6	1.4	100.0%	-3.8
4833	AT5G25190.1   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr5:8706793-8707739 REVERSE   Aliases: F21J6.103, F21J6_103	2.9	3.1	-0.2	-1.4	100.0%	-4.4
4834	AT5G11480.1   expressed protein   chr5:3669198-3671575 REVERSE   Aliases: F15N18.70, F15N18_70	8.1	8.6	-0.5	-1.4	100.0%	-3.8
4835	AT4G24370.1   expressed protein   chr4:12611038-12612141 REVERSE   Aliases: T22A6.200, T22A6_200	4.6	4.2	0.5	1.4	100.0%	-3.9
4836	AT4G34265.2   expressed protein   chr4:16402284-16403827 FORWARD   Aliases: None	8.0	7.3	0.8	1.4	100.0%	-3.7
4837	AT2G25170.1   Symbol: PKL   chromatin remodeling factor CHD3 (PICKLE), identical to chromatin remodeling factor CHD3 (Arabidopsis thaliana) GI:6478518   chr2:10721485-10731065 FORWARD   Aliases: CHD3, CHD3 PROTEIN, F13D4.130, F13D4_130, GYM, GYMNOS, PICKLE	7.2	7.8	-0.6	-1.4	100.0%	-4.0
4838	AT5G08580.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:2780513-2783067 REVERSE   Aliases: MAH20.14, MAH20_14	6.5	7.1	-0.6	-1.4	100.0%	-4.0
4839	AT1G17870.1   S2P-like putative metalloprotease, also contain transmembrane helices near their C-termini and many of them, five of seven, contain a conserved zinc-binding motif HEXXH. Homolog of EGY1. Each of the EGY1 and EGY-like proteins share two additional highly conserved motifs, the previously reported NPDG motif (aa 442??454 in EGY1, Rudner et al., 1999) and a newly defined GNLR motif (aa 171??179 in EGY1). The GNLR motif is a novel signature motif unique to EGY1 and EGY-like proteins as well as other EGY1 orthologs found in cyanobacteria.   chr1:6150029-6152215 REVERSE   Aliases: ATEGY3, F2H15.10, F2H15_10	4.8	4.5	0.3	1.4	100.0%	-4.2
4840	AT2G24060.1   translation initiation factor 3 (IF-3) family protein, similar to SP:P33319 Translation initiation factor IF-3 {Proteus vulgaris}; contains Pfam profiles PF00707: Translation initiation factor IF-3, C-terminal domain, PF05198: Translation initiation factor IF-3, N-terminal domain	7.9	8.6	-0.7	-1.4	100.0%	-3.7
4841	AT5G57280.1   expressed protein   chr5:23221696-23223877 FORWARD   Aliases: MJB24.9, MJB24_9	8.2	8.8	-0.5	-1.4	100.0%	-3.8
4842	AT4G15955.1   epoxide hydrolase-related, similar to epoxide hydrolase GI:1109600 from (Arabidopsis thaliana)   chr4:9043727-9045613 REVERSE   Aliases: None	2.5	2.3	0.2	1.4	100.0%	-4.5
4843	AT3G48500.1   Symbol: PDE312	5.1	5.6	-0.5	-1.4	100.0%	-4.0
4844	AT4G30660.1   hydrophobic protein, putative / low temperature and salt responsive protein, putative, similar to SP:Q9ZNQ7 Hydrophobic protein RC12A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}; contains Pfam profile PF01679: Uncharacterized protein family   chr4:14955453-14956069 FORWARD   Aliases: T10C21.10, T10C21_10	9.3	8.9	0.4	1.4	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4845	AT1G61490.1   S-locus protein kinase, putative, similar to KI domain interacting kinase 1 (Zea mays) gi:2735017:gb:AAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954	3.1	3.4	-0.3	-1.4	100.0%	-4.6
4846	AT2G20950.4   expressed protein   chr2:9010220-9013019 FORWARD   Aliases: F26H11.29	6.2	5.3	1.0	1.4	100.0%	-3.6
4847	AT2G22200.1   encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.   chr2:9450208-9451503 REVERSE   Aliases: T26C19.14, T26C19_14	2.8	2.6	0.2	1.4	100.0%	-4.7
4848	AT1G34200.1   oxidoreductase family protein, similar to AX110P (Daucus carota) GI:285739; contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain	4.6	4.3	0.4	1.4	100.0%	-3.9
4849	AT1G30510.3   ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative, strong similarity to SP:P41345 Ferredoxin--NADP reductase, root isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) {Oryza sativa}, ferredoxin-NADP reductase precursor (Zea mays) GI:500751   chr1:10806968-10809144 REVERSE   Aliases: F26G16.13, F26G16_13	9.8	9.3	0.5	1.4	100.0%	-3.9
4850	AT5G40540.1   protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi:1054633:emb:CAA63387   chr5:16254609-16256818 FORWARD   Aliases: MNF13.60, MNF13_60	7.0	6.6	0.4	1.4	100.0%	-3.9
4851	AT4G10050.1   hydrolase, alpha/beta fold family protein, similar to protein phosphatase methylesterase-1 (Homo sapiens) GI:5533003; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:6284447-6287287 REVERSE   Aliases: F28M11.4	9.1	9.7	-0.6	-1.4	100.0%	-3.9
4852	AT2G28510.1   Dof-type zinc finger domain-containing protein, similar to elicitor-responsive Dof protein ERDP GI:6092016 from (Pisum sativum)   chr2:12206175-12207842 REVERSE   Aliases: T17D12.7, T17D12_7	5.2	5.5	-0.3	-1.4	100.0%	-4.4
4853	AT3G16857.2   Symbol: ARR1   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain; similar to ARR1 protein GB:BAA74528 from (Arabidopsis thaliana) (Plant Cell Physiol. (1998) 39 (11), 1232-1239)   chr3:5755930-5759376 FORWARD   Aliases: ARABIDOPSIS RESPONSE REGULATOR 1, MUH15.5	4.4	4.1	0.4	1.4	100.0%	-4.0
4854	AT4G17215.1   expressed protein   chr4:9655848-9656588 FORWARD   Aliases: None	3.5	4.1	-0.5	-1.4	100.0%	-3.8
4855	AT1G21190.1   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to SWISS-PROT:Q9Y4Z1 U6 snRNA-associated Sm-like protein LSm3 (MDS017) (Mouse)   chr1:7419667-7420892 REVERSE   Aliases: F16F4.12, F16F4_12	6.5	6.1	0.5	1.4	100.0%	-3.8
4856	AT3G66652.1   fip1 motif-containing protein, contains Pfam profile PF05182: Fip1 motif	4.6	5.3	-0.7	-1.4	100.0%	-3.9
4857	AT5G24010.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:8113798-8116618 FORWARD   Aliases: MZF18.11, MZF18_11	6.5	6.0	0.5	1.4	100.0%	-3.9
4858	AT2G02960.5   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger); contains PROSITE PS00190: Cytochrome c family heme-binding site signature   chr2:862086-864358 REVERSE   Aliases: T17M13.13, T17M13_13	6.5	6.0	0.5	1.4	100.0%	-3.9
4859	AT5G19310.1   homeotic gene regulator, putative, similar to SP:P25439 Homeotic gene regulator (Brahma protein) {Drosophila melanogaster}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain	4.1	5.6	-1.5	-1.4	100.0%	-3.8
4860	AT1G78580.1   Symbol: ATTPS1	7.2	6.7	0.5	1.4	100.0%	-4.0
4861	AT1G08350.1   endomembrane protein 70 family protein, KNOLLE; similar to putative endosomal protein GB:AAD20090 GI:4406780 from (Arabidopsis thaliana)	4.6	4.8	-0.3	-1.4	100.0%	-4.3
4862	AT4G02940.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to A. thaliana hypothetical protein T13L16.2, GenBank accession number 2708738; contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily   chr4:1306503-1310938 FORWARD   Aliases: T4I9.18, T4I9_18	5.6	5.1	0.5	1.4	100.0%	-3.8
4863	AT4G14150.1   Symbol: PAKRP1	6.1	7.0	-0.9	-1.4	100.0%	-3.8
4864	AT1G17080.1   expressed protein   chr1:5839679-5841559 REVERSE   Aliases: F20D23.22, F20D23_22	9.4	8.8	0.6	1.4	100.0%	-4.0
4865	AT4G15470.1   expressed protein, low similarity to N-methyl-D-aspartate receptor-associated protein (Drosophila melanogaster) GI:567104; contains Pfam profile PF01027: Uncharacterized protein family UPF0005	11.4	10.6	0.8	1.4	100.0%	-4.1
4866	AT3G59650.1   mitochondrial ribosomal protein L51/S25/CI-B8 family protein, low similarity to mitochondrial ribosomal protein bMRP36a (Mus musculus) GI:13559406; contains Pfam profile PF05047: Mitochondrial ribosomal protein L51 / S25 / CI-B8 domain   chr3:22044152-22045134 FORWARD   Aliases: T16L24.200	7.2	7.7	-0.6	-1.4	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4867	AT3G44940.1   expressed protein   chr3:16424319-16426226 REVERSE   Aliases: F14D17.10	3.0	2.8	0.2	1.4	100.0%	-4.6
4868	AT5G51820.1   Symbol: PGM   phosphoglucomutase, chloroplast (PGM) (PGMP) / glucose phosphomutase, identical to SP:Q9SCY0 Phosphoglucomutase, chloroplast precursor (EC 5.4.2.2) (Glucose phosphomutase) (PGM) {Arabidopsis thaliana}   chr5:21080594-21085283 REVERSE   Aliases: ATPGMP, MIO24.4, MIO24_4, PGM1, PHOSPHOGLUCOMUTASE, STARCH FREE 1, STF1	8.1	8.7	-0.6	-1.4	100.0%	-3.7
4869	AT4G12990.1   expressed protein   chr4:7595041-7595445 REVERSE   Aliases: F25G13.80, F25G13_80	6.5	5.5	1.0	1.4	100.0%	-3.8
4870	AT5G51990.1   Symbol: CBF4   encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF4). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to drought stress and abscisic acid treatment, but not to low temperature.   chr5:21134339-21135013 REVERSE   Aliases: CBF4, MSG15.8, MSG15_8	3.4	3.0	0.4	1.4	100.0%	-4.0
4871	AT4G17870.1   expressed protein   chr4:9928691-9929531 FORWARD   Aliases: T6K21.50, T6K21_50	7.6	7.0	0.7	1.4	100.0%	-3.9
4872	AT4G31520.1   SDA1 family protein, contains Pfam profile PF05285: SDA1	3.2	2.9	0.2	1.4	100.0%	-4.6
4873	AT1G65070.1   DNA mismatch repair MutS family protein, contains Pfam profile PF00488: MutS domain V   chr1:24176795-24179907 REVERSE   Aliases: F16G16.7, F16G16_7	4.0	4.5	-0.5	-1.4	100.0%	-3.9
4874	AT4G31400.1   expressed protein   chr4:15237417-15239062 FORWARD   Aliases: F3L17.7	3.3	3.7	-0.4	-1.4	100.0%	-4.1
4875	AT4G19660.1   Symbol: NPR4   ankyrin repeat family protein / BTB/POZ domain-containing protein, contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain   chr4:10696276-10698253 REVERSE   Aliases: NPR1 LIKE PROTEIN 4, T16H5.20, T16H5_20	4.0	4.6	-0.5	-1.4	100.0%	-3.8
4876	AT3G44890.1   Symbol: RPL9   50S ribosomal protein L9, chloroplast (CL9), contains Pfam profile PF03948: Ribosomal protein L9, C-terminal domain; contains Pfam profile PF01281: ribosomal protein L9, N-terminal domain; contains TIGRfam profile TIGR00158: ribosomal protein L9   chr3:16397420-16399451 FORWARD   Aliases: F28D10.80, RP19	6.9	7.6	-0.7	-1.4	100.0%	-3.6
4877	AT3G06750.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:2129629-2130321 REVERSE   Aliases: F3E22.11	5.8	5.4	0.5	1.4	100.0%	-4.0
4878	AT3G21230.1   4-coumarate--CoA ligase, putative / 4-coumaroyl-CoA synthase, putative (4CL), similar to 4CL2 (gi:12229665) and 4CL1 (gi:12229649) from (Arabidopsis thaliana), 4CL1 (gi:12229631) from Nicotiana tabacum   chr3:7448046-7452006 REVERSE   Aliases: MXL8.9	8.1	8.7	-0.6	-1.4	100.0%	-4.0
4879	AT3G27010.1   Symbol: AT TCP20   TCP family transcription factor, putative, similar to PCF2 ((GI:2580440) Oryza sativa)   chr3:9958619-9960135 REVERSE   Aliases: MOJ10.8, PCF1	5.4	5.1	0.3	1.4	100.0%	-4.1
4880	AT5G08540.1   expressed protein, similar to unknown protein (pir::T27191)   chr5:2763824-2766156 FORWARD   Aliases: MAH20.10, MAH20_10	6.9	7.6	-0.7	-1.4	100.0%	-3.8
4881	AT3G58010.1   expressed protein   chr3:21486790-21488475 REVERSE   Aliases: T10K17.220	6.4	6.9	-0.4	-1.4	100.0%	-3.9
4882	AT3G12550.1   XH/XS domain-containing protein / XS zinc finger domain-containing protein, contains Pfam domains PF03469: XH domain, PF03468: XS domain and PF03470: XS zinc finger domain   chr3:3978676-3981379 FORWARD   Aliases: T2E22.14	3.1	3.4	-0.3	-1.4	100.0%	-4.3
4883	AT4G25490.1   Symbol: CBF1   Transcriptional activator that binds to the DRE/CRT regulatory element and induces COR (cold-regulated) gene expression increasing plant freezing tolerance. It encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (CBF1). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. This gene is involved in response to low temperature and abscisic acid.   chr4:13021790-13022735 REVERSE   Aliases: C REPEAT/DRE BINDING FACTOR 1, DREB1B, T30C3.11, TRANSCRIPTIONAL ACTIVATOR CBF1	3.4	3.2	0.3	1.4	100.0%	-4.2
4884	AT3G16240.1   Symbol: DELTA TIP   delta tonoplast integral protein (delta-TIP), identical to delta tonoplast integral protein (delta-TIP) (GI:9279707)(GB:U39485) (Arabidopsis thaliana) (Plant Cell 8 (4), 587-599 (1996))   chr3:5505430-5507056 FORWARD   Aliases: AQP1, ATTIP2;1, DELTA TIP1, MYA6.10, MYA6_10, TIP2;1	5.9	6.4	-0.4	-1.4	100.0%	-4.0
4885	AT1G26130.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Homo sapiens (SP:Q9Y2Q0, SP:O43520), Mus musculus (SP:P98200, SP:P70704), {Bos taurus} SP:Q29449; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:9033587-9038233 FORWARD   Aliases: F28B23.19, F28B23_19	3.2	3.5	-0.2	-1.4	100.0%	-4.4
4886	AT1G20330.1   Symbol: SMT2   S-adenosyl-methionine-sterol-C-methyltransferase, identical to sterol-C-methyltransferase GI:1061040 from (Arabidopsis thaliana)	7.4	6.6	0.8	1.4	100.0%	-3.8
4887	AT1G01600.1   Symbol: CYP86A4   cytochrome P450, putative, similar to cytochrome P450 GI:10442763 from (Triticum aestivum)   chr1:219131-221286 FORWARD   Aliases: F22L4.14, F22L4_14	5.0	4.6	0.4	1.4	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4888	AT5G24600.1   expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599   chr5:8421632-8423483 REVERSE   Aliases: K18P6.13, K18P6_13	5.0	4.5	0.5	1.4	100.0%	-3.8
4889	AT4G19400.1   expressed protein   chr4:10580838-10582000 REVERSE   Aliases: T5K18.180, T5K18_180	7.5	7.9	-0.4	-1.4	100.0%	-4.1
4890	AT1G61430.1   S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida) gi:836954:gb:AAC23542; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22668334-22672025 REVERSE   Aliases: T1F9.8, T1F9_8	2.8	2.9	-0.2	-1.4	100.0%	-5.0
4891	AT1G77630.1   peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	3.1	3.5	-0.4	-1.4	100.0%	-4.1
4892	AT1G29220.1   transcriptional regulator family protein, similar to Transcriptional regulator protein HCNGP (Swiss-Prot:Q02614) (Mus musculus)   chr1:10210506-10212679 REVERSE   Aliases: F28N24.10, F28N24_10	6.6	6.2	0.4	1.4	100.0%	-3.9
4893	AT5G41770.1   crooked neck protein, putative / cell cycle protein, putative, similar to Swiss-Prot:P17886 crooked neck protein (Drosophila melanogaster)   chr5:16735224-16738450 FORWARD   Aliases: K16L22.5, K16L22_5	5.9	6.6	-0.7	-1.4	100.0%	-3.9
4894	AT2G17880.1   DNAJ heat shock protein, putative, similar to J11 protein (Arabidopsis thaliana) GI:9843641; contains Pfam profile PF00226 DnaJ domain   chr2:7774047-7775013 REVERSE   Aliases: T13L16.10, T13L16_10	2.6	2.4	0.2	1.4	100.0%	-4.5
4895	AT1G27300.1   expressed protein   chr1:9483250-9484576 FORWARD   Aliases: F17L21.9, F17L21_9	7.1	6.7	0.4	1.4	100.0%	-3.8
4896	AT5G66060.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Rattus norvegicus (GI:474940), Mus musculus (SP:Q60715), Homo sapiens (GI:18073925); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr5:26436707-26438156 FORWARD   Aliases: K2A18.14, K2A18_14	3.7	3.3	0.4	1.4	100.0%	-4.1
4897	AT2G39980.1   transferase family protein, contains Pfam profile PF02458 transferase family   chr2:16695379-16697034 REVERSE   Aliases: T28M21.14, T28M21_14	6.2	5.4	0.9	1.4	100.0%	-3.9
4898	AT1G67490.2   Symbol: GCS1   similar to alpha-glucosidase, putative [Arabidopsis thaliana] (TAIR:At1g24320.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG11506.1); contains InterPro domain Glycoside hydrolase, family 63 (InterPro:IPR004888)   chr1:25284114-25290274 REVERSE   Aliases: GLUCOSIDASE 1, KNF, KNOPF, T1F15.4, T1F15_4	5.4	5.8	-0.4	-1.4	100.0%	-4.2
4899	AT3G25620.1   ABC transporter family protein, similar to GB:AAC61893 from (Bactrocera tryoni) (Insect Mol. Biol. 6 (4), 343-356 (1997))   chr3:9317311-9320805 REVERSE   Aliases: T5M7.11	4.5	4.9	-0.4	-1.4	100.0%	-3.8
4900	AT5G02450.1   60S ribosomal protein L36 (RPL36C), 60S ribosomal protein L36, Arabidopsis thaliana, EMBL:AC004684   chr5:533119-534635 FORWARD   Aliases: T22P11.40, T22P11_40	11.0	11.3	-0.4	-1.4	100.0%	-4.4
4901	AT1G27090.1   glycine-rich protein   chr1:9403898-9406243 REVERSE   Aliases: T7N9.15, T7N9_15	5.7	5.1	0.6	1.4	100.0%	-3.8
4902	AT5G24300.1   starch synthase, putative, similar to starch synthase I-1 GI:9369334 from (Triticum aestivum)   chr5:8266802-8271199 FORWARD   Aliases: MOP9.12, MOP9_12	9.2	8.5	0.7	1.4	100.0%	-3.7
4903	AT5G60220.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr5:24266183-24267291 FORWARD   Aliases: F15L12.11, F15L12_11	3.2	3.0	0.3	1.4	100.0%	-4.3
4904	AT3G05327.1   similar to cyclin family protein [Arabidopsis thaliana] (TAIR:At3g21870.1); similar to PREG-like protein [Picea mariana] (GB:AAC32127.1); contains InterPro domain Cyclin, N-terminal domain (InterPro:IPR006671)   chr3:1517587-1518405 REVERSE   Aliases: None	2.6	2.4	0.2	1.4	100.0%	-4.4
4905	AT2G04370.1   hypothetical protein   chr2:1523760-1524118 REVERSE   Aliases: T23O15.2	2.4	2.6	-0.2	-1.4	100.0%	-5.1
4906	AT3G43150.1   hypothetical protein   chr3:15154683-15155333 FORWARD   Aliases: T6L19.10	2.4	2.2	0.2	1.4	100.0%	-4.6
4907	AT1G29080.1   peptidase C1A papain family protein, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas); contains Pfam profile PF00112: Papain family cysteine protease   chr1:10157480-10158660 REVERSE   Aliases: F28N24.27, F28N24_27	2.3	2.1	0.2	1.4	100.0%	-4.7
4908	AT2G46650.1   Symbol: B5 #1   cytochrome b5, putative, similar to cytochrome b5 GI:2695711 from (Olea europaea)   chr2:19158723-19159663 FORWARD   Aliases: T3A4.3, T3A4_3	5.0	4.0	1.0	1.4	100.0%	-3.6
4909	AT1G63130.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23416395-23418814 FORWARD   Aliases: F16M19.5, F16M19_5	6.5	7.0	-0.6	-1.4	100.0%	-3.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4910	AT2G19180.1   expressed protein   chr2:8331798-8333040 FORWARD   Aliases: T20K24.20, T20K24_20	2.7	2.5	0.2	1.4	100.0%	-4.5
4911	AT5G16880.3   VHS domain-containing protein / GAT domain-containing protein, weak similarity to hepatocyte growth factor-regulated tyrosine kinase substrate (Homo sapiens) GI:2731383; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain   chr5:5548993-5551466 FORWARD   Aliases: F2K13.30, F2K13_30	8.0	7.3	0.7	1.4	100.0%	-3.9
4912	AT5G22540.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr5:7481497-7482902 REVERSE   Aliases: MQJ16.8, MQJ16_8	2.9	3.1	-0.3	-1.4	100.0%	-4.3
4913	AT3G15040.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr3:5064711-5066697 REVERSE   Aliases: K15M2.18	6.1	5.8	0.3	1.4	100.0%	-4.0
4914	AT4G02640.2   Symbol: BZO2H1	7.0	6.3	0.7	1.4	100.0%	-3.8
4915	AT5G66040.2   senescence-associated family protein, almost identical to ketoconazole resistant protein GI:928938 from (Arabidopsis thaliana) full-length cDNA: Ceres:101608.   chr5:26427756-26428553 FORWARD   Aliases: K2A18.11, K2A18_11	6.8	6.2	0.6	1.4	100.0%	-3.7
4916	AT4G18050.1   ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter; similar to multidrug-resistant protein CjMDR1 GI:14715462 from (Coptis japonica)	2.8	2.6	0.3	1.4	100.0%	-4.3
4917	AT4G33310.1   expressed protein   chr4:16056160-16056420 FORWARD   Aliases: F17M5.70, F17M5_70	4.7	4.3	0.5	1.4	100.0%	-3.9
4918	AT3G46430.1   expressed protein   chr3:17098672-17099482 FORWARD   Aliases: F18L15.150, F18L15_150	10.1	10.6	-0.5	-1.4	100.0%	-4.2
4919	AT5G25450.1   ubiquinol-cytochrome C reductase complex 14 kDa protein, putative, similar to SP:P48502 Ubiquinol-cytochrome C reductase complex 14 kDa protein (EC 1.10.2.2) (CR14) {Solanum tuberosum}; contains Pfam profile PF02271: Ubiquinol-cytochrome C reductase complex 14kD subunit   chr5:8857039-8858479 FORWARD   Aliases: F18G18.190, F18G18_190	7.8	7.3	0.6	1.4	100.0%	-3.8
4920	AT5G20885.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:7083968-7084736 REVERSE   Aliases: None	5.8	5.3	0.5	1.4	100.0%	-4.2
4921	AT1G22690.1   gibberellin-responsive protein, putative, similar to SP:P46688 Gibberellin-regulated protein 2 precursor {Arabidopsis thaliana}; contains Pfam profile PF02704: Gibberellin regulated protein   chr1:8027294-8028114 FORWARD   Aliases: T22J18.14, T22J18_14	2.6	2.4	0.1	1.4	100.0%	-5.0
4922	AT1G26110.1   expressed protein   chr1:9024332-9027745 REVERSE   Aliases: F14G11.8, F14G11_8	8.8	7.8	0.9	1.4	100.0%	-3.8
4923	AT1G76540.1   Symbol: CDKB2;1   cell division control protein, putative, similar to SWISS-PROT:Q38775, cell division control protein 2 homolog D (Antirrhinum majus); contains protein kinase domain, Pfam:PF00069   chr1:28725222-28727415 REVERSE   Aliases: CDKB2;1, Cyclin dependent kinase B2;1, F14G6.14, F14G6_14	4.3	4.8	-0.6	-1.4	100.0%	-4.0
4924	AT1G52220.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g46820.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_478022.1)   chr1:19457238-19458366 REVERSE   Aliases: F9I5.10, F9I5_10	6.5	5.9	0.7	1.4	100.0%	-3.5
4925	AT1G07790.1   histone H2B, putative, strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP:O22582, Lycopersicon esculentum GI:3021489, Capsicum annuum SP:O49118; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:2412977-2413705 FORWARD   Aliases: F24B9.10, F24B9_10	6.6	7.4	-0.8	-1.4	100.0%	-3.6
4926	AT5G53760.2   Symbol: MLO11   similar to seven transmembrane MLO family protein / MLO-like protein 14 (MLO14) [Arabidopsis thaliana] (TAIR:At1g26700.1); similar to seven transmembrane protein Mlo9 [Zea mays] (GB:AAK38345.1); contains InterPro domain Mlo-related protein (InterPro:IPR004326)   chr5:21839760-21843677 FORWARD   Aliases: MGN6.12, MGN6_12	5.8	6.3	-0.5	-1.4	100.0%	-3.8
4927	AT4G05090.1   inositol monophosphatase family protein, low similarity to SP:Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) (DPNPase) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family   chr4:2609140-2611735 FORWARD   Aliases: C17L7.10, C17L7_10	5.7	5.5	0.3	1.4	100.0%	-4.4
4928	AT3G17930.1   expressed protein   chr3:6141834-6143316 REVERSE   Aliases: MEB5.15	8.9	8.3	0.5	1.4	100.0%	-3.7
4929	AT1G67140.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g22795.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD45833.1)   chr1:25104571-25121035 REVERSE   Aliases: F5A8.12, F5A8_12	3.5	4.1	-0.6	-1.4	100.0%	-3.9
4930	AT5G17370.1   WD-40 repeat family protein, contains 1 significant, 2 weak WD-40 repeats (PF00400); similar to transducin beta-like 1 protein.(SP:O60907) (Homo sapiens)   chr5:5721803-5724721 REVERSE   Aliases: MKP11.21, MKP11_21	3.7	4.0	-0.3	-1.4	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4931	AT1G13950.1   Symbol: EIF 5A	6.2	5.6	0.6	1.4	100.0%	-4.0
4932	AT1G53645.1   hydroxyproline-rich glycoprotein family protein   chr1:20029841-20032303 REVERSE   Aliases: None	7.0	7.5	-0.5	-1.3	100.0%	-3.8
4933	AT1G64170.1   Symbol: ATCHX16   cation/hydrogen exchanger, putative (CHX16), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr1:23818839-23821956 REVERSE   Aliases: CHX16, F22C12.7, F22C12_7	4.1	4.5	-0.4	-1.3	100.0%	-4.0
4934	AT5G20720.2   Symbol: CPN20   20 kDa chaperonin, chloroplast (CPN21) (CHCPN10) (CPN20), identical to chloroplast 20 kDa chaperonin, chloroplast precursor (Protein Cpn21), chloroplast protein Cpn10, chloroplast chaperonin 10 (Ch-CPN10), SP:O65282 from (Arabidopsis thaliana); identical to cDNA chaperonin 20 GI:14587372   chr5:7014688-7016476 FORWARD   Aliases: ATCPN21, CHAPERONIN 10, CHAPERONIN 20, CHCPN10, CHLOROPLAST CHAPERONIN 10, CPN10, CPN21, T1M15.120, T1M15_120	11.1	11.6	-0.5	-1.3	100.0%	-4.0
4935	AT5G11210.1   Symbol: ATGLR2.5   glutamate receptor family protein (GLR2.5), plant glutamate receptor family, PMID:11379626   chr5:3571215-3574538 REVERSE   Aliases: F2I11.100, F2I11_100, GLR2.5	2.3	2.5	-0.2	-1.3	100.0%	-4.8
4936	AT5G05390.1   laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)   chr5:1594754-1597043 FORWARD   Aliases: K18I23.20, K18I23_20	3.3	3.5	-0.2	-1.3	100.0%	-4.4
4937	AT5G59000.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) ;contains PROSITE PS00190: Cytochrome c family heme-binding site signature   chr5:23835980-23837463 FORWARD   Aliases: K19M22.19, K19M22_19	5.3	4.8	0.5	1.3	100.0%	-3.7
4938	AT1G62770.1   invertase/pectin methylesterase inhibitor family protein, similar to pectinesterase from Arabidopsis thaliana SP:Q42534, Lycopersicon esculentum SP:Q43143, Phaseolus vulgaris SP:Q43111; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	3.6	3.8	-0.2	-1.3	100.0%	-4.7
4939	AT2G40540.1   Symbol: KT2   potassium transporter, putative (KT2), identical to putative potassium transporter AtKT2p (Arabidopsis thaliana) gi:2384671:gb:AAC49845, strong similarity to potassium transporter HAK2p (Mesembryanthemum crystallinum) GI:14091471; KUP/HAK/KT Transporter family member, PMID:11500563   chr2:16937942-16941666 FORWARD   Aliases: ATK2, ATK2P, ATKUP2, KUP2, POTASSIUM TRANSPORTER 2, SHY3, T2P4.11, T2P4_11, TRK2	4.9	5.2	-0.4	-1.3	100.0%	-4.2
4940	AT1G29860.1   Symbol: WRKY71	3.0	3.3	-0.3	-1.3	100.0%	-4.2
4941	AT5G42540.1   Symbol: XRN2   5'-3' exoribonuclease (XRN2), identical to XRN2 (Arabidopsis thaliana) GI:11875630; contains Pfam domain PF03159: Putative 5'-3' exonuclease domain   chr5:17024661-17032029 FORWARD   Aliases: EXORIBONUCLEASE 2, K16E1.2, K16E1_2	5.4	6.1	-0.7	-1.3	100.0%	-3.9
4942	AT3G56910.1   expressed protein   chr3:21080395-21081312 REVERSE   Aliases: T8M16.240	9.3	9.7	-0.4	-1.3	100.0%	-4.1
4943	AT1G64230.2   similar to ubiquitin-conjugating enzyme E2-17 kDa 9 (UBC9) [Arabidopsis thaliana] (TAIR:At4g27960.1); similar to ubiquitin-conjugating enzyme E2-17 kDa 9 (UBC9) [Arabidopsis thaliana] (TAIR:At4g27960.2); similar to ubiquitin-conjugating enzyme OsUBC5b [Oryza sativa (japonica cultivar-group)] (GB:XP_464900.1); similar to ubiquitin-conjugating enzyme E2 [Gossypium raimondii] (GB:AAL99225.1); similar to ubiquitin-conjugating enzyme 8 [Capsicum annuum] (GB:AAR83891.1); similar to ubiquitin carrier protein (GB:AAA34125.1); contains InterPro domain Ubiquitin-conjugating enzymes (InterPro:IPR000608)   chr1:23837231-23839199 FORWARD   Aliases: F22C12.2, F22C12_2	11.9	11.5	0.4	1.3	100.0%	-4.5
4944	AT5G15470.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr5:5021013-5024745 REVERSE   Aliases: T20K14.80, T20K14_80	3.0	3.3	-0.4	-1.3	100.0%	-4.1
4945	AT3G25520.1   Symbol: ATL5   60S ribosomal protein L5, similar to 60S ribosomal protein L5 GB:P49625 from (Oryza sativa)   chr3:9270524-9272626 REVERSE   Aliases: A. THALIANA RIBOSOMAL PROTEIN L5, MWL2.17, RIBOSOMAL PROTEIN L5	9.6	10.5	-0.9	-1.3	100.0%	-3.7
4946	AT5G22280.1   expressed protein   chr5:7373998-7375722 REVERSE   Aliases: T6G21.7	5.8	6.5	-0.7	-1.3	100.0%	-3.7
4947	AT5G66210.2   Symbol: CPK28   calcium-dependent protein kinase family protein / CDPK family protein, contains Pfam domains, PF00069: Protein kinase domain and PF00036: EF hand   chr5:26473517-26476696 REVERSE   Aliases: K2A18.29, K2A18_29	4.8	4.4	0.5	1.3	100.0%	-4.0
4948	AT5G15540.1   expressed protein, low similarity to DNA repair and meiosis protein Rad9 (Coprinus cinereus) GI:1353390, SP:Q09725 Sister chromatid cohesion protein mis4 {Schizosaccharomyces pombe}   chr5:5047676-5057414 REVERSE   Aliases: T20K14.150, T20K14_150	3.6	4.0	-0.4	-1.3	100.0%	-4.2
4949	AT3G21210.1   similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At1g34480.1); similar to universal stress protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD53290.1); contains InterPro domain Zn-finger-like, PHD finger (InterPro:IPR001965); contains InterPro domain Usp domain (InterPro:IPR006016); contains InterPro domain DC1 domain (InterPro:IPR004146)   chr3:7437593-7440832 REVERSE   Aliases: MXL8.6	2.3	2.5	-0.2	-1.3	100.0%	-4.6
4950	AT4G12220.1   expressed protein   chr4:7283242-7283733 REVERSE   Aliases: T4C9.60, T4C9_60	2.4	2.2	0.2	1.3	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4951	AT5G44870.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18131893-18135835 FORWARD   Aliases: K21C13.4, K21C13_4	3.0	2.9	0.2	1.3	100.0%	-4.7
4952	AT5G04560.1   Symbol: DME   DEMETER protein (DME), identical to DEMETER protein (Arabidopsis thaliana) GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein   chr5:1309194-1318387 FORWARD   Aliases: AT5G04570, AT5G04580, DEMETER, DME1, T32M21.160, T32M21_160	3.9	4.2	-0.3	-1.3	100.0%	-4.5
4953	AT5G49590.1   hypothetical protein, similar to unknown protein (pir::T02348)   chr5:20145962-20146780 FORWARD   Aliases: K6M13.15, K6M13_15	2.9	3.1	-0.2	-1.3	100.0%	-5.1
4954	AT1G56610.2   similar to F-box family protein [Arabidopsis thaliana] (TAIR:At4g14096.1); contains InterPro domain FBD (InterPro:IPR006566)   chr1:21215620-21218227 FORWARD   Aliases: F25P12.94, F25P12_94	4.0	4.4	-0.4	-1.3	100.0%	-4.0
4955	AT4G11300.1   expressed protein   chr4:6872182-6873537 REVERSE   Aliases: F8L21.90, F8L21_90	4.5	4.0	0.6	1.3	100.0%	-3.8
4956	AT3G05000.1   transport protein particle (TRAPP) component Bet3 family protein, similar to Transport protein particle 33 kDa subunit (TRAPP 33 kDa subunit) (Swiss-Prot:Q99394) (Saccharomyces cerevisiae); contains Pfam profile PF04051: Transport protein particle (TRAPP) component, Bet3   chr3:1387181-1388741 REVERSE   Aliases: T9J14.5, T9J14_5	7.0	6.4	0.6	1.3	100.0%	-3.9
4957	AT5G60260.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr5:24272660-24273511 REVERSE   Aliases: F15L12.14, F15L12_14	3.1	2.9	0.3	1.3	100.0%	-4.5
4958	AT5G62740.1   band 7 family protein, strong similarity to hypersensitive-induced response protein (Zea mays) GI:7716470; contains Pfam profile PF01145: SPFH domain / Band 7 family; supporting cDNA gi:17065547:gb:AY062850.1   chr5:25218173-25219982 FORWARD   Aliases: MQB2.40, MQB2_40	8.1	7.4	0.7	1.3	100.0%	-4.0
4959	AT2G39810.1   Symbol: HOS1   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_469639.1); contains domain CYS_RICH (PS50311)   chr2:16619883-16625135 FORWARD   Aliases: T5I7.11, T5I7_11	4.0	4.4	-0.3	-1.3	100.0%	-4.2
4960	AT5G07280.1   Symbol: EMS1   leucine-rich repeat protein kinase, putative / extra sporogenous cells (ESP), identical to extra sporogenous cells (Arabidopsis thaliana) gi:23304947:emb:CAD42912; contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:2285041-2288687 FORWARD   Aliases: EXCESS MICROSPOROCTES1, EXS, EXTRA SPOROGENOUS CELL, T28J14.220, T28J14_220	2.8	3.2	-0.4	-1.3	100.0%	-4.2
4961	AT1G54440.1   similar to 3'-5' exonuclease domain-containing protein / helicase and RNase D C-terminal domain-containing protein / HRDC domain-containing protein [Arabidopsis thaliana] (TAIR:At5g35910.1); similar to Putative nucleolar protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470252.1); contains InterPro domain HRDC domain (InterPro:IPR002121); contains InterPro domain 3'-5' exonuclease (InterPro:IPR002562)   chr1:20326715-20331736 FORWARD   Aliases: F20D21.26, F20D21_26	5.6	6.1	-0.5	-1.3	100.0%	-4.1
4962	AT1G63780.1   Symbol: IMP4   brix domain-containing protein, contains Pfam domain, PF04427: Brix domain   chr1:23668536-23671015 REVERSE   Aliases: F24D7.3	6.4	6.8	-0.3	-1.3	100.0%	-4.1
4963	AT1G60420.1   DC1 domain-containing protein, contains Pfam domain PF03107: DC1 domain   chr1:22265573-22268324 FORWARD   Aliases: T13D8.29, T13D8_29	9.0	9.6	-0.6	-1.3	100.0%	-4.2
4964	AT3G02720.1   DJ-1 family protein / protease-related, similar to Intracellular Protease (Pyrococcus horikoshii) GI:11513902; contains Pfam profile: PF01965 Thij/Pfpl family   chr3:586270-588270 FORWARD   Aliases: F16B3.36	8.1	7.8	0.3	1.3	100.0%	-4.2
4965	AT2G04740.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:1657118-1659669 FORWARD   Aliases: F28I8.22, F28I8_22	5.3	5.7	-0.4	-1.3	100.0%	-4.0
4966	AT3G51630.1   Symbol: WNK5   protein kinase family protein, contains Pfam profile: PF00069 protein kinase domain   chr3:19159886-19163172 FORWARD   Aliases: T18N14.10, ZIK1	6.7	6.4	0.3	1.3	100.0%	-4.1
4967	AT5G20120.1   expressed protein   chr5:6795891-6797155 FORWARD   Aliases: F5O24.10, F5O24_10	5.6	5.1	0.4	1.3	100.0%	-3.9
4968	AT1G61460.1   S-locus protein kinase, putative, contains similarity to KI domain interacting kinase 1 (Zea mays) gi:2735017:gb:AAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22677863-22681378 REVERSE   Aliases: T1F9.5, T1F9_5	3.6	3.9	-0.3	-1.3	100.0%	-4.4
4969	AT3G46000.1   Symbol: ADF2   actin-depolymerizing factor, putative (ADF2), strong similarity to SP:Q9ZSK3 Actin-depolymerizing factor 4 (ADF-4) (AtADF4) {Arabidopsis thaliana}; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein   chr3:16918466-16919980 REVERSE   Aliases: ACTIN DEPOLYMERIZING FACTOR 2, F16L2.210	10.6	10.1	0.6	1.3	100.0%	-4.3
4970	AT5G47930.1   40S ribosomal protein S27 (RPS27D)   chr5:19423403-19424624 REVERSE   Aliases: K16F13.2, K16F13_2	11.9	12.3	-0.4	-1.3	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4971	AT3G22620.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:8008541-8010024 FORWARD   Aliases: F16J14.17	3.3	4.0	-0.7	-1.3	100.0%	-3.6
4972	AT5G63450.1   Symbol: CYP94B1   cytochrome P450, putative   chr5:25426121-25427799 REVERSE   Aliases: MLE2.8, MLE2_8	3.9	3.6	0.2	1.3	100.0%	-4.6
4973	AT5G06550.1   similar to transcription factor jumonji (jmiC) domain-containing protein [Arabidopsis thaliana] (TAIR:At1g78280.1); similar to hypothetical protein [Neurospora crassa] (GB:XP_327705.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Transcription factor jumonji, jmiC (InterPro:IPR003347)   chr5:2001147-2003076 REVERSE   Aliases: F15M7.8, F15M7_8	4.5	4.9	-0.3	-1.3	100.0%	-4.0
4974	AT2G23530.1   expressed protein, ; expression supported by MPSS   chr2:10027732-10029875 REVERSE   Aliases: F26B6.18, F26B6_18	7.4	6.8	0.6	1.3	100.0%	-3.7
4975	AT1G28960.5   similar to MutT/nudix family protein [Arabidopsis thaliana] (TAIR:At2g33980.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_476134.1); contains InterPro domain NUDIX hydrolase (InterPro:IPR000086)   chr1:10109580-10111646 REVERSE   Aliases: F1K23.5, F1K23_5	6.8	6.3	0.5	1.3	100.0%	-3.9
4976	AT5G23390.1   expressed protein, contains Pfam profile: PF04842 plant protein of unknown function (DUF639)   chr5:7870516-7874508 REVERSE   Aliases: T32G24.2, T32G24_2	5.5	6.3	-0.8	-1.3	100.0%	-3.9
4977	AT4G31615.1   transcriptional factor B3 family protein, low similarity to reproductive meristem gene 1 from (Brassica oleracea var. botrytis) GI:3170424, (Arabidopsis thaliana) GI:13604227; contains Pfam profile PF02362: B3 DNA binding domain   chr4:15320403-15322200 REVERSE   Aliases: None	2.4	2.3	0.1	1.3	100.0%	-5.2
4978	AT4G23410.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr4:12223963-12225235 FORWARD   Aliases: F16G20.110, F16G20_110	3.8	3.3	0.5	1.3	100.0%	-3.7
4979	AT1G79690.1   MutT/nudix family protein, contains Pfam NUDIX domain (PF00293); very low similarity to Chain A and Chain B of Escherichia coli isopentenyl diphosphate:dimethylallyl diphosphate isomerase (gi:15826361) (gi:15826360)   chr1:29990223-29996035 FORWARD   Aliases: F20B17.11, F20B17_11	9.5	9.8	-0.3	-1.3	100.0%	-4.4
4980	AT5G04160.1   phosphate translocator-related, low similarity to SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275   chr5:1142783-1144913 REVERSE   Aliases: F21E1.80, F21E1_80	4.6	5.1	-0.5	-1.3	100.0%	-4.0
4981	AT3G54060.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g37960.1)   chr3:20029639-20031904 REVERSE   Aliases: F24B22.20	2.2	2.3	-0.1	-1.3	100.0%	-4.9
4982	AT4G01030.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:448336-449838 REVERSE   Aliases: F3I3.50, F3I3_50	3.3	3.1	0.2	1.3	100.0%	-4.7
4983	AT5G23290.1   c-myc binding protein, putative / prefoldin, putative, similar to Swiss-Prot:Q99471 prefoldin subunit 5 (C-myc binding protein Mm-1) (Myc modulator 1) (Homo sapiens)   chr5:7846084-7847626 FORWARD   Aliases: MKD15.15, MKD15_15	7.0	6.5	0.6	1.3	100.0%	-3.7
4984	AT1G33390.1   helicase domain-containing protein, similar to kurz protein (Drosophila melanogaster) GI:5869803; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr1:12099462-12104088 REVERSE   Aliases: F10C21.6	4.7	4.9	-0.3	-1.3	100.0%	-4.3
4985	AT5G38780.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292), caffeine synthase (Camellia sinensis)(GI:9967143), SAM:benzoic acid carboxyl methyltransferase (Antirrhinum majus)(GI:9789277)   chr5:15547245-15548752 FORWARD   Aliases: MKD10.80, MKD10_80	2.7	2.5	0.2	1.3	100.0%	-4.8
4986	AT3G46540.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Chain A Of The Epsin N-Terminal Homology (Enth) Domain (GI:8569264) (Rattus Norvegicus); similar to Af10-protein (GI:1724114) (Avena fatua)   chr3:17145076-17146572 REVERSE   Aliases: F12A12.60	4.8	5.4	-0.6	-1.3	100.0%	-4.1
4987	AT1G12270.1   stress-inducible protein, putative, similar to sti (stress inducible protein) (Glycine max) GI:872116; contains Pfam profile PF00515 TPR Domain   chr1:4172073-4174773 FORWARD   Aliases: F5O11.2, F5O11_2	6.0	7.0	-1.0	-1.3	100.0%	-4.0
4988	AT2G28320.1   pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein, contains Pfam profiles PF01852: START domain, PF00169: PH domain   chr2:12101823-12106721 FORWARD   Aliases: T1B3.16, T1B3_16	6.3	6.7	-0.4	-1.3	100.0%	-4.1
4989	AT3G25730.1   AP2 domain-containing transcription factor, putative, contains Pfam profile: PF00847 AP2 domain; similar to RAV1 (DNA-binding protein) GB:BAA34250 (Arabidopsis thaliana) (Nucleic Acids Res. 27 (2), 470-478 (1999))   chr3:9397657-9398896 FORWARD   Aliases: K13N2.14	8.0	7.6	0.3	1.3	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
4990	AT4G14690.1   Symbol: ELIP2   chlorophyll A-B binding family protein / early light-induced protein, putative, strong similarity to early light-induced protein; ELIP (Arabidopsis thaliana) GI:1872544; contains Pfam profile: PF00504 chlorophyll A-B binding protein   chr4:8418278-8419258 FORWARD   Aliases: DL3385W, EARLY LIGHT INDUCIBLE PROTEIN 2, FCAALL.232	8.2	8.8	-0.6	-1.3	100.0%	-3.5
4991	AT3G54400.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr3:20151036-20153620 REVERSE   Aliases: T14E10.1	6.8	5.9	0.9	1.3	100.0%	-3.7
4992	AT5G12900.1   expressed protein   chr5:4071922-4074622 REVERSE   Aliases: T24H18.70, T24H18_70	3.8	4.1	-0.3	-1.3	100.0%	-4.3
4993	AT1G11730.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr1:3957473-3960113 FORWARD   Aliases: F25C20.12, F25C20_12	3.6	4.0	-0.4	-1.3	100.0%	-4.1
4994	AT1G07020.1   expressed protein   chr1:2154900-2156007 REVERSE   Aliases: F10K1.34, F10K1_34	6.0	6.4	-0.4	-1.3	100.0%	-4.0
4995	AT5G10700.1   expressed protein   chr5:3378054-3378868 REVERSE   Aliases: MAJ23.60, MAJ23_60	5.4	5.0	0.4	1.3	100.0%	-3.8
4996	AT1G35680.1   50S ribosomal protein L21, chloroplast / CL21 (RPL21), identical to 50S ribosomal protein L21, chloroplast precursor (CL21) (Arabidopsis thaliana) SWISS-PROT:P51412   chr1:13209965-13211630 FORWARD   Aliases: F15O4.7	7.9	8.6	-0.7	-1.3	100.0%	-3.6
4997	AT2G18520.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr2:8040964-8042445 REVERSE   Aliases: F24H14.13, F24H14_13	3.5	3.8	-0.3	-1.3	100.0%	-4.3
4998	AT3G26110.1   expressed protein   chr3:9542720-9543351 FORWARD   Aliases: MPE11.5	3.5	3.3	0.2	1.3	100.0%	-4.6
4999	AT2G07740.1   zinc knuckle (CCHC-type) family protein, similar to zinc finger protein GB:AAA75253; some members of this protein family have a weak CCHC zinc fingers that is mostly from retroviral gag proteins (nucleocapsid)   chr2:3570258-3571570 REVERSE   Aliases: T12J2.6	3.4	3.0	0.4	1.3	100.0%	-4.4
5000	AT1G31550.2   similar to lipase, putative [Arabidopsis thaliana] (TAIR:At1g28600.1); similar to lipase-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_917247.1); contains InterPro domain Lipolytic enzyme, G-D-S-L family (InterPro:IPR001087)   chr1:11295506-11297266 REVERSE   Aliases: T8E3.19, T8E3_19	3.7	3.4	0.3	1.3	100.0%	-4.3
5001	AT3G30460.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:12106895-12107355 FORWARD   Aliases: MSJ3.9	3.6	3.2	0.3	1.3	100.0%	-4.2
5002	AT2G22740.2   Symbol: SUVH6   SET domain-containing protein (SUVH6), identical to SUVH6 (Arabidopsis thaliana) GI:13517753; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain   chr2:9669718-9674061 REVERSE   Aliases: T9I22.18, T9I22_18	6.7	7.0	-0.4	-1.3	100.0%	-4.1
5003	AT1G66330.2   senescence-associated family protein, similar to senescence-associated protein (GI:12836895) (Ipomoea batatas)   chr1:24733292-24736125 REVERSE   Aliases: T27F4.8, T27F4_8	6.1	5.5	0.7	1.3	100.0%	-3.9
5004	AT4G35750.1   Rho-GTPase-activating protein-related, contains weak similarity to Rho-GTPase-activating protein 1 (GTPase-activating protein rhoOGAP) (Rho-related small GTPase protein activator) (CDC42 GTPase-activating protein) (p50-rhoGAP) (Swiss-Prot:Q07960) (Homo sapiens)   chr4:16940512-16941867 REVERSE   Aliases: F4B14.4	6.2	5.0	1.2	1.3	100.0%	-3.6
5005	AT5G42670.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr5:17125490-17127463 FORWARD   Aliases: MJB21.4, MJB21_4	6.0	6.6	-0.6	-1.3	100.0%	-3.8
5006	AT2G16760.1   expressed protein   chr2:7282783-7284314 FORWARD   Aliases: T24I21.17, T24I21_17	4.7	5.0	-0.3	-1.3	100.0%	-4.0
5007	AT4G19550.1   expressed protein   chr4:10659391-10661109 REVERSE   Aliases: F24J7.110, F24J7_110	3.9	3.4	0.4	1.3	100.0%	-4.1
5008	AT1G06550.1   enoyl-CoA hydratase/isomerase family protein, similar to CHY1 (gi:8572760); contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein   chr1:2003653-2006563 REVERSE   Aliases: F12K11.12, F12K11_12	7.8	9.0	-1.2	-1.3	100.0%	-3.9
5009	AT1G75050.1   thaumatin-like protein, putative / pathogenesis-related protein, putative, similar to thaumatin-like protein (Arabidopsis thaliana) GI:2435406, SP:P28493 Pathogenesis-related protein 5 precursor (PR-5) {Arabidopsis thaliana}; contains Pfam profile: PF00314 Thaumatin family   chr1:28183749-28184766 FORWARD   Aliases: F9E10.10, F9E10_10	3.6	3.8	-0.3	-1.3	100.0%	-4.3
5010	AT2G22650.1   FAD-dependent oxidoreductase family protein   chr2:9631702-9634041 REVERSE   Aliases: T9I22.9, T9I22_9	5.5	5.9	-0.4	-1.3	100.0%	-4.2
5011	AT5G23140.1   Symbol: CLPP2   ATP-dependent Clp protease proteolytic subunit, putative, nClpP2/nClpP7; similar to SP:Q9X6W8 ATP-dependent Clp protease proteolytic subunit (EC 3.4.21.92) (Endopeptidase Clp) from (Azospirillum brasilense)   chr5:7783761-7785500 FORWARD   Aliases: MYJ24.13, MYJ24_13, NCLPP2	5.2	5.5	-0.3	-1.3	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5012	AT2G45920.1   U-box domain-containing protein, contains Pfam profile PF04564: U-box domain   chr2:18906288-18908376 FORWARD   Aliases: F4I18.10	4.0	4.6	-0.6	-1.3	100.0%	-3.9
5013	AT1G68160.1   expressed protein   chr1:25549471-25552557 REVERSE   Aliases: T22E19.21, T22E19_21	5.3	5.0	0.3	1.3	100.0%	-4.1
5014	AT4G37000.1   Symbol: ACD2   accelerated cell death 2 (ACD2), identical to accelerated cell death 2 (ACD2) GI:12484129 from (Arabidopsis thaliana)   chr4:17442606-17443844 FORWARD   Aliases: ACCELERATED CELL DEATH 2, AP22.36, AP22_36	6.8	6.2	0.6	1.3	100.0%	-3.9
5015	AT2G26500.2   cytochrome b6f complex subunit (petM), putative, nearly identical to cytochrome b6f complex subunit (GI:3090403) (Arabidopsis thaliana); alternative splice forms exist   chr2:11277353-11278031 FORWARD   Aliases: T9J22.17, T9J22_17	10.8	10.2	0.6	1.3	100.0%	-3.7
5016	AT4G32720.2   similar to La domain-containing protein [Arabidopsis thaliana] (TAIR:At1g79880.1); similar to putative RNA recognition motif (RRM)-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466667.1); contains InterPro domain RNA-binding protein Lupus Lal (InterPro:IPR006630); contains InterPro domain Lupus La protein (InterPro:IPR002344); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr4:15787218-15789982 FORWARD   Aliases: F4D11.80, F4D11_80	7.5	8.0	-0.5	-1.3	100.0%	-3.8
5017	AT1G70750.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593; supporting cDNA gi:4101563:gb:AF004556.1:AF004556	6.4	5.6	0.8	1.3	100.0%	-3.8
5018	AT2G01410.1   expressed protein   chr2:174777-176398 REVERSE   Aliases: F10A8.30	6.7	6.4	0.3	1.3	100.0%	-4.5
5019	AT5G58540.3   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr5:23680362-23682905 FORWARD   Aliases: MQJ2.16, MQJ2_16	3.2	2.9	0.3	1.3	100.0%	-4.1
5020	AT4G36650.1   transcription factor IIB (TFIIB) family protein, contains Pfam domain, PF00382: Transcription factor TFIIB repeat   chr4:17283288-17285532 REVERSE   Aliases: AP22.23, AP22_23	3.2	3.0	0.2	1.3	100.0%	-4.5
5021	AT4G13820.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591   chr4:8007990-8010739 REVERSE   Aliases: F18A5.210, F18A5_210	3.4	3.1	0.3	1.3	100.0%	-4.1
5022	AT3G05800.1   expressed protein   chr3:1727347-1728246 FORWARD   Aliases: F10A16.9, F10A16_9	3.5	4.0	-0.5	-1.3	100.0%	-3.9
5023	AT1G73980.1   phosphoribulokinase/uridine kinase family protein, weak similarity to SP:Q59190 Uridine kinase (EC 2.7.1.48) (Uridine monophosphokinase) (Cytidine monophosphokinase) {Borrelia burgdorferi}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family	7.4	7.9	-0.5	-1.3	100.0%	-3.9
5024	AT3G22210.1   expressed protein   chr3:7838791-7839474 REVERSE   Aliases: MKA23.19	4.5	5.1	-0.6	-1.3	100.0%	-3.8
5025	AT3G13550.2   Symbol: FUS9   similar to ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] (TAIR:At2g16740.1); similar to Ubiquitin-conjugating enzyme E2E 3 [Danio rerio] (GB:AAH67146.1); contains InterPro domain Ubiquitin-conjugating enzymes (InterPro:IPR000608)   chr3:4423697-4424890 REVERSE   Aliases: CIN4, CONSTITUTIVE PHOTOMORPHOGENIC 10, COP10, CYTOKININ INSENSITIVE 4, E2 UBIQUITIN CONJUGATING ENZYME, EMB144, EMBRYO DEFECTIVE 144, FUSCA 9, MRP15.21	6.7	5.9	0.7	1.3	100.0%	-3.8
5026	AT5G02020.2   expressed protein   chr5:386079-388120 REVERSE   Aliases: T7H20.70, T7H20_70	5.8	5.2	0.5	1.3	100.0%	-3.7
5027	AT3G28230.1   hypothetical protein   chr3:10530551-10531436 FORWARD   Aliases: MZF16.2	2.7	2.8	-0.1	-1.3	100.0%	-5.0
5028	AT4G35570.1   Symbol: HMGB5   high mobility group protein delta (HMGdelta) / HMG protein delta, identical to HMG protein (HMGdelta) (Arabidopsis thaliana) GI:2832363	7.6	8.0	-0.4	-1.3	100.0%	-4.0
5029	AT5G52590.1   RabGAP/TBC domain-containing protein, contains similarity to SP:P48365 GTPase-activating protein GYP7 {Saccharomyces cerevisiae}; contains Pfam profile PF00566: TBC domain   chr5:21356854-21360210 FORWARD   Aliases: F6N7.7, F6N7_7	6.9	6.2	0.7	1.3	100.0%	-3.8
5030	AT5G11450.1   oxygen-evolving complex-related, 23 kDa polypeptide of water-oxidizing complex of photosystem II, Nicotiana tabacum, EMBL:NT23WOP2B   chr5:3654431-3656556 FORWARD   Aliases: F15N18.40, F15N18_40	7.0	7.6	-0.6	-1.3	100.0%	-3.7
5031	AT2G01910.2   similar to microtubule associated protein (MAP65/ASE1) family protein [Arabidopsis thaliana] (TAIR:At1g14690.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470643.1); contains InterPro domain MAP65/ASE1 (InterPro:IPR007145)   chr2:417439-420586 FORWARD   Aliases: T23K3.10, T23K3_10	6.0	6.7	-0.7	-1.3	100.0%	-3.9
5032	AT3G04530.1   Symbol: PPCK2   phosphoenolpyruvate carboxylase kinase 2 (PPCK2), phosphoenolpyruvate carboxylase kinase 2 (Arabidopsis thaliana) gi:13877128:gb:AAK43710; contains protein kinase domain, Pfam:PF00069	4.7	3.9	0.7	1.3	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5033	AT4G29340.1   Symbol: PRF4   profilin 3 (PRO3) (PFN3), identical to profilin 3 SP:Q38904 GI:1353765 from (Arabidopsis thaliana)   chr4:14447653-14448704 FORWARD   Aliases: F17A13.160, F17A13_160, PROFILIN 4	3.5	2.9	0.6	1.3	100.0%	-3.7
5034	AT1G04520.1   33 kDa secretory protein-related, contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa secretory proteins   chr1:1231577-1234005 FORWARD   Aliases: F19P19.1, F19P19_1	3.5	3.8	-0.3	-1.3	100.0%	-4.1
5035	AT3G01160.1   expressed protein   chr3:54548-57469 REVERSE   Aliases: T4P13.15, T4P13_15	4.6	5.3	-0.7	-1.3	100.0%	-3.8
5036	AT2G01870.1   expressed protein   chr2:389469-390376 REVERSE   Aliases: T23K3.6, T23K3_6	3.7	3.4	0.3	1.3	100.0%	-4.4
5037	AT4G29060.2   Symbol: EMB2726   similar to translation elongation factor Ts (EF-Ts), putative [Arabidopsis thaliana] (TAIR:At4g11120.1); similar to elongation factor TS [Synechocystis sp. PCC 6803] (GB:NP_441466.1); contains InterPro domain Elongation factor Ts (InterPro:IPR001816); contains InterPro domain Ubiquitin-associated domain (InterPro:IPR000449); contains InterPro domain RNA binding S1 (InterPro:IPR003029); contains InterPro domain Ribosomal protein S1 (InterPro:IPR000110)   chr4:14317262-14321573 FORWARD   Aliases: EMB2726, EMBRYO DEFECTIVE 2726, F19B15.90, F19B15_90	7.6	8.7	-1.0	-1.3	100.0%	-3.8
5038	AT2G27190.1   Symbol: PAP1   iron(III)-zinc(II) purple acid phosphatase (PAP12), identical to iron(III)-zinc(II) purple acid phosphatase (precursor) SP:Q38924 from (Arabidopsis thaliana)   chr2:11628304-11630534 REVERSE   Aliases: PURPLE ACID PHOSPHATASE 1, SECRETED PURPLE ACID PHOSPHATASE PRECURSOR, T22O13.4, T22O13_4	9.4	9.6	-0.2	-1.3	100.0%	-4.6
5039	AT1G04600.1   Symbol: XIA   myosin, putative, similar to myosin (GI:499047) (Arabidopsis thaliana)   chr1:1262122-1272375 FORWARD   Aliases: ATXIA, T1G11.15, T1G11_15	3.0	3.2	-0.2	-1.3	100.0%	-4.6
5040	AT5G15010.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:4857262-4858962 FORWARD   Aliases: F2G14.130, F2G14_130	3.3	3.7	-0.4	-1.3	100.0%	-4.6
5041	AT1G54850.1   expressed protein, contains similarity to LMW heat shock protein GI:2326354 from (Arabidopsis thaliana)   chr1:20458056-20459887 FORWARD   Aliases: F14C21.42, F14C21_42	3.9	4.1	-0.2	-1.3	100.0%	-4.5
5042	AT2G25870.1   haloacid dehalogenase-like hydrolase family protein, contains Pfam profiles PF00702: haloacid dehalogenase-like hydrolase, PF02130: Uncharacterized protein family UPF0054   chr2:11038193-11041532 FORWARD   Aliases: AT2G25860, F17H15.10, F17H15_10	6.1	6.5	-0.4	-1.3	100.0%	-3.9
5043	AT5G57020.1   Symbol: NMT1   myristoyl-CoA:protein N-myristoyltransferase 1 (NMT1), identical to N-myristoyltransferase 1 (NMT1) (Arabidopsis thaliana) GI:7339834   chr5:23092093-23094127 FORWARD   Aliases: ATNMT1, MHM17.15, MHM17_15, N MYRISTOYLTRANSFERASE 1	7.7	8.3	-0.6	-1.3	100.0%	-3.9
5044	AT5G17250.1   phosphatidylinositolglycan class O (PIG-O) family protein, similar to Pig-o (Mus musculus) GI:8099973   chr5:5668902-5673518 REVERSE   Aliases: MKP11.10, MKP11_10	3.5	3.2	0.3	1.3	100.0%	-4.2
5045	AT5G57180.3   Symbol: CIA2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g25990.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g25990.2); similar to putative CIL [Oryza sativa (japonica cultivar-group)] (GB:BAD53999.1)	3.4	3.8	-0.4	-1.3	100.0%	-4.1
5046	AT5G02590.1   chloroplast lumen common family protein, various predicted proteins, Arabidopsis thaliana   chr5:583084-584177 FORWARD   Aliases: T22P11.180, T22P11_180	4.8	5.3	-0.5	-1.3	100.0%	-3.8
5047	AT4G03990.1   hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At3g30450, At5g34895, At3g47270, At2g02200   chr4:1916459-1917814 REVERSE   Aliases: T24H24.2, T24H24_2	2.7	2.9	-0.2	-1.3	100.0%	-5.0
5048	AT1G11430.1   plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	9.6	10.0	-0.4	-1.3	100.0%	-3.8
5049	AT2G40810.2   WD-40 repeat protein family, similar to Gsa12p(GI:18307769)(Pichia pastoris); contains 3 Pfam PF00400: WD domain, G-beta repeats	5.5	5.0	0.5	1.3	100.0%	-4.0
5050	AT5G37980.1   NADP-dependent oxidoreductase, putative, similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana   chr5:15148590-15150315 FORWARD   Aliases: K18L3.140, K18L3_140	5.6	5.9	-0.4	-1.3	100.0%	-4.1
5051	AT2G42390.1   protein kinase C substrate, heavy chain-related, similar to Protein kinase C substrate, 80 kDa protein, heavy chain (PKCSH) (80K-H protein) (Swiss-Prot:P14314) (Homo sapiens); contains 1 transmembrane domain;	7.3	6.9	0.3	1.3	100.0%	-4.0
5052	AT3G02910.1   expressed protein, contains Pfam domain PF03674: Uncharacterised protein family (UPF0131)   chr3:649821-650928 FORWARD   Aliases: F13E7.14, F13E7_14	9.3	8.3	1.1	1.3	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5053	AT4G29000.1   tesmin/TSO1-like CXC domain-containing protein, similar to CXC domain containing TSO1-like protein 1 (SOL1) (Arabidopsis thaliana) GI:7767427, SP:Q9Y4I5 Tesmin (Metallothionein-like 5, testis-specific) {Homo sapiens}; contains Pfam profile PF03638: Tesmin/TSO1-like CXC domain   chr4:14293519-14297072 FORWARD   Aliases: F19B15.30, F19B15_30	2.4	2.5	-0.2	-1.3	100.0%	-4.9
5054	AT3G02990.1   Symbol: ATHSFA1E   heat shock factor protein 2 (HSF2) / heat shock transcription factor 2 (HSTF2), identical to heat shock transcription factor 2 (HSF2) SP:Q96320 from	3.9	3.7	0.2	1.3	100.0%	-4.4
5055	AT1G48000.1   Symbol: MYB112	3.6	3.3	0.3	1.3	100.0%	-4.5
5056	AT3G18490.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr3:6348761-6350674 REVERSE   Aliases: MYF24.39	9.1	9.7	-0.5	-1.3	100.0%	-4.0
5057	AT5G15390.1   tRNA/rRNA methyltransferase (SpoU) family protein, similar to SP:P19396 tRNA (Guanosine-2'-O-)-methyltransferase (EC 2.1.1.34) {Escherichia coli O157:H7}; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family   chr5:4995158-4997398 FORWARD   Aliases: T20K14.1	7.1	6.7	0.5	1.3	100.0%	-3.8
5058	AT4G00200.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr4:82445-84694 REVERSE   Aliases: F6N15.24, F6N15_24	4.4	4.2	0.2	1.3	100.0%	-4.7
5059	AT1G71830.1   Symbol: SERK1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr1:27021820-27025774 FORWARD   Aliases: ATSERK1, F14O23.21, F14O23_21, SOMATIC EMBRYOGENESIS RECEPTOR LIKE KINASE 1	6.5	7.0	-0.5	-1.3	100.0%	-4.2
5060	AT1G69680.1   expressed protein, similar to MOG1 isoform A (GI:9864064) (Homo sapiens)	5.6	5.1	0.4	1.3	100.0%	-3.9
5061	AT1G34140.1   Symbol: PAB1   polyadenylate-binding protein, putative / PABP, putative, non-consensus splice donor TA at exon 1; similar to polyadenylate-binding protein (poly(A)-binding protein) from (Triticum aestivum) GI:1737492, (Nicotiana tabacum) GI:7673355, {Arabidopsis thaliana} SP:P42731; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM). Only member of the class IV PABP family.	2.2	2.3	-0.1	-1.3	100.0%	-5.1
5062	AT5G51350.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:20885086-20887847 REVERSE   Aliases: MFG13.5, MFG13_5	5.4	5.8	-0.4	-1.3	100.0%	-4.1
5063	AT3G23820.1   Symbol: GAE6   NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile: PF01370 NAD dependent epimerase/dehydratase family   chr3:8603451-8605469 FORWARD   Aliases: F14O13.9, UDP D GLUCURONATE 4 EPIMERASE 6	11.2	10.9	0.2	1.3	100.0%	-4.6
5064	AT2G40280.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr2:16832578-16835476 REVERSE   Aliases: T7M7.24	7.2	7.6	-0.5	-1.3	100.0%	-3.8
5065	AT2G18400.1   ribosomal protein L6 family protein   chr2:7996561-7997668 REVERSE   Aliases: T30D6.9, T30D6_9	9.4	9.9	-0.4	-1.3	100.0%	-3.9
5066	AT5G67290.1   FAD-dependent oxidoreductase family protein, contains Pfam profile PF01266: FAD dependent oxidoreductase	5.2	4.9	0.3	1.3	100.0%	-4.2
5067	AT5G53990.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	3.8	4.3	-0.5	-1.3	100.0%	-3.8
5068	AT1G64460.1   phosphatidylinositol 3- and 4-kinase family protein, contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase	3.9	3.4	0.5	1.3	100.0%	-3.9
5069	AT3G53610.2   Symbol: ATRAB8	6.1	6.5	-0.4	-1.3	100.0%	-3.9
5070	AT4G38870.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr4:18132577-18133857 REVERSE   Aliases: F19H22.2	2.2	2.0	0.2	1.3	100.0%	-5.0
5071	AT1G02500.2   Symbol: SAM1   S-adenosylmethionine synthetase 1 (SAM1), identical to S-adenosylmethionine synthetase 1 (Methionine adenosyltransferase 1, AdoMet synthetase 1) (Arabidopsis thaliana) SWISS-PROT:P23686   chr1:518254-520437 FORWARD   Aliases: SAM 1, T14P4.17, T14P4_17	7.1	8.0	-0.9	-1.3	100.0%	-3.7
5072	AT1G13740.1   expressed protein   chr1:4713671-4715404 FORWARD   Aliases: F21F23.17, F21F23_17	6.8	7.5	-0.7	-1.3	100.0%	-3.9
5073	AT1G04230.1   expressed protein   chr1:1125571-1128167 FORWARD   Aliases: F19P19.34	5.1	4.7	0.3	1.3	100.0%	-4.1
5074	AT1G36390.2   co-chaperone grpE family protein, similar to co-chaperone CGE1 precursor isoform b (Chlamydomonas reinhardtii) GI:15384279; contains Pfam profile PF01025: co-chaperone GrpE   chr1:13702613-13704782 REVERSE   Aliases: F7F23.11, F7F23_11	4.2	4.7	-0.5	-1.3	100.0%	-4.1
5075	AT5G52420.1   expressed protein   chr5:21298999-21300507 FORWARD   Aliases: K24M7.17, K24M7_17	5.5	5.1	0.3	1.3	100.0%	-4.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5076	AT2G43460.1   60S ribosomal protein L38 (RPL38A)   chr2:18053081-18054478 REVERSE   Aliases: T1O24.20	10.4	10.8	-0.4	-1.3	100.0%	-4.2
5077	AT3G01980.2   short-chain dehydrogenase/reductase (SDR) family protein, contains Pfam profiles: PF00106 short chain dehydrogenase, PF00678 short chain dehydrogenase/reductase C-terminus   chr3:327634-328971 REVERSE   Aliases: F1C9.24, F1C9_24	5.0	5.8	-0.8	-1.3	100.0%	-4.0
5078	AT5G21070.1   expressed protein   chr5:7156175-7157768 FORWARD   Aliases: T10F18.100, T10F18_100	4.8	4.3	0.5	1.3	100.0%	-4.2
5079	AT5G59600.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:24028227-24030251 REVERSE   Aliases: F2O15.13, F2O15_13	3.5	3.7	-0.3	-1.3	100.0%	-4.2
5080	AT2G34570.1   expressed protein, contains Pfam profile: PF04900 protein of unknown function, DUF652   chr2:14569980-14571861 REVERSE   Aliases: T31E10.9, T31E10_9	6.1	6.4	-0.4	-1.3	100.0%	-4.0
5081	AT3G05570.1   expressed protein   chr3:1616271-1616642 REVERSE   Aliases: F18C1.16, F18C1_16	7.5	7.9	-0.4	-1.3	100.0%	-3.8
5082	AT3G15260.2   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase type 2C GB:AAD17805 from (Lotus japonicus)   chr3:5138703-5142651 FORWARD   Aliases: K7L4.6	8.0	7.5	0.4	1.3	100.0%	-4.1
5083	AT5G16830.1   Symbol: SYP21   syntaxin 21 (SYP21) / PEP12 homolog, identical to Syntaxin homolog (PEP12 homolog) (SP:Q39233) and syntaxin of plants 21 (GP:899122) {Arabidopsis thaliana}; contains Pfam profiles PF05739:SNARE domain and PF00804: Syntaxin	9.0	8.2	0.8	1.3	100.0%	-3.9
5084	AT1G01720.1   Symbol: ATAF1   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain protein NAM GB:AAD17313 GI:4325282 from (Arabidopsis thaliana)   chr1:268330-269819 FORWARD   Aliases: ANAC002, T1N6.12, T1N6_12	6.1	5.3	0.9	1.3	100.0%	-3.7
5085	AT1G77810.2   galactosyltransferase family protein, contains Pfam profile PF01762: Galactosyltransferase   chr1:29265515-29267895 REVERSE   Aliases: T32E8.14	6.6	6.2	0.4	1.3	100.0%	-4.0
5086	AT2G31170.1   tRNA synthetase class I (C) family protein, similar to cysteine-tRNA ligase (Escherichia coli) GI:41203; contains Pfam profile PF01406: tRNA synthetases class I (C)   chr2:13289458-13292722 REVERSE   Aliases: T16B12.16	3.0	3.2	-0.2	-1.3	100.0%	-4.5
5087	AT1G54200.1   expressed protein   chr1:20239379-20240732 FORWARD   Aliases: F20D21.2, F20D21_2	3.6	3.9	-0.3	-1.3	100.0%	-4.1
5088	AT4G11340.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr4:6894203-6899125 REVERSE   Aliases: F8L21.130, F8L21_130	2.6	2.8	-0.2	-1.3	100.0%	-4.7
5089	AT1G14990.1   expressed protein   chr1:5167147-5168238 REVERSE   Aliases: T15D22.3, T15D22_3	7.4	6.8	0.6	1.3	100.0%	-4.1
5090	AT4G12740.1   adenine-DNA glycosylase-related / MYH-related, similar to MYH (GI:18845094) (Rattus norvegicus); similar to adenine-DNA glycosylase (GI:12656850) (Mus musculus); contains TIGRFAM profile TIGR01084: A/G-specific adenine glycosylase (hits below the trusted cutoff)   chr4:7494575-7497593 REVERSE   Aliases: T20K18.90, T20K18_90	3.8	4.1	-0.3	-1.3	100.0%	-4.1
5091	AT3G45060.1   Symbol: ATNRT2.6   high-affinity nitrate transporter, putative, similar to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362   chr3:16488656-16490467 REVERSE   Aliases: F14D17.130	4.9	4.5	0.4	1.3	100.0%	-4.0
5092	AT5G43850.1   acireductone dioxygenase (ARD/ARD') family protein, similar to iron-deficiency induced gene (Hordeum vulgare) GI:14522834, SIPL (Homo sapiens) GI:16551383; contains Pfam profile PF03079: ARD/ARD' family   chr5:17644412-17646385 REVERSE   Aliases: MQD19.21, MQD19_21	10.0	9.7	0.4	1.3	100.0%	-4.4
5093	AT4G16820.1   lipase class 3 family protein, similar to DEFECTIVE IN ANTHOR DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase   chr4:9467582-9469135 FORWARD   Aliases: DL4435W, FCAALL.42	3.3	3.9	-0.6	-1.3	100.0%	-4.0
5094	AT3G02320.1   similar to N2,N2-dimethylguanosine tRNA methyltransferase family protein [Arabidopsis thaliana] (TAIR:At5g15810.1); similar to putative N2,N2-dimethylguanosine tRNA methyltransferase [Oryza sativa (japonica cultivar-group)] (GB:AAT75242.1); contains InterPro domain N2,N2-dimethylguanosine tRNA methyltransferase (InterPro:IPR002905); contains InterPro domain SAM (and some other nucleotide) binding motif (InterPro:IPR000051)   chr3:469941-473695 FORWARD   Aliases: F11A12.1, F11A12_1	5.2	5.4	-0.3	-1.3	100.0%	-4.1
5095	AT1G63160.1   replication factor C 40 kDa, putative, similar to SWISS-PROT:Q9WUK4 activator 1 40 kDa subunit (Replication factor C 40 kDa subunit, A1 40 kDa subunit, RF-C 40 kDa subunit, RFC40) (Mus musculus)   chr1:23425529-23427478 REVERSE   Aliases: F16M19.6, F16M19_6	3.5	3.9	-0.4	-1.3	100.0%	-4.0
5096	AT2G40460.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr2:16903985-16908358 FORWARD   Aliases: T2P4.19, T2P4_19	5.5	6.0	-0.5	-1.3	100.0%	-3.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5097	AT1G68710.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from {Mus musculus} SP:P98200, {Bos taurus} SP:Q29449, {Homo sapiens} SP:O43520; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:25796870-25801638 REVERSE   Aliases: F24J5.6, F24J5_6	4.5	3.8	0.7	1.3	100.0%	-3.8
5098	AT3G45160.1   expressed protein   chr3:16544436-16545063 REVERSE   Aliases: T14D3.100	8.9	9.7	-0.8	-1.3	100.0%	-4.0
5099	AT3G51580.1   expressed protein   chr3:19141813-19144259 REVERSE   Aliases: T18N14.6	6.5	6.2	0.3	1.3	100.0%	-4.2
5100	AT4G26270.1   phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase   chr4:13300804-13304356 REVERSE   Aliases: T25K17.80, T25K17_80	7.4	6.9	0.5	1.3	100.0%	-4.0
5101	AT5G05780.1   Symbol: ATHMOV34   26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory subunit S12, putative / MOV34 protein, putative, contains similarity to 26s proteasome regulatory subunit s12 (proteasome subunit p40) (mov34 protein) SP:P26516 from (Mus musculus); contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr5:1735734-1738493 FORWARD   Aliases: MJJ3.19, MJJ3_19, PUTATIVE 26S PROTEASOME SUBUNIT ATHMOV34	6.9	8.0	-1.0	-1.3	100.0%	-3.9
5102	AT1G63960.1   hypothetical protein   chr1:23741864-23742169 FORWARD   Aliases: T12P18.2, T12P18_2	3.9	3.6	0.3	1.3	100.0%	-4.2
5103	AT5G22875.2   expressed protein, similar to hypothetical protein [Ipomoea trifida] (GB:AAS79573.1)   chr5:7650585-7651779 FORWARD   Aliases: None	4.9	4.5	0.4	1.3	100.0%	-4.2
5104	AT5G20930.1   Symbol: TSL   protein kinase, putative, nearly identical to protein kinase tousled gi:433052:gb:AAA32874   chr5:7097910-7103200 FORWARD   Aliases: F22D1.100, F22D1_100, PROTEIN KINASE TSL, TOUSLED	6.5	6.9	-0.4	-1.3	100.0%	-4.2
5105	AT5G05100.1   expressed protein   chr5:1505123-1507203 REVERSE   Aliases: MUG13.4, MUG13_4	9.6	9.4	0.2	1.3	100.0%	-4.7
5106	AT5G64030.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr5:25641263-25645701 FORWARD   Aliases: MBM17.13, MBM17_13	8.1	8.6	-0.5	-1.3	100.0%	-4.2
5107	AT2G39920.1   acid phosphatase class B family protein, weak similarity to pod storage protein (Phaseolus vulgaris GI:2627233 SP:P10743 STEM 31 kDa glycoprotein precursor (Vegetative storage protein B) {Glycine max}); contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr2:16670102-16671616 REVERSE   Aliases: T28M21.8, T28M21_8	3.2	2.9	0.3	1.3	100.0%	-4.4
5108	AT3G19300.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:6690124-6693290 REVERSE   Aliases: MLD14.2	4.4	5.0	-0.6	-1.3	100.0%	-3.9
5109	AT5G38020.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri) and to SAM:benzoic acid carboxyl methyltransferase (BAMT)(GI:9789277)(Antirrhinum majus)   chr5:15182882-15184959 REVERSE   Aliases: F16F17.20, F16F17_20	2.9	3.2	-0.3	-1.3	100.0%	-4.3
5110	AT5G55050.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	4.7	5.3	-0.5	-1.3	100.0%	-3.9
5111	AT4G31090.1   expressed protein   chr4:15122235-15123492 FORWARD   Aliases: F6E21.10, F6E21_10	4.8	4.0	0.8	1.3	100.0%	-4.0
5112	AT5G01470.1   expressed protein   chr5:190927-192610 FORWARD   Aliases: T10O8.180, T10O8_180	4.9	5.3	-0.4	-1.3	100.0%	-3.9
5113	AT3G25870.1   expressed protein   chr3:9464553-9465520 REVERSE   Aliases: MPE11.2	4.1	3.6	0.5	1.3	100.0%	-4.0
5114	AT5G59990.1   expressed protein, ; expression supported by MPSS   chr5:24168432-24170310 REVERSE   Aliases: MMN10.24, MMN10_24	2.7	2.5	0.2	1.3	100.0%	-4.8
5115	AT1G19130.1   expressed protein   chr1:6609360-6610593 REVERSE   Aliases: F14D16.29, F14D16_29	8.8	9.3	-0.4	-1.3	100.0%	-3.9
5116	AT1G10690.1   expressed protein   chr1:3549993-3550633 REVERSE   Aliases: T16B5.17, T16B5_17	3.7	3.3	0.4	1.3	100.0%	-4.3
5117	AT5G50310.1   kelch repeat-containing protein, similar to Kelch repeats protein 3 (SP:Q08979) (Saccharomyces cerevisiae); contains Pfam PF01344: Kelch motif (6 repeats)   chr5:20491713-20496641 FORWARD   Aliases: MXI22.1, MXI22_1	6.7	7.2	-0.5	-1.3	100.0%	-4.1
5118	AT3G23600.2   similar to dienelactone hydrolase family protein [Arabidopsis thaliana] (TAIR:At3g23570.1); similar to 'putative endo-1,3;1,4-beta-D-glucanase' [Oryza sativa (japonica cultivar-group)] (GB:AAU10803.1); contains InterPro domain Dienelactone hydrolase (InterPro:IPR002925)   chr3:8473802-8475895 FORWARD   Aliases: MDB19.8	10.8	11.4	-0.6	-1.3	100.0%	-4.3
5119	AT2G20470.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr2:8833358-8836578 REVERSE   Aliases: T13C7.6, T13C7_6	2.7	2.9	-0.2	-1.3	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5120	AT1G64980.1   expressed protein   chr1:24141180-24142924 REVERSE   Aliases: F13O11.28, F13O11_28	6.6	6.3	0.3	1.3	100.0%	-4.3
5121	AT5G06265.1   hyaluronan mediated motility receptor-related, contains weak similarity to hyaluronan mediated motility receptor (Intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility) (CD168 antigen) (Swiss-Prot:O75330) (Homo sapiens)   chr5:1905293-1908168 FORWARD   Aliases: None	6.0	5.6	0.4	1.3	100.0%	-4.1
5122	AT3G51450.1   strictosidine synthase family protein, similar to hemomucin (Drosophila melanogaster)(GI:1280434), strictosidine synthase (Rauvolfia serpentina)(SP:P15324)   chr3:19101947-19103482 FORWARD   Aliases: F26O13.90	5.8	6.1	-0.3	-1.3	100.0%	-4.2
5123	AT3G06240.1   F-box family protein, contains F-box domain Pfam:PF00646	7.0	6.4	0.6	1.3	100.0%	-4.1
5124	AT5G26830.1   threonyl-tRNA synthetase / threonine--tRNA ligase (THRRS), identical to SP:O04630 Threonyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS) {Arabidopsis thaliana}	8.1	8.4	-0.3	-1.3	100.0%	-4.3
5125	AT4G01450.3   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr4:608456-610705 FORWARD   Aliases: F11O4.14, F11O4_14	7.7	7.3	0.4	1.3	100.0%	-4.2
5126	AT2G44880.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:18512314-18513981 FORWARD   Aliases: T13E15.11	2.7	2.5	0.1	1.3	100.0%	-4.8
5127	AT1G20270.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus (GI:212530), Rattus norvegicus (GI:474940), Mus musculus (SP:Q60715); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:7020742-7023057 REVERSE   Aliases: F14O10.12, F14O10_12	4.0	3.7	0.3	1.3	100.0%	-4.3
5128	AT3G48120.1   expressed protein   chr3:17783122-17785724 FORWARD   Aliases: T24C20.2	4.7	4.3	0.4	1.3	100.0%	-4.0
5129	AT5G02200.1   phytochrome A specific signal transduction component-related, contains weak similarity to phytochrome A specific signal transduction component PAT3 (Arabidopsis thaliana) gi:19421998:gb:AAL87850 and far-red elongated hypocotyl protein 1 (Arabidopsis thaliana) gi:17148773:gb:AAL35819   chr5:437458-438892 FORWARD   Aliases: T7H20.250, T7H20_250	3.8	3.5	0.4	1.3	100.0%	-4.5
5130	AT1G06060.1   RanBPM-related, similar to RANBPM {GI:13194576}(Homo sapiens)   chr1:1832942-1835576 FORWARD   Aliases: T21E18.11, T21E18_11	3.6	3.8	-0.3	-1.3	100.0%	-4.2
5131	AT4G17490.1   Symbol: ATERF6	4.7	3.8	0.8	1.3	100.0%	-3.8
5132	AT5G49320.1   expressed protein   chr5:20012251-20013440 REVERSE   Aliases: K21P3.22, K21P3_22	4.9	4.5	0.4	1.3	100.0%	-4.0
5133	AT5G13790.1   Symbol: AGL15   floral homeotic protein AGL-15 (AGL15)   chr5:4449017-4450846 REVERSE   Aliases: AGAMOUS LIKE 15, MADS BOX PROTEIN AGL15, MXE10.8, MXE10_8	3.0	3.2	-0.2	-1.3	100.0%	-4.7
5134	AT1G10360.1   Symbol: ATGSTU18   glutathione S-transferase, putative, similar to glutathione S-transferase (sp:Q03666:GTX4_TOBAC); similar to EST gb:H36275 gb:AB039930.   chr1:3395560-3396851 REVERSE   Aliases: F14N23.24, F14N23_24, GLUTATHIONE S TRANSFERASE 29, GST29	6.2	5.6	0.7	1.3	100.0%	-3.6
5135	AT4G34030.1   Symbol: MCCB   methylcrotonyl-CoA carboxylase beta chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 2 (MCCB), identical to SP:Q9LDD8 Methylcrotonyl-CoA carboxylase beta chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 2) (MCCase beta subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase beta subunit) {Arabidopsis thaliana}; contains Pfam profile: PF01039 carboxyl transferase domain   chr4:16301198-16304031 FORWARD   Aliases: 3 METHYLCROTONYL COA CARBOXYLASE, F28A23.210, F28A23_210	10.2	10.5	-0.3	-1.3	100.0%	-4.5
5136	AT4G30580.1   Symbol: ATS2   phospholipid/glycerol acyltransferase family protein   chr4:14932347-14934525 REVERSE   Aliases: EMB1995, EMBRYO DEFECTIVE 1995, F17I23.80, F17I23_80	6.6	6.2	0.4	1.3	100.0%	-4.2
5137	AT3G21470.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:7563614-7565254 FORWARD   Aliases: MIL23.2	2.7	2.9	-0.2	-1.3	100.0%	-4.7
5138	AT3G15020.1   malate dehydrogenase (NAD), mitochondrial, putative, similar to mitochondrial NAD-dependent malate dehydrogenase GB:CAA10320 SP:Q9ZP06 (Arabidopsis thaliana); contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr3:5056083-5058255 FORWARD   Aliases: K15M2.16	9.3	10.1	-0.8	-1.3	100.0%	-3.9
5139	AT2G17930.1   FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein, contains Pfam profiles PF02259 FAT domain, PF00454 Phosphatidylinositol 3- and 4-kinase, PF02260: FATC domain   chr2:7791458-7809312 REVERSE   Aliases: T13L16.5, T13L16_5	5.3	5.8	-0.5	-1.3	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5140	AT3G57550.2   Symbol: AGK2   similar to guanylate kinase 1 (GK-1) [Arabidopsis thaliana] (TAIR:At2g41880.1); similar to guanylate kinase [Nicotiana tabacum] (GB:AAG12251.1); contains InterPro domain Guanylate kinase (InterPro:IPR008144); contains InterPro domain Guanylate kinase/L-type calcium channel region (InterPro:IPR008145)   chr3:21317700-21320441 FORWARD   Aliases: GK 2, GUANYLATE KINAS, T8H10.150	6.9	7.7	-0.8	-1.3	100.0%	-3.9
5141	AT3G01690.1   expressed protein   chr3:256562-258554 FORWARD   Aliases: F4P13.23, F4P13_23	10.1	9.8	0.3	1.3	100.0%	-4.2
5142	AT4G00330.1   Symbol: CRCK2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:142622-144523 REVERSE   Aliases: A_IG005I10.8, A_IG005I10_8, F5I10.8, F5I10_8	5.8	5.5	0.3	1.3	100.0%	-4.5
5143	AT3G09720.1   DEAD/DEAH box helicase, putative, similar to RNA helicase involved in rRNA processing GB:6321267 from (Saccharomyces cerevisiae)c, contains DEAD and DEAH box domain   chr3:2980236-2983578 REVERSE   Aliases: F11F8.31	4.2	4.4	-0.2	-1.3	100.0%	-4.3
5144	AT5G13020.1   emsy N terminus domain-containing protein / ENT domain-containing protein, contains Pfam profile PF03735: ENT domain   chr5:4129362-4132092 REVERSE   Aliases: T19L5.3	5.8	5.2	0.6	1.3	100.0%	-3.9
5145	AT4G39280.1   phenylalanyl-tRNA synthetase, putative / phenylalanine--tRNA ligase, putative, similar to SP:Q9Y285 Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phenylalanine- tRNA ligase alpha chain) (PheRS) {Homo sapiens}; contains Pfam profile PF01409: tRNA synthetases class II core domain (F)   chr4:18281456-18284843 REVERSE   Aliases: T22F8.180, T22F8_180	8.8	9.6	-0.8	-1.3	100.0%	-3.8
5146	AT4G09730.1   DEAD/DEAH box helicase, putative, RNA helicase -Mus musculus,PIR2:I84741	3.8	4.2	-0.4	-1.3	100.0%	-4.2
5147	AT2G33490.1   hydroxyproline-rich glycoprotein family protein, Common family member:At3g26910 (Arabidopsis thaliana)   chr2:14190628-14194945 FORWARD   Aliases: F4P9.26, F4P9_26	3.8	4.1	-0.3	-1.3	100.0%	-4.2
5148	AT1G30300.1   expressed protein, similar to putative hydrolase GI:7270684 from (Arabidopsis thaliana); similar to PhnP protein (GI:15620485) (Rickettsia conorii)   chr1:10673002-10675350 FORWARD   Aliases: F12P21.8, F12P21_8	4.0	4.2	-0.2	-1.3	100.0%	-4.3
5149	AT1G78810.2   expressed protein   chr1:29633206-29635446 REVERSE   Aliases: F9K20.15, F9K20_15	7.2	7.7	-0.5	-1.3	100.0%	-3.9
5150	AT4G08670.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:5536696-5538207 REVERSE   Aliases: T3F12.2, T3F12_2	2.8	2.6	0.2	1.3	100.0%	-4.5
5151	AT2G24280.1   serine carboxypeptidase S28 family protein, contains Pfam profile: PF05577 Serine carboxypeptidase S28   chr2:10340364-10344161 FORWARD   Aliases: F27D4.19, F27D4_19	4.0	3.6	0.4	1.3	100.0%	-4.0
5152	AT1G51380.1   eukaryotic translation initiation factor 4A, putative / eIF-4A, putative	4.6	5.0	-0.3	-1.3	100.0%	-4.0
5153	AT3G07160.1   Symbol: ATGSL10   glycosyl transferase family 48 protein, similar to glucan synthase GB:AAD11794 (Filobasidiella neoformans var. neoformans)   chr3:2264963-2279389 REVERSE   Aliases: GLUCAN SYNTHASE LIKE 10, GSL10, T1B9.18	6.8	7.3	-0.5	-1.3	100.0%	-4.1
5154	AT4G14930.1   acid phosphatase survival protein SurE, putative, similar to Swiss-Prot:P36664 acid phosphatase surE (EC 3.1.3.2) (Stationary-phase survival protein surE) (Escherichia coli O157:H7); contains Pfam domain PF01975: Survival protein SurE   chr4:8538582-8541895 FORWARD   Aliases: DL3505W, FCAALL.200	6.6	7.2	-0.7	-1.3	100.0%	-3.9
5155	AT1G05960.1   expressed protein, similar to hypothetical protein GB:AAF80120 GI:8810459 from (Arabidopsis thaliana)   chr1:1807972-1815463 REVERSE   Aliases: T21E18.21, T21E18_21	6.5	6.0	0.4	1.3	100.0%	-4.0
5156	AT1G64390.1   endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-beta-1,4-glucanase GI:4972236 from (Fragaria x ananassa) (Plant Mol. Biol. 40, 323-332 (1999))   chr1:23914782-23918892 FORWARD   Aliases: F15H21.9, F15H21_9	3.9	4.7	-0.7	-1.3	100.0%	-4.1
5157	AT3G06770.3   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to polygalacturonase (Persea americana) GI:166951; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr3:2134806-2136918 REVERSE   Aliases: F3E22.9	4.0	4.6	-0.6	-1.3	100.0%	-4.2
5158	AT2G20450.1   60S ribosomal protein L14 (RPL14A)   chr2:8820947-8822332 FORWARD   Aliases: T13C7.4, T13C7_4	9.2	9.7	-0.5	-1.3	100.0%	-4.0
5159	AT1G17480.1   calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr1:6006454-6008259 REVERSE   Aliases: F28G4.3, F28G4_3	3.5	3.2	0.2	1.3	100.0%	-4.5
5160	AT5G67210.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr5:26836245-26837198 FORWARD   Aliases: K21H1.17, K21H1_17	5.7	6.1	-0.4	-1.3	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5161	AT1G70420.1   expressed protein   chr1:26543237-26544425 REVERSE   Aliases: F1707.4, F1707_4	4.8	4.4	0.5	1.3	100.0%	-4.5
5162	AT5G04290.1   KOW domain-containing transcription factor family protein   chr5:1196070-1202654 FORWARD   Aliases: T19N18.20, T19N18_20	8.7	8.0	0.6	1.3	100.0%	-4.5
5163	AT3G29280.1   expressed protein, ; expression supported by MPSS   chr3:11237942-11239184 REVERSE   Aliases: MMF24.3	6.1	6.6	-0.5	-1.3	100.0%	-3.8
5164	AT4G02930.1   elongation factor Tu, putative / EF-Tu, putative, similar to mitochondrial elongation factor Tu (Arabidopsis thaliana) gi:1149571:emb:CAA61511   chr4:1295409-1298397 REVERSE   Aliases: T4I9.19	9.6	10.3	-0.7	-1.3	100.0%	-3.8
5165	AT4G39870.1   expressed protein, hypothetical protein, Schizosaccharomyces cerevisiae, Z99168   chr4:18501889-18504422 FORWARD   Aliases: T5J17.40, T5J17_40	5.3	5.0	0.4	1.3	100.0%	-4.0
5166	AT1G21570.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:7557251-7560272 REVERSE   Aliases: F24J8.21, F24J8_21	9.2	8.6	0.6	1.3	100.0%	-4.1
5167	AT2G39390.1   60S ribosomal protein L35 (RPL35B)   chr2:16457738-16458956 REVERSE   Aliases: F12L6.5, F12L6_5	10.6	11.0	-0.3	-1.3	100.0%	-4.3
5168	AT2G03420.1   expressed protein   chr2:1034995-1035966 REVERSE   Aliases: T4M8.15, T4M8_15	4.5	5.0	-0.5	-1.3	100.0%	-3.7
5169	AT5G60630.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:24386876-24387630 REVERSE   Aliases: MUP24.5, MUP24_5	4.8	5.3	-0.5	-1.3	100.0%	-3.8
5170	AT5G62940.1   Dof-type zinc finger domain-containing protein, Dof zinc finger protein, Oryza sativa, EMBL:AB028129   chr5:25274145-25275907 REVERSE   Aliases: MQB2.26, MQB2_26	4.3	4.5	-0.3	-1.3	100.0%	-4.3
5171	AT1G25290.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr1:8867144-8869079 FORWARD   Aliases: F4F7.32, F4F7_32	5.0	4.7	0.2	1.3	100.0%	-4.4
5172	AT2G36410.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g52920.2); similar to unknown [Oryza sativa (japonica cultivar-group)] (GB:AAO72703.1); contains InterPro domain Protein of unknown function DUF662 (InterPro:IPR007033)   chr2:15285848-15287683 FORWARD   Aliases: F1O11.4, F1O11_4	6.1	5.3	0.8	1.3	100.0%	-3.8
5173	AT1G01550.2   Symbol: BPS1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g46080.1); similar to OSJNBa0018M05.6 [Oryza sativa (japonica cultivar-group)] (GB:XP_474319.1)   chr1:199792-201775 FORWARD   Aliases: BYPASS 1, F22L4.9, F22L4_9	10.2	9.6	0.6	1.3	100.0%	-4.1
5174	AT1G08970.4   Symbol: HAP5C   CCAAT-box binding transcription factor Hap5a, putative   chr1:2882546-2884285 FORWARD   Aliases: F7G19.16, F7G19_16, HAP5C, HEME ACTIVATED PROTEIN 5C	9.8	8.9	0.8	1.3	100.0%	-3.9
5175	AT5G43960.2   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein, contains Pfam profiles PF02136: Nuclear transport factor 2 (NTF2) domain, PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr5:17706015-17709114 REVERSE   Aliases: MRH10.6, MRH10_6	5.8	6.2	-0.4	-1.3	100.0%	-4.0
5176	AT4G11410.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr4:6944919-6947328 REVERSE   Aliases: F25E4.30, F25E4_30	7.1	6.4	0.7	1.3	100.0%	-3.9
5177	AT1G69390.1   chloroplast division protein, putative (MinE1), identical to chloroplast division protein homolog MinE1 GI:17511220 from (Arabidopsis thaliana)   chr1:26088317-26090144 FORWARD   Aliases: F23O10.25, F23O10_25	7.1	6.5	0.5	1.3	100.0%	-3.9
5178	AT5G49970.2   pyridoxamine 5'-phosphate oxidase-related, contains weak similarity to Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5) (PNP/PMP oxidase) (PNPOx). (Swiss-Prot:P28225) (Shigella flexneri)	7.3	7.9	-0.6	-1.3	100.0%	-4.0
5179	AT3G21310.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr3:7497296-7499158 FORWARD   Aliases: MXL8.19	3.2	3.1	0.2	1.3	100.0%	-5.0
5180	AT4G14465.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr4:8320626-8322185 FORWARD   Aliases: None	5.6	5.3	0.3	1.3	100.0%	-4.1
5181	AT4G31330.1   expressed protein, contains Pfam profile PF04654: Protein of unknown function, DUF599   chr4:15202302-15203437 FORWARD   Aliases: F8F16.150, F8F16_150	5.7	5.2	0.5	1.3	100.0%	-4.0
5182	AT5G36250.1   protein phosphatase 2C, putative / PP2C, putative   chr5:14299333-14301811 FORWARD   Aliases: T30G6.11, T30G6_11	4.6	4.1	0.5	1.3	100.0%	-4.1
5183	AT5G24750.1   expressed protein   chr5:8490575-8494590 REVERSE   Aliases: T4C12.20	5.2	5.5	-0.3	-1.3	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5184	AT1G48280.1   hydroxyproline-rich glycoprotein family protein   chr1:17838756-17841385 FORWARD   Aliases: F11A17.16, F11A17_16	4.3	4.7	-0.4	-1.3	100.0%	-4.0
5185	AT3G15160.1   expressed protein   chr3:5104374-5108457 FORWARD   Aliases: F4B12.7	5.0	5.3	-0.3	-1.3	100.0%	-4.2
5186	AT3G08620.1   KH domain-containing protein   chr3:2617774-2620579 FORWARD   Aliases: F17O14.9	4.5	4.1	0.4	1.3	100.0%	-4.0
5187	AT5G22360.1   Symbol: ATVAMP714   synaptobrevin family protein, similar to Synaptobrevin-like protein 1 (SP:P51809) (Homo sapiens)   chr5:7404014-7405657 REVERSE   Aliases: MWD9.16, MWD9_16, VAMP714	6.6	6.1	0.6	1.3	100.0%	-4.2
5188	AT1G72250.1   kinesin motor protein-related   chr1:27196564-27201976 FORWARD   Aliases: T9N14.6, T9N14_6	3.1	2.9	0.2	1.3	100.0%	-4.4
5189	AT1G48170.1   expressed protein   chr1:17792455-17793762 FORWARD   Aliases: F21D18.10	6.5	5.9	0.5	1.3	100.0%	-4.0
5190	AT5G51720.1   expressed protein   chr5:21026822-21027571 FORWARD   Aliases: MIO24.14, MIO24_14	6.5	5.7	0.8	1.3	100.0%	-3.6
5191	AT1G32400.3   Symbol: TOM2A   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g20230.1); similar to senescence-associated protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_480197.1); contains InterPro domain CD9/CD37/CD63 antigen (InterPro:IPR000301)   chr1:11689088-11691445 REVERSE   Aliases: F5D14.17, F5D14_17, TOBAMOVIRUS MULTIPLICATION 2A	9.4	8.8	0.6	1.3	100.0%	-4.2
5192	AT5G25070.1   expressed protein   chr5:8641001-8643494 REVERSE   Aliases: T11H3.80, T11H3_80	5.7	6.2	-0.5	-1.3	100.0%	-4.0
5193	AT4G20480.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr4:11034283-11035885 REVERSE   Aliases: F9F13.130, F9F13_130	8.4	7.8	0.5	1.3	100.0%	-4.1
5194	AT3G14770.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr3:4957363-4959709 REVERSE   Aliases: T21E2.6	2.7	2.4	0.3	1.3	100.0%	-4.1
5195	ATCG00350.1   Symbol: PSAA   Encodes psaA protein comprising the reaction center for photosystem I along with psaB protein; hydrophobic protein encoded by the chloroplast genome.   chrC:39605-41857 REVERSE   Aliases: PSAA	4.7	4.3	0.4	1.3	100.0%	-4.3
5196	AT2G42780.1   expressed protein   chr2:17807590-17809893 FORWARD   Aliases: F7D19.22, F7D19_22	7.6	7.9	-0.3	-1.3	100.0%	-4.2
5197	AT5G12850.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat   chr5:4056194-4059583 FORWARD   Aliases: T24H18.20, T24H18_20	4.3	4.7	-0.4	-1.3	100.0%	-4.1
5198	AT3G11040.1   glycosyl hydrolase family 85 protein, contains similarity to endo-b-N-acetylglucosaminidase GI:13774138 from (Mucor hiemalis)   chr3:3460149-3463318 FORWARD   Aliases: F9F8.14	3.2	3.5	-0.3	-1.3	100.0%	-4.3
5199	AT3G23240.1   Symbol: ATERF1/ERF1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family (ERF1). The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5. EREBP like protein that binds GCC box of ethylene regulated promoters such as basic chitinases. Constitutive expression of ERF1 phenocopies ethylene over production. Involved in ethylene signaling cascade, downstream of EIN2 and EIN3.   chr3:8295651-8296611 FORWARD   Aliases: ATERF1, ERF1, ETHYLENE RESPONSE FACTOR 1, K14B15.4	3.6	3.4	0.2	1.3	100.0%	-4.7
5200	AT3G14690.1   Symbol: CYP72A15   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4937386-4939472 FORWARD   Aliases: MIE1.19	7.4	6.6	0.8	1.3	100.0%	-3.9
5201	AT2G37190.1   60S ribosomal protein L12 (RPL12A)   chr2:15626486-15627198 REVERSE   Aliases: T2N18.5, T2N18_5	8.8	9.4	-0.6	-1.3	100.0%	-3.8
5202	AT5G48230.2   Symbol: EMB1276   acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative, strong similarity to Acetoacetyl-coenzyme A thiolase (E.C. 2.3.1.9) (Raphanus sativus) GI:1542941; contains InterPro accession IPR002155: Thiolase   chr5:19569241-19572755 REVERSE   Aliases: EMB1276, EMBRYO DEFECTIVE 1276, MIF21.12, MIF21_12	7.6	8.6	-0.9	-1.3	100.0%	-4.1
5203	AT4G04860.1   Der1-like family protein / degradation in the ER-like family protein, contains Pfam profile: PF04511 Der1-like family   chr4:2459878-2461737 FORWARD   Aliases: T4B21.2, T4B21_2	6.1	5.6	0.5	1.3	100.0%	-4.2
5204	AT3G23605.1   UBX domain-containing protein, contains Pfam profile PF00789: UBX domain	6.5	6.0	0.5	1.3	100.0%	-4.0
5205	AT5G38730.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:15528131-15529921 FORWARD   Aliases: MKD10.5, MKD10_5	5.2	4.9	0.4	1.3	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5206	AT4G16330.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonone-3-hydroxylase (naringenin,2-oxoglutarate 3-dioxygenase) from Malus domestica (SP:Q06942), Pyrus communis (GI:20269881); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily	10.8	10.4	0.4	1.3	100.0%	-4.5
5207	AT3G28050.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575; contains Pfam profile PF00892: Integral membrane protein   chr3:10444054-10446622 FORWARD   Aliases: MMG15.22	5.5	4.7	0.8	1.3	100.0%	-3.8
5208	AT5G16660.1   expressed protein   chr5:5465490-5467066 REVERSE   Aliases: MTG13.11, MTG13_11	8.4	8.1	0.3	1.3	100.0%	-4.2
5209	AT5G66780.1   expressed protein   chr5:26680799-26681629 FORWARD   Aliases: MUD21.2, MUD21_2	3.8	4.3	-0.5	-1.3	100.0%	-3.7
5210	AT5G09660.2   Symbol: PMDH2   similar to malate dehydrogenase, glyoxysomal, putative [Arabidopsis thaliana] (TAIR:At2g22780.1); similar to malate dehydrogenase 1 [Brassica napus] (GB:CAB43994.1); contains InterPro domain Malate dehydrogenase, active site (InterPro:IPR001252); contains InterPro domain Lactate/malate dehydrogenase (InterPro:IPR001236)   chr5:2993445-2995308 REVERSE   Aliases: F17I14.150, F17I14_150, PEROXISOMAL NAD MALATE DEHYDROGENASE 2, PMDH2	7.2	6.5	0.7	1.3	100.0%	-3.5
5211	AT3G06150.1   expressed protein   chr3:1861803-1864122 REVERSE   Aliases: F28L1.9, F28L1_9	4.9	5.1	-0.2	-1.3	100.0%	-4.5
5212	AT1G73130.1   expressed protein   chr1:27502696-27505557 FORWARD   Aliases: T18K17.21, T18K17_21	4.9	5.3	-0.4	-1.3	100.0%	-4.1
5213	AT1G67370.1   Symbol: ASY1   meiotic asynaptic mutant 1 (ASY1), identical to meiotic asynaptic mutant 1 (Arabidopsis thaliana) GI:7939627; contains Pfam profiles PF02301: DNA-binding HORMA domain, PF04433: SWIRM domain   chr1:25242780-25247500 REVERSE   Aliases: ASY1, ASYNAPTIC 1, F1N21.19	4.3	3.9	0.3	1.3	100.0%	-4.1
5214	AT5G05290.1   Symbol: ATEXPA2   expansin, putative (EXP2), identical to expansin At-EXP2 (Arabidopsis thaliana) gi:1041708:gb:AAB38073; alpha-expansin gene family, PMID:11641069   chr5:1568695-1569865 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A2, ATEXP2, ATHEXP ALPHA 1.12, EXP2, EXPANSIN 2, K18I23.9, K18I23_9	3.8	3.5	0.3	1.3	100.0%	-4.3
5215	AT3G09150.3   Symbol: HY2   phytochromobilin:ferredoxin oxidoreductase, chloroplast / phytochromobilin synthase (HY2), identical to SP:Q9SR43 Phytochromobilin:ferredoxin oxidoreductase, chloroplast precursor (EC 1.3.7.4) (Phytochromobilin synthase) (PFB synthase) (PPhiB synthase) {Arabidopsis thaliana}; identical to cDNA for phytochromobilin synthase HY2 protein, GI:13359272   chr3:2803615-2805569 FORWARD   Aliases: ELONGATED HYPOCOTYL 2, F3L24.1, GENOMES UNCOUPLED 3, GUN3, PHYTOCHROMOBILIN SYNTHASE	4.7	5.2	-0.5	-1.3	100.0%	-3.8
5216	AT5G08740.1   pyridine nucleotide-disulphide oxidoreductase family protein, similar to DhnA (Synechococcus sp. PCC 7942) GI:15620546; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr5:2848507-2851424 REVERSE   Aliases: None	4.2	4.5	-0.3	-1.3	100.0%	-4.4
5217	AT5G65350.1   histone H3, nearly identical to histone H3 from Zea mays SP:P05203, Medicago sativa GI:166384, Encephalartos altensteinii SP:P08903, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:26136437-26137051 REVERSE   Aliases: MNA5.8, MNA5_8	3.0	2.8	0.2	1.3	100.0%	-4.6
5218	AT4G08930.1   Symbol: ATAPRL6   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily. This protein also belongs to the adenosine 5'-phosphosulfate reductase-like (APRL) group.   chr4:5729189-5730858 FORWARD   Aliases: APR LIKE 6, ATAPRL6, T3H13.4, T3H13_4	5.8	5.3	0.5	1.3	100.0%	-3.8
5219	AT3G01290.1   band 7 family protein, similar to hypersensitive-induced response protein (Zea mays) GI:7716470; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr3:88064-89429 REVERSE   Aliases: T22N4.8, T22N4_8	4.0	3.4	0.7	1.3	100.0%	-3.6
5220	AT5G11490.1   adaptin family protein, similar to SP:Q9WV76 Adapter-related protein complex 4 beta 1 subunit (Beta subunit of AP- 4) {Mus musculus}, beta-adaptin Drosophila 1 {Drosophila melanogaster} GI:434902; contains Pfam profile: PF01602 Adaptin N terminal region   chr5:3671838-3676305 FORWARD   Aliases: F15N18.80, F15N18_80	6.3	6.7	-0.4	-1.3	100.0%	-3.9
5221	AT5G03740.1   Symbol: HD2C   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:981896-984201 FORWARD   Aliases: F17C15.160, F17C15_160, HISTONE DEACETYLASE 2C	9.2	9.5	-0.3	-1.3	100.0%	-4.3
5222	AT2G46750.1   FAD-binding domain-containing protein, low similarity to SP:P58710 L-gulonolactone oxidase (EC 1.1.3.8) {Mus musculus}; contains Pfam profile PF01565: FAD binding domain   chr2:19215390-19218028 REVERSE   Aliases: F19D11.3	3.3	3.9	-0.5	-1.3	100.0%	-3.7
5223	AT1G66750.1   Symbol: CDKD1;2   cell division protein kinase, putative, similar to cell division protein kinase 7 (Homo sapiens) SWISS-PROT:P50613   chr1:24898399-24900911 FORWARD   Aliases: CDKD1;2, Cyclin dependent kinase D1;2, F4N21.12, F4N21_12	5.2	5.6	-0.4	-1.3	100.0%	-4.2
5224	AT4G20460.1   NAD-dependent epimerase/dehydratase family protein, similar to UDP-galactose 4-epimerase from Cyamopsis tetragonoloba GI:3021357 (EMBL:AJ005082), Bacillus subtilis SP:P55180; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family   chr4:11029747-11031583 REVERSE   Aliases: F9F13.110, F9F13_110	4.4	4.9	-0.5	-1.3	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5225	AT3G55870.1   anthranilate synthase, alpha subunit, putative, similar to anthranilate synthase alpha subunit, Ruta graveolens, EMBL:RGANTSYNB (gi:960291), Arabidopsis thaliana (SP:P32068)   chr3:20741837-20744882 FORWARD   Aliases: F27K19.50	3.2	3.1	0.2	1.3	100.0%	-4.7
5226	AT5G08139.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:2616346-2617865 FORWARD   Aliases: None	5.9	5.5	0.3	1.3	100.0%	-4.3
5227	AT2G19290.1   expressed protein   chr2:8373001-8374104 REVERSE   Aliases: F27F23.9, F27F23_9	2.5	2.4	0.2	1.3	100.0%	-5.0
5228	AT4G03410.2   peroxisomal membrane protein-related, contains weak similarity to Swiss-Prot:P42925 22 kDa peroxisomal membrane protein (Mus musculus)   chr4:1501167-1503560 FORWARD   Aliases: F9H3.2	4.1	3.8	0.3	1.3	100.0%	-4.1
5229	AT3G49890.1   expressed protein, lea32, Arabidopsis thaliana, EMBL:ATH131342   chr3:18510221-18511705 FORWARD   Aliases: T16K5.240	4.9	5.6	-0.7	-1.3	100.0%	-4.0
5230	AT1G44810.1   expressed protein, contains Pfam profile: PF04504 protein of unknown function, DUF573   chr1:16925983-16927261 FORWARD   Aliases: T12C22.8, T12C22_8	6.1	5.8	0.3	1.3	100.0%	-4.3
5231	AT1G49700.1   expressed protein, ; expression supported by MPSS   chr1:18392460-18393976 REVERSE   Aliases: F14J22.9, F14J22_9	3.5	3.2	0.3	1.3	100.0%	-4.4
5232	AT3G21780.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:7675058-7676353 REVERSE   Aliases: MSD21.11	3.8	3.4	0.4	1.3	100.0%	-3.9
5233	AT5G09930.1   Symbol: ATGCN2	2.9	2.8	0.2	1.3	100.0%	-4.7
5234	AT5G13810.1   glutaredoxin family protein   chr5:4455354-4457022 FORWARD   Aliases: MAC12.24, MAC12_24	6.6	6.2	0.4	1.3	100.0%	-4.2
5235	AT3G04840.1   40S ribosomal protein S3A (RPS3aA), similar to 40S ribosomal protein S3A (S phase specific protein GBIS289) GB:P49396 (Brassica rapa)   chr3:1329699-1331581 FORWARD   Aliases: T9J14.21, T9J14_21	10.1	10.6	-0.5	-1.3	100.0%	-4.2
5236	AT5G09850.1   transcription elongation factor-related, low similarity to SP:P10712 Transcription elongation factor S-II (Transcription elongation factor A) {Mus musculus}   chr5:3063252-3065890 REVERSE   Aliases: MYH9.6, MYH9_6	4.9	5.5	-0.6	-1.3	100.0%	-4.0
5237	AT3G58450.2   universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family   chr3:21632979-21634131 FORWARD   Aliases: F14P22.40	3.4	3.1	0.3	1.3	100.0%	-4.4
5238	AT3G44520.1   esterase/lipase/thioesterase family protein, similar to SP:Q02104 Lipase 1 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Psychrobacter immobilis}; contains Interpro entry IPR000379   chr3:16121387-16122126 REVERSE   Aliases: F14L2.70	2.9	2.7	0.2	1.3	100.0%	-4.6
5239	AT5G19280.1   Symbol: KAPP   kinase associated protein phosphatase (KAPP), identical to Kinase associated protein phosphatase (SP:P46014) (Arabidopsis thaliana); contains Pfam PF00481: Protein phosphatase 2C domain; contains Pfam PF00498: FHA domain   chr5:6488365-6493441 FORWARD   Aliases: F7K24.30, F7K24_30, KAPP, KINASE ASSOCIATED PROTEIN PHOSPHATASE, RAG1, ROOT ALTERNATED GROWTH 1, T24G5.3	6.4	6.0	0.4	1.3	100.0%	-4.0
5240	AT4G01320.1   Symbol: ATSTE24   CAAX protease, putative (STE24), contains Pfam domain, PF01435: Peptidase family M48   chr4:545796-549261 FORWARD   Aliases: ATSTE24, F2N1.21, F2N1_21, STE24	8.5	9.0	-0.5	-1.3	100.0%	-4.2
5241	AT1G04830.1   RabGAP/TBC domain-containing protein, low similarity to SP:Q08484 GTPase-activating protein GYP1 {Saccharomyces cerevisiae}; contains Pfam profile PF00566: TBC domain   chr1:1358916-1361980 REVERSE   Aliases: F13M7.18, F13M7_18	5.6	5.2	0.4	1.3	100.0%	-4.1
5242	AT2G04340.1   expressed protein   chr2:1513555-1515400 FORWARD   Aliases: T23O15.19	5.9	5.5	0.5	1.3	100.0%	-4.1
5243	AT4G20440.3   Symbol: SMB   similar to small nuclear ribonucleoprotein associated protein B, putative / snRNP-B, putative / Sm protein B, putative [Arabidopsis thaliana] (TAIR:At5g44500.1); similar to small nuclear ribonucleoprotein B' [Macropus eugenii] (GB:AAF40115.1); similar to small nuclear ribonucleoprotein-associated protein N - rat (GB:A35448); similar to small nuclear ribonucleoprotein polypeptide B/B' isoform B' [Bos taurus] (GB:AAX46330.1); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Small nuclear ribonucleoprotein (Sm protein) (InterPro:IPR001163)	4.7	5.5	-0.7	-1.3	100.0%	-3.9
5244	AT2G04430.1   similar to MutT/nudix family protein [Arabidopsis thaliana] (TAIR:At2g04450.1); similar to OSJNBa0079A21.19 [Oryza sativa (japonica cultivar-group)] (GB:XP_473408.1); contains InterPro domain Anti-sense to fibroblast growth factor protein GFG (InterPro:IPR003293); contains InterPro domain NUDIX hydrolase (InterPro:IPR000086)   chr2:1538898-1541091 FORWARD   Aliases: T1O3.16, T1O3_16	4.5	4.1	0.5	1.3	100.0%	-3.9
5245	AT3G07350.1   expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506)   chr3:2347474-2348797 FORWARD   Aliases: F21O3.6	5.2	5.6	-0.4	-1.3	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5246	AT5G01610.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:231042-232198 FORWARD   Aliases: F7A7.130, F7A7_130	4.4	3.8	0.5	1.3	100.0%	-3.8
5247	AT3G03860.1   Symbol: ATAPRL5   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily. This protein also belongs to the adenosine 5'-phosphosulfate reductase-like (APRL) group.   chr3:992135-994587 FORWARD   Aliases: APR LIKE 5, ATAPRL5, F20H23.9, F20H23_9	6.1	5.6	0.5	1.3	100.0%	-4.0
5248	AT1G07590.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr1:2336520-2339388 REVERSE   Aliases: F22G5.3, F22G5_3	8.5	8.1	0.3	1.3	100.0%	-4.2
5249	AT1G79710.1   integral membrane transporter family protein, similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554) (Leishmania tarentolae); Interpro IPR001991/ PR00173 Sodium:dicarboxylate symporter family   chr1:30000030-30001881 FORWARD   Aliases: F19K16.31, F19K16_31	5.5	5.0	0.5	1.3	100.0%	-4.1
5250	AT2G15530.2   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:6779996-6784353 FORWARD   Aliases: F9O13.8	6.1	6.3	-0.2	-1.3	100.0%	-4.3
5251	AT1G77580.2   myosin heavy chain-related, low similarity to SP:P08799 Myosin II heavy chain, non muscle {Dictyostelium discoideum}   chr1:29148921-29152478 REVERSE   Aliases: T5M16.17, T5M16_17	3.1	3.3	-0.3	-1.3	100.0%	-4.5
5252	AT1G56660.1   expressed protein   chr1:21241553-21244223 FORWARD   Aliases: F25P12.91, F25P12_91	6.9	6.0	1.0	1.3	100.0%	-4.0
5253	AT5G52660.2   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA-binding domain   chr5:21376285-21379384 REVERSE   Aliases: F6N7.15, F6N7_15	3.9	3.4	0.4	1.3	100.0%	-4.0
5254	AT2G17260.1   Symbol: GLR2   glutamate receptor family protein (GLR3.1) (GLR2), identical to putative glutamate receptor GLR2 (Arabidopsis thaliana) gi:4185740:gb:AAD09174; plant glutamate receptor family, PMID:11379626   chr2:7511838-7515476 FORWARD   Aliases: ATGLR2, ATGLR3.1, F5J6.2, F5J6_2, GLR3.1, GLUTAMATE RECEPTOR 2	4.9	4.6	0.3	1.3	100.0%	-4.1
5255	AT4G36870.2   Symbol: BLH2   similar to BEL1-like homeobox 4 protein (BLH4) [Arabidopsis thaliana] (TAIR:At2g23760.1); similar to BEL1-like homeobox 4 protein (BLH4) [Arabidopsis thaliana] (TAIR:At2g23760.2); similar to BEL1-related homeotic protein 13 [Solanum tuberosum] (GB:AAN03623.1); contains InterPro domain POX (InterPro:IPR006563); contains InterPro domain Homeobox (InterPro:IPR001356)   chr4:17368964-17373927 FORWARD   Aliases: AP22.90, AP22_90, BEL1 LIKE HOMEODOMAIN 2	2.6	2.3	0.3	1.3	100.0%	-4.4
5256	AT3G18180.1   expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)   chr3:6230276-6231884 FORWARD   Aliases: MRC8.18	2.7	2.4	0.2	1.3	100.0%	-4.4
5257	AT1G55970.1   histone acetyltransferase 4 (HAC4), similar to CREB-binding protein GB:AAC51770 GI:2443859 from (Homo sapiens); contains Pfam PF02135: TAZ zinc finger profile; contains Pfam PF00569: Zinc finger, ZZ type domain; identical to histone acetyltransferase HAC4 (GI:14794966) {Arabidopsis thaliana}   chr1:20935794-20941955 REVERSE   Aliases: F14J16.27, F14J16_27	2.7	2.5	0.2	1.3	100.0%	-4.7
5258	AT1G69350.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535: PPR repeat   chr1:26073545-26075908 FORWARD   Aliases: F10D13.4, F10D13_4	2.7	3.0	-0.2	-1.3	100.0%	-4.6
5259	AT1G50740.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)   chr1:18811340-18812667 FORWARD   Aliases: F4M15.3, F4M15_3	8.0	7.7	0.3	1.3	100.0%	-4.4
5260	AT4G23460.1   beta-adaptin, putative, strong similarity to SP:Q10567 Adapter-related protein complex 1 beta 1 subunit (Beta-adaptin 1) (Homo sapiens), beta-adaptin (Drosophila melanogaster) GI:434902; contains Pfam profile: PF01602 Adaptin N terminal region   chr4:12243681-12248960 REVERSE   Aliases: F16G20.160, F16G20_160	6.0	6.6	-0.6	-1.3	100.0%	-3.9
5261	AT3G48960.1   60S ribosomal protein L13 (RPL13C), 60S ribosomal protein L13 (BBC1), Arabidopsis thaliana, gb:X75162   chr3:18161429-18162397 REVERSE   Aliases: T2J13.200	2.7	2.9	-0.2	-1.3	100.0%	-4.6
5262	AT1G59980.1   DNAJ heat shock N-terminal domain-containing protein, similar to Altered Response to Gravity (Arabidopsis thaliana) GI:4249662; contains Pfam profile PF00226 DnaJ domain   chr1:22084454-22087316 FORWARD   Aliases: T2K10.3, T2K10_3	3.4	3.7	-0.3	-1.3	100.0%	-4.2
5263	AT1G80420.2   DNA repair protein, putative (XRCC1), identical to putative DNA repair protein XRCC1 (Arabidopsis thaliana) GI:11181954; contains Pfam domain, PF00533: BRCA1 C Terminus (BRCT) domain   chr1:30240115-30242576 REVERSE   Aliases: T21F11.25, T21F11_25	3.9	4.9	-1.0	-1.3	100.0%	-4.0
5264	AT2G40530.1   expressed protein   chr2:16934580-16935274 FORWARD   Aliases: T2P4.12, T2P4_12	2.7	2.9	-0.2	-1.3	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5265	AT4G18230.1   expressed protein, predicted gene M02B7.4, Caenorhabditis elegans, PID:G1572781   chr4:10080368-10081950 REVERSE   Aliases: T9A21.80, T9A21_80	4.8	4.3	0.4	1.3	100.0%	-3.9
5266	AT1G24575.1   expressed protein   chr1:8711023-8711515 REVERSE   Aliases: None	2.5	2.3	0.1	1.3	100.0%	-5.2
5267	AT4G22753.1   Symbol: SMO1 3	2.3	2.4	-0.2	-1.3	100.0%	-4.6
5268	AT5G20900.1   expressed protein   chr5:7090751-7092541 FORWARD   Aliases: F22D1.70, F22D1_70	9.7	8.9	0.8	1.3	100.0%	-4.2
5269	AT1G09540.1   Symbol: MYB61   myb family transcription factor (MYB61), contains Pfam profile: myb DNA-binding domain PF00249   chr1:3086163-3087914 FORWARD   Aliases: ATMYB61, F14J9.20, F14J9_20	3.6	4.1	-0.5	-1.3	100.0%	-4.0
5270	AT5G57220.1   Symbol: CYP81F2   cytochrome P450, putative, similar to	4.3	4.7	-0.3	-1.3	100.0%	-4.4
5271	AT5G51600.1   Symbol: PLE   microtubule associated protein (MAP65/ASE1) family protein, low similarity to SP:P50275 Anaphase spindle elongation protein {Saccharomyces cerevisiae}, protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr5:20978137-20981306 REVERSE   Aliases: ATMAP65 3, K17N15.15, K17N15_15, PLEIADE	4.3	4.0	0.4	1.3	100.0%	-4.0
5272	AT5G26600.2   expressed protein, weak similarity to SP:P18549 Isopenicillin N epimerase (EC 5.-.-) {Streptomyces clavuligerus}   chr5:9377405-9379800 FORWARD   Aliases: None	7.4	7.1	0.3	1.3	100.0%	-4.3
5273	AT2G43760.1   molybdopterin biosynthesis MoaE family protein, contains Pfam profile: PF02391 molybdopterin converting factor, subunit 2   chr2:18140026-18141047 FORWARD   Aliases: F18O19.13	8.0	7.5	0.5	1.3	100.0%	-4.0
5274	AT1G07880.2   Symbol: ATMPK13   similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK6) [Arabidopsis thaliana] (TAIR:At2g43790.1); similar to NRK1 MAPK [Nicotiana tabacum] (GB:BA32406.1); similar to p43Nft6 serine/threonine protein kinase [Nicotiana tabacum] (GB:CAA58760.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain MAP kinase (InterPro:IPR003527); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:2434056-2435742 REVERSE   Aliases: F24B9.3, F24B9_3	3.7	4.0	-0.3	-1.3	100.0%	-4.3
5275	AT2G32940.1   PAZ domain-containing protein / piwi domain-containing protein, similar to SP:O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}, SP:Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain   chr2:13979295-13983933 REVERSE   Aliases: T21L14.12, T21L14_12	2.2	2.3	-0.1	-1.3	100.0%	-5.0
5276	AT3G52580.1   40S ribosomal protein S14 (RPS14C), ribosomal protein S14 -Zea mays, PIR2:A30097   chr3:19514203-19515902 FORWARD   Aliases: F3C22.6	10.3	10.9	-0.6	-1.3	100.0%	-4.0
5277	AT4G22250.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:11767525-11768464 REVERSE   Aliases: T10I14.80, T10I14_80	3.3	3.6	-0.3	-1.3	100.0%	-4.2
5278	AT1G23050.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:8168432-8169256 FORWARD   Aliases: F19G10.1	3.7	3.4	0.3	1.3	100.0%	-4.4
5279	AT3G07050.1   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function   chr3:2229608-2232352 REVERSE   Aliases: F17A9.21	6.9	8.1	-1.2	-1.3	100.0%	-3.9
5280	AT2G23250.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains similarity to glucosyltransferases   chr2:9904889-9906205 REVERSE   Aliases: T20D16.12, T20D16_12	2.3	2.2	0.1	1.3	100.0%	-5.0
5281	AT3G06510.1   Symbol: SFR2   glycosyl hydrolase family 1 protein, similar to Beta-galactosidase (SP:P22498) (Sulfolobus solfataricus); almost identical to beta-glucosidase GB:AAF23823 GI:6685165 from (Arabidopsis thaliana)   chr3:2016443-2019680 FORWARD   Aliases: F5E6.16, F5E6_16, SENSITIVE TO FREEZING 2	5.7	6.4	-0.6	-1.3	100.0%	-4.3
5282	AT1G72730.1   eukaryotic translation initiation factor 4A, putative / eIF-4A, putative, similar to Eukaryotic initiation factor 4A-10 GB:P41382 (Nicotiana tabacum); identical to (putative) RNA helicase GB:CAA09211 (Arabidopsis thaliana) (Nucleic Acids Res. 27 (2), 628-636 (1999))   chr1:27381460-27383844 REVERSE   Aliases: F28P22.8, F28P22_8	4.7	5.1	-0.3	-1.3	100.0%	-4.4
5283	AT1G64750.2   DSS1/SEM1 family protein, contains Pfam profile PF05160: DSS1/SEM1 family   chr1:24056244-24057568 REVERSE   Aliases: F13O11.6, F13O11_6	8.5	9.0	-0.5	-1.3	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5284	AT3G18130.1   guanine nucleotide-binding family protein / activated protein kinase C receptor (RACK1), identical to guanine nucleotide-binding protein; activated protein kinase C receptor; RACK1 (GI:9294068) {Arabidopsis thaliana}; contains Pfam profile: PF00400 WD domain, G-beta repeat (7 copies)   chr3:6210912-6212439 REVERSE   Aliases: MRC8.11	9.6	10.3	-0.7	-1.3	100.0%	-3.8
5285	AT5G01400.1   expressed protein, contains low similarity to symplekin SP:Q92797 from (Homo sapiens)   chr5:162549-171071 REVERSE   Aliases: T1008.110, T1008_110	4.9	5.5	-0.6	-1.3	100.0%	-4.0
5286	AT1G10570.2   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to EST gb:N96456	5.3	5.7	-0.4	-1.3	100.0%	-4.1
5287	AT1G44835.2   similar to 25.7 kDa protein [Cicer arietinum] (GB:CAB81546.1); contains InterPro domain YbaK/prolyl-tRNA synthetase associated region (InterPro:IPR007214)   chr1:16942246-16944949 FORWARD   Aliases: T12C22.11, T12C22_11	5.7	6.0	-0.4	-1.3	100.0%	-4.1
5288	AT1G43980.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:16688272-16691942 REVERSE   Aliases: F9C16.15, F9C16_15	2.7	2.9	-0.2	-1.3	100.0%	-4.8
5289	AT1G18870.1   isochorismate synthase, putative / isochorismate mutase, putative, similar to GI:17223087   chr1:6515657-6519273 FORWARD   Aliases: F6A14.3, F6A14_3	2.8	3.0	-0.2	-1.3	100.0%	-4.7
5290	AT5G21105.1   L-ascorbate oxidase, putative, similar to L-ascorbate oxidase from {Nicotiana tabacum} SP:Q40588, {Cucurbita pepo var. melopepo} SP:P37064; contains Pfam profile PF00394: Multicopper oxidase; supported by cDNA gi_15215753_gb_AY050406.1; A false intron was added between exons 4 and 5 to circumvent the single nucleotide insertion in this BAC which, otherwise, causes a frameshift.   chr5:7172777-7177749 FORWARD   Aliases: None	8.3	7.1	1.1	1.3	100.0%	-3.6
5291	AT3G27740.1   Symbol: CARA   carbamoyl-phosphate synthase (glutamine-hydrolyzing) (CARA) / glutamine-dependent carbamoyl-phosphate synthase small subunit, identical to carbamoyl phosphate synthetase small subunit GI:2462781 (Arabidopsis thaliana)   chr3:10282498-10285103 REVERSE   Aliases: CARBAMOYL PHOSPHATE SYNTHETASE A, CARBAMOYL PHOSPHATE SYNTHETASE SMALL SUBUNIT, MGF10.14	7.9	8.6	-0.8	-1.3	100.0%	-3.9
5292	AT3G02350.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr3:479013-481481 FORWARD   Aliases: F11A12.4, F11A12_4	5.6	6.3	-0.6	-1.3	100.0%	-3.9
5293	AT1G21480.2   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr1:7518980-7521461 REVERSE   Aliases: F24J8.10, F24J8_10	5.7	6.0	-0.3	-1.3	100.0%	-4.3
5294	AT5G60710.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to SP:P97280 Inter-alpha-trypsin inhibitor heavy chain H3 precursor {Mesocricetus auratus}; contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF00092: von Willebrand factor type A domain   chr5:24427944-24432294 REVERSE   Aliases: MUP24.2, MUP24_2	3.9	3.5	0.4	1.3	100.0%	-4.1
5295	AT4G04350.1   Symbol: EMB2369   leucyl-tRNA synthetase, putative / leucine--tRNA ligase, putative, similar to SP:P36430 Leucyl-tRNA synthetase (EC 6.1.1.4) (Leucine--tRNA ligase) (LeuRS) {Bacillus subtilis}; contains Pfam profile PF00133: tRNA synthetases class I (I, L, M and V)   chr4:2128088-2133126 FORWARD   Aliases: EMB2369, EMBRYO DEFECTIVE 2369, T19B17.7, T19B17_7	6.0	6.5	-0.4	-1.3	100.0%	-4.2
5296	AT5G57080.1   expressed protein   chr5:23116185-23116594 FORWARD   Aliases: MUL3.2, MUL3_2	3.6	3.9	-0.4	-1.3	100.0%	-4.1
5297	AT1G09400.1   12-oxophytodienoate reductase, putative, similar to OPR1 (GI:3882355) and OPR2 (GI:3882356)   chr1:3033603-3035038 REVERSE   Aliases: F14J9.6, F14J9_6	2.7	2.5	0.2	1.3	100.0%	-4.5
5298	AT5G54095.1   expressed protein   chr5:21969959-21970723 REVERSE   Aliases: None	2.7	2.5	0.2	1.3	100.0%	-4.6
5299	AT3G25230.1   Symbol: ROF1   peptidyl-prolyl cis-trans isomerase / FK506-binding protein (ROF1), identical to rotamase FKBP (ROF1) GB:U49453 (Arabidopsis thaliana) (Mol. Gen. Genet. 252 (5), 510-517 (1996))   chr3:9189444-9192642 FORWARD   Aliases: MJL12.21, ROTAMASE FKBP 1	9.7	10.5	-0.8	-1.3	100.0%	-4.2
5300	AT3G12250.4   Symbol: TGA6   similar to bZIP transcription factor HBP-1b homolog [Arabidopsis thaliana] (TAIR:At5g06950.1); similar to bZIP transcription factor HBP-1b homolog [Arabidopsis thaliana] (TAIR:At5g06950.2); similar to TGA-type basic leucine zipper protein TGA2.1 [Phaseolus vulgaris] (GB:AAK84889.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr3:3906358-3908590 FORWARD   Aliases: BZIP45, F28J15.6	3.9	3.4	0.5	1.3	100.0%	-3.9
5301	AT1G64190.1   6-phosphogluconate dehydrogenase family protein, contains Pfam profiles: PF00393 6-phosphogluconate dehydrogenase C-terminal domain, PF03446 NAD binding domain of 6-phosphogluconate   chr1:23828991-23830799 REVERSE   Aliases: F22C12.5, F22C12_5	11.2	11.4	-0.3	-1.3	100.0%	-4.7
5302	AT1G60730.2   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:22361700-22363814 REVERSE   Aliases: F8A5.24, F8A5_24	4.4	4.9	-0.4	-1.3	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5303	AT3G27050.1   expressed protein   chr3:9979396-9980901 REVERSE   Aliases: MOJ10.12	8.6	8.2	0.5	1.3	100.0%	-4.2
5304	AT3G08660.1   phototropic-responsive protein, putative, contains similarity to root phototropism RPT2 (Arabidopsis thaliana) gi:6959488:gb:AAF33112, a signal transducer of phototropic response PMID:10662859	3.2	3.0	0.1	1.3	100.0%	-5.0
5305	AT1G16820.1   vacuolar ATP synthase catalytic subunit-related / V-ATPase-related / vacuolar proton pump-related, similar to Vacuolar ATP synthase catalytic subunit A (V-ATPase A subunit) (Vacuolar proton pump alpha subunit) (V-ATPase 69 kDa subunit) (SP:O23654) (Arabidopsis thaliana)   chr1:5756401-5758457 REVERSE   Aliases: F17F16.15	3.6	3.4	0.3	1.3	100.0%	-4.2
5306	AT1G20700.1   homeobox-leucine zipper family protein, strong similarity to homeodomain protein PALE-2 (GI:20152544) (Arabidopsis thaliana); contains Pfam profile: PF00046 homeobox domain   chr1:7182548-7183999 FORWARD   Aliases: F2D10.19, F2D10_19	5.1	4.7	0.4	1.3	100.0%	-3.9
5307	AT1G23380.2   Symbol: KNAT6   homeobox transcription factor (KNAT6), nearly identical to homeodomain transcription factor KNAT6 (KNAT6L) GI:15991302 (Arabidopsis thaliana), homeodomain transcription factor KNAT6 (KNAT6S) (Arabidopsis thaliana) GI:15991300   chr1:8297280-8302472 REVERSE   Aliases: F26F24.32, F26F24_32, KNAT6L, KNAT6S	5.3	4.8	0.6	1.3	100.0%	-4.2
5308	AT4G22720.2   glycoprotease M22 family protein, similar to sialylglycoprotease (Haemophilus ducreyi) GI:6942294; contains Pfam profile PF00814: Glycoprotease family   chr4:11937075-11938977 FORWARD   Aliases: T12H17.110, T12H17_110	7.3	7.6	-0.3	-1.3	100.0%	-4.2
5309	AT3G44620.1   similar to protein tyrosine phosphatase-like protein [Oryza sativa (japonica cultivar-group)] (GB:AAO72543.1); contains InterPro domain Low molecular weight phosphotyrosine protein phosphatase (InterPro:IPR000106)   chr3:16204816-16206820 FORWARD   Aliases: T18B22.20	4.0	4.4	-0.4	-1.3	100.0%	-4.1
5310	AT4G26130.1   expressed protein   chr4:13240015-13241292 REVERSE   Aliases: F20B18.240, F20B18_240	2.9	2.7	0.2	1.3	100.0%	-5.0
5311	AT4G35560.1   expressed protein   chr4:16881567-16887024 FORWARD   Aliases: F8D20.70, F8D20_70	5.1	5.7	-0.6	-1.3	100.0%	-3.8
5312	AT3G54300.1   Symbol: ATVAMP727   synaptobrevin family protein, similar to vesicle-associated membrane protein 7B (At VAMP7B), Arabidopsis thaliana, EMBL:AF025333   chr3:20119187-20121624 REVERSE   Aliases: F24B22.260, VAMP727	9.3	8.3	1.0	1.3	100.0%	-3.7
5313	AT5G49010.1   DNA replication protein-related, similar to Sld5 (Xenopus laevis) GI:29365477; contains Pfam profile PF05916: Eukaryotic protein of unknown function (DUF873)   chr5:19883690-19885367 FORWARD   Aliases: K19E20.14, K19E20_14	7.0	7.7	-0.7	-1.3	100.0%	-3.7
5314	AT3G09630.2   similar to 60S ribosomal protein L4/L1 (RPL4D) [Arabidopsis thaliana] (TAIR:At5g02870.1); similar to PREDICTED OJ1014_E09.28 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_507356.1); contains InterPro domain Ribosomal protein L4/L1e (InterPro:IPR002136)   chr3:2953742-2955753 FORWARD   Aliases: F11F8.22	12.1	12.5	-0.4	-1.3	100.0%	-4.7
5315	AT3G14600.1   60S ribosomal protein L18A (RPL18aC), similar to GB:CAA08791 from (Podocoryne carnea)   chr3:4910704-4912180 FORWARD   Aliases: MIE1.10	10.0	10.6	-0.6	-1.3	100.0%	-3.9
5316	AT1G55690.3   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus) and Phosphatidylinositol Transfer Protein GB:2780955 GI:2780955 (Saccharomyces cerevisiae)	4.1	4.4	-0.3	-1.3	100.0%	-4.1
5317	AT5G66440.1   expressed protein   chr5:26547461-26548323 REVERSE   Aliases: K1F13.9, K1F13_9	9.4	8.7	0.7	1.3	100.0%	-3.9
5318	AT1G53340.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr1:19902596-19904599 REVERSE   Aliases: F12M16.24, F12M16_24	4.8	4.0	0.9	1.3	100.0%	-3.8
5319	AT5G44020.1   acid phosphatase class B family protein, similar to SP:P15490 STEM 28 kDa glycoprotein precursor (Vegetative storage protein A) {Glycine max}, acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr5:17729638-17731563 FORWARD   Aliases: MRH10.13, MRH10_13	3.5	3.2	0.3	1.3	100.0%	-4.1
5320	AT1G72160.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to GI:807956 from (Saccharomyces cerevisiae) similar to polyphosphoinositide binding protein Ssh2p (GI:2739046) {Glycine max}; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus   chr1:27157243-27159326 REVERSE   Aliases: T9N14.8, T9N14_8	6.1	6.8	-0.7	-1.3	100.0%	-3.8
5321	AT3G01770.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr3:275418-278792 REVERSE   Aliases: F28J7.10	10.0	10.4	-0.4	-1.3	100.0%	-4.3
5322	AT5G08640.1   Symbol: FLS   flavonol synthase 1 (FLS1), identical to SP:Q96330; contains PF03171 2OG-Fe(II) oxygenase superfamily   chr5:2803959-2805448 FORWARD   Aliases: FLAVONOL SYNTHASE, T2K12.5	3.6	4.2	-0.6	-1.3	100.0%	-3.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5323	AT4G14190.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At3g42630.1); similar to pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_483365.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr4:8183539-8185182 REVERSE   Aliases: DL3135C, FCAALL.115	5.0	4.7	0.3	1.3	100.0%	-4.2
5324	AT2G46450.1   Symbol: ATCNGC12   cyclic nucleotide-regulated ion channel, putative (CNGC12), similar to cyclic nucleotide and calmodulin-regulated ion channel (cngc3) Gl:4581201 from (Arabidopsis thaliana)	6.9	6.3	0.6	1.3	100.0%	-3.8
5325	AT1G51950.1   Symbol: IAA18   auxin-responsive protein / indoleacetic acid-induced protein 18 (IAA18), identical to SP:O24408:AXII_ARATH Auxin-responsive protein IAA18 (Indoleacetic acid-induced protein 18) {Arabidopsis thaliana}	6.2	5.8	0.4	1.3	100.0%	-4.0
5326	AT4G21850.2   methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein, low similarity to pilin-like transcription factor (Homo sapiens) Gl:5059062, SP:P14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) {Neisseria gonorrhoeae}; contains Pfam profile PF01641: SelR domain   chr4:11591128-11592250 REVERSE   Aliases: T8O5.60, T8O5_60	5.0	4.3	0.7	1.3	100.0%	-3.7
5327	AT1G12910.1   Symbol: AN11   flower pigmentation protein (AN11), contains 3 WD-40 repeats (PF00400); identical to GB:AAC18912 from (Arabidopsis thaliana) (Genes Dev. 11 (11), 1422-1434 (1997))   chr1:4394899-4396289 REVERSE   Aliases: ATAN11, F13K23.16, F13K23_16	9.5	8.8	0.7	1.3	100.0%	-4.3
5328	AT3G09250.1   expressed protein   chr3:2839007-2840871 FORWARD   Aliases: F3L24.12	6.0	5.7	0.3	1.3	100.0%	-4.1
5329	AT5G27650.1   PWWP domain-containing protein, hypothetical protein F22F7.12 - Arabidopsis thaliana, EMBL:AC009606   chr5:9785410-9789235 FORWARD   Aliases: T1G16.4	4.4	4.7	-0.3	-1.3	100.0%	-4.4
5330	AT5G67230.1   glycosyl transferase family 43 protein, low similarity to Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1, Homo sapiens (SP:Q9P2W7), Rattus norvegicus (SP:O35789); contains Pfam domain Glycosyltransferase family 43 (PF03360)   chr5:26839704-26841905 FORWARD   Aliases: K21H1.19, K21H1_19	3.9	3.7	0.3	1.3	100.0%	-4.3
5331	AT1G24140.1   matrixin family protein, similar to matrix metalloproteinase (Cucumis sativus) Gl:7159629; contains InterPro accession IPR001818: Matrixin   chr1:8536034-8537376 REVERSE   Aliases: F3I6.6, F3I6_6	3.0	3.3	-0.2	-1.3	100.0%	-4.5
5332	AT3G14620.1   Symbol: CYP72A8   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4914921-4917083 FORWARD   Aliases: MIE1.12	5.0	4.5	0.5	1.3	100.0%	-3.8
5333	AT2G38100.1   proton-dependent oligopeptide transport (POT) family protein, low similarity to SP:P46032 Peptide transporter PTR2-B (Histidine transporting protein) {Arabidopsis thaliana}; contains Pfam profile PF00854: POT family   chr2:15955562-15957306 REVERSE   Aliases: F16M14.3, F16M14_3	3.6	3.4	0.2	1.3	100.0%	-4.7
5334	AT3G25290.2   similar to auxin-responsive protein, putative [Arabidopsis thaliana] (TAIR:At4g12980.1); similar to putative auxin-induced protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483411.1); contains InterPro domain Cytochrome b561 / ferric reductase transmembrane (InterPro:IPR006593); contains InterPro domain Protein of unknown function DUF568 (InterPro:IPR007613); contains InterPro domain DOMON domain (InterPro:IPR005018)   chr3:9210178-9211824 FORWARD   Aliases: MJL12.25	6.4	7.0	-0.6	-1.3	100.0%	-3.8
5335	AT1G08110.4   similar to lactoylglutathione lyase, putative / glyoxalase I, putative [Arabidopsis thaliana] (TAIR:At1g67280.1); similar to Glyoxalase I [Cicer arietinum] (GB:CAA12028.1); contains InterPro domain Glyoxalase I (InterPro:IPR004361); contains InterPro domain Glyoxalase/Bleomycin resistance protein/dioxygenase domain (InterPro:IPR004360)   chr1:2535368-2537928 FORWARD   Aliases: T6D22.20, T6D22_20	10.5	9.5	0.9	1.3	100.0%	-3.8
5336	AT5G14640.1   protein kinase family protein, similar to glycogen synthase kinase-3 homolog MsK-3 SP:P51139 from (Medicago sativa); contains Pfam profile PF00069: Protein kinase domain   chr5:4719087-4722282 REVERSE   Aliases: T15N1.130, T15N1_130	6.1	5.7	0.4	1.3	100.0%	-4.3
5337	AT1G02640.1   Symbol: BXL2   glycosyl hydrolase family 3 protein, similar to beta-xylosidase GB:Z84377 Gl:2102655 from (Aspergillus niger)   chr1:564205-567769 FORWARD   Aliases: ATBXL2, BETA XYLOSIDASE 2, T14P4.8, T14P4_8	4.9	5.7	-0.8	-1.3	100.0%	-4.0
5338	AT2G16390.1   Symbol: DRD1   SNF2 domain-containing protein / helicase domain-containing protein, low similarity to RAD54 (Drosophila melanogaster) Gl:1765914; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr2:7104720-7108178 FORWARD   Aliases: CHR35, F16F14.11, F16F14_11	3.3	3.5	-0.2	-1.3	100.0%	-4.4
5339	AT1G71070.1   glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, similar to glucosaminyl (N-acetyl) transferase GB:4758422 from (Homo sapiens)   chr1:26810850-26813166 REVERSE   Aliases: F23N20.6, F23N20_6	4.9	5.5	-0.6	-1.3	100.0%	-4.1
5340	AT5G35970.1   DNA-binding protein, putative, similar to SWISS-PROT:Q60560 DNA-binding protein SMUBP-2 (Immunoglobulin MU binding protein 2, SMUBP-2) (Mesocricetus auratus)   chr5:14136124-14140570 REVERSE   Aliases: MEE13.8, MEE13_8	6.4	6.1	0.3	1.3	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5341	AT2G18630.1   expressed protein, unusual splice site at second intron; GA instead of conserved GT at donor site; similar to At14a GI:11994571 and GI:11994573 (Arabidopsis thaliana)   chr2:8087640-8089721 FORWARD   Aliases: F24H14.1	6.3	6.8	-0.6	-1.3	100.0%	-3.8
5342	AT5G57410.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g18876.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG08075.1)   chr5:23282130-23285030 REVERSE   Aliases: MSF19.7, MSF19_7	5.7	6.3	-0.6	-1.3	100.0%	-3.9
5343	AT1G68680.1   expressed protein   chr1:25789169-25790587 FORWARD   Aliases: F24J5.21, F24J5_21	7.6	8.1	-0.5	-1.3	100.0%	-4.0
5344	AT5G64950.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr5:25971070-25972386 FORWARD   Aliases: MXK3.18, MXK3_18	6.1	6.4	-0.4	-1.3	100.0%	-4.1
5345	AT3G55090.1   ABC transporter family protein, ATP-binding cassette-sub-family G-member 2, Mus musculus, EMBL:AF140218   chr3:20427319-20429481 REVERSE   Aliases: T15C9.80	3.0	3.5	-0.4	-1.3	100.0%	-3.9
5346	AT1G03270.1   expressed protein, contains Pfam profile PF01595: Domain of unknown function   chr1:799191-802436 FORWARD   Aliases: F15K9.13, F15K9_13	5.0	5.8	-0.8	-1.3	100.0%	-3.9
5347	AT3G27120.1   spastin ATPase, putative, similar to SWISS-PROT:Q9QYY8 spastin (Fragment) (Mus musculus); contains Pfam domain, PF00004: ATPase, AAA family   chr3:10000931-10003372 REVERSE   Aliases: MOJ10.20	3.6	3.9	-0.2	-1.3	100.0%	-4.4
5348	AT1G14700.1   purple acid phosphatase, putative, contains Pfam profile: PF00149 calcineurin-like phosphoesterase; similar to purple acid phosphatase (GI:20257479) (Arabidopsis thaliana)   chr1:5058675-5061052 FORWARD   Aliases: F10B6.10, F10B6_10	2.4	2.6	-0.2	-1.3	100.0%	-4.8
5349	AT1G06640.2   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967); contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family   chr1:2032344-2034013 FORWARD   Aliases: F12K11.27, F12K11_27	10.9	10.5	0.4	1.3	100.0%	-4.6
5350	AT2G02660.1   expressed protein   chr2:738503-739768 FORWARD   Aliases: T8K22.4, T8K22_4	2.6	2.7	-0.1	-1.3	100.0%	-5.3
5351	AT4G25960.1   similar to multidrug resistance P-glycoprotein, putative [Arabidopsis thaliana] (TAIR:At1g28010.1); similar to multidrug resistance P-glycoprotein (PGP1) [Arabidopsis thaliana] (TAIR:At2g36910.1); similar to P-glycoprotein, putative [Arabidopsis thaliana] (TAIR:At1g10680.1); similar to multidrug resistance P-glycoprotein, putative [Arabidopsis thaliana] (TAIR:At3g28860.1); similar to multidrug resistance P-glycoprotein, putative [Arabidopsis thaliana] (TAIR:At1g27940.1); similar to OSJNBa0036B21.21 [Oryza sativa (japonica cultivar-group)] (GB:XP_472741.1); similar to MDR-like ABC transporter [Oryza sativa (japonica cultivar-group)] (GB:CAD59581.1); similar to P-glycoprotein [Solanum tuberosum] (GB:AAD10836.1); similar to MDR-like ABC transporter [Oryza sativa (japonica cultivar-group)] (GB:XP_467259.1); similar to OSJNBb0079B02.13 [Oryza sativa (japonica cultivar-group)] (GB:XP_474071.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain ABC transporter (InterPro:IPR003439); contains InterPro domain ABC transporter, transmembrane region (InterPro:IPR001140); contains InterPro domain ATP/GTP-binding site motif A (P-loop) (InterPro:IPR001687)   chr4:13177418-13183640 FORWARD   Aliases: F20B18.70, F20B18_70	2.2	2.3	-0.1	-1.3	100.0%	-5.1
5352	AT2G30350.2   endo/excinuclease amino terminal domain-containing protein, contains Pfam domain PF01541: Endo/excinuclease amino terminal domain   chr2:12941314-12942824 REVERSE   Aliases: T9D9.16, T9D9_16	6.2	6.9	-0.7	-1.3	100.0%	-3.7
5353	AT5G64360.4   similar to DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] (TAIR:At5g09540.1); similar to putative AT hook-containing MAR binding protein 1(AHM1) [Oryza sativa (japonica cultivar-group)] (GB:XP_482959.1); contains InterPro domain Heat shock protein DnaJ, N-terminal (InterPro:IPR001623)   chr5:25753566-25755828 REVERSE   Aliases: MSJ1.20, MSJ1_20	5.6	5.1	0.5	1.3	100.0%	-4.0
5354	AT3G24110.1   calcium-binding EF hand family protein, contains Pfam profile: PF00036 EF hand, similar to calcium-modulated proteins   chr3:8704436-8705420 REVERSE   Aliases: MUJ8.1	4.1	4.5	-0.4	-1.3	100.0%	-4.0
5355	AT1G80900.1   magnesium transporter CorA-like family protein (MGT1) (MRS2), low similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg2+ transporter protein   chr1:30403042-30405232 REVERSE   Aliases: F23A5.26, F23A5_26	4.4	4.2	0.2	1.3	100.0%	-4.5
5356	AT3G11500.1   small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein G, putative, similar to SWISS-PROT:Q15357 small nuclear ribonucleoprotein G (snRNP-G, Sm protein G, Sm-G, SmG) (Homo sapiens)   chr3:3621415-3622598 REVERSE   Aliases: F24K9.17	8.5	8.9	-0.3	-1.3	100.0%	-4.3
5357	AT3G21720.1   isocitrate lyase, putative, similar to isocitrate lyase GI:167144 from (Brassica napus)   chr3:7652511-7655950 REVERSE   Aliases: MSD21.4	4.8	4.5	0.3	1.3	100.0%	-4.4
5358	AT2G32920.1   Symbol: ATPDIL2 3   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	5.0	6.1	-1.1	-1.3	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5359	AT2G33390.1   expressed protein   chr2:14158655-14159820 FORWARD   Aliases: F4P9.16, F4P9_16	7.8	7.0	0.8	1.3	100.0%	-4.1
5360	AT3G23940.1   dehydratase family, contains Pfam profile: PF00920 dehydratase family   chr3:8648712-8652564 FORWARD   Aliases: F14O13.18	10.9	11.3	-0.4	-1.3	100.0%	-4.0
5361	AT3G15520.1   peptidyl-prolyl cis-trans isomerase TLP38, chloroplast / thylakoid lumen PPIase of 38 kDa / cyclophilin / rotamase, cyclophylin-type; identical to SP:P82869 Thylakoid lumenal 38 kDa protein, chloroplast precursor (P38) {Arabidopsis thaliana}   chr3:5248936-5252439 REVERSE   Aliases: MJK13.18	4.2	4.5	-0.3	-1.3	100.0%	-4.1
5362	AT5G02910.1   F-box family protein, similar to ribosomal RNA apurinic site specific lyase (Triticum aestivum) GI:6505722; contains F-box domain Pfam:PF00646   chr5:677085-679041 FORWARD   Aliases: F9G14.220, F9G14_220	5.0	4.6	0.3	1.3	100.0%	-4.0
5363	AT5G10070.2   RNase L inhibitor protein-related, contains Pfam profiles PF04034: Domain of unknown function (DUF367), PF04068: Possible metal-binding domain in RNase L inhibitor, RLI	6.5	6.0	0.5	1.3	100.0%	-3.9
5364	AT1G76590.1   zinc-binding family protein, similar to zinc-binding protein (Pisum sativum) GI:16117799; contains Pfam profile PF04640 : Protein of unknown function, DUF597   chr1:28745585-28747101 FORWARD   Aliases: F14G6.19, F14G6_19	4.1	3.3	0.8	1.3	100.0%	-3.7
5365	AT3G56330.1   N2,N2-dimethylguanosine tRNA methyltransferase family protein, low similarity to SP:Q9P804 N(2),N(2)-dimethylguanosine tRNA methyltransferase (EC 2.1.1.32) (tRNA(guanine-26,N(2)-N(2)) methyltransferase) {Schizosaccharomyces pombe}; contains Pfam profile PF02005: N2,N2-dimethylguanosine tRNA methyltransferase   chr3:20901229-20902923 FORWARD   Aliases: T5P19.2	3.8	4.1	-0.3	-1.3	100.0%	-4.3
5366	AT1G79940.2   similar to DNAJ heat shock N-terminal domain-containing protein / sec63 domain-containing protein [Arabidopsis thaliana] (TAIR:At4g21180.1); similar to DNAJ-like Sec63 homologue [Plasmodium falciparum 3D7] (GB:NP_705096.1); contains InterPro domain Heat shock protein DnaJ (InterPro:IPR003095); contains InterPro domain Heat shock protein DnaJ, N-terminal (InterPro:IPR001623); contains InterPro domain Sec63 domain (InterPro:IPR004179)   chr1:30074497-30078232 FORWARD   Aliases: F19K16.10, F19K16_10	9.5	9.9	-0.4	-1.3	100.0%	-4.6
5367	AT4G11350.2   similar to fringe-related protein [Arabidopsis thaliana] (TAIR:At4g23490.1); similar to fringe-related protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD29388.1)   chr4:6901677-6904220 FORWARD   Aliases: F8L21.140, F8L21_140	4.9	5.3	-0.4	-1.3	100.0%	-3.9
5368	AT5G63220.1   expressed protein, contains Pfam PF04190: Protein of unknown function (DUF410)   chr5:25370285-25372707 REVERSE   Aliases: MDC12.19, MDC12_19	2.7	2.9	-0.2	-1.3	100.0%	-4.9
5369	AT2G44030.1   kelch repeat-containing F-box family protein, low similarity to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:18227162-18228304 FORWARD   Aliases: F6E13.16	4.0	3.7	0.3	1.3	100.0%	-4.3
5370	AT1G69690.1   TCP family transcription factor, putative, similar to PCF1 (GI:2580438) and PCF2 ((GI:2580440) Oryza sativa)   chr1:26219887-26221514 FORWARD   Aliases: T6C23.11, T6C23_11	2.8	3.0	-0.2	-1.3	100.0%	-4.5
5371	AT2G36350.1   protein kinase, putative, similar to protein kinase KIPK (KCBP-interacting protein kinase) (Arabidopsis thaliana) gi:7716430:gb:AAF68383	4.3	4.6	-0.4	-1.3	100.0%	-4.0
5372	AT4G28180.1   expressed protein   chr4:13982917-13983687 REVERSE   Aliases: F26K10.60, F26K10_60	3.0	3.2	-0.2	-1.3	100.0%	-4.6
5373	AT5G23830.1   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain   chr5:8033743-8034892 FORWARD   Aliases: MRO11.13, MRO11_13	8.2	7.8	0.5	1.3	100.0%	-4.2
5374	AT5G41410.1   Symbol: BEL1   homeodomain protein (BEL1), identical to cDNA homeobox protein (BEL1) GI:28202124   chr5:16597272-16601236 FORWARD   Aliases: BEL1, BELL 1, MYC6.12, MYC6_12	3.2	2.9	0.3	1.3	100.0%	-4.4
5375	AT5G47170.1   expressed protein, similar to unknown protein (gb AAF26469.1)   chr5:19175735-19176187 REVERSE   Aliases: MQL5.2, MQL5_2	3.6	3.2	0.3	1.3	100.0%	-4.3
5376	AT1G79510.2   expressed protein   chr1:29912906-29914881 REVERSE   Aliases: T8K14.7, T8K14_7	3.9	3.4	0.5	1.3	100.0%	-4.1
5377	AT3G19480.1   D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative, similar to SP:O04130 from (Arabidopsis thaliana)   chr3:6752537-6754791 FORWARD   Aliases: MLD14.34	4.3	3.9	0.4	1.3	100.0%	-3.8
5378	AT2G03060.1   MADS-box family protein   chr2:901613-903568 FORWARD   Aliases: T17M13.23, T17M13_23	2.9	2.7	0.2	1.3	100.0%	-4.8
5379	AT5G13600.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000; contains BTB/POZ domain, Pfam:PF00651   chr5:4380435-4382500 FORWARD   Aliases: T6I14.9	3.9	3.6	0.3	1.3	100.0%	-4.3
5380	AT1G60620.1   Symbol: ATRPAC43   DNA-directed RNA polymerase, putative, identical to RNA polymerase subunit (Arabidopsis thaliana) GI:514324; contains Pfam profile PF01000: RNA polymerase Rpb3/RpoA insert domain   chr1:22334771-22337189 FORWARD   Aliases: RNA POLYMERASE I SUBUNIT 43	5.2	5.5	-0.3	-1.3	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5381	AT1G19000.2   myb family transcription factor, similar to MybSt1 GI:7705206 from (Solanum tuberosum)   chr1:6560783-6562772 REVERSE   Aliases: F14D16.15, F14D16_15	7.1	6.3	0.8	1.3	100.0%	-3.9
5382	AT3G02500.1   expressed protein   chr3:519371-521754 FORWARD   Aliases: F16B3.13, F16B3_13	2.9	3.1	-0.3	-1.3	100.0%	-4.6
5383	AT5G06910.1   Symbol: ATJ6   DNAJ heat shock protein, putative (J6), identical to DnaJ homologue (Arabidopsis thaliana) GI:2689720; contains Pfam profile PF00226 DnaJ domain	7.1	7.9	-0.7	-1.3	100.0%	-3.9
5384	AT1G20300.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr1:7029619-7031525 FORWARD   Aliases: F14O10.10, F14O10_10	5.8	6.1	-0.4	-1.3	100.0%	-4.2
5385	AT2G26360.1   similar to mitochondrial substrate carrier family protein [Arabidopsis thaliana] (TAIR:At2g35800.1); similar to MGC82075 protein [Xenopus laevis] (GB:AAH82409.1); contains InterPro domain Mitochondrial substrate carrier (InterPro:IPR001993); contains InterPro domain Mitochondrial carrier protein (InterPro:IPR002067)   chr2:11227795-11230291 REVERSE   Aliases: T9J22.3, T9J22_3	5.1	5.4	-0.3	-1.3	100.0%	-4.1
5386	AT1G48570.1   zinc finger (Ran-binding) family protein, contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others   chr1:17958528-17961387 REVERSE   Aliases: T1N15.19, T1N15_19	5.0	5.5	-0.5	-1.3	100.0%	-3.8
5387	AT3G20860.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	3.1	4.1	-1.0	-1.3	100.0%	-3.6
5388	AT5G16270.1   Rad21/Rec8-like family protein, weak similarity to cohesion family protein SYN2 (Arabidopsis thaliana) GI:12006360; contains Pfam profiles PF04824: Conserved region of Rad21 / Rec8 like protein, PF04825: N terminus of Rad21 / Rec8 like protein; supporting cDNA gi:18157648:gb:AF400129.1:AF400129   chr5:5316302-5322699 FORWARD   Aliases: T21H19.190, T21H19_190	7.4	6.9	0.5	1.3	100.0%	-4.1
5389	AT2G35950.1   expressed protein   chr2:15111863-15113167 FORWARD   Aliases: F11F19.14, F11F19_14	2.0	2.1	-0.1	-1.3	100.0%	-5.1
5390	AT3G10300.4   similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At5g04170.1); similar to putative fiber protein Fb1 [Oryza sativa (japonica cultivar-group)] (GB:XP_483756.1); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr3:3186326-3188232 FORWARD   Aliases: F14P13.10	5.6	5.2	0.4	1.3	100.0%	-4.2
5391	AT1G62290.2   similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:At1g11910.1); similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:At4g04460.1); similar to aspartic proteinase (EC 3.4.23.-) - cowpea (GB:T11686); similar to ASPR_CUCPE Aspartic proteinase precursor (GB:O04057); similar to aspartic proteinase [Vigna unguiculata] (GB:AAB03843.2); similar to aspartic proteinase [Theobroma cacao] (GB:CAC86004.1); similar to aspartic proteinase 1 [Glycine max] (GB:BAB62890.1); contains InterPro domain Eukaryotic/viral aspartic protease, active site (InterPro:IPR001969); contains InterPro domain Saposin B subdomain (InterPro:IPR008140); contains InterPro domain Saposin-like type B, 2 (InterPro:IPR008138); contains InterPro domain Saposin B (InterPro:IPR008139); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461); contains InterPro domain Saposin-like type B, 1 (InterPro:IPR007856)   chr1:23013576-23017193 REVERSE   Aliases: F19K23.21, F19K23_21	8.7	8.2	0.5	1.3	100.0%	-3.7
5392	AT4G05520.2   calcium-binding EF hand family protein, similar to EH-domain containing protein 1 from {Mus musculus} SP:Q9WVK4, {Homo sapiens} SP:Q9H4M9, receptor-mediated endocytosis 1 from (Caenorhabditis elegans) GI:13487775, GI:13487777, GI:13487779; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:2804448-2807926 FORWARD   Aliases: T1J24.10, T1J24_10	5.7	6.3	-0.6	-1.3	100.0%	-4.0
5393	AT2G26960.1   myb family transcription factor (MYB81), contains PFAM profile: myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB81) mRNA, partial cds GI:3941513   chr2:11513143-11514503 REVERSE   Aliases: T20P8.1, T20P8_1	2.4	2.3	0.1	1.3	100.0%	-5.0
5394	AT5G26710.1   glutamate-tRNA ligase, putative / glutamyl-tRNA synthetase, putative / GluRS, putative, identical to gi:3435196   chr5:9305600-9308774 FORWARD   Aliases: None	10.5	11.0	-0.5	-1.3	100.0%	-4.4
5395	AT5G61240.1   similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:At1g13910.1); similar to Hcr2-0B [Lycopersicon esculentum] (GB:AAC78593.1); similar to putative leucine-rich repeat resistance protein [Solanum demissum] (GB:AAT38740.1); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr5:24646613-24649812 FORWARD   Aliases: MFB13.23, MFB13_23	7.2	7.9	-0.6	-1.3	100.0%	-3.9
5396	AT1G15410.1   aspartate-glutamate racemase family, contains Pfam profile PF:01177 Aspartate-glutamate racemase family; contains TIGRFAM TIGR00035: aspartate racemase; similar to aspartate racemase (GI:5458794){Pyrococcus abyssi}   chr1:5298939-5300898 FORWARD   Aliases: F9L1.36, F9L1_36	5.3	5.0	0.3	1.3	100.0%	-4.2
5397	AT1G78200.2   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase 2C GB:CAA72341 (Medicago sativa); contains Pfam profile: PF00481 Protein phosphatase 2C   chr1:29425231-29426755 FORWARD   Aliases: T11I11.14, T11I11_14	7.3	7.0	0.3	1.3	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5398	AT5G48090.1   expressed protein, ; expression supported by MPSS   chr5:19502460-19505609 FORWARD   Aliases: MDN11.17, MDN11_17	2.9	3.1	-0.2	-1.3	100.0%	-4.6
5399	AT5G06610.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr5:2029898-2033724 FORWARD   Aliases: F15M7.14, F15M7_14	5.4	4.8	0.6	1.3	100.0%	-4.0
5400	AT2G19570.1   Symbol: CDA1   cytidine deaminase (CDD) / cytidine aminohydrolase, identical to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700   chr2:8477460-8478726 REVERSE   Aliases: AT CDA1, CYTIDINE DEAMINASE 1, DESZ, F3P11.17, F3P11_17	7.1	7.4	-0.4	-1.3	100.0%	-4.2
5401	AT1G64530.1   RWP-RK domain-containing protein, similar to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	4.6	5.0	-0.4	-1.3	100.0%	-4.2
5402	AT5G39990.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr5:16021520-16023968 FORWARD   Aliases: MYH19.150, MYH19_150	4.5	5.0	-0.5	-1.3	100.0%	-4.2
5403	AT2G35720.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:O54946 Dnaj homolog subfamily B member 6 (Heat shock protein J2) Mus musculus; contains Pfam profile PF00226 Dnaj domain   chr2:15023749-15027090 FORWARD   Aliases: T20F21.9, T20F21_9	4.7	5.1	-0.3	-1.3	100.0%	-4.1
5404	AT2G47400.1   Symbol: CP12 1	9.4	9.0	0.5	1.3	100.0%	-3.9
5405	AT1G60610.2   expressed protein   chr1:22331577-22333941 REVERSE   Aliases: F8A5.13, F8A5_13	6.4	6.1	0.3	1.3	100.0%	-4.4
5406	AT3G22845.1   emp24/gp25L/p24 protein-related, contains weak similarity to transmembrane protein (GI:1212965) (Homo sapiens)   chr3:8087314-8088754 FORWARD   Aliases: F5N5.1	8.6	9.1	-0.5	-1.3	100.0%	-4.1
5407	AT2G18900.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); related to LACK protective antigen (GI:13625467) (Leishmania donovani)   chr2:8195339-8199567 REVERSE   Aliases: F19F24.10, F19F24_10	5.0	5.3	-0.3	-1.3	100.0%	-4.0
5408	AT1G80940.2   expressed protein   chr1:30415667-30417021 FORWARD   Aliases: F23A5.30, F23A5_30	5.0	4.5	0.5	1.3	100.0%	-3.9
5409	AT2G01280.1   transcription factor IIB (TFIIB) family protein, contains Pfam domain, PF00382: Transcription factor TFIIB repeat   chr2:145675-148783 FORWARD   Aliases: F10A8.16, F10A8_16	2.2	2.1	0.1	1.3	100.0%	-5.1
5410	AT4G32600.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING finger protein 38 (Homo sapiens) GI:21666412; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:15723468-15726105 FORWARD   Aliases: F4D11.200, F4D11_200	7.0	6.7	0.3	1.3	100.0%	-4.3
5411	AT5G11810.1   expressed protein   chr5:3808721-3810749 FORWARD   Aliases: F14F18.1	7.3	7.9	-0.6	-1.3	100.0%	-4.3
5412	AT3G46720.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:17221840-17223333 REVERSE   Aliases: T6H20.250	4.0	4.2	-0.3	-1.3	100.0%	-4.5
5413	AT2G26660.1   SPX (SYG1/Pho81/XPR1) domain-containing protein, low similarity to NUC-2 (Neurospora crassa) GI:1399532, xenotropic and polytropic murine leukemia virus receptor (Mus musculus castaneus) GI:6093320; contains Pfam profile PF03105: SPX domain	6.5	6.2	0.3	1.3	100.0%	-4.1
5414	AT5G27320.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr5:9629095-9631213 FORWARD   Aliases: F21A20.30, F21A20_30	4.4	4.0	0.4	1.3	100.0%	-4.2
5415	AT1G07630.1   protein phosphatase 2C family protein / PP2C family protein, similar to protein phosphatase-2c (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain   chr1:2349094-2351564 FORWARD   Aliases: F24B9.31, F24B9_31	4.7	5.2	-0.5	-1.3	100.0%	-3.8
5416	AT2G14900.1   gibberellin-regulated family protein, similar to SP:P46690 Gibberellin-regulated protein 4 precursor {Arabidopsis thaliana} GASA4; contains Pfam profile PF02704: Gibberellin regulated protein   chr2:6411259-6412412 FORWARD   Aliases: T26I20.6, T26I20_6	3.3	4.0	-0.7	-1.3	100.0%	-3.6
5417	AT4G14270.2   similar to dehydration-induced protein (ERD15) [Arabidopsis thaliana] (TAIR:At2g41430.2); similar to dehydration-induced protein (ERD15) [Arabidopsis thaliana] (TAIR:At2g41430.3); similar to dehydration-induced protein (ERD15) [Arabidopsis thaliana] (TAIR:At2g41430.4); similar to dehydration-induced protein (ERD15) [Arabidopsis thaliana] (TAIR:At2g41430.1); similar to early response to dehydration 15-like protein [Pseudotsuga menziesii var. menziesii] (GB:AAV92278.1); similar to early response to dehydration 15-like protein [Pseudotsuga menziesii var. menziesii] (GB:AAV92296.1)	8.0	7.6	0.4	1.3	100.0%	-4.2
5418	AT5G47440.1   expressed protein, strong similarity to unknown protein (pir::G71442)   chr5:19260797-19262431 REVERSE   Aliases: MNJ7.2, MNJ7_2	3.1	2.9	0.2	1.3	100.0%	-4.7
5419	AT5G16290.2   acetolactate synthase small subunit, putative, similar to gi:5931761 from Nicotiana plumbaginifolia   chr5:5333830-5337747 FORWARD   Aliases: MQK4.1, MQK4_1	7.2	7.8	-0.6	-1.3	100.0%	-3.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5420	AT4G24280.1   Symbol: CPHSC70 1   heat shock protein 70, putative / HSP70, putative, strong similarity to heat shock protein 70 (Arabidopsis thaliana) GI:6746592; similar to heat shock 70 protein - Spinacia oleracea,PID:g2654208   chr4:12589998-12593640 FORWARD   Aliases: CPHSC70 1, T22A6.110, T22A6_110	8.8	9.2	-0.4	-1.3	100.0%	-4.4
5421	AT4G19070.1   cadmium-responsive protein / cadmium induced protein (AS8), identical to cadmium induced protein AS8 SP:P42735 from (Arabidopsis thaliana)   chr4:10446351-10448201 REVERSE   Aliases: T18B16.3	5.2	4.9	0.3	1.3	100.0%	-4.3
5422	AT2G24240.1   potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain   chr2:10317728-10319408 FORWARD   Aliases: F27D4.15, F27D4_15	5.1	5.7	-0.6	-1.3	100.0%	-3.7
5423	AT2G46330.2   Symbol: AGP16   arabinogalactan-protein (AGP16), identical to gi:10880509:gb:AAG24284   chr2:19025581-19026328 REVERSE   Aliases: ARABINO GALACTAN PROTEIN 16, F11C10.2	9.2	8.7	0.6	1.3	100.0%	-4.0
5424	AT5G09430.1   hydrolase, alpha/beta fold family protein, low similarity to hydrolases from Rhodococcus sp. EtbD1 GI:3273239, EtbD2 GI:3273241; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:2932163-2933363 FORWARD   Aliases: T5E8.230, T5E8_230	3.1	3.4	-0.3	-1.3	100.0%	-4.5
5425	AT5G61150.2   Symbol: VIP4   leo1-like family protein, weak similarity to SP:P38439 LEO1 protein {Saccharomyces cerevisiae}; contains Pfam profile PF04004: Leo1-like protein; supporting cDNA gi:21929714:gb:AF490422.1:   chr5:24620882-24624951 REVERSE   Aliases: MAF19.15, MAF19_15, VERNALIZATION INDEPENDENCE 4	6.2	6.8	-0.7	-1.3	100.0%	-4.1
5426	AT1G25470.2   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr1:8944596-8946601 REVERSE   Aliases: F2J7.8, F2J7_8	4.9	5.3	-0.4	-1.3	100.0%	-4.1
5427	AT1G10110.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)	2.8	2.9	-0.1	-1.3	100.0%	-5.1
5428	AT1G21120.1   O-methyltransferase, putative, similar to GI:2781394   chr1:7395221-7396738 REVERSE   Aliases: T22I11.5, T22I11_5	3.8	4.3	-0.5	-1.3	100.0%	-4.1
5429	AT1G02840.3   Symbol: SR1   pre-mRNA splicing factor SF2 (SF2) / SR1 protein, identical to SP:O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}   chr1:626741-629819 FORWARD   Aliases: ATSRP34, F22D16.16, F22D16_16, SRP34	10.1	9.8	0.3	1.3	100.0%	-4.5
5430	AT1G76040.2   Symbol: CPK29   similar to calcium-dependent protein kinase, putative / CDPK, putative [Arabidopsis thaliana] (TAIR:At1g50700.1); similar to calmodulin-domain protein kinase isoform 9 (CPK9) [Arabidopsis thaliana] (TAIR:At3g20410.1); similar to calcium-dependent protein kinase, putative / CDPK, putative [Arabidopsis thaliana] (TAIR:At4g04720.1); similar to calcium-dependent protein kinase, putative / CDPK, putative [Arabidopsis thaliana] (TAIR:At4g21940.1); similar to calcium-dependent protein kinase, putative / CDPK, putative [Arabidopsis thaliana] (TAIR:At1g61950.1); similar to calcium-dependent protein kinase [Oryza sativa (japonica cultivar-group)] (GB:CAA57157.1); similar to Ca2+-dependent protein kinase [Mesembryanthemum crystallinum] (GB:AAD17800.1); similar to calmodulin-like domain protein kinase isoenzyme gamma [Glycine max] (GB:AAB80693.1); similar to calcium-dependent protein kinase [Nicotiana tabacum] (GB:AAC25423.1); similar to PREDICTED P0048D08.105 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_506365.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr1:28542567-28545531 FORWARD   Aliases: T4O12.25, T4O12_25	6.2	5.5	0.7	1.3	100.0%	-4.0
5431	AT5G05370.1   ubiquinol-cytochrome C reductase complex ubiquinone-binding protein, putative / ubiquinol-cytochrome C reductase complex 8.2 kDa protein, putative, strong similarity to SP:P46269 Ubiquinol-cytochrome C reductase complex ubiquinone-binding protein QP-C (EC 1.10.2.2) (Ubiquinol-cytochrome C reductase complex 8.2 kDa protein) {Solanum tuberosum}	10.9	11.1	-0.2	-1.3	100.0%	-4.5
5432	AT5G58160.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, low similarity to SP:Q05858 Formin (Limb deformity protein) {Gallus gallus}; contains Pfam profile PF02181: Formin Homology 2 (FH2) Domain   chr5:23551169-23556691 FORWARD   Aliases: MCK7.3, MCK7_3	3.9	4.3	-0.4	-1.3	100.0%	-4.4
5433	AT3G52090.1   Symbol: ATRPB13.6   DNA-directed RNA polymerase II 13.6 kDa subunit (RPB13.6), identical to SP:Q38859 DNA-directed RNA polymerase II 13.6 kDa polypeptide (EC 2.7.7.6) {Arabidopsis thaliana}   chr3:19328832-19330030 REVERSE   Aliases: F4F15.200, RNA POLYMERASE II 13.6 KDA SUBUNIT	9.9	10.3	-0.4	-1.3	100.0%	-4.4
5434	AT3G18230.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, contains Pfam profile PF00564: PB1 domain   chr3:6251489-6254227 FORWARD   Aliases: MIE15.2	5.9	5.6	0.3	1.3	100.0%	-4.3
5435	AT5G04170.1   calcium-binding EF hand family protein, low similarity to peflin (Homo sapiens) GI:6015440; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:1145432-1147782 FORWARD   Aliases: F21E1.90, F21E1_90	6.5	6.0	0.5	1.3	100.0%	-3.8
5436	AT1G01620.1   Symbol: PIP1C   plasma membrane intrinsic protein 1C (PIP1C) / aquaporin PIP1.3 (PIP1.3) / transmembrane protein B (TMPB), identical to plasma membrane intrinsic protein 1c SP:Q08733 from (Arabidopsis thaliana)   chr1:225722-227302 REVERSE   Aliases: F22L4.16, F22L4_16, PIP1;3, TMP B	3.4	3.8	-0.5	-1.3	100.0%	-4.1
5437	AT3G16780.1   60S ribosomal protein L19 (RPL19B), similar to ribosomal protein L19 GB:CAA45090 from (Homo sapiens)   chr3:5708931-5710415 FORWARD   Aliases: MGL6.7	9.0	9.5	-0.5	-1.3	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5438	AT2G20140.1   26S protease regulatory complex subunit 4, putative, similar to Swiss-Prot:P48601 26S protease regulatory subunit 4 (P26S4) (Drosophila melanogaster)   chr2:8699781-8702160 FORWARD   Aliases: T2G17.6, T2G17_6	7.1	7.8	-0.6	-1.3	100.0%	-3.9
5439	AT2G18320.1   hypothetical protein   chr2:7963302-7964613 FORWARD   Aliases: T30D6.17, T30D6_17	3.1	3.4	-0.3	-1.3	100.0%	-4.6
5440	AT1G68750.1   Symbol: ATPPC4	3.4	3.2	0.2	1.3	100.0%	-4.4
5441	AT5G47090.1   expressed protein   chr5:19144486-19145996 FORWARD   Aliases: K14A3.4, K14A3_4	9.0	8.1	0.9	1.3	100.0%	-3.8
5442	AT3G61540.1   peptidase family protein, similar to prolyl aminopeptidase (proline iminopeptidase) from Aeromonas sobria SP:P46547, Propionibacterium freudenreichii subsp. shermanii GI:2415704, Hafnia alvei GI:1754489   chr3:22784361-22786802 FORWARD   Aliases: F2A19.140	6.8	7.4	-0.5	-1.3	100.0%	-4.3
5443	AT3G52040.1   expressed protein   chr3:19315151-19315839 REVERSE   Aliases: F4F15.150	7.8	8.4	-0.5	-1.3	100.0%	-3.8
5444	AT4G20930.1   3-hydroxyisobutyrate dehydrogenase, putative, similar to SP:P29266 3-hydroxyisobutyrate dehydrogenase, mitochondrial precursor (EC 1.1.1.31) {Rattus norvegicus}; contains Pfam profile PF03446: NAD binding domain of 6-phosphogluconate dehydrogenase   chr4:11198417-11201084 REVERSE   Aliases: T13K14.90, T13K14_90	4.1	4.4	-0.3	-1.3	100.0%	-4.2
5445	AT4G40010.1   serine/threonine protein kinase, putative, similar to serine-threonine protein kinase (Triticum aestivum) gi:2055374:gb:AAB58348	5.2	4.2	0.9	1.3	100.0%	-3.6
5446	AT4G32690.1   Symbol: GLB3   2-on-2 hemoglobin (GLB3), identical to 2-on-2 hemoglobin (GLB3) GI:14165163 from (Arabidopsis thaliana)   chr4:15765436-15766990 FORWARD   Aliases: F4D11.1	7.6	6.8	0.8	1.3	100.0%	-4.0
5447	AT2G42370.1   expressed protein   chr2:17650412-17652611 FORWARD   Aliases: MHK10.9, MHK10_9	3.5	4.2	-0.7	-1.3	100.0%	-4.2
5448	AT2G27170.1   Symbol: TTN7   similar to SMC2-like condensin, putative (SMC2) (TITAN3) [Arabidopsis thaliana] (TAIR:At5g62410.1); similar to cohesin complex subunit [Gallus gallus] (GB:NP_989848.1); similar to chondroitin sulfate proteoglycan 6 [Mus musculus] (GB:NP_031816.2); similar to putative SMC3 protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464029.1); similar to putative SMC3 protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464028.1); similar to chondroitin sulfate proteoglycan 6 (bamacan) [Homo sapiens] (GB:CAI16576.1); contains InterPro domain Structural maintenance of chromosome protein SMC, C-terminal (InterPro:IPR003405); contains InterPro domain SMC protein, N-terminal (InterPro:IPR003395)   chr2:11616397-11624509 REVERSE   Aliases: SMC3, T22O13.6, TITAN7	3.2	4.1	-1.0	-1.3	100.0%	-4.0
5449	AT2G27390.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr2:11727562-11727966 REVERSE   Aliases: F12K2.3, F12K2_3	2.5	2.3	0.2	1.3	100.0%	-4.5
5450	AT1G53210.1   sodium/calcium exchanger family protein / calcium-binding EF hand family protein, contains Pfam profiles: PF01699 sodium/calcium exchanger protein, PF00036 EF hand   chr1:19848300-19851504 FORWARD   Aliases: F12M16.12, F12M16_12	9.7	9.2	0.5	1.3	100.0%	-4.2
5451	AT1G63440.1   copper-exporting ATPase, putative / responsive-to-antagonist 1, putative / copper-transporting ATPase, putative, similar to ATP dependent copper transporter SP:Q9S7J8 (Arabidopsis thaliana)   chr1:23531320-23534774 FORWARD   Aliases: F2K11.18, F2K11_18	7.3	7.6	-0.3	-1.3	100.0%	-4.2
5452	AT3G28345.1   ABC transporter family protein, similar to P-glycoprotein (Arabidopsis thaliana) GI:3849833; contains Pfam profiles PF00005: ABC transporter, PF00664: ABC transporter transmembrane region   chr3:10595158-10600012 REVERSE   Aliases: MFJ20.7	2.4	2.3	0.1	1.3	100.0%	-5.1
5453	AT2G38185.4   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:16007115-16013339 FORWARD   Aliases: None	2.7	2.6	0.2	1.3	100.0%	-4.9
5454	AT3G11630.1   2-cys peroxiredoxin, chloroplast (BAS1), identical to SP:Q96291 2-cys peroxiredoxin BAS1, chloroplast precursor {Arabidopsis thaliana}; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family   chr3:3672126-3674081 FORWARD   Aliases: F24K9.28, F24K9_28, T19F11.3	10.0	10.9	-1.0	-1.3	100.0%	-4.0
5455	AT2G35940.3   Symbol: BLH1   similar to BEL1-like homeobox 4 protein (BLH4) [Arabidopsis thaliana] (TAIR:At2g23760.1); similar to BEL1-like homeobox 4 protein (BLH4) [Arabidopsis thaliana] (TAIR:At2g23760.2); similar to bell-like homeodomain protein 2 [Lycopersicon esculentum] (GB:AAP47025.1); contains InterPro domain POX (InterPro:IPR006563); contains InterPro domain Homeobox (InterPro:IPR001356)   chr2:15095911-15099027 REVERSE   Aliases: BEL1 like homeodomain 1, F11F19.15, F11F19_15	5.2	4.9	0.4	1.3	100.0%	-4.2
5456	AT4G36750.1   quinone reductase family protein, similar to 1,4-benzoquinone reductase (Phanerochaete chrysosporium)(GI:4454993); similar to Trp repressor binding protein (Escherichia coli)(SP:P30849); contains flavodoxin domain PF00258   chr4:17324575-17326462 FORWARD   Aliases: AP22.84, AP22_84	8.3	7.9	0.4	1.3	100.0%	-4.3
5457	AT4G32320.1   peroxidase family protein, similar to L-ascorbate peroxidase (Arabidopsis thaliana) gi:1523789:emb:CAA66925; contains Pfam profile PF00141: Peroxidase   chr4:15602727-15605348 FORWARD   Aliases: F10M6.50, F10M6_50	4.9	4.6	0.3	1.3	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5458	AT2G45350.1   Symbol: CRR4   Encodes a member of a PCMP (plant combinatorial and modular protein) family (PCMP-E subfamily) with 11 pentatricopeptide (PPR) repeats. The protein is involved in RNA editing of the initiation codon of ndhD in the chloroplast.   chr2:18701890-18703710 REVERSE   Aliases: CHLORORESPIRATORY REDUCTION 4, CRR4, F4L23.14	2.9	2.8	0.1	1.3	100.0%	-4.9
5459	AT5G22460.2   esterase/lipase/thioesterase family protein, low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (Rhodococcus sp. RHA1) GI:8978311, SP:Q02104 Lipase 1 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Psychrobacter immobilis}; contains Interpro entry IPR000379   chr5:7443511-7445403 REVERSE   Aliases: MWD9.26, MWD9_26	2.9	2.7	0.2	1.3	100.0%	-4.8
5460	AT1G10130.1   Symbol: ECA3   calcium-transporting ATPase 3, endoplasmic reticulum-type (ACA6) (ECA3), nearly identical to SP:Q9SY55 Calcium-transporting ATPase 3, endoplasmic reticulum-type (EC 3.6.3.8) {Arabidopsis thaliana}; contains InterPro Accession IPR006069: Cation transporting ATPase   chr1:3310932-3322215 FORWARD   Aliases: ATECA3, ENDOPLASMIC RETICULUM TYPE CALCIUM TRANSPORTING ATPASE 3, T2711.16, T2711_16	4.3	4.8	-0.5	-1.3	100.0%	-4.1
5461	AT1G52930.1   brix domain-containing protein, contains Pfam domain, PF04427: Brix domain   chr1:19714905-19716898 FORWARD   Aliases: F14G24.20, F14G24_20	7.5	8.2	-0.7	-1.3	100.0%	-3.9
5462	AT1G15900.1   expressed protein   chr1:5464350-5464691 FORWARD   Aliases: F7H2.24, F7H2_24	3.1	2.9	0.2	1.3	100.0%	-4.8
5463	AT1G18550.1   kinesin motor protein-related, contains similarity to kinesin-related protein GI:4493964 from (Plasmodium falciparum)   chr1:6380922-6384333 REVERSE   Aliases: F25I16.11, F25I16_11	3.7	4.1	-0.4	-1.3	100.0%	-3.8
5464	AT3G15490.1   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	2.4	2.3	0.1	1.3	100.0%	-5.2
5465	AT1G61840.1   DC1 domain-containing protein, similar to hypothetical protein GI:3184279 from (Arabidopsis thaliana); contains Pfam profile PF03107: DC1 domain	3.3	3.1	0.3	1.3	100.0%	-4.7
5466	AT5G52130.1   expressed protein   chr5:21199694-21201101 REVERSE   Aliases: F17P19.2, F17P19_2	2.4	2.3	0.1	1.3	100.0%	-5.0
5467	AT3G15860.1   expressed protein   chr3:5361214-5361726 REVERSE   Aliases: MSJ11.26	2.3	2.2	0.1	1.3	100.0%	-5.1
5468	AT1G69790.1   protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) SWISS-PROT:Q06548   chr1:26270422-26272646 FORWARD   Aliases: T6C23.1, T6C23_1	4.1	3.4	0.7	1.3	100.0%	-3.8
5469	AT2G26160.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.4	0.1	1.3	100.0%	-5.1
5470	AT4G31040.1   proton extrusion protein-related, contains weak similarity to Proton extrusion protein pcxA (Swiss-Prot:P75028) (Synechocystis sp.)   chr4:15111491-15114132 REVERSE   Aliases: F6I18.50, F6I18_50	7.3	7.0	0.3	1.3	100.0%	-4.3
5471	AT3G22230.1   60S ribosomal protein L27 (RPL27B), similar to 60S RIBOSOMAL PROTEIN L27 GB:P41101 from (Solanum tuberosum)   chr3:7843974-7844604 REVERSE   Aliases: MKA23.22	8.9	9.5	-0.5	-1.3	100.0%	-4.0
5472	AT5G03380.2   similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:At2g36950.1); similar to GMFP5 [Glycine max] (GB:AAD09514.1); contains InterPro domain Heavy metal binding (InterPro:IPR006191); contains InterPro domain Heavy metal transport/detoxification protein (InterPro:IPR006121)   chr5:832103-834284 REVERSE   Aliases: F12E4.120, F12E4_120	8.9	8.2	0.8	1.3	100.0%	-3.9
5473	AT3G03490.1   peroxisomal protein PEX19 family protein, contains Pfam profile: PF04614 Pex19 protein family   chr3:830172-831853 REVERSE   Aliases: T21P5.9, T21P5_9	9.4	9.1	0.3	1.3	100.0%	-4.3
5474	AT3G08860.1   alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative, similar to similar to SP:Q64565 Alanine--glyoxylate aminotransferase 2, mitochondrial precursor (EC 2.6.1.44) (AGT 2) (Beta-alanine-pyruvate aminotransferase) {Rattus norvegicus}; contains Pfam profile PF00202: aminotransferase, class III   chr3:2696565-2699164 REVERSE   Aliases: T16O11.21	2.6	2.8	-0.2	-1.3	100.0%	-4.9
5475	AT5G35320.1   expressed protein   chr5:13539049-13540655 FORWARD   Aliases: T26D22.2, T26D22_2	4.6	4.2	0.4	1.3	100.0%	-4.4
5476	AT3G42670.1   Symbol: CHR38   SNF2 domain-containing protein / helicase domain-containing protein, low similarity to SP:P41410 DNA repair protein rhp54 (RAD54 homolog) {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr3:14766784-14771071 REVERSE   Aliases: CHR38, T12K4.120	3.8	4.1	-0.3	-1.3	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5477	AT1G44350.1   Symbol: ILL6   IAA-amino acid hydrolase 6, putative (ILL6) / IAA-Ala hydrolase, putative, virtually identical to gr1-protein from (Arabidopsis thaliana) GI:3559811; similar to IAA-amino acid hydrolase GI:3421384 from (Arabidopsis thaliana); contains TIGRfam profile TIGR01891: amidohydrolase; contains Pfam profile PF01546: Peptidase family M20/M25/M40; identical to cDNA IAA-amino acid conjugate hydrolase-like protein (ILL6), partial cds GI:17978837   chr1:16836650-16840726 REVERSE   Aliases: T18F15.9, T18F15_9	4.7	4.4	0.3	1.3	100.0%	-4.0
5478	AT1G75820.1   Symbol: CLV1   CLAVATA1 receptor kinase (CLV1), identical to receptor kinase (CLV1) GB:AAB58929 GI:2160756 (Arabidopsis thaliana)   chr1:28467123-28470632 REVERSE   Aliases: CLAVATA 1, CLV1 RECEPTOR KINASE PRECURSOR, FAS3, FASCIATA 3, FLO5, FLOWER DEVELOPMENT 5, T4O12.5, T4O12_5	4.5	4.0	0.6	1.3	100.0%	-3.6
5479	AT1G08580.1   expressed protein   chr1:2715086-2716387 REVERSE   Aliases: F22O13.6, F22O13_6	8.6	9.1	-0.5	-1.3	100.0%	-3.9
5480	AT1G48560.1   expressed protein   chr1:17956533-17958973 FORWARD   Aliases: T1N15.18, T1N15_18	4.5	4.8	-0.3	-1.3	100.0%	-4.0
5481	AT4G10810.1   expressed protein   chr4:6645712-6646332 REVERSE   Aliases: F25I24.20, F25I24_20	7.3	6.6	0.7	1.3	100.0%	-3.9
5482	AT5G52180.1   expressed protein   chr5:21217281-21218835 REVERSE   Aliases: F17P19.8, F17P19_8	6.6	6.2	0.4	1.3	100.0%	-4.3
5483	AT1G48830.2   40S ribosomal protein S7 (RPS7A), similar to 40S ribosomal protein S7 homolog GI:5532505 from (Brassica oleracea)   chr1:18063304-18064925 REVERSE   Aliases: F11I4.1, F11I4_1	12.0	12.4	-0.4	-1.3	100.0%	-4.7
5484	AT2G24420.2   DNA repair ATPase-related, contains 2 transmembrane domains; similar to DNA double-strand break repair rad50 ATPase. (Swiss-Prot:O33600) (Sulfolobus acidocaldarius)   chr2:10387117-10390480 FORWARD   Aliases: T28I24.15, T28I24_15	5.2	4.6	0.7	1.3	100.0%	-4.1
5485	AT3G53970.2   proteasome inhibitor-related, similar to proteasome inhibitor PI31 subunit (hPI31) SP:Q92530 from (Homo sapiens)	6.8	6.0	0.8	1.2	100.0%	-4.0
5486	AT2G35600.1   expressed protein   chr2:14948171-14952407 REVERSE   Aliases: T32F12.2, T32F12_2	2.7	2.9	-0.1	-1.2	100.0%	-4.9
5487	AT4G21590.1   bifunctional nuclease, putative, similar to bifunctional nuclease (Zinnia elegans) gi:4099833/gb:AAD00694. Activated by AGAMOUS in a cal-1, ap1-1 background. Expressed in the floral meristem and during stamen development.   chr4:11480379-11482726 FORWARD   Aliases: F17L22.50	3.2	3.0	0.2	1.2	100.0%	-4.5
5488	AT1G16780.1   Symbol: AVPL1   vacuolar-type H <sup>+</sup> -translocating inorganic pyrophosphatase, putative, similar to vacuolar-type H <sup>+</sup> -translocating inorganic pyrophosphatase GI:6901676 from (Arabidopsis thaliana)   chr1:5739292-5743562 REVERSE   Aliases: AVPL1, F17F16.2, F17F16_2, VACUOLAR PYROPHOSPHATASE LIKE PROTEIN 1	5.6	6.1	-0.5	-1.2	100.0%	-3.9
5489	AT4G04620.2   autophagy 8b (APG8b), identical to autophagy 8b (Arabidopsis thaliana) GI:19912153; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3   chr4:2328506-2330134 REVERSE   Aliases: F4H6.14, F4H6_14	8.2	7.7	0.5	1.2	100.0%	-4.4
5490	AT1G64820.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family; contains 12 transmembrane domains, PMID: 11152613   chr1:24092268-24094221 FORWARD   Aliases: F13O11.12, F13O11_12	3.9	3.7	0.2	1.2	100.0%	-4.7
5491	AT5G54160.1   Symbol: ATOMT1	12.4	12.9	-0.5	-1.2	100.0%	-4.7
5492	AT1G10970.1   Symbol: ZIP4   metal transporter, putative (ZIP4), similar to Zn and Cd transporter ZNT1 (Thlaspi caerulescens) gi:7381054/gb:AAF61374; member of the Zinc (Zn <sup>2+</sup> )-Iron (Fe <sup>2+</sup> ) permease (ZIP) family, PMID:11500563   chr1:3665089-3667139 REVERSE   Aliases: T19D16.11, T19D16_11, ZRT, IRT LIKE PROTEIN	5.1	4.6	0.4	1.2	100.0%	-3.8
5493	AT3G18430.1   calcium-binding EF hand family protein, similar to Calcineurin B subunit (Protein phosphatase 2B regulatory subunit) (Calcineurin regulatory subunit) SP:P42322 from (Naegleria gruberi); contains Pfam profile PF00036: EF hand	9.1	8.8	0.3	1.2	100.0%	-4.7
5494	AT3G23280.2   zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) and Pfam profile: PF00023 ankyrin repeat   chr3:8321371-8324435 FORWARD   Aliases: K14B15.19	9.4	8.8	0.7	1.2	100.0%	-4.0
5495	AT5G60140.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:24231303-24232581 REVERSE   Aliases: MGO3.2, MGO3_2	2.9	2.6	0.2	1.2	100.0%	-4.6
5496	AT1G22650.1   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr1:8013371-8015968 REVERSE   Aliases: T22J18.18, T22J18_18	3.8	4.2	-0.3	-1.2	100.0%	-4.3
5497	AT5G10830.1   embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531   chr5:3423687-3425468 FORWARD   Aliases: T30N20.100, T30N20_100	6.8	7.2	-0.4	-1.2	100.0%	-4.2
5498	AT1G78960.1   Symbol: ATLUP2	4.4	3.9	0.4	1.2	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5499	AT4G28600.1   Symbol: NPGR2   calmodulin-binding protein, similar to pollen-specific calmodulin-binding protein MPCBP GI:10086260 from (Zea mays)   chr4:14129421-14132805 FORWARD   Aliases: NO POLLEN GERMINATION RELATED 2, T5F17.50, T5F17_50	6.0	5.5	0.5	1.2	100.0%	-4.3
5500	AT5G63560.1   transferase family protein, similar to hypersensitivity-related gene product HSR201 - Nicotiana tabacum, EMBL:X95343; contains Pfam transferase family domain PF00248   chr5:25466707-25468640 FORWARD   Aliases: MBK5.2, MBK5_2	4.0	4.3	-0.3	-1.2	100.0%	-4.2
5501	AT3G23060.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:8200647-8203240 FORWARD   Aliases: MXC7.9	2.9	2.6	0.3	1.2	100.0%	-4.5
5502	AT1G48580.1   expressed protein   chr1:17961931-17964278 REVERSE   Aliases: T1N15.20, T1N15_20	3.8	4.1	-0.3	-1.2	100.0%	-4.2
5503	AT3G49850.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:18500030-18501981 FORWARD   Aliases: T16K5.200	4.8	5.3	-0.5	-1.2	100.0%	-3.9
5504	AT1G10200.1   transcription factor LIM, putative, strong similarity to transcription factor Ntlm1 (Nicotiana tabacum) GI:5689136, LIM domain protein WLIM-1 (Helianthus annuus) GI:5070280; contains Pfam profile PF00412: LIM domain	7.2	6.5	0.7	1.2	100.0%	-4.3
5505	AT3G47340.3   Symbol: ASN1   asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1), identical to SP:P49078 Asparagine synthetase (glutamine-hydrolyzing) (EC 6.3.5.4) (Glutamine- dependent asparagine synthetase) {Arabidopsis thaliana}   chr3:17448869-17452227 REVERSE   Aliases: AT ASN1, DARK INDUCIBLE 6, DIN6, GLUTAMINE DEPENDENT ASPARAGINE SYNTHETASE, T21L8.90	2.9	3.3	-0.4	-1.2	100.0%	-4.3
5506	AT4G19820.1   glycosyl hydrolase family 18 protein, similar to chitinase/lysozyme GI:467689 from (Nicotiana tabacum)   chr4:10767446-10768624 REVERSE   Aliases: T16H5.180, T16H5_180	2.3	2.5	-0.2	-1.2	100.0%	-4.7
5507	AT4G38620.1   Symbol: MYB4   myb family transcription factor (MYB4), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr4:18053545-18054993 FORWARD   Aliases: ATMYB4, T9A14.11	6.3	6.7	-0.4	-1.2	100.0%	-4.0
5508	AT4G39640.2   gamma-glutamyltranspeptidase family protein, similar to SP:P19440 Gamma-glutamyltranspeptidase 1 precursor (EC 2.3.2.2) (Gamma-glutamyltransferase 1) (CD224 antigen) {Homo sapiens}; contains Pfam profile PF01019: Gamma-glutamyltranspeptidase	3.9	3.6	0.3	1.2	100.0%	-4.3
5509	AT2G42520.1   DEAD box RNA helicase, putative, similar to SP:O00571 DEAD-box protein 3 (Helicase-like protein 2) {Homo sapiens}, DEAD box RNA helicase DDX3 (Homo sapiens) GI:3523150; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr2:17711913-17716025 FORWARD   Aliases: F14N22.21, F14N22_21	5.5	5.3	0.2	1.2	100.0%	-4.5
5510	AT4G08280.1   expressed protein, hypothetical protein ssr1391 - Synechocystis sp. (strain PCC 6803),PIR2:S75571   chr4:5230323-5232128 FORWARD   Aliases: T12G13.120, T12G13_120	6.1	5.4	0.7	1.2	100.0%	-3.9
5511	AT1G73640.1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 ras family Pfam profile: PF00071 Ras family   chr1:27690653-27691788 FORWARD   Aliases: F25P22.5, F25P22_5	4.5	5.1	-0.6	-1.2	100.0%	-3.9
5512	AT4G33460.1   Symbol: ATNAP13   ABC transporter family protein, ABC-type transport protein sll1623 -Synechocystis,PIR2:S74812	6.0	5.5	0.5	1.2	100.0%	-4.0
5513	AT1G04430.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr1:1198136-1201526 FORWARD   Aliases: F19P19.11, F19P19_11	9.5	10.0	-0.5	-1.2	100.0%	-4.2
5514	AT1G01140.3   Symbol: CIPK9   CBL-interacting protein kinase 9 (CIPK9), identical to CBL-interacting protein kinase 9 (Arabidopsis thaliana) gi:13249117:gb:AAK16684; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 9 (CIPK9) GI:13249116   chr1:64167-67625 REVERSE   Aliases: CBL INTERACTING PROTEIN KINASE 9, F6F3.28, PKS6	6.4	5.9	0.5	1.2	100.0%	-3.9
5515	AT4G18250.1   receptor serine/threonine kinase, putative, similar to to receptor serine/threonine kinase PR5K gi:1235680:gb:AAC49208   chr4:10087354-10091974 REVERSE   Aliases: T9A21.100, T9A21_100	2.5	2.8	-0.2	-1.2	100.0%	-4.6
5516	AT4G04950.1   thioredoxin family protein, similar to PKCq-interacting protein PICOT from (Mus musculus) GI:6840949, (Rattus norvegicus) GI:6840951; contains Pfam profile PF00085: Thioredoxin	6.3	7.1	-0.7	-1.2	100.0%	-4.0
5517	AT1G02690.2   importin alpha-2 subunit, putative, similar to importin alpha-2 subunit (Karyopherin alpha-2 subunit) (KAP alpha) SP:O04294 from (Arabidopsis thaliana)   chr1:584260-587219 FORWARD   Aliases: T14P4.3, T14P4_3	5.9	6.3	-0.4	-1.2	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5518	AT4G26090.1   Symbol: RPS2   disease resistance protein RPS2 (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. identical to RPS2 (gi:13661831)   chr4:13224347-13227881 FORWARD   Aliases: DISEASE RESISTANCE PROTEIN RPS2, F20B18.200, F20B18_200, RESISTANT TO P. SYRINGAE 2	3.3	3.0	0.3	1.2	100.0%	-4.2
5519	AT5G42760.1   expressed protein, similar to hypothetical protein [Streptomyces sp. KO-3988] (GB:BAD86809.1); contains InterPro domain Protein of unknown function DUF142 (InterPro:IPR003455)   chr5:17166151-17167514 FORWARD   Aliases: MJB21.14, MJB21_14	4.8	4.2	0.5	1.2	100.0%	-4.1
5520	AT5G48020.1   expressed protein   chr5:19479884-19482183 REVERSE   Aliases: MDN11.10, MDN11_10	8.5	9.1	-0.5	-1.2	100.0%	-3.9
5521	AT3G15250.1   similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g53165.1); contains domain SER_RICH (PS50324)   chr3:5136269-5137202 REVERSE   Aliases: K7L4.5	2.1	2.0	0.1	1.2	100.0%	-5.0
5522	AT4G35760.1   expressed protein   chr4:16942326-16944665 REVERSE   Aliases: F4B14.2	5.6	5.2	0.5	1.2	100.0%	-4.1
5523	AT5G06970.1   expressed protein   chr5:2158229-2166399 REVERSE   Aliases: MOJ9.14, MOJ9_14	6.5	6.8	-0.3	-1.2	100.0%	-4.3
5524	AT5G67020.1   expressed protein   chr5:26767076-26768475 FORWARD   Aliases: K8A10.9, K8A10_9	3.8	4.0	-0.2	-1.2	100.0%	-4.4
5525	AT3G42310.1   expressed protein   chr3:14470804-14472483 FORWARD   Aliases: T14K23.20	5.5	4.8	0.8	1.2	100.0%	-3.5
5526	AT5G58490.1   cinnamoyl-CoA reductase family, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Eucalyptus gunnii (GI:2058311)   chr5:23660248-23661824 FORWARD   Aliases: MQJ2.6, MQJ2_6	9.2	9.9	-0.7	-1.2	100.0%	-4.0
5527	AT3G26520.1   Symbol: TIP2   tonoplast intrinsic protein, putative, similar to tonoplast intrinsic protein GI:5081419 from (Brassica napus)   chr3:9723680-9725052 REVERSE   Aliases: GAMMA TIP2, MFE16.17, SALT STRESS INDUCIBLE PROTEIN, SITIP, TIP1;2, TONOPLAST INTRINSIC PROTEIN 2	4.1	3.6	0.5	1.2	100.0%	-3.9
5528	AT4G00960.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:414361-416180 FORWARD   Aliases: A_TM018A10.19, A_TM018A10_19, T18A10.6, T18A10_6	3.3	3.0	0.3	1.2	100.0%	-4.7
5529	AT3G04480.1   endoribonuclease L-PSP family protein, contains Pfam domain PF01902: Domain of unknown function   chr3:1193636-1197403 REVERSE   Aliases: T27C4.13, T27C4_13	5.1	5.4	-0.4	-1.2	100.0%	-4.2
5530	AT1G71340.1   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family   chr1:26889162-26892000 REVERSE   Aliases: F3I17.1, F3I17_1	6.7	6.0	0.7	1.2	100.0%	-4.1
5531	AT1G32290.1   expressed protein   chr1:11650202-11650547 REVERSE   Aliases: F27G20.4	8.8	8.4	0.4	1.2	100.0%	-4.5
5532	AT3G63240.1   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr3:23374859-23378567 REVERSE   Aliases: F16M2.90	2.5	3.1	-0.5	-1.2	100.0%	-4.2
5533	AT2G48070.2   expressed protein   chr2:19669920-19671535 FORWARD   Aliases: T9J23.22	3.5	3.3	0.2	1.2	100.0%	-4.6
5534	AT3G27270.1   expressed protein   chr3:10074517-10075397 FORWARD   Aliases: K17E12.9	4.3	4.6	-0.4	-1.2	100.0%	-4.1
5535	AT2G37320.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:15674302-15675804 FORWARD   Aliases: F3G5.11, F3G5_11	3.2	3.1	0.1	1.2	100.0%	-4.8
5536	AT2G24320.1   expressed protein   chr2:10352739-10353909 REVERSE   Aliases: T28I24.5, T28I24_5	2.6	2.8	-0.2	-1.2	100.0%	-4.7
5537	AT5G66170.2   similar to senescence-associated family protein [Arabidopsis thaliana] (TAIR:At2g17850.1); similar to A Chain A, Solution Structure Of At5g66040, A Putative Protein From Arabidopsis Thaliana (GB:1TQ1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)   chr5:26464874-26465953 FORWARD   Aliases: K2A18.25, K2A18_25	7.6	7.2	0.5	1.2	100.0%	-4.0
5538	AT1G33360.1   ATP-dependent Clp protease ATP-binding subunit ClpX, putative, similar to CLP protease regulatory subunit CLPX GI:2674203 from (Arabidopsis thaliana)   chr1:12091857-12096005 FORWARD   Aliases: F10C21.5	4.7	5.1	-0.4	-1.2	100.0%	-3.9
5539	AT1G04050.1   SET domain-containing protein / suppressor of variegation related 1 (SUVR1), identical to suppressor of variegation related 1 (Arabidopsis thaliana) GI:15004614; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif; identical to cDNA trithorax 3 (ATX3) partial cds GI:15217142   chr1:1045597-1048751 REVERSE   Aliases: AT1G04060, F21M11.35, F21M11_35	3.4	3.6	-0.2	-1.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5540	AT1G61930.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr1:22896766-22897635 FORWARD   Aliases: F8K4.12, F8K4_12	6.1	5.5	0.6	1.2	100.0%	-4.1
5541	AT4G30330.1   small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative, similar to SWISS-PROT:P08578 small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E, Sm-E, SmE) (Chicken)   chr4:14836558-14838024 REVERSE   Aliases: F17I23.330, F17I23_330	7.4	7.9	-0.6	-1.2	100.0%	-3.9
5542	AT1G67780.1   hypothetical protein   chr1:25416479-25419193 FORWARD   Aliases: F12A21.9, F12A21_9	2.6	2.7	-0.1	-1.2	100.0%	-5.3
5543	AT2G04620.1   cation efflux family protein, potential member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, see PMID:11500563	4.5	4.9	-0.4	-1.2	100.0%	-4.3
5544	AT3G63350.1   Symbol: AT HSFA7B   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr3:23410443-23411787 FORWARD   Aliases: HSFA7B, MAA21.4	2.6	2.4	0.2	1.2	100.0%	-4.7
5545	AT1G16270.1   protein kinase family protein, contains PF:00069 Eukaryotic protein kinase domain. ESTs gb:H37741, gb:T43005 and gb:AI100340 come from this gene	3.9	4.2	-0.3	-1.2	100.0%	-4.4
5546	AT1G79570.1   protein kinase family protein, low similarity to EDR1 (Arabidopsis thaliana) GI:11127925	3.9	4.2	-0.3	-1.2	100.0%	-4.4
5547	AT4G35010.1   Symbol: BGAL11	2.4	2.6	-0.2	-1.2	100.0%	-4.9
5548	AT2G21410.1   vacuolar proton ATPase, putative, similar to vacuolar proton ATPase 100-kDa subunit from Dictyostelium discoideum P:1384136:gb:AAB49621   chr2:9169700-9175532 FORWARD   Aliases: F3K23.17, F3K23_17	7.0	6.7	0.2	1.2	100.0%	-4.5
5549	AT5G52560.1   This gene was shown to have sequence similarities with pea PsUSP gene, encoding an UDP-sugar pyrophosphorylase. UDP-N-acetylglucosamine pyrophosphorylase-related, contains weak similarity to UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) (Swiss-Prot:O74933) (Candida albicans).   chr5:21347924-21352037 FORWARD   Aliases: F6N7.4, F6N7_4	7.0	7.8	-0.8	-1.2	100.0%	-4.0
5550	AT1G55110.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:20563951-20566838 REVERSE   Aliases: T7N22.5, T7N22_5	3.2	3.5	-0.2	-1.2	100.0%	-4.5
5551	AT3G54390.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189   chr3:20148719-20150120 REVERSE   Aliases: T14E10.5	5.5	5.1	0.4	1.2	100.0%	-4.1
5552	AT3G16280.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr3:5518356-5519252 FORWARD   Aliases: MYA6.14	4.0	3.8	0.2	1.2	100.0%	-4.6
5553	AT5G47120.1   Symbol: ATBI 1	10.0	9.2	0.8	1.2	100.0%	-4.4
5554	AT3G22740.1   Symbol: HMT3   homocysteine S-methyltransferase 3 (HMT-3), identical to homocysteine S-methyltransferase HMT-3 (Arabidopsis thaliana) GI:9966515; similar to homocysteine S-methyltransferase AtHMT-2 (GI:6685163) (Arabidopsis thaliana); similar to selenocysteine methyltransferase GB:P56707 from (Astragalus bisulcatus)   chr3:8032966-8035816 REVERSE   Aliases: MWI23.11	2.4	2.3	0.1	1.2	100.0%	-5.0
5555	AT3G01120.1   Symbol: MTO1   cystathionine gamma-synthase, chloroplast / O-succinylhomoserine (Thiol)-lyase (CGS), identical to SP:P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}	12.2	11.7	0.5	1.2	100.0%	-4.5
5556	AT3G53770.1   late embryogenesis abundant protein-related / LEA protein-related, contains weak similarity to Swiss-Prot:P46521 late embryogenesis abundant protein Lea5-A (Gossypium hirsutum)	2.2	2.3	-0.1	-1.2	100.0%	-5.2
5557	AT5G40970.1   expressed protein   chr5:16431266-16431732 FORWARD   Aliases: MEE6.4, MEE6_4	6.4	5.6	0.8	1.2	100.0%	-3.9
5558	AT3G10050.1   Symbol: OMR1   threonine ammonia-lyase / threonine dehydratase / threonine deaminase (OMR1), identical to SP:Q9ZSS6 Threonine dehydratase biosynthetic, chloroplast precursor (EC 4.3.1.19, formerly EC 4.2.1.16) (Threonine deaminase) (TD) {Arabidopsis thaliana}   chr3:3098730-3101766 REVERSE   Aliases: L O METHYLTHREONINE RESISTANT 1, T22K18.12, THREONINE DEHYDRATASE/DEAMINASE	6.2	6.9	-0.7	-1.2	100.0%	-3.9
5559	AT1G79080.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:29751865-29753837 REVERSE   Aliases: YUP8H12R.30, YUP8H12R_30	4.0	4.5	-0.5	-1.2	100.0%	-3.9
5560	AT3G21360.1   expressed protein   chr3:7522810-7524586 FORWARD   Aliases: MHC9.4	6.7	6.3	0.4	1.2	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5561	AT4G24330.1   expressed protein, hypothetical protein - <i>Caenorhabditis elegans</i> ,PID:e1350884   chr4:12603531-12606338 REVERSE   Aliases: T22A6.160, T22A6_160	9.9	10.3	-0.4	-1.2	100.0%	-4.7
5562	AT1G76580.1   similar to squamosa promoter-binding protein-like 1 (SPL1) [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g47070.1); similar to putative SBP-domain protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_470314.1); contains domain SER_RICH (PS50324)   chr1:28740222-28743811 FORWARD   Aliases: F14G6.18, F14G6_18	4.1	3.9	0.2	1.2	100.0%	-4.7
5563	AT5G20700.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) ( <i>Arabidopsis thaliana</i> );   chr5:7005860-7007119 REVERSE   Aliases: T1M15.100, T1M15_100	7.7	7.1	0.5	1.2	100.0%	-4.4
5564	AT5G08010.1   expressed protein, condensin subunit SMC4, <i>Drosophila melanogaster</i> , EMBL:AF186472   chr5:2569607-2571735 FORWARD   Aliases: F13G24.210, F13G24_210	6.6	7.0	-0.3	-1.2	100.0%	-4.4
5565	AT2G45770.1   Symbol: CPFTSY	4.6	4.9	-0.3	-1.2	100.0%	-4.2
5566	AT1G34300.1   lectin protein kinase family protein, contains Pfam domains, PF01453: Lectin (probable mannose binding) and PF00069: Protein kinase domain   chr1:12503384-12506026 FORWARD   Aliases: F23M19.5, F23M19_5	6.6	6.3	0.3	1.2	100.0%	-4.1
5567	AT5G23710.1   expressed protein   chr5:7996531-7997223 REVERSE   Aliases: MQM1.2, MQM1_2	5.9	5.6	0.4	1.2	100.0%	-4.0
5568	AT2G32460.1   myb family transcription factor (MYB101), identical to putative transcription factor MYB101 GI:18087348 from ( <i>Arabidopsis thaliana</i> )   chr2:13789285-13791548 REVERSE   Aliases: T32F6.1	2.4	2.6	-0.1	-1.2	100.0%	-4.9
5569	AT2G04350.2   long-chain-fatty-acid--CoA ligase family protein / long-chain acyl-CoA synthetase family protein (LACS8), similar to LACS 4 (SP:O35547) from <i>Rattus norvegicus</i> , LACS 4 (SP:O60488) from <i>Homo sapiens</i> ; contains Pfam HMM hit: AMP-binding enzymes PF00501	11.0	11.4	-0.4	-1.2	100.0%	-4.7
5570	AT3G17410.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 GB:AAC61805 from ( <i>Lycopersicon esculentum</i> )	7.3	6.7	0.6	1.2	100.0%	-4.0
5571	AT1G69480.1   EXS family protein / ERD1/XPR1/SYG1 family protein, similar to PHO1 protein ( <i>Arabidopsis thaliana</i> ) GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family	3.1	2.9	0.2	1.2	100.0%	-4.5
5572	AT2G01930.2   expressed protein   chr2:427116-428682 REVERSE   Aliases: F23I14.2, F23I14_2	5.0	4.6	0.4	1.2	100.0%	-4.3
5573	AT1G22730.1   MA3 domain-containing protein, contains Pfam profile PF02847: MA3 domain; low similarity to programmed cell death 4 protein ( <i>Gallus gallus</i> ) GI:12958564   chr1:8046142-8049028 FORWARD   Aliases: T22J18.10, T22J18_10	4.8	5.2	-0.4	-1.2	100.0%	-4.2
5574	AT4G29830.1   Symbol: VIP3   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); G protein beta subunit-like protein, <i>Schistosoma mansoni</i> , gb:U30261	7.5	7.9	-0.4	-1.2	100.0%	-4.0
5575	AT3G20040.1   similar to hexokinase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g50460.1); similar to putative hexokinase [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_463697.1); contains InterPro domain Hexokinase (InterPro:IPR001312)   chr3:6994900-6998177 FORWARD   Aliases: MAL21.4	4.1	4.6	-0.5	-1.2	100.0%	-4.0
5576	AT3G18000.1   Symbol: NMT1   phosphoethanolamine N-methyltransferase 1 / PEAMT 1 (NMT1), identical to Phosphoethanolamine N-methyltransferase 1 (EC 2.1.1.103) (PEAMT 1) (AtNMT1) (SP:Q9FR44){ <i>Arabidopsis thaliana</i> }; strong similarity to phosphoethanolamine N-methyltransferase from ( <i>Spinacia oleracea</i> ) GI:7407189, ( <i>Triticum aestivum</i> ) GI:17887465; contains Pfam profile PF01209: methyltransferase, UbiE/COQ5 family   chr3:6154369-6157558 FORWARD   Aliases: AT3G17990, MEB5.22, N METHYLTRANSFERASE 1, S ADENOSYLMETHIONINE:PHOSPHO ETHANOLAMINE	4.4	4.7	-0.3	-1.2	100.0%	-4.2
5577	AT5G47510.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to phosphatidylinositol transfer-like protein IV (GI:14486707) ( <i>Lotus japonicus</i> ), SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PCTP) (SP:P24859) ( <i>Kluyveromyces lactis</i> ) and to SEC14 cytosolic factor (SP:P53989) ( <i>Candida glabrata</i> )	3.1	3.3	-0.2	-1.2	100.0%	-5.0
5578	AT5G47310.1   expressed protein   chr5:19218088-19220148 FORWARD   Aliases: MQL5.17, MQL5_17	7.4	6.8	0.6	1.2	100.0%	-4.2
5579	AT3G26450.1   major latex protein-related / MLP-related, low similarity to major latex protein { <i>Papaver somniferum</i> }(GI:294060) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr3:9682535-9684605 REVERSE   Aliases: F20C19.24	3.7	3.9	-0.2	-1.2	100.0%	-4.4
5580	AT1G71740.1   expressed protein   chr1:26990907-26991299 FORWARD   Aliases: F14O23.12, F14O23_12	3.6	4.3	-0.6	-1.2	100.0%	-3.6
5581	AT3G58050.1   expressed protein   chr3:21503516-21508134 FORWARD   Aliases: T10K17.260	4.4	4.6	-0.3	-1.2	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5582	AT3G02310.1   Symbol: SEP2   developmental protein SEPALLATA2 / floral homeotic protein (AGL4) (SEP2), identical to developmental protein SEPALLATA2 / floral homeotic protein AGL4 GB:P29384 (Arabidopsis thaliana), Pfam HMM hit: SRF-type transcription factors (DNA-binding and dimerization domain)   chr3:464286-467081 REVERSE   Aliases: AGL4, F14P3.4, F14P3_4, SEPALLATA2, TRANSCRIPTION FACTOR	2.9	2.8	0.2	1.2	100.0%	-4.8
5583	AT3G50620.1   nodulation protein-related, contains weak similarity to nodulation protein H (EC 2.8.2.-) (Host-specificity of nodulation protein D) (Swiss-Prot:P06237) (Rhizobium meliloti)   chr3:18795777-18797864 REVERSE   Aliases: T20E23.220	4.4	4.7	-0.3	-1.2	100.0%	-4.2
5584	AT1G79470.1   inosine-5'-monophosphate dehydrogenase, identical to inosine-5'-monophosphate dehydrogenase SP:P47996 {Arabidopsis thaliana}   chr1:29899491-29901650 REVERSE   Aliases: T8K14.11, T8K14_11	7.2	7.8	-0.5	-1.2	100.0%	-4.3
5585	AT4G22260.1   Symbol: IM   alternative oxidase, putative / immutans protein (IM), identical to IMMUTANS from Arabidopsis thaliana (gi:4138855); contains Pfam profile PF01786 alternative oxidase   chr4:11769768-11772526 REVERSE   Aliases: IM1, IMMUTANS, T10I14.90, T10I14_90	6.9	6.4	0.5	1.2	100.0%	-4.1
5586	AT2G41800.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr2:17443607-17445106 REVERSE   Aliases: T11A7.10, T11A7_10	4.6	4.9	-0.4	-1.2	100.0%	-4.0
5587	AT5G48720.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g01990.1); similar to P0413C03.27 [Oryza sativa (japonica cultivar-group)] (GB:NP_914850.1)	4.1	3.7	0.3	1.2	100.0%	-4.3
5588	AT1G21980.1   Symbol: ATPIP5K1   1-phosphatidylinositol-4-phosphate 5-kinase, putative / PIP kinase, putative / PtdIns(4)P-5-kinase, putative / diphosphoinositide kinase, putative, strong similarity to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr1:7734754-7738645 FORWARD   Aliases: PHOSPHATIDYLINOSITOL 4 PHOSPHATE 5 KINASE	7.7	8.2	-0.5	-1.2	100.0%	-4.2
5589	AT5G13700.1   polyamine oxidase, putative, similar to SP:O64411 Polyamine oxidase precursor (EC 1.5.3.11) from Zea mays   chr5:4419924-4423036 REVERSE   Aliases: MSH12.17, MSH12_17	4.4	4.2	0.2	1.2	100.0%	-4.4
5590	AT1G19100.1   ATP-binding region, ATPase-like domain-containing protein-related, low similarity to microrchidia (Homo sapiens) GI:5410257; contains non-consensus splice site (GC) at intron 8	4.1	4.4	-0.3	-1.2	100.0%	-4.2
5591	AT5G06720.1   peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:1491617:emb:CAA68212   chr5:2077430-2079006 REVERSE   Aliases: MPH15.8, MPH15_8	7.1	7.7	-0.6	-1.2	100.0%	-3.8
5592	AT4G21326.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr4:11346991-11349664 FORWARD   Aliases: None	2.9	3.1	-0.2	-1.2	100.0%	-4.4
5593	AT3G25110.1   acyl-(acyl carrier protein) thioesterase / acyl-ACP thioesterase / oleoyl-(acyl-carrier protein) hydrolase / S-acyl fatty acid synthase thioesterase, identical to acyl-(acyl carrier protein) thioesterase (Arabidopsis thaliana) GI:804946   chr3:9146281-9148493 REVERSE   Aliases: MJL12.9	4.5	5.0	-0.6	-1.2	100.0%	-4.3
5594	AT1G17440.2   transcription initiation factor IID (TFIID) subunit A family protein, similar to SP:Q16514 Transcription initiation factor TFIID 20/15 kDa subunits (TAFII-20/TAFII-15) {Homo sapiens}; contains Pfam profile PF03847: Transcription initiation factor TFIID subunit A   chr1:5984154-5987764 REVERSE   Aliases: F1L3.13	4.7	4.3	0.4	1.2	100.0%	-4.1
5595	AT2G30800.1   Symbol: HVT1   DEIH-box RNA/DNA helicase, putative, similar to DEIH-box RNA/DNA helicase (Arabidopsis thaliana) GI:5881579; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr2:13127430-13133846 REVERSE   Aliases: ATVT 1, HELICASE IN VASCULAR TISSUE AND TAPETUM, T11J7.19	3.8	4.2	-0.4	-1.2	100.0%	-4.3
5596	AT5G12410.1   THUMP domain-containing protein, contains Pfam profile PF02926: THUMP domain   chr5:4021816-4023989 REVERSE   Aliases: None	6.9	7.5	-0.5	-1.2	100.0%	-4.1
5597	AT2G28000.1   Symbol: CPN60A	9.9	10.3	-0.4	-1.2	100.0%	-4.1
5598	AT5G15950.2   similar to adenosylmethionine decarboxylase family protein [Arabidopsis thaliana] (TAIR:At3g02470.1); similar to S-adenosyl-L-methionine decarboxylase [Brassica juncea] (GB:AAB88273.1); contains InterPro domain S-adenosylmethionine decarboxylase (InterPro:IPR001985)   chr5:5206159-5208039 FORWARD   Aliases: F1N13.90, F1N13_90	4.4	4.0	0.3	1.2	100.0%	-4.2
5599	AT1G77460.1   C2 domain-containing protein / armadillo/beta-catenin repeat family protein, similar to CCLS 65 (Silene latifolia) GI:2570102; contains Pfam profiles PF00514: Armadillo/beta-catenin-like repeat, PF00168: C2 domain   chr1:29109442-29116474 FORWARD   Aliases: T5M16.5, T5M16_5	3.9	4.2	-0.3	-1.2	100.0%	-4.3
5600	AT3G56160.1   expressed protein   chr3:20848423-20852520 REVERSE   Aliases: F18O21.120	3.7	3.5	0.2	1.2	100.0%	-4.8
5601	AT5G45800.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:18592809-18596324 REVERSE   Aliases: MRA19.24, MRA19_24	3.8	4.3	-0.6	-1.2	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5602	AT2G25450.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967)   chr2:10836995-10838733 REVERSE   Aliases: F13B15.11, F13B15_11	8.6	7.7	0.9	1.2	100.0%	-4.0
5603	AT1G34290.1   leucine-rich repeat family protein, conatins leucine rich repeat (LRR) domains, Pfam:PF00560; contains similarity to disease resistance protein GI:3894383 from (Lycopersicon esculentum)   chr1:12497978-12498778 FORWARD   Aliases: F23M19.6, F23M19_6	2.3	2.4	-0.1	-1.2	100.0%	-5.0
5604	AT3G13800.1   metallo-beta-lactamase family protein, similar to Metal Dependent Hydrolase GB:AAD18619 from (Chlamydomophila pneumoniae)	4.9	4.6	0.3	1.2	100.0%	-4.3
5605	AT5G44580.1   expressed protein   chr5:17996538-17997634 FORWARD   Aliases: K15C23.2, K15C23_2	2.8	2.5	0.3	1.2	100.0%	-4.6
5606	AT4G13010.1   oxidoreductase, zinc-binding dehydrogenase family protein, low similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430); contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family   chr4:7600548-7602726 FORWARD   Aliases: F25G13.100, F25G13_100	10.5	9.8	0.6	1.2	100.0%	-4.1
5607	AT2G46700.1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase homolog MCK1 (Zea mays) gi:1839597:gb:AAB47181   chr2:19189794-19193648 REVERSE   Aliases: T3A4.8	5.3	5.6	-0.3	-1.2	100.0%	-4.2
5608	AT4G39520.1   GTP-binding protein, putative, similar to SP:Q9Y295 Developmentally regulated GTP-binding protein 1 (DRG 1) {Homo sapiens}; contains Pfam profiles PF02824: TGS domain, PF01018: GTP1/OBG family	7.0	7.6	-0.7	-1.2	100.0%	-4.1
5609	AT3G48730.1   glutamate-1-semialdehyde 2,1-aminomutase 2 (GSA 2) / glutamate-1-semialdehyde aminotransferase 2 (GSA-AT 2), identical to GSA2 (SP:Q42522)   chr3:18060608-18062687 FORWARD   Aliases: T8P19.240	8.4	9.3	-0.9	-1.2	100.0%	-3.7
5610	AT1G12120.1   expressed protein, contains Pfam domain PF05904: Plant protein of unknown function (DUF863)   chr1:4114769-4117592 REVERSE   Aliases: T28K15.14, T28K15_14	7.5	7.9	-0.5	-1.2	100.0%	-4.2
5611	AT3G03780.2   5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase, putative / vitamin-B12-independent methionine synthase, putative / cobalamin-independent methionine synthase, putative, very strong similarity to SP:O50008 5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14) (Vitamin-B12-independent methionine synthase isozyme) (Cobalamin-independent methionine synthase isozyme) {Arabidopsis thaliana}; contains Pfam profile PF01717: Methionine synthase, vitamin-B12 independent   chr3:957095-960985 FORWARD   Aliases: F20H23.19, F20H23_19	8.0	10.6	-2.5	-1.2	100.0%	-4.5
5612	AT5G17920.1   Symbol: ATCIMS	8.0	10.6	-2.5	-1.2	100.0%	-4.5
5613	AT5G47410.1   expressed protein   chr5:19249442-19249813 FORWARD   Aliases: MQL5.27, MQL5_27	7.0	7.6	-0.7	-1.2	100.0%	-4.2
5614	AT1G18490.1   expressed protein   chr1:6367061-6368842 FORWARD   Aliases: F15H18.26, F15H18_26	7.6	8.1	-0.5	-1.2	100.0%	-4.1
5615	AT3G57100.1   expressed protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana); contains Pfam PF05055 : Protein of unknown function (DUF677); contains Prosite PS00453: FKBP-type peptidyl-prolyl cis-trans isomerase signature 1; contains one transmembrane domain   chr3:21144235-21145314 REVERSE   Aliases: F24I3.180	4.9	4.5	0.4	1.2	100.0%	-4.2
5616	AT5G64080.2   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:25662489-25663954 REVERSE   Aliases: MHJ24.6, MHJ24_6	7.1	7.9	-0.8	-1.2	100.0%	-3.5
5617	AT5G42280.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	3.1	-0.2	-1.2	100.0%	-4.9
5618	AT5G24650.1   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr5:8437088-8439107 FORWARD   Aliases: K18P6.19, K18P6_19	7.1	7.9	-0.8	-1.2	100.0%	-3.9
5619	AT3G16640.1   Symbol: TCTP   translationally controlled tumor family protein, similar to translationally controlled tumor protein GB:AAD10032 from (Hevea brasiliensis)   chr3:5669379-5670823 REVERSE   Aliases: MGL6.19, TRANSLATIONALLY CONTROLLED TUMOR PROTEIN	10.9	10.5	0.4	1.2	100.0%	-4.3
5620	AT5G66360.2   ribosomal RNA adenine dimethylase family protein, similar to SP:P41819 Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl(rRNA) dimethyltransferase) {Saccharomyces cerevisiae}; contains Pfam profile PF00398: ribosomal RNA adenine dimethylase family protein	5.9	6.4	-0.5	-1.2	100.0%	-4.1
5621	AT5G16320.1   Symbol: FRL1   expressed protein   chr5:5344505-5346022 FORWARD   Aliases: FRIGIDA LIKE 1, MQK4.4, MQK4_4	4.1	3.8	0.2	1.2	100.0%	-4.5
5622	AT2G32590.1   barren family protein, low similarity to SP:Q9Y7R3 Condensin complex subunit 2 (p105) {Schizosaccharomyces pombe}; contains Pfam profile PF05786: Barren protein	4.4	4.8	-0.5	-1.2	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5623	AT4G33500.1   protein phosphatase 2C-related / PP2C-related, YHR077c (NMD2,IFS1) protein -Saccharomyces cerevisiae,PID:g555939	6.5	6.1	0.4	1.2	100.0%	-4.0
5624	AT1G10700.1   ribose-phosphate pyrophosphokinase 3 / phosphoribosyl diphosphate synthetase 3 (PRS3), nearly identical to phosphoribosyl diphosphate synthase GI:4902470 from (Arabidopsis thaliana)   chr1:3554116-3556504 FORWARD   Aliases: T16B5.16	5.3	5.7	-0.3	-1.2	100.0%	-4.5
5625	AT2G25660.1   Symbol: EMB2410   expressed protein   chr2:10923281-10934468 REVERSE   Aliases: EMB2410, EMBRYO DEFECTIVE 2410, F3N11.11, F3N11_11	4.8	5.1	-0.3	-1.2	100.0%	-4.4
5626	AT3G54770.2   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At1g20880.1); similar to putative RRM-containing protein [Oryza sativa (japonica cultivar-group)] (GB:BAD37252.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr3:20284762-20286802 REVERSE   Aliases: T5N23.130	2.3	2.6	-0.2	-1.2	100.0%	-4.3
5627	AT3G02790.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr3:604852-605428 FORWARD   Aliases: F13E7.27, F13E7_27	11.6	11.3	0.3	1.2	100.0%	-4.2
5628	AT5G14900.1   helicase associated (HA2) domain-containing protein, similar to SP:P53131 Pre-mRNA splicing factor RNA helicase PRP43 (Helicase JA1) {Saccharomyces cerevisiae}; contains Pfam profile PF04408: Helicase associated domain (HA2)	2.0	2.1	-0.1	-1.2	100.0%	-5.4
5629	AT4G22560.1   expressed protein   chr4:11880189-11880983 FORWARD   Aliases: F7K2.140, F7K2_140	5.2	4.6	0.5	1.2	100.0%	-4.1
5630	AT1G67500.1   Symbol: ATREV3	6.8	7.3	-0.4	-1.2	100.0%	-4.3
5631	AT2G40935.2   expressed protein, low similarity to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614	8.3	7.9	0.4	1.2	100.0%	-4.1
5632	AT3G62950.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.3	2.2	0.2	1.2	100.0%	-4.8
5633	AT5G66680.1   Symbol: DGL1   dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48kDa subunit family protein, similar to SP:Q05052 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 48 kDa subunit precursor (EC 2.4.1.119) (Oligosaccharyl transferase 48 kDa subunit) {Canis familiaris}; contains Pfam profile PF03345: Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 48kD subunit   chr5:26634770-26637893 REVERSE   Aliases: MSN2.7, MSN2_7	10.4	10.7	-0.4	-1.2	100.0%	-4.4
5634	AT2G35320.1   Symbol: ATEYA   homologue of the animal Eys Absent genes. encodes a tyrosine-specific phosphatase. the protein sequence lacks the cys-containing signature of the classical tyrosine phosphatases. belongs to the aspartate-based phosphatases. The enzyme activity is strictly metal-dependent.   chr2:14873911-14875939 REVERSE   Aliases: ATEYA, T4C15.1, T4C15_1	6.0	6.3	-0.3	-1.2	100.0%	-4.2
5635	AT5G05250.1   expressed protein   chr5:1557038-1557999 REVERSE   Aliases: K18I23.5, K18I23_5	8.4	7.8	0.6	1.2	100.0%	-4.0
5636	AT3G53140.1   O-diphenol-O-methyl transferase, putative, similar to GI:6688808 (Medicago sativa subsp. x varia), caffeic acid O-methyltransferase (homt1), Populus kitakamiensis, EMBL:PKHOMT1A   chr3:19706621-19708520 FORWARD   Aliases: T4D2.70	3.4	3.7	-0.3	-1.2	100.0%	-4.6
5637	AT3G50560.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily   chr3:18772069-18774994 REVERSE   Aliases: T20E23.160	3.7	3.4	0.3	1.2	100.0%	-4.4
5638	AT5G61480.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:24741767-24745068 REVERSE   Aliases: MCI2.4, MCI2_4	5.4	5.7	-0.3	-1.2	100.0%	-4.5
5639	AT3G48425.1   endonuclease/exonuclease/phosphatase family protein, similar to SP:P51173:APEA_DICDI DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18)(Class II apurinic/apyrimidinic(AP)-endonuclease) {Dictyostelium discoideum}; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr3:17942803-17945729 FORWARD   Aliases: None	5.0	5.4	-0.3	-1.2	100.0%	-4.1
5640	AT5G02220.1   expressed protein   chr5:441705-442144 REVERSE   Aliases: T7H20.270, T7H20_270	6.3	5.7	0.6	1.2	100.0%	-3.9
5641	AT1G50670.1   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr1:18778532-18780621 REVERSE   Aliases: F17J6.19, F17J6_19	9.3	9.7	-0.3	-1.2	100.0%	-4.6
5642	AT3G55760.2   expressed protein   chr3:20711414-20714035 FORWARD   Aliases: F1I16.170	7.1	6.4	0.7	1.2	100.0%	-4.2
5643	AT5G65720.1   cysteine desulfurase, mitochondrial (NIFS), identical to Cysteine desulfurase, mitochondrial precursor (SP:O49543) {Arabidopsis thaliana}; identical to cDNA GI:12656131; contains Pfam profile PF00266: aminotransferase, class V   chr5:26313479-26315298 FORWARD   Aliases: MPA24.7, MPA24_7	8.7	8.3	0.4	1.2	100.0%	-4.3
5644	AT5G24840.1   expressed protein, contains Pfam profile PF02390: Putative methyltransferase   chr5:8533790-8535046 REVERSE   Aliases: F6A4.50, F6A4_50	7.7	8.1	-0.4	-1.2	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5645	AT4G13235.1   Encodes a defensin-like (DEFL) family protein.   chr4:7677520-7678243 REVERSE   Aliases: None	7.2	7.4	-0.2	-1.2	100.0%	-4.6
5646	AT5G57720.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:23407153-23408752 REVERSE   Aliases: MRI1.8, MRI1_8	2.7	2.4	0.2	1.2	100.0%	-4.6
5647	AT4G35190.1   expressed protein, contains Pfam profile PF03641: decarboxylase family protein   chr4:16746604-16748266 FORWARD   Aliases: T12J5.60, T12J5_60	4.4	4.7	-0.3	-1.2	100.0%	-4.3
5648	AT1G77350.2   similar to Krtcap2 protein [Mus musculus] (GB:AAH43030.1); similar to keratinocytes associated protein 2 [Mus musculus] (GB:NP_079603.1); similar to ENSANGP00000016671 [Anopheles gambiae str. PEST] (GB:XP_312812.2)   chr1:29075214-29076793 FORWARD   Aliases: F2P24.6, F2P24_6	9.4	9.0	0.5	1.2	100.0%	-4.3
5649	AT3G62840.1   small nuclear ribonucleoprotein D2, putative / snRNP core protein D2, putative / Sm protein D2, putative, similar to small nuclear ribonucleoprotein Sm D2 (snRNP core protein D2) (Sm-D2) (Mus musculus) SWISS-PROT:P43330   chr3:23246086-23247791 REVERSE   Aliases: F26K9.270	10.9	11.2	-0.3	-1.2	100.0%	-4.3
5650	AT3G26590.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family   chr3:9762938-9766552 REVERSE   Aliases: MFE16.12	4.7	4.9	-0.3	-1.2	100.0%	-4.6
5651	AT2G45700.1   sterile alpha motif (SAM) domain-containing protein, similar to SNM1 protein (Mus musculus) GI:7595835; contains Pfam profile PF00536: SAM domain (Sterile alpha motif)   chr2:18834074-18837600 REVERSE   Aliases: F4I18.32	5.2	5.5	-0.3	-1.2	100.0%	-4.0
5652	AT2G46360.1   expressed protein   chr2:19035561-19036088 FORWARD   Aliases: F11C10.5	2.4	2.2	0.1	1.2	100.0%	-5.2
5653	AT3G50150.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function; expression supported by MPSS   chr3:18606792-18608534 REVERSE   Aliases: F3A4.230	2.0	2.1	-0.1	-1.2	100.0%	-5.3
5654	AT4G25500.2   Symbol: ATRSP35   arginine/serine-rich splicing factor RSP40 (RSP40), identical to SP:P92965 Arginine/serine-rich splicing factor RSP40 {Arabidopsis thaliana}   chr4:13026028-13027422 FORWARD   Aliases: ARGININE/SERINE RICH SPLICING FACTOR, ATRSP40, SPLICING FACTOR AT SRP40, T30C3.9	7.9	7.3	0.6	1.2	100.0%	-4.0
5655	AT3G18680.2   aspartate/glutamate/uridylate kinase family protein, similar to UMP-kinase GB:CAB38122 gi:4468612 from (Lactococcus lactis) ; contains Pfam profile PF00696: Amino acid kinase family   chr3:6427413-6429658 FORWARD   Aliases: MVE11.4	6.8	7.3	-0.6	-1.2	100.0%	-3.7
5656	AT5G47320.1   Symbol: RPS19   30S ribosomal protein S19, mitochondrial (RPS19)   chr5:19220379-19222499 FORWARD   Aliases: MQL5.18, MQL5_18	8.3	8.9	-0.5	-1.2	100.0%	-4.0
5657	AT5G65710.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:26309598-26312666 FORWARD   Aliases: MPA24.6, MPA24_6	5.9	6.4	-0.5	-1.2	100.0%	-3.8
5658	AT1G06810.1   expressed protein, contains Pfam PF04396: Protein of unknown function, DUF537   chr1:2091920-2092527 REVERSE   Aliases: F4H5.25, F4H5_25	3.9	4.1	-0.3	-1.2	100.0%	-4.6
5659	AT4G18890.1   brassinosteroid signalling positive regulator-related, contains similarity to BZR1 protein (Arabidopsis thaliana) gi:20270971:gb:AAM18490   chr4:10352633-10355566 FORWARD   Aliases: F13C5.60, F13C5_60	3.4	3.1	0.2	1.2	100.0%	-4.4
5660	AT5G66530.1   aldose 1-epimerase family protein, similar to apospory-associated protein C; APOC (Chlamydomonas reinhardtii) GI:6970044; contains Pfam profile PF01263: Aldose 1-epimerase   chr5:26570973-26572902 REVERSE   Aliases: K1F13.19, K1F13_19	8.9	9.4	-0.5	-1.2	100.0%	-4.0
5661	AT3G04570.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr3:1230992-1232334 FORWARD   Aliases: F7O18.4, F7O18_4	5.4	5.0	0.4	1.2	100.0%	-4.1
5662	AT5G61890.1   encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	4.5	4.9	-0.4	-1.2	100.0%	-3.8
5663	AT2G30950.1   Symbol: VAR2   FtsH protease (VAR2), identical to zinc dependent protease VAR2 GI:7650138 from (Arabidopsis thaliana)   chr2:13181402-13184300 FORWARD   Aliases: F7F1.16, F7F1_16, FTSH2, VAR2, VARIEGATED 2, YELLOW VARIEGATED	10.3	9.8	0.5	1.2	100.0%	-4.3
5664	AT5G65260.1   polyadenylate-binding protein family protein / PABP family protein, low similarity to poly(A)-binding protein II (Drosophila melanogaster) GI:6007612; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain   chr5:26097457-26100243 REVERSE   Aliases: MQN23.21, MQN23_21	8.0	7.4	0.6	1.2	100.0%	-4.2
5665	AT2G25490.1   Symbol: EBF1   F-box family protein (FBL6), contains similarity to grr1 GI:2407790 from (Glycine max)   chr2:10854461-10857606 REVERSE   Aliases: EIN3 BINDING F BOX PROTEIN 1, F13B15.15, F13B15_15, FBL6	3.8	3.3	0.5	1.2	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5666	AT2G25940.1   Symbol: ALPHA VPE   vacuolar processing enzyme alpha / alpha-VPE, identical to SP:P49047 Vacuolar processing enzyme, alpha-isozyme precursor (EC 3.4.22.-) (Alpha-VPE) {Arabidopsis thaliana}   chr2:11069798-11073106 REVERSE   Aliases: ALPHAVPE, F17H15.4	5.2	4.6	0.7	1.2	100.0%	-3.8
5667	AT5G55130.2   Symbol: CNX5   similar to SUMO activating enzyme 2 (SAE2) [Arabidopsis thaliana] (TAIR:At2g21470.1); similar to SUMO activating enzyme 2 (SAE2) [Arabidopsis thaliana] (TAIR:At2g21470.2); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG09882.1); contains InterPro domain UBA/THIF-type NAD/FAD binding fold (InterPro:IPR000594); contains InterPro domain Rhodanese-like (InterPro:IPR001763); contains InterPro domain MoeZ/MoeB (InterPro:IPR007901)	6.4	6.8	-0.4	-1.2	100.0%	-4.3
5668	AT5G59960.1   expressed protein   chr5:24159240-24162559 REVERSE   Aliases: MMN10.21, MMN10_21	5.6	5.1	0.5	1.2	100.0%	-4.2
5669	AT1G16340.2   similar to 2-dehydro-3-deoxyphosphooctonate aldolase / phospho-2-dehydro-3-deoxyoctonate aldolase / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase (KDSA) [Arabidopsis thaliana] (TAIR:At1g79500.1); similar to 2-dehydro-3-deoxyphosphooctonate aldolase / phospho-2-dehydro-3-deoxyoctonate aldolase / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase (KDSA) [Arabidopsis thaliana] (TAIR:At1g79500.3); similar to 2-dehydro-3-deoxyphosphooctonate aldolase / phospho-2-dehydro-3-deoxyoctonate aldolase / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase (KDSA) [Arabidopsis thaliana] (TAIR:At1g79500.2); similar to 3-desoxy-D-manno octulosonic acid-8-phosphate synthase [Lycopersicon esculentum] (GB:CAC35366.1); similar to putative 2-dehydro-3-deoxyphosphooctonate aldolase [Oryza sativa (japonica cultivar-group)] (GB:AAO72599.1); contains InterPro domain DAHP synthetase I/KDSA superfamily (InterPro:IPR006218); contains InterPro domain 2-dehydro-3-deoxyphosphooctonate aldolase (InterPro:IPR006269)	8.9	9.5	-0.6	-1.2	100.0%	-3.8
5670	AT4G11150.1   Symbol: TUF   vacuolar ATP synthase subunit E / V-ATPase E subunit / vacuolar proton pump E subunit (VATE), identical to SP:Q39258 Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E subunit) (Vacuolar proton pump E subunit) {Arabidopsis thaliana}   chr4:6799958-6801927 FORWARD   Aliases: EMB2448, EMBRYO DEFECTIVE 2448, T22B4.130, T22B4_130, TUFF, VACUOLAR H+ ATPASE SUBUNIT E ISOFORM 1, VHA E1	10.3	10.7	-0.4	-1.2	100.0%	-4.1
5671	AT1G11800.1   endonuclease/exonuclease/phosphatase family protein, contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr1:3985224-3987289 REVERSE   Aliases: F25C20.3, F25C20_3	5.8	6.2	-0.4	-1.2	100.0%	-4.0
5672	AT5G27610.1   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At3g05380.1); similar to P0671B11.29 [Oryza sativa (japonica cultivar-group)] (GB:NP_914584.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)   chr5:9764138-9769906 FORWARD   Aliases: F15A18.70, F15A18_70	3.9	3.7	0.2	1.2	100.0%	-4.6
5673	AT3G05690.1   Symbol: HAP2B   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr3:1676552-1678938 REVERSE   Aliases: ATHAP2B, F18C1.4, F18C1_4, HAP2	4.9	5.4	-0.5	-1.2	100.0%	-4.1
5674	AT2G23320.2   Symbol: WRKY15	5.3	5.7	-0.4	-1.2	100.0%	-4.0
5675	AT3G14520.1   terpene synthase/cyclase family protein, similar to terpene synthase GB:CAA72074 from (Arabidopsis thaliana)   chr3:4875755-4878340 REVERSE   Aliases: MIE1.2	3.0	3.1	-0.2	-1.2	100.0%	-4.9
5676	AT5G23760.1   heavy-metal-associated domain-containing protein, Pfam profile PF00403: Heavy-metal-associated domain   chr5:8013090-8014231 REVERSE   Aliases: MRO11.20, MRO11_20	9.8	9.4	0.4	1.2	100.0%	-4.2
5677	AT4G25740.2   similar to 40S ribosomal protein S10 (RPS10C) [Arabidopsis thaliana] (TAIR:At5g52650.1); similar to RS10_ORYSA 40S ribosomal protein S10 (GB:Q9AYP4); contains InterPro domain Plectin/S10, N-terminal (InterPro:IPR005326)   chr4:13107273-13108822 REVERSE   Aliases: F14M19.20, F14M19_20	9.7	10.2	-0.5	-1.2	100.0%	-3.9
5678	AT2G44230.1   expressed protein   chr2:18293601-18295476 FORWARD   Aliases: F4I1.4	2.9	3.2	-0.2	-1.2	100.0%	-4.5
5679	AT3G14880.1   DNA-binding protein-related, low similarity to tumor-related protein (Nicotiana glauca x Nicotiana langsdorffii) GI:688423, SP:O24160 TGACG-sequence specific DNA-binding protein TGA-2.1 {Nicotiana tabacum}   chr3:5006572-5007696 FORWARD   Aliases: K15M2.2	4.7	4.4	0.3	1.2	100.0%	-4.2
5680	AT3G19510.1   homeobox protein (HAT 3.1), identical to homeotic protein HAT 3.1 (GI:11994474) (Arabidopsis thaliana)   chr3:6762770-6766570 REVERSE   Aliases: MLD14.37	4.6	5.1	-0.6	-1.2	100.0%	-4.2
5681	AT5G02500.1   Symbol: HSC70 1   heat shock cognate 70 kDa protein 1 (HSC70-1) (HSP70-1), identical to SP:P22953 Heat shock cognate 70 kDa protein 1 (Hsc70.1) {Arabidopsis thaliana}   chr5:553743-556437 REVERSE   Aliases: AT HSC70 1, HSC70, HSP70 1, T22P11.90, T22P11_90	10.9	11.2	-0.3	-1.2	100.0%	-4.7
5682	AT1G70290.1   Symbol: ATTPS8	6.5	6.1	0.4	1.2	100.0%	-4.2
5683	AT4G23990.1   Symbol: ATCSLG3   cellulose synthase family protein, similar to cellulose synthase catalytic subunit from Arabidopsis thaliana (gi:5230423), cellulose synthase-5 from Zea mays (gi:9622882)   chr4:12456534-12460763 FORWARD   Aliases: CSLG3, T32A16.160, T32A16_160	6.0	5.4	0.6	1.2	100.0%	-3.8
5684	AT3G25020.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-0B (Lycopersicon esculentum) gi:3894387;gb:AAC78593   chr3:9116875-9119547 REVERSE   Aliases: K3G3.7	3.0	3.2	-0.2	-1.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5685	AT5G62000.3   Symbol: ARF2   transcriptional factor B3 family protein / auxin-responsive factor, putative (ARF1), contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA ARF1 (auxin response factor) binding protein GI:2245393   chr5:24927608-24932431 FORWARD   Aliases: ARF1 BINDING PROTEIN, ARF1 BP, AT5G62010, AUXIN RESPONSE FACTOR 2, HLS1 SUPPRESSOR, HSS, MTG10.1, MTG10_1	4.5	4.2	0.2	1.2	100.0%	-4.3
5686	AT5G11540.1   FAD-binding domain-containing protein, similar to hypothetical protein (Oryza sativa (japonica))(GI:18844891); contains PF01565 FAD binding domain   chr5:3703003-3704982 REVERSE   Aliases: F15N18.130, F15N18_130	5.0	5.3	-0.3	-1.2	100.0%	-4.3
5687	AT1G62350.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23060318-23061600 FORWARD   Aliases: F24O1.37, F24O1_37	3.6	3.9	-0.4	-1.2	100.0%	-4.4
5688	AT2G04830.1   F-box family protein, similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana); confirmed by FLcDNA GI:16604421; contains uncharacterized Arabidopsis domain shared by 33 Arabidopsis proteins   chr2:1695352-1695853 FORWARD   Aliases: F28I8.13, F28I8_13	2.7	2.8	-0.1	-1.2	100.0%	-5.1
5689	AT1G30290.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:10670304-10672722 REVERSE   Aliases: F12P21.10, F12P21_10	6.0	6.4	-0.4	-1.2	100.0%	-4.0
5690	AT5G02710.1   expressed protein, contains Pfam PF03692: Uncharacterised protein family (UPF0153)   chr5:612606-614418 FORWARD   Aliases: F9G14.8	3.7	3.3	0.3	1.2	100.0%	-4.2
5691	AT1G36730.1   eukaryotic translation initiation factor 5, putative / eIF-5, putative, similar to SP:P55876 Eukaryotic translation initiation factor 5 (eIF-5) {Zea mays}; contains Pfam profiles PF02020: eIF4-gamma/eIF5/eIF2-epsilon, PF01873: Domain found in IF2B/IF5   chr1:13899422-13902025 REVERSE   Aliases: T15P17.7, T15P17_7	6.1	5.4	0.7	1.2	100.0%	-3.9
5692	AT3G09100.2   mRNA capping enzyme family protein, similar to mRNA capping enzyme (Xenopus laevis) GI:7239232; contains Pfam profiles PF01331: mRNA capping enzyme catalytic domain, PF00782: Dual specificity phosphatase catalytic domain   chr3:2787986-2793537 REVERSE   Aliases: MZB10.13	4.9	5.2	-0.3	-1.2	100.0%	-4.5
5693	AT2G20940.1   expressed protein   chr2:9009113-9009782 REVERSE   Aliases: F26H11.30, F26H11_30	6.2	6.9	-0.7	-1.2	100.0%	-3.7
5694	AT2G32560.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SKIP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr2:13831871-13834063 FORWARD   Aliases: AT2G32570, T26B15.12, T26B15_12	3.1	2.9	0.2	1.2	100.0%	-5.1
5695	AT5G45410.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g25030.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g25030.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_476693.1)   chr5:18419135-18421010 REVERSE   Aliases: MFC19.8, MFC19_8	9.6	8.2	1.4	1.2	100.0%	-3.8
5696	AT3G15110.1   expressed protein   chr3:5084295-5085836 REVERSE   Aliases: F4B12.2	4.2	3.9	0.3	1.2	100.0%	-4.3
5697	AT3G26330.1   Symbol: CYP71B37   similar to cytochrome P450 family protein [Arabidopsis thaliana] (TAIR:At3g26300.1); similar to cytochrome P450 family protein [Arabidopsis thaliana] (TAIR:At3g26310.1); similar to cytochrome P450 71B26, putative (CYP71B26) [Arabidopsis thaliana] (TAIR:At3g26290.1); similar to cytochrome P450 family protein [Arabidopsis thaliana] (TAIR:At2g02580.1); similar to cytochrome P450 71B10 [Arabidopsis thaliana] (TAIR:At5g57260.1); similar to cytochrome P450 [Citrus sinensis] (GB:AAL24049.1); contains InterPro domain E-class P450, group I (InterPro:IPR002401); contains InterPro domain Cytochrome P450 (InterPro:IPR001128)	5.0	4.6	0.4	1.2	100.0%	-4.0
5698	AT5G03940.1   Symbol: FFC   signal recognition particle 54 kDa protein, chloroplast / 54 chloroplast protein / SRP54 (FFC), identical to Swiss-Prot:P37107 signal recognition particle 54 kDa protein, chloroplast precursor (SRP54) (54 chloroplast protein) (54CP) (FFC) (Arabidopsis thaliana)   chr5:1059503-1063318 REVERSE   Aliases: 54CP, CPSRP54, F8F6.150, F8F6_150, FIFTY FOUR CHLOROPLAST HOMOLOGUE, SIGNAL RECOGNITION PARTICLE 54 KDA SUBUNIT, SRP54CP	7.7	8.3	-0.6	-1.2	100.0%	-4.1
5699	AT3G14840.2   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain; contains 2 predicted transmembrane domains   chr3:4988278-4994065 FORWARD   Aliases: T21E2.2	6.6	7.0	-0.4	-1.2	100.0%	-4.2
5700	AT2G27285.1   expressed protein, weak similarity to maeb1 (GI:20087019) (Plasmodium falciparum), chimeric erythrocyte-binding protein MAEBL (GI:22086284) (Plasmodium falciparum)   chr2:11683038-11685178 REVERSE   Aliases: None	8.7	9.4	-0.7	-1.2	100.0%	-4.2
5701	AT2G21060.1   Symbol: ATGRP2B   cold-shock DNA-binding family protein / glycine-rich protein (GRP2), identical to Glycine-rich protein 2b (AtGRP2b) (Arabidopsis thaliana) SWISS-PROT:Q38896; contains Pfam domains PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle   chr2:9043874-9044731 REVERSE   Aliases: F26H11.18, F26H11_18, GLYCINE RICH PROTEIN 2B	8.4	7.9	0.6	1.2	100.0%	-4.1
5702	AT5G01020.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:5916-8443 REVERSE   Aliases: F7J8.5, F7J8_5	7.7	7.1	0.5	1.2	100.0%	-4.2
5703	AT1G44120.1   C2 domain-containing protein / armadillo/beta-catenin repeat family protein, similar to CCLS 65 (Silene latifolia) GI:2570102; contains Pfam profiles PF00514: Armadillo/beta-catenin-like repeat, PF00168: C2 domain   chr1:16783050-16789854 FORWARD   Aliases: T7O23.25, T7O23_25	3.0	2.8	0.1	1.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5704	AT2G41080.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:17139931-17141671 FORWARD   Aliases: T3K9.15, T3K9_15	3.5	3.7	-0.2	-1.2	100.0%	-4.4
5705	AT4G30530.1   defense-related protein, putative, strong similarity to defense-related protein (Brassica carinata) GI:14009290; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr4:14920540-14922464 FORWARD   Aliases: F17I23.130, F17I23_130	8.1	8.8	-0.7	-1.2	100.0%	-4.0
5706	AT4G29910.1   origin recognition complex subunit 5-related (ORC5), contains weak similarity to Origin recognition complex subunit 5 (Swiss-Prot:Q9WUV0) (Mus musculus)	4.6	5.0	-0.4	-1.2	100.0%	-3.9
5707	AT3G62240.1   zinc finger (C2H2 type) family protein, contains Pfam PF00096: Zinc finger, C2H2 type   chr3:23044417-23047740 REVERSE   Aliases: T17J13.200	6.9	7.5	-0.6	-1.2	100.0%	-4.0
5708	AT2G15440.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr2:6750695-6751912 REVERSE   Aliases: F26H6.4, F26H6_4	5.2	5.0	0.3	1.2	100.0%	-4.4
5709	AT3G47670.1   similar to pectinesterase family protein [Arabidopsis thaliana] (TAIR:At1g53840.1); similar to pectin methylesterase [Lycopersicon esculentum] (GB:AAL02367.1); contains InterPro domain Plant invertase/pectin methylesterase inhibitor (InterPro:IPR007186); contains InterPro domain Pectinesterase inhibitor (InterPro:IPR006501)   chr3:17585770-17586865 REVERSE   Aliases: F1P2.220	4.0	3.7	0.3	1.2	100.0%	-4.4
5710	AT4G39850.1   Symbol: PXA1   peroxisomal ABC transporter (PXA1), identical to peroxisomal ABC transporter PXA1 GI:15320529 from (Arabidopsis thaliana); contains Pfam profile PF00005: ABC transporter;   chr4:18488513-18497130 FORWARD   Aliases: COMATOSE, CTS, PED3, PEROXISOMAL ABC TRANSPORTER 1, PEROXISOME DEFECTIVE 3, T5J17.20, T5J17_20	6.7	7.2	-0.4	-1.2	100.0%	-4.2
5711	AT4G23910.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr4:12426718-12429297 FORWARD   Aliases: T32A16.80, T32A16_80	5.6	5.1	0.4	1.2	100.0%	-4.1
5712	AT1G68100.1   Symbol: IAR1   IAA-alanine resistance protein 1, putative, similar to IAA-alanine resistance protein 1 (Arabidopsis thaliana) SWISS-PROT:Q9M647; contains ZIP Zinc transporter domain, Pfam:PF02535; identical to cDNA IAA-alanine resistance protein 1 mRNA GI:6942042	6.1	5.8	0.3	1.2	100.0%	-4.1
5713	AT1G48050.1   Symbol: KU80   Ku80 family protein, identical to Ku80-like protein (Arabidopsis thaliana) GI:12006422; contains Pfam profiles: PF02197 Regulatory subunit of type II PKA R-subunit, PF02735: Ku70/Ku80 beta-barrel domain, PF03731: Ku70/Ku80 N-terminal alpha/beta domain, PF03730: Ku70/Ku80 C-terminal arm   chr1:17727121-17730712 FORWARD   Aliases: ATKU80, KU80 LIKE PROTEIN, T2J15.4	5.4	5.7	-0.3	-1.2	100.0%	-4.2
5714	AT3G27700.2   RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif   chr3:10258354-10263211 REVERSE   Aliases: MGF10.11	4.1	4.4	-0.3	-1.2	100.0%	-4.4
5715	AT1G50660.1   expressed protein, similar to liver stage antigen-1 (GI:510184) (Plasmodium falciparum); similar to Myosin II heavy chain, non muscle (Swiss-Prot:P08799) (Dictyostelium discoideum); similar to liver stage antigen (GI:9916) (Plasmodium falciparum); similar to Kinesin-like protein KLPA (Swiss-Prot:P28739) (Emericella nidulans)   chr1:18774605-18778354 FORWARD   Aliases: F17J6.18, F17J6_18	3.9	4.3	-0.4	-1.2	100.0%	-3.9
5716	AT5G51970.2   sorbitol dehydrogenase, putative / L-iditol 2-dehydrogenase, putative, similar to NAD-dependent sorbitol dehydrogenase from Malus x domestica (gi:4519539)   chr5:21128820-21130629 FORWARD   Aliases: MSG15.7, MSG15_7	12.4	11.9	0.5	1.2	100.0%	-4.3
5717	AT1G71220.1   UDP-glucose:glycoprotein glucosyltransferase, putative, similar to UDP-glucose:glycoprotein glucosyltransferase precursor GB:Q09332 (SP:Q09332) from Drosophila melanogaster, (gi:7670746) and (gi:11346464) from Homo sapiens   chr1:26845326-26855583 FORWARD   Aliases: F3I17.13, F3I17_13	6.5	7.0	-0.5	-1.2	100.0%	-4.1
5718	AT1G20630.1   Symbol: CAT1   catalase 1, identical to catalase 1 GI:2511725 from (Arabidopsis thaliana)   chr1:7146720-7149967 FORWARD   Aliases: CATALASE 1, F5M15.31, F5M15_31	8.0	8.8	-0.9	-1.2	100.0%	-4.0
5719	ATCG00420.1   Symbol: NDHJ   NADH dehydrogenase subunit   chrC:48677-49153 REVERSE   Aliases: NDHJ	6.8	5.8	1.0	1.2	100.0%	-3.9
5720	AT1G22170.1   phosphoglycerate/bisphosphoglycerate mutase family protein, similar to SP:P31217 Phosphoglycerate mutase 1 (EC 5.4.2.1) {Escherichia coli O157:H7}; contains Pfam profile PF00300: phosphoglycerate mutase family   chr1:7826278-7828307 FORWARD   Aliases: F16L1.10, F16L1_10	4.8	5.1	-0.3	-1.2	100.0%	-4.4
5721	AT2G38130.2   Symbol: ATMAK3	7.4	7.1	0.3	1.2	100.0%	-4.3
5722	AT3G16810.1   pumilio/Puf RNA-binding domain-containing protein, contains Pfam profile:PF00806 Pumilio-family RNA binding domains   chr3:5723255-5727626 REVERSE   Aliases: K20I9.3	5.9	6.2	-0.3	-1.2	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5723	AT4G22590.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPA) GI:2944178; contains Pfam profile PF02358: Trehalose-phosphatase   chr4:11893559-11896464 REVERSE   Aliases: F7K2.170, F7K2_170	5.8	5.3	0.6	1.2	100.0%	-4.0
5724	AT5G26100.1   hypothetical protein   chr5:9117293-9117820 REVERSE   Aliases: T1N24.107, T1N24_107	2.7	2.9	-0.2	-1.2	100.0%	-4.7
5725	AT2G43160.4   similar to epsin N-terminal homology (ENTH) domain-containing protein [Arabidopsis thaliana] (TAIR:At3g59290.1); similar to OSJNBa0083N12.8 [Oryza sativa (japonica cultivar-group)] (GB:XP_473754.1); contains InterPro domain Epsin N-terminal homology (InterPro:IPR001026)   chr2:17955139-17960798 FORWARD   Aliases: F14B2.10	5.8	5.5	0.3	1.2	100.0%	-4.3
5726	AT2G35690.1   Symbol: ACX5   acyl-CoA oxidase, putative, strong similarity to acyl-CoA oxidase (Arabidopsis thaliana) GI:3044214   chr2:15006833-15010145 FORWARD   Aliases: ACYL COA OXIDASE 5, T20F21.12, T20F21_12	4.0	4.4	-0.4	-1.2	100.0%	-4.3
5727	AT1G27930.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr1:9731252-9732706 REVERSE   Aliases: F13K9.4, F13K9_4	7.3	6.9	0.4	1.2	100.0%	-4.3
5728	AT2G47680.1   zinc finger (CCCH type) helicase family protein, similar to SP:Q28141 ATP-dependent RNA helicase A (Nuclear DNA helicase II) (DEAD-box protein 9) {Bos taurus}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:19552898-19557975 REVERSE   Aliases: F17A22.7	3.6	3.8	-0.3	-1.2	100.0%	-4.4
5729	AT5G26680.1   endonuclease, putative, similar to Swiss-Prot:P39748 FLAP endonuclease-1 (Maturation factor 1) (MF1) (Homo sapiens)   chr5:9311885-9315478 REVERSE   Aliases: None	3.9	4.3	-0.4	-1.2	100.0%	-3.9
5730	AT2G43360.1   Symbol: BIO2   biotin synthase (BioB) (BIO2), identical to SP:P54967 Pfam profile PF04055: radical SAM domain protein   chr2:18017828-18020315 REVERSE   Aliases: BIOB, BIOTIN AUXOTROPH 2, BIOTIN AUXOTROPH B, BIOTIN SYNTHASE, T1O24.10	12.1	11.6	0.5	1.2	100.0%	-4.1
5731	AT2G38690.1   expressed protein   chr2:16183554-16184741 REVERSE   Aliases: T6A23.11, T6A23_11	2.4	2.6	-0.2	-1.2	100.0%	-4.8
5732	AT5G50340.1   DNA repair protein-related, similar to RadA (Pseudomonas aeruginosa) GI:1881700   chr5:20508643-20512982 REVERSE   Aliases: MXI22.5, MXI22_5	4.0	3.8	0.3	1.2	100.0%	-4.3
5733	AT2G25800.1   expressed protein   chr2:11012980-11016817 REVERSE   Aliases: F17H15.17, F17H15_17	4.6	5.1	-0.4	-1.2	100.0%	-4.2
5734	AT3G63150.1   GTP-binding protein-related, low similarity to SP:Q38912 RAC-like GTP binding protein ARAC3 (GTP-binding protein ROP6) {Arabidopsis thaliana}; contains Pfam profile PF00036: EF hand (domain)   chr3:23339903-23343704 REVERSE   Aliases: T20O10.250	8.2	8.6	-0.3	-1.2	100.0%	-4.2
5735	AT2G04063.1   glycine-rich protein   chr2:1349755-1350174 REVERSE   Aliases: F3L12.1, F3L12_1	4.9	4.4	0.5	1.2	100.0%	-4.2
5736	AT1G09130.2   similar to ATP-dependent Clp protease proteolytic subunit (ClpR1) (nClpP5) [Arabidopsis thaliana] (TAIR:At1g49970.1); similar to COG0740: Protease subunit of ATP-dependent Clp proteases [Nostoc punctiforme PCC 73102] (GB:ZP_00108611.1); contains InterPro domain Clp protease (InterPro:IPR001907)   chr1:2939928-2942269 REVERSE   Aliases: F7G19.1, F7G19_1	9.3	8.5	0.8	1.2	100.0%	-3.8
5737	AT4G00810.2   60S acidic ribosomal protein P1 (RPP1B), similar to acidic ribosomal protein p1   chr4:345952-347192 REVERSE   Aliases: A_TM018A10.9, A_TM018A10_9, T18A10.8, T18A10_8	10.0	10.7	-0.6	-1.2	100.0%	-3.8
5738	AT2G42610.2   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr2:17754994-17757517 FORWARD   Aliases: F14N22.12, F14N22_12	2.9	2.8	0.2	1.2	100.0%	-4.8
5739	AT5G23640.1   expressed protein   chr5:7968262-7968505 REVERSE   Aliases: MQM1.10, MQM1_10	3.1	3.0	0.2	1.2	100.0%	-5.2
5740	AT1G52740.1   histone H2A, putative, similar to histone H2A.F/Z Arabidopsis thaliana GI:2407800; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:19648963-19650099 FORWARD   Aliases: F14G24.1, F14G24_1	9.7	9.2	0.5	1.2	100.0%	-4.4
5741	AT5G37480.1   expressed protein   chr5:14901561-14903198 REVERSE   Aliases: MPA22.2, MPA22_2	7.7	7.4	0.4	1.2	100.0%	-4.3
5742	AT1G31250.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; similar to prolin rich protein GB:S44189 GI:433706 from (Zea mays)   chr1:11166538-11167493 REVERSE   Aliases: T19E23.3, T19E23_3	2.2	2.3	-0.1	-1.2	100.0%	-5.3
5743	AT2G41530.1   esterase, putative, similar to SP:P10768 Esterase D (EC 3.1.1.1) {Homo sapiens}; contains Pfam profile: PF00756 putative esterase   chr2:17330573-17332689 REVERSE   Aliases: T32G6.5, T32G6_5	10.2	10.7	-0.6	-1.2	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5744	AT3G55050.2   serine/threonine protein phosphatase 2C (PP2C6), identical to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain; contains TIGRFAM TIGR01573 : CRISPR-associated protein Cas2   chr3:20411465-20413572 REVERSE   Aliases: T15C9.50	9.0	8.6	0.4	1.2	100.0%	-4.1
5745	AT4G09430.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:5970929-5975372 FORWARD   Aliases: T15G18.150, T15G18_150	2.7	2.9	-0.2	-1.2	100.0%	-4.8
5746	AT3G17380.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:5950206-5953699 FORWARD   Aliases: MGD8.22	7.0	7.9	-0.9	-1.2	100.0%	-3.9
5747	AT3G11850.2   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr3:3738903-3741720 REVERSE   Aliases: F26K24.14	4.9	5.2	-0.3	-1.2	100.0%	-4.2
5748	AT1G78380.1   Symbol: ATGSTU19   glutathione S-transferase, putative, similar to glutathione transferase GI:2853219 from (Carica papaya)   chr1:29491306-29492799 REVERSE   Aliases: F3F9.11, F3F9_11, GLUTATHIONE TRANSFERASE 8, GST8	10.8	11.3	-0.5	-1.2	100.0%	-4.4
5749	AT1G31830.2   amino acid permease family protein, weak similarity to y+LAT1a (amino acid transporter) (Mus musculus) GI:3970791; contains Pfam profile PF00324: Amino acid permease   chr1:11418606-11420703 REVERSE   Aliases: F5M6.16, F5M6_16	7.8	7.3	0.5	1.2	100.0%	-4.2
5750	AT2G40180.1   protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain; identical to protein phosphatase 2C (GI:4587992) (Arabidopsis thaliana)   chr2:16789600-16791225 FORWARD   Aliases: ATHPP2C5, T7M7.17	3.0	3.4	-0.4	-1.2	100.0%	-4.4
5751	AT2G01630.1   glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis)   chr2:279283-282122 REVERSE   Aliases: T8O11.20, T8O11_20	4.3	4.6	-0.2	-1.2	100.0%	-4.5
5752	AT1G52980.1   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function   chr1:19741161-19744016 FORWARD   Aliases: F14G24.25, F14G24_25	7.3	7.7	-0.5	-1.2	100.0%	-3.9
5753	AT1G72900.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27435226-27437443 FORWARD   Aliases: F3N23.10, F3N23_10	4.5	3.8	0.6	1.2	100.0%	-4.2
5754	AT4G29220.1   phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase   chr4:14403041-14406511 REVERSE   Aliases: F17A13.40, F17A13_40	4.3	5.0	-0.7	-1.2	100.0%	-3.7
5755	AT2G05755.1   integral membrane family protein, contains Pfam PF00892: Integral membrane protein domain   chr2:2170890-2173757 FORWARD   Aliases: None	5.4	5.1	0.3	1.2	100.0%	-4.3
5756	AT3G22550.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana)   chr3:7991653-7993461 REVERSE   Aliases: F16J14.11	5.0	4.6	0.3	1.2	100.0%	-4.1
5757	AT1G79460.1   Symbol: GA2   ent-kaurene synthase / ent-kaurene synthetase B (KS) (GA2), identical to GI:3056725 (PMID:9536043); formerly called ent-kaurene synthetase B   chr1:29895285-29899428 FORWARD   Aliases: ATKS, ENT KAURENE SYNTHASE, GA REQUIRING 2, KS, T8K14.12, T8K14_12	5.2	5.4	-0.3	-1.2	100.0%	-4.4
5758	AT2G38770.1   expressed protein   chr2:16210041-16217416 REVERSE   Aliases: T6A23.3, T6A23_3	3.6	3.4	0.2	1.2	100.0%	-4.5
5759	AT2G05840.2   Symbol: PAA2   similar to 20S proteasome alpha subunit A1 (PAA1) (PRC1) [Arabidopsis thaliana] (TAIR:At5g35590.1); similar to proteasome IOTA subunit [Glycine max] (GB:AAC28135.1); contains InterPro domain Proteasome subunit, A-type (InterPro:IPR000426); contains InterPro domain Multispecific proteasome protease (InterPro:IPR001353)   chr2:2234089-2236287 FORWARD   Aliases: 20S PROTEASOME SUBUNIT PAA2, T6P5.4, T6P5_4	11.1	11.5	-0.3	-1.2	100.0%	-4.7
5760	AT5G35590.1   Symbol: PAA1   20S proteasome alpha subunit A1 (PAA1) (PRC1), identical to proteasome subunit alpha type 6-1 SP:O81146 GI:12643647 from (Arabidopsis thaliana); identical to cDNA proteasome subunit prc1 GI:2511587   chr5:13782400-13785047 REVERSE   Aliases: 20S PROTEASOME SUBUNIT PAA1, K2K18.4, K2K18_4	11.1	11.5	-0.3	-1.2	100.0%	-4.7
5761	AT4G33540.1   metallo-beta-lactamase family protein   chr4:16130876-16133963 FORWARD   Aliases: T16L1.30, T16L1_30	8.8	8.1	0.7	1.2	100.0%	-4.1
5762	AT1G22620.1   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248;gb:AAG29810; contains Pfam domain, PF02383: SacI homology domain; identical to cDNA SAC domain protein 1 (SAC1) SAC1-FRA7 allele, GI:31415718   chr1:7997665-8002933 REVERSE   Aliases: F12K8.3	5.7	5.9	-0.3	-1.2	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5763	AT1G73260.1   trypsin and protease inhibitor family protein / Kunitz family protein, similar to trypsin inhibitor propeptide (Brassica oleracea) GI:841208; contains Pfam profile PF00197: Trypsin and protease inhibitor   chr1:27550935-27551851 REVERSE   Aliases: T18K17.7, T18K17_7	5.0	5.6	-0.6	-1.2	100.0%	-3.6
5764	AT4G15975.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:9052187-9053164 FORWARD   Aliases: None	2.8	3.0	-0.1	-1.2	100.0%	-5.0
5765	AT1G05620.1   inosine-uridine preferring nucleoside hydrolase family protein, similar to Chain A, Crystal Structure Of Nucleoside Hydrolase From Leishmania MajorGI:8569431; contains Pfam profile PF01156: Inosine-uridine preferring nucleoside hydrolase   chr1:1679165-1681705 FORWARD   Aliases: F3F20.7, F3F20_7	7.1	7.5	-0.4	-1.2	100.0%	-4.2
5766	AT3G14560.1   expressed protein   chr3:4889079-4890166 FORWARD   Aliases: MIE1.6	4.1	3.3	0.8	1.2	100.0%	-3.7
5767	AT4G17420.1   expressed protein, contains Pfam domain, PF01987: Protein of unknown function   chr4:9722451-9724652 REVERSE   Aliases: DL4745C, FCAALL.389	7.7	7.3	0.4	1.2	100.0%	-4.0
5768	AT2G17560.2   Symbol: HMGB4   similar to high mobility group protein delta (HMGdelta) / HMG protein delta [Arabidopsis thaliana] (TAIR:At4g35570.1); similar to HMG-1 like protein gene [Glycine max] (GB:CAA41200.1); similar to high mobility group protein [Solanum tuberosum] (GB:CAA05365.1); contains InterPro domain HMG1/2 (high mobility group) box (InterPro:IPR000910)   chr2:7649247-7650749 REVERSE   Aliases: HIGH MOBILITY GROUP B 4, HMG GAMMA, MJB20.12, MJB20_12, NFD04, NFD4	7.3	8.1	-0.8	-1.2	100.0%	-3.9
5769	AT3G08680.2   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profile: PF00069 Eukaryotic protein kinase domain, PF00560 leucine Rich Repeat (5 copies)   chr3:2637603-2640844 FORWARD   Aliases: F17O14.15	5.4	5.8	-0.4	-1.2	100.0%	-4.4
5770	AT3G58990.1   aconitase C-terminal domain-containing protein, contains Pfam profile PF00694: Aconitase C-terminal domain   chr3:21808035-21809280 REVERSE   Aliases: F17J16.40	4.2	3.6	0.6	1.2	100.0%	-3.6
5771	AT5G55200.1   co-chaperone grpE protein, putative, similar to chaperone GrpE type 2 (Nicotiana tabacum) GI:3851640; contains Pfam profile PF01025: co-chaperone GrpE   chr5:22411860-22413777 FORWARD   Aliases: MCO15.15, MCO15_15	8.7	9.1	-0.4	-1.2	100.0%	-4.4
5772	AT1G14687.1   zinc finger homeobox family protein / ZF-HD homeobox family protein   chr1:5047798-5048607 FORWARD   Aliases: None	4.0	3.6	0.3	1.2	100.0%	-4.2
5773	AT5G09800.1   U-box domain-containing protein, low similarity to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain	5.5	5.2	0.3	1.2	100.0%	-4.4
5774	AT5G16850.1   Symbol: ATTERT	2.4	2.6	-0.2	-1.2	100.0%	-4.9
5775	AT5G50460.1   protein transport protein SEC61 gamma subunit, putative, similar to Swiss-Prot:Q19967 protein transport protein SEC61 gamma subunit (Caenorhabditis elegans)   chr5:20568663-20569792 REVERSE   Aliases: MBA10.8	9.7	10.4	-0.7	-1.2	100.0%	-4.2
5776	AT5G26670.2   pectinacylesterase, putative, similar to pectinacylesterase precursor GI:1431629 from (Vigna radiata)   chr5:9318283-9320990 FORWARD   Aliases: None	5.7	6.1	-0.4	-1.2	100.0%	-4.0
5777	AT4G10090.1   expressed protein   chr4:6305439-6307514 FORWARD   Aliases: F28M11.10, F28M11_10	4.5	4.7	-0.2	-1.2	100.0%	-4.5
5778	AT5G61070.1   histone deacetylase family protein (HDA18), identical to HDA18 (Arabidopsis thaliana) GI:21105769; similar to SP:Q9UBN7 Histone deacetylase 6 (HD6) {Homo sapiens}; contains Pfam profile PF00850: Histone deacetylase family   chr5:24588397-24591598 REVERSE   Aliases: MAF19.8, MAF19_8	3.1	3.3	-0.2	-1.2	100.0%	-4.6
5779	AT2G41090.1   calmodulin-like calcium-binding protein, 22 kDa (CaBP-22), identical to SP:P30187 22 kDa calmodulin-like calcium-binding protein (CABP-22) (Arabidopsis thaliana)   chr2:17142862-17143930 FORWARD   Aliases: T3K9.14, T3K9_14	4.0	3.7	0.3	1.2	100.0%	-4.2
5780	AT4G03270.1   Symbol: CYCD6;1   cyclin family protein, similar to CycD3;2 (Lycopersicon esculentum) GI:6434199 ; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr4:1432375-1433691 REVERSE   Aliases: CYCD6;1, Cyclin D6;1, F4C21.20, F4C21_20	2.9	3.1	-0.1	-1.2	100.0%	-4.9
5781	AT5G44320.1   eukaryotic translation initiation factor 3 subunit 7, putative / eIF-3 zeta, putative / eIF3d, putative, similar to initiation factor 3d (Arabidopsis thaliana) GI:12407755, SP:O15371 Eukaryotic translation initiation factor 3 subunit 7 (eIF-3 zeta) (eIF3 p66) (eIF3d) {Homo sapiens}; contains Pfam profile PF05091: Eukaryotic translation initiation factor 3 subunit 7 (eIF-3)   chr5:17871816-17873907 REVERSE   Aliases: K9L2.10, K9L2_10	8.4	8.7	-0.3	-1.2	100.0%	-4.6
5782	AT3G26850.2   expressed protein   chr3:9896779-9899243 REVERSE   Aliases: MDJ14.17	4.0	4.1	-0.1	-1.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5783	AT1G05055.1   basic transcription factor 2, 44kD subunit-related, contains weak similarity to Swiss-Prot:Q13888 TFIIF basal transcription factor complex p44 subunit (Basic transcription factor 2 44 kDa subunit, BTF2-p44, General transcription factor IIF polypeptide 2) (Homo sapiens)   chr1:1448718-1450855 REVERSE   Aliases: AT1G05050	6.2	6.5	-0.3	-1.2	100.0%	-4.2
5784	AT4G12540.1   expressed protein   chr4:7429873-7431599 REVERSE   Aliases: T1P17.130, T1P17_130	3.1	3.4	-0.3	-1.2	100.0%	-4.3
5785	AT4G18850.1   hypothetical protein   chr4:10342074-10342253 REVERSE   Aliases: F13C5.20, F13C5_20	2.4	2.3	0.1	1.2	100.0%	-5.2
5786	AT3G01630.1   similar to nodulin-related [Arabidopsis thaliana] (TAIR:At1g31470.1); similar to P0031D02.33 [Oryza sativa (japonica cultivar-group)] (GB:NP_915291.1)   chr3:237246-239120 FORWARD   Aliases: F4P13.17, F4P13_17	3.0	2.8	0.2	1.2	100.0%	-4.8
5787	AT5G19100.1   extracellular dermal glycoprotein-related / EDGP-related, low similarity to extracellular dermal glycoprotein EDGP precursor (Daucus carota) GI:285741, SP:P13917 Basic 7S globulin precursor {Glycine max}   chr5:6408244-6409419 REVERSE   Aliases: T16G12.140, T16G12_140	3.6	3.4	0.2	1.2	100.0%	-4.4
5788	AT1G55850.1   Symbol: ATCSLE1   cellulose synthase family protein, similar to cellulose synthase catalytic subunit (gi:13925881) from Nicotiana glauca, cellulose synthase-5 (gi:9622882) from Zea mays   chr1:20880365-20883146 FORWARD   Aliases: CSLE1, F14J16.9, F14J16_9	7.1	7.5	-0.4	-1.2	100.0%	-4.1
5789	AT2G39990.1   Symbol: EIF2   eukaryotic translation initiation factor 3 subunit 5 / eIF-3 epsilon / eIF3f (TIF3F1), identical to SP:O04202 Eukaryotic translation initiation factor 3 subunit 5 (eIF-3 epsilon) (eIF3 p32 subunit) (eIF3f) {Arabidopsis thaliana}; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr2:16705174-16707090 REVERSE   Aliases: T28M21.15, T28M21_15, TRANSLATION INITIATION FACTOR EIF2 P47 SUBUNIT HOMOLOG	8.6	9.3	-0.8	-1.2	100.0%	-4.0
5790	AT4G13070.1   group II intron splicing factor CRS1-related, contains weak similarity to CRS1 (Zea mays) gi:9837550:gb:AAG00595	4.3	4.7	-0.4	-1.2	100.0%	-4.3
5791	AT3G58560.1   endonuclease/exonuclease/phosphatase family protein, similar to SP:P31384 Glucose-repressible alcohol dehydrogenase transcriptional effector (Carbon catabolite repressor protein 4) {Saccharomyces cerevisiae}; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr3:21661573-21665177 REVERSE   Aliases: F14P22.150	5.6	6.3	-0.7	-1.2	100.0%	-4.2
5792	AT5G42190.1   Symbol: ASK2   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At2) / UFO-binding protein (UIP2), E3 ubiquitin ligase; skp1b; identical to UIP2 GI:3719211 from (Arabidopsis thaliana); contains Pfam profiles PF01466: Skp1 family, dimerisation domain and PF03931:Skp1 family, tetramerisation domain; identical to cDNA UFO binding protein UIP2 mRNA, partial cds GI:3719210   chr5:16870883-16872793 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 2, MJC20.30, MJC20_30, SKP1B	11.3	10.6	0.7	1.2	100.0%	-4.0
5793	AT4G12640.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr4:7462598-7467859 FORWARD   Aliases: T1P17.230, T1P17_230	3.7	3.9	-0.2	-1.2	100.0%	-4.7
5794	AT2G41710.2   ovule development protein, putative, similar to ovule development protein AINTEGUMENTA (GI:1209099) (Arabidopsis thaliana);Pfam domain (PF00847)	6.0	5.6	0.4	1.2	100.0%	-4.1
5795	AT5G27820.1   ribosomal protein L18 family protein, similar to SP:P52863 50S ribosomal protein L18 (Aeromonas proteolytica) {Vibrio proteolyticus}   chr5:9859858-9861133 FORWARD   Aliases: T1G16.150, T1G16_150	5.2	5.8	-0.6	-1.2	100.0%	-3.7
5796	AT5G06850.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr5:2126976-2129325 REVERSE   Aliases: MOJ9.2, MOJ9_2	4.1	3.7	0.4	1.2	100.0%	-4.0
5797	AT5G64640.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:25853953-25856279 FORWARD   Aliases: MUB3.16, MUB3_16	4.4	4.8	-0.3	-1.2	100.0%	-4.2
5798	AT3G46580.1   Symbol: MBD5   methyl-CpG-binding domain-containing protein, weak similarity to SP:P51608 Methyl-CpG-binding protein 2 (MeCP-2 protein) (MeCP2) {Homo sapiens}; contains Pfam profile PF01429: Methyl-CpG binding domain   chr3:17159327-17160574 FORWARD   Aliases: F12A12.100	5.0	5.4	-0.4	-1.2	100.0%	-4.0
5799	AT1G31814.1   Symbol: FRL2   expressed protein   chr1:11412589-11414414 REVERSE   Aliases: F5M6.26, F5M6_26, FRIGIDA LIKE 2	3.4	3.2	0.2	1.2	100.0%	-4.6
5800	AT4G01860.2   transducin family protein / WD-40 repeat family protein, contains ten G-protein beta-subunit (beta-transducin) WD-40 repeats   chr4:801032-808060 REVERSE   Aliases: T7B11.12, T7B11_12	2.6	2.9	-0.3	-1.2	100.0%	-4.7
5801	AT3G01850.2   ribulose-phosphate 3-epimerase, cytosolic, putative / pentose-5-phosphate 3-epimerase, putative, strong similarity to D-ribulose-5-phosphate 3-epimerase (Oryza sativa) GI:6007803; contains Pfam profile PF00834: Ribulose-phosphate 3 epimerase family; contains non-consensus splice sites at exon 1 and exon2   chr3:300047-302044 REVERSE   Aliases: F28J7.18, F28J7_18	5.5	4.9	0.6	1.2	100.0%	-3.9
5802	AT3G48030.1   hypoxia-responsive family protein / zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHX1a (Arabidopsis thaliana) GI:3790591; contains Pfam profiles PF00097: Zinc finger C3HC4 type (RING finger), PF04588: Hypoxia induced protein conserved region   chr3:17736395-17738939 REVERSE   Aliases: T17F15.100	2.2	2.4	-0.2	-1.2	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5803	AT3G25560.2   protein kinase family protein, contains Prosite:PS00108: Serine/Threonine protein kinases active-site signature and PS00107: Protein kinases ATP-binding region signature   chr3:9280750-9283924 REVERSE   Aliases: MWL2.18	6.3	6.0	0.2	1.2	100.0%	-4.4
5804	AT5G34460.1   replication protein-related, weak similarity to Replication Protein A 70	2.6	2.7	-0.1	-1.2	100.0%	-5.2
5805	AT3G59400.1   Symbol: GUN4   expressed protein   chr3:21959694-21960687 REVERSE   Aliases: F25L23.260	3.4	3.0	0.4	1.2	100.0%	-4.0
5806	AT3G16180.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:5481331-5485100 REVERSE   Aliases: MSL1.22	5.2	4.7	0.5	1.2	100.0%	-4.1
5807	AT3G17465.1   Symbol: RPL3P   ribosomal protein L3 family protein   chr3:5977823-5979578 REVERSE   Aliases: MKP6.7, RIBOSOMAL PROTEIN L3 PLASTID	6.4	7.0	-0.5	-1.2	100.0%	-3.8
5808	AT1G42580.1   hypothetical protein, contains similarity to hypothetical proteins   chr1:15994136-15994615 REVERSE   Aliases: F8D11.4, F8D11_4	3.1	2.9	0.2	1.2	100.0%	-4.9
5809	AT4G21510.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr4:11445868-11447175 REVERSE   Aliases: F18E5.130, F18E5_130	4.9	4.7	0.3	1.2	100.0%	-4.4
5810	AT2G45660.1   Symbol: AGL20   MADS-box protein (AGL20)   chr2:18814612-18818094 REVERSE   Aliases: AGAMOUS LIKE 20, AGL20, F17K2.19, MADS BOX PROTEIN AGL20, SOC1, SUPPRESSOR OF OVEREXPRESSION OF CO 1	5.4	5.1	0.3	1.2	100.0%	-4.4
5811	AT3G52940.2   Symbol: FK   C-14 sterol reductase / delta(14)-sterol reductase / FACKEL (FK), identical to gi:9082182   chr3:19641176-19644261 REVERSE   Aliases: ELL1, EXTRA LONG LIFESPAN 1, F8J2.111, FACKEL, HYD2	6.7	7.1	-0.4	-1.2	100.0%	-4.1
5812	AT4G11450.1   expressed protein   chr4:6958676-6962041 REVERSE   Aliases: F25E4.70, F25E4_70	3.1	3.2	-0.2	-1.2	100.0%	-4.7
5813	AT3G29640.1   hypothetical protein, contains similarity to hypothetical proteins   chr3:11490525-11491040 FORWARD   Aliases: T13J10.7	2.5	2.3	0.2	1.2	100.0%	-4.7
5814	AT4G36670.1   mannitol transporter, putative, similar to mannitol transporter (Apium graveolens var. dulce) GI:12004316; contains Pfam profile PF00083: major facilitator superfamily protein   chr4:17287503-17289594 REVERSE   Aliases: AP22.86, AP22_86	4.4	5.1	-0.6	-1.2	100.0%	-3.9
5815	AT4G16420.3   Symbol: ADA2B   transcriptional adaptor (ADA2b), identical to transcriptional adaptor ADA2b (Arabidopsis thaliana) gi:13591700:gb:AAK31320   chr4:9262690-9266078 REVERSE   Aliases: DL4235C, FCAALL.57, PROPORZ1, PRZ1	7.9	7.6	0.3	1.2	100.0%	-4.3
5816	AT5G40150.1   peroxidase, putative, identical to peroxidase ATP26a {Arabidopsis thaliana} GP:1890317:emb:CAA72487   chr5:16076737-16078271 REVERSE   Aliases: MSN9.50, MSN9_50	3.8	4.1	-0.2	-1.2	100.0%	-4.5
5817	AT3G44950.1   glycine-rich protein   chr3:16432030-16432271 FORWARD   Aliases: F14D17.20	7.2	6.8	0.4	1.2	100.0%	-4.0
5818	AT1G59960.1   aldo/keto reductase, putative, similar to NADPH-dependent codeinone reductase GI:6478210 (Papaver somniferum), NAD(P)H dependent 6'-deoxychalcone synthase (Glycine max)(GI:18728)   chr1:22074961-22076812 REVERSE   Aliases: F23H11.27, F23H11_27	10.2	10.8	-0.5	-1.2	100.0%	-4.5
5819	AT4G23100.2   Symbol: RML1   similar to gamma-glutamylcysteine synthetase [Brassica juncea] (GB:CAA06613.1); similar to glutamate-cysteine ligase [Brassica juncea] (GB:CAD91714.1); similar to gamma-glutamylcysteine synthetase precursor [Pisum sativum] (GB:AAF22137.1); similar to gamma-glutamylcysteine synthetase [Lotus corniculatus var. japonicus] (GB:AAO27827.1); similar to glutamate-cysteine ligase [Brassica juncea] (GB:CAD91713.1); contains InterPro domain Glutamate--cysteine ligase, plant (InterPro:IPR006336)   chr4:12103172-12107310 REVERSE   Aliases: CAD2, CADMIUM SENSITIVE 2, F7H19.290, F7H19_290, GAMMA GLUTAMYL CYSTEINE SYNTHETASE, GAMMA GLUTAMYL CYSTEINE SYNTHETASE 1, GAMMA GLUTAMYL CYSTEINE SYNTHETASE, GSH1, ROOT MERISTEMLESS 1	11.6	10.6	1.0	1.2	100.0%	-3.9
5820	AT1G68070.1   zinc finger (C3HC4-type RING finger) family protein, very low similarity to RING-H2 finger protein RHG1a (Arabidopsis thaliana) GI:3822225; contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	5.6	5.4	0.2	1.2	100.0%	-4.5
5821	AT5G67110.1   Symbol: ALC   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain   chr5:26802333-26803609 REVERSE   Aliases: ALCATRAZ, K21H1.7, K21H1_7	2.9	2.7	0.2	1.2	100.0%	-4.8
5822	AT5G21060.3   similar to bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative [Arabidopsis thaliana] (TAIR:At4g19710.2); similar to COG0460: Homoserine dehydrogenase [Rubrobacter xylanophilus DSM 9941] (GB:ZP_00199840.1); contains InterPro domain Homoserine dehydrogenase (InterPro:IPR001342)   chr5:7148980-7152866 REVERSE   Aliases: T10F18.90, T10F18_90	7.6	8.2	-0.6	-1.2	100.0%	-3.9
5823	AT5G17330.1   Symbol: GAD   glutamate decarboxylase 1 (GAD 1), sp:Q42521   chr5:5711070-5715077 FORWARD   Aliases: GAD1, GLUTAMATE DECARBOXYLASE, MKP11.30, MKP11_30	8.2	9.3	-1.1	-1.2	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5824	AT2G21940.2   shikimate kinase, putative, similar to shikimate kinase precursor from <i>Lycopersicon esculentum</i> (SP:Q00497); contains Pfam shikimate kinase domain PF01202   chr2:9357926-9360235 FORWARD   Aliases: F7D8.26, F7D8_26	6.0	5.4	0.6	1.2	100.0%	-4.1
5825	AT4G19050.1   mob1/phocein family protein, contains Pfam PF03637: Mob1/phocein family; contains Pfam F00560: Leucine Rich Repeats; contains TIGRFAMS profile TIGR01612: reticulocyte binding protein; hypothetical protein YIL106w, <i>Saccharomyces cerevisiae</i> , PIR2:S48466   chr4:10438224-10443797 REVERSE   Aliases: T18B16.1	5.0	4.7	0.3	1.2	100.0%	-4.4
5826	AT2G13730.1   hypothetical protein   chr2:5732639-5733085 REVERSE   Aliases: F13J11.8, F13J11_8	2.4	2.5	-0.1	-1.2	100.0%	-5.2
5827	AT4G00500.2   lipase class 3 family protein / calmodulin-binding heat-shock protein-related   chr4:224992-227195 REVERSE   Aliases: F6N23.21, F6N23_21	4.4	4.1	0.3	1.2	100.0%	-4.1
5828	AT5G40530.2   expressed protein, contains Pfam profile PF05148: Protein of unknown function (DUF691)   chr5:16251740-16253450 FORWARD   Aliases: MNF13.4, MNF13_4	5.6	6.1	-0.5	-1.2	100.0%	-4.4
5829	AT5G48590.1   expressed protein   chr5:19715647-19717173 FORWARD   Aliases: K15N18.6, K15N18_6	6.0	5.7	0.2	1.2	100.0%	-4.6
5830	AT4G15100.1   Symbol: SCPL30	2.7	2.6	0.1	1.2	100.0%	-4.9
5831	AT1G22890.1   expressed protein   chr1:8102807-8103521 FORWARD   Aliases: F19G10.22, F19G10_22	2.8	3.0	-0.2	-1.2	100.0%	-5.2
5832	AT5G10290.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:3235296-3238720 REVERSE   Aliases: F18D22.60, F18D22_60	7.3	7.8	-0.5	-1.2	100.0%	-4.6
5833	AT5G14390.1   expressed protein   chr5:4637315-4639759 REVERSE   Aliases: F18O22.180, F18O22_180	5.9	5.6	0.3	1.2	100.0%	-4.3
5834	AT5G01510.1   expressed protein, contains Pfam domain, PF04884: Protein of unknown function, DUF647   chr5:201605-205380 FORWARD   Aliases: F7A7.30, F7A7_30	3.6	3.8	-0.2	-1.2	100.0%	-4.6
5835	AT5G17640.1   expressed protein   chr5:5810189-5813286 REVERSE   Aliases: K10A8.120, K10A8_120	5.3	4.8	0.5	1.2	100.0%	-4.0
5836	AT2G17250.1   expressed protein, weak similarity to Ribosome biogenesis protein MAK21 (Swiss-Prot:Q12176) ( <i>Saccharomyces cerevisiae</i> )   chr2:7506559-7510207 FORWARD   Aliases: T23A1.11, T23A1_11	6.9	7.3	-0.4	-1.2	100.0%	-4.2
5837	AT4G02130.3   similar to glycosyl transferase family 8 protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g02720.2); similar to glycosyl transferase family 8 protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g02720.1); similar to putative glycosyltransferase [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_479332.1); similar to OSJNBa0074L08.24 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_473276.1); contains InterPro domain Glycosyl transferase, family 8 (InterPro:IPR002495)   chr4:944360-947085 REVERSE   Aliases: T10M13.14, T10M13_14	4.5	4.2	0.3	1.2	100.0%	-4.2
5838	AT5G27000.1   Symbol: ATK4   kinesin motor protein-related, non-consensus AT donor splice site at exon 12; non-consensus AC acceptor splice site at exon 13   chr5:9498055-9503137 FORWARD   Aliases: ARABIDOPSIS THALIANA KINESIN 4, F2P16.12, F2P16_12, KATD, KINESIN LIKE PROTEIN D	3.2	3.5	-0.3	-1.2	100.0%	-4.3
5839	AT3G15070.1   zinc finger (C3HC4-type RING finger) family protein, similar to C-terminal zinc-finger (Glycine max) GI:558543; contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:5069620-5073324 REVERSE   Aliases: K15M2.22	3.7	3.3	0.4	1.2	100.0%	-4.3
5840	AT4G32540.1   Symbol: YUC   flavin-containing monooxygenase / FMO (YUCCA), identical to gi:16555352   chr4:15700910-15702876 FORWARD   Aliases: L23H3.20, L23H3_20, YUCCA	5.1	5.6	-0.5	-1.2	100.0%	-3.9
5841	AT5G16750.1   Symbol: TOZ   transducin family protein / WD-40 repeat family protein, contains 8 WD-40 repeats (PF00400); similar to transducin homolog sazD - <i>Homo sapiens</i> , EMBL:U02609   chr5:5504349-5509345 REVERSE   Aliases: F5E19.90, F5E19_90, TORMOZ, TORMOZEMBRYO DEFECTIVE	5.2	5.5	-0.4	-1.2	100.0%	-4.2
5842	AT2G04890.1   Symbol: SCL21   scarecrow-like transcription factor 21 (SCL21)   chr2:1719778-1722378 REVERSE   Aliases: F1O13.2, F1O13_2, SCARECROW LIKE 21, SCL21	6.3	5.9	0.4	1.2	100.0%	-4.2
5843	AT4G04930.1   Symbol: DES 1 LIKE   fatty acid desaturase family protein, similar to <i>D. melanogaster</i> Des-1 protein, GenBank accession number X94180; contains Pfam profile PF00487 Fatty acid desaturase domain   chr4:2509131-2511060 FORWARD   Aliases: DES 1 LIKE TRANSMEMBRANE PROTEIN, T1J1.1, T1J1_1	2.7	2.9	-0.2	-1.2	100.0%	-4.7
5844	AT1G14410.1   DNA-binding protein-related, similar to DNA-binding protein p24 GI:9651810 from ( <i>Solanum tuberosum</i> )   chr1:4929118-4930888 REVERSE   Aliases: F14L17.18, F14L17_18	5.8	6.3	-0.5	-1.2	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5845	AT5G24340.1   3'-5' exonuclease domain-containing protein, contains Pfam profile PF01612: 3'-5' exonuclease   chr5:8297308-8300377 FORWARD   Aliases: K16H17.2, K16H17_2	3.5	3.3	0.2	1.2	100.0%	-4.7
5846	AT1G64185.1   lactoylglutathione lyase family protein / glyoxalase I family protein, contains Pfam domain PF00903: glyoxalase family protein   chr1:23828177-23829447 FORWARD   Aliases: None	4.9	5.3	-0.4	-1.2	100.0%	-4.1
5847	AT4G39140.4   expressed protein   chr4:18229325-18232034 REVERSE   Aliases: T22F8.40, T22F8_40	5.0	4.6	0.4	1.2	100.0%	-4.0
5848	AT3G54840.1   Symbol: ARA6   Rab GTPase (ARA6), identical to small GTPase Ara6 (Arabidopsis thaliana) GI:13160603   chr3:20329480-20331970 FORWARD   Aliases: F28P10.180	9.2	8.2	1.0	1.2	100.0%	-4.1
5849	AT1G36030.1   F-box family protein, similar to hypothetical protein GB:AAC61810   chr1:13437798-13438040 FORWARD   Aliases: T22A15.5, T22A15_5	2.4	2.5	-0.1	-1.2	100.0%	-5.3
5850	AT5G62080.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to tapetum-specific protein a9 precursor {Brassica napus} SP:Q05772; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234; supported by full-length cDNA Ceres:27795   chr5:24950822-24951671 REVERSE   Aliases: MTG10.3, MTG10_3	2.3	2.4	-0.1	-1.2	100.0%	-4.9
5851	AT1G60850.3   Symbol: ATRPAC42   DNA-directed RNA polymerase, putative, identical to RNA polymerase subunit (Arabidopsis thaliana) GI:514322; contains Pfam profile PF01000: RNA polymerase Rpb3/RpoA insert domain   chr1:22401581-22403834 REVERSE   Aliases: AAC42, F23C21.3, F23C21_3, RNA POLYMERASE I SUBUNIT 42	6.3	6.8	-0.5	-1.2	100.0%	-4.0
5852	AT1G74800.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr1:28105629-28108773 REVERSE   Aliases: F25A4.23, F25A4_23	4.4	4.8	-0.4	-1.2	100.0%	-4.1
5853	AT3G60130.2   similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At5g44640.1); similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At2g44450.1); similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At5g42260.1); similar to putative prunasin hydrolase precursor [Prunus serotina] (GB:AAL07490.1); similar to putative prunasin hydrolase isoform PH-L1 precursor [Prunus serotina] (GB:AAF34651.2); similar to prunasin hydrolase isoform PH B precursor [Prunus serotina] (GB:AAL39079.1); similar to prunasin hydrolase isoform PH B precursor [Prunus serotina] (GB:AAL06338.1); contains InterPro domain Glycoside hydrolase, family 1 (InterPro:IPR001360)   chr3:22221409-22224792 FORWARD   Aliases: T2O9.110	3.4	4.0	-0.6	-1.2	100.0%	-3.7
5854	AT2G25460.1   expressed protein   chr2:10839838-10842561 REVERSE   Aliases: F13B15.12, F13B15_12	4.1	3.9	0.2	1.2	100.0%	-4.6
5855	AT2G20320.1   DENN (AEX-3) domain-containing protein, contains Pfam domain PF02141: DENN (AEX-3) domain   chr2:8774187-8779217 FORWARD   Aliases: F11A3.13, F11A3_13	5.4	5.0	0.3	1.2	100.0%	-4.2
5856	AT1G08380.1   expressed protein   chr1:2640858-2641825 REVERSE   Aliases: T27G7.25, T27G7_25	7.9	7.3	0.6	1.2	100.0%	-3.7
5857	AT2G32210.1   expressed protein   chr2:13685063-13685907 FORWARD   Aliases: F22D22.4, F22D22_4	2.6	2.4	0.2	1.2	100.0%	-5.2
5858	AT3G57810.2   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr3:21426805-21428925 FORWARD   Aliases: T10K17.20	6.7	7.1	-0.4	-1.2	100.0%	-4.0
5859	AT3G05650.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4A protein (Lycopersicon esculentum) gi:3097197:emb:CAA73187   chr3:1645686-1648579 REVERSE   Aliases: F18C1.8, F18C1_8	2.7	2.6	0.2	1.2	100.0%	-4.7
5860	AT4G05330.1   zinc finger and C2 domain protein, putative, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)	4.6	5.0	-0.4	-1.2	100.0%	-3.9
5861	AT3G47550.6   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:17534483-17536888 FORWARD   Aliases: F1P2.100	5.3	4.8	0.4	1.2	100.0%	-4.3
5862	AT4G35290.2   Symbol: GLUR2   glutamate receptor family protein (GLR3.2) (GLUR2), identical to putative glutamate receptor like-protein GLUR2 (Arabidopsis thaliana) gi:13160471:gb:AAK13248; plant glutamate receptor family, PMID:11379626   chr4:16789726-16793685 FORWARD   Aliases: ATGLR3.2, ATGLUR2, F23E12.150, F23E12_150, GLR3.2	2.9	3.0	-0.2	-1.2	100.0%	-4.7
5863	AT2G42630.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:17765609-17767786 REVERSE   Aliases: F14N22.10, F14N22_10	3.9	4.2	-0.3	-1.2	100.0%	-4.4
5864	AT5G50000.1   protein kinase, putative, similar to protein kinase ATMRK1 (Arabidopsis thaliana) gi:2351097:dbj:BAA22079   chr5:20359813-20362359 REVERSE   Aliases: MPF21.1, MPF21_1	7.4	8.1	-0.7	-1.2	100.0%	-4.0
5865	AT5G53020.1   expressed protein   chr5:21517125-21519627 FORWARD   Aliases: MNB8.8, MNB8_8	4.5	4.2	0.3	1.2	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5866	AT4G03150.1   expressed protein   chr4:1393614-1394574 REVERSE   Aliases: F4C21.13	3.9	3.7	0.1	1.2	100.0%	-5.0
5867	AT1G53310.3   Symbol: ATPPC1	8.5	9.8	-1.3	-1.2	100.0%	-4.3
5868	AT1G24610.1   SET domain-containing protein, low similarity to SP:Q43088 Ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N- methyltransferase, chloroplast precursor (EC 2.1.1.127) {Pisum sativum}; contains Pfam profile PF00856: SET domain   chr1:8720177-8722732 REVERSE   Aliases: F21J9.27	8.8	8.3	0.5	1.2	100.0%	-4.0
5869	AT2G45120.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:18610693-18611826 FORWARD   Aliases: T14P1.7	2.6	2.5	0.1	1.2	100.0%	-4.9
5870	AT5G54310.1   ARF GAP-like zinc finger-containing protein ZIGA3 (ZIGA3), nearly identical to ARF GAP-like zinc finger-containing protein ZIGA3 GI:10441352 from (Arabidopsis thaliana); contains InterPro accession IPR001164: Human Rev interacting-like protein (hRIP)   chr5:22074278-22078457 REVERSE   Aliases: MDK4.13, MDK4_13	7.4	7.9	-0.5	-1.2	100.0%	-4.3
5871	AT3G10080.1   germin-like protein, putative, similar to germin-like protein 2 (Oryza sativa) GI:2655287   chr3:3107281-3108182 REVERSE   Aliases: T22K18.9	3.5	3.8	-0.4	-1.2	100.0%	-4.0
5872	AT4G33780.1   expressed protein   chr4:16201833-16203643 REVERSE   Aliases: T16L1.270, T16L1_270	8.8	8.3	0.5	1.2	100.0%	-4.1
5873	AT1G53970.1   hypothetical protein   chr1:20152087-20152566 FORWARD   Aliases: T18A20.21	1.8	1.9	-0.1	-1.2	100.0%	-5.4
5874	AT3G05120.1   expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873   chr3:1430483-1432784 FORWARD   Aliases: T12H1.8, T12H1_8	5.4	5.1	0.3	1.2	100.0%	-4.3
5875	AT3G14060.1   expressed protein   chr3:4657053-4657608 REVERSE   Aliases: MDC16.20	3.8	4.3	-0.5	-1.2	100.0%	-3.8
5876	AT4G38370.1   phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family   chr4:17969521-17971289 REVERSE   Aliases: F22I13.140, F22I13_140	8.4	8.9	-0.5	-1.2	100.0%	-3.9
5877	AT1G78750.1   F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.1	0.2	1.2	100.0%	-4.7
5878	AT4G39160.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28770.1); similar to myb domain-containing protein [Dictyostelium discoideum] (GB:EAL65687.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)   chr4:18236822-18239738 FORWARD   Aliases: T22F8.60, T22F8_60	4.8	5.1	-0.4	-1.2	100.0%	-4.3
5879	AT5G47970.1   nitrogen regulation family protein, strong similarity to unknown protein (emb:CAB87804.1) ; contains Pfam domain PF01207: Dihydrouridine synthase (Dus); similar to (SP:P45672) NIFR3-like protein (SP:P45672) (Azospirillum brasilense)	4.6	4.9	-0.3	-1.2	100.0%	-4.2
5880	AT4G27780.1   Symbol: ACBP2   acyl-CoA binding protein 2 (ACBP2), identical to acyl-CoA binding protein 2 (Arabidopsis thaliana) gi:12039034:gb:AAG46057   chr4:13847555-13849893 FORWARD   Aliases: ACYL COA BINDING PROTEIN ACBP 2, ACYL COA BINDING PROTEIN ACBP2, T27E11.20, T27E11_20	6.6	6.1	0.4	1.2	100.0%	-4.2
5881	AT2G22840.1   Symbol: AtGRF1	3.1	3.7	-0.5	-1.2	100.0%	-4.2
5882	AT2G17900.1   Symbol: SDG37   zinc finger (MYND type) family protein / SET domain-containing protein, contains Pfam profiles PF00856: SET domain, PF01753: MYND zinc finger (ZnF) domain; confirmed by cDNA (Paola Vittorioso--accession not assigned yet (paola.vittorioso@uniroma1.it)   chr2:7780410-7783765 REVERSE   Aliases: SET DOMAIN GROUP 37, T13L16.8, T13L16_8	4.5	4.8	-0.3	-1.2	100.0%	-4.3
5883	AT3G54630.1   expressed protein, weak similarity to retinoblastoma-associated protein HEC (Homo sapiens) GI:2501873   chr3:20232075-20234006 REVERSE   Aliases: T14E10.200	5.3	5.9	-0.5	-1.2	100.0%	-4.1
5884	AT1G18900.2   pentatricopeptide (PPR) repeat-containing protein, low similarity to 67kD chloroplastic RNA-binding protein, P67 (Arabidopsis thaliana) GI:9755842; contains Pfam profile PF01535: PPR repeat   chr1:6529037-6532605 FORWARD   Aliases: F14D16.2, F14D16_2	5.1	5.6	-0.5	-1.2	100.0%	-4.2
5885	AT3G54030.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:20021931-20024671 FORWARD   Aliases: F5K20.330	4.5	4.9	-0.4	-1.2	100.0%	-4.5
5886	AT5G10210.1   expressed protein   chr5:3206237-3206830 FORWARD   Aliases: F18D22.2	4.2	3.6	0.6	1.2	100.0%	-4.0
5887	AT2G30810.1   gibberellin-regulated family protein, similar to GASAS5 (Arabidopsis thaliana) GI:1289320; contains Pfam profile PF02704: Gibberellin regulated protein   chr2:13134904-13135732 REVERSE   Aliases: F7F1.2, F7F1_2	2.5	2.4	0.1	1.2	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5888	AT1G02960.3   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g02965.1)   chr1:666872-669805 REVERSE   Aliases: F22D16.4, F22D16_4	6.6	6.2	0.4	1.2	100.0%	-4.2
5889	AT1G48840.1   expressed protein, contains Pfam profile: PF04842 plant protein of unknown function (DUF639)   chr1:18065203-18068948 FORWARD   Aliases: T24P22.6, T24P22_6	4.3	4.6	-0.3	-1.2	100.0%	-4.2
5890	AT5G03555.1   permease, cytosine/purines, uracil, thiamine, allantoin family protein, contains Pfam PF02133: permease, cytosine/purines, uracil, thiamine, allantoin family   chr5:898240-900158 REVERSE   Aliases: None	5.3	4.7	0.6	1.2	100.0%	-4.0
5891	AT4G10100.2   Symbol: CNX7/SIR5   molybdenum cofactor synthesis family protein, similar to Molybdenum cofactor synthesis protein 2 small subunit (Molybdopterin-synthase small subunit) (MOCS2A) (MOCO1-A) (Swiss-Prot:O96033) (Homo sapiens); contains TIGRFAM TIGR01682: molybdopterin converting factor, subunit 1; contains Pfam PF02597: ThiS family   chr4:6308712-6309504 FORWARD   Aliases: CNX7, F28M11.20, F28M11_20, MOLYBDOPTERIN SYNTHASE, SIR5	12.0	11.8	0.2	1.2	100.0%	-5.0
5892	AT4G02210.1   expressed protein   chr4:973924-976129 REVERSE   Aliases: T2H3.2	4.7	4.5	0.2	1.2	100.0%	-4.6
5893	AT4G08460.2   expressed protein   chr4:5377140-5380615 REVERSE   Aliases: T15F16.1, T15F16_1	5.9	5.7	0.3	1.2	100.0%	-4.4
5894	AT4G00760.1   Symbol: APRR8   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain   chr4:327025-329048 REVERSE   Aliases: A_TM018A10.20, A_TM018A10_20, PRR8, PSEUDO RESPONSE REGULATOR 8, T18A10.1, T18A10_1	4.5	4.1	0.4	1.2	100.0%	-4.3
5895	AT1G28760.1   expressed protein, ; expression supported by MPSS   chr1:10103144-10104574 FORWARD   Aliases: F1K23.6, F1K23_6	4.4	4.7	-0.3	-1.2	100.0%	-4.1
5896	AT1G73200.1   expressed protein   chr1:27527115-27530234 REVERSE   Aliases: T18K17.13, T18K17_13	4.3	4.6	-0.3	-1.2	100.0%	-4.4
5897	AT3G24050.1   GATA transcription factor 1 (GATA-1), identical to GATA transcription factor 1 (AtGATA-1) GB:Y13648 (Arabidopsis thaliana)   chr3:8685929-8687684 FORWARD   Aliases: F14O13.7	4.9	4.1	0.8	1.2	100.0%	-3.9
5898	AT3G01520.1   universal stress protein (USP) family protein, similar to ER6 protein (GI:5669654) (Lycopersicon esculentum); contains Pfam profile PF00582: universal stress protein family   chr3:208446-210110 FORWARD   Aliases: F4P13.7, F4P13_7	9.9	9.2	0.7	1.2	100.0%	-3.9
5899	AT1G70530.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:26592413-26595042 REVERSE   Aliases: F24J13.10, F24J13_10	4.5	5.0	-0.4	-1.2	100.0%	-4.3
5900	AT2G33580.1   protein kinase family protein / peptidoglycan-binding LysM domain-containing protein, protein kinase (Arabidopsis thaliana) GI:2852449; contains Pfam profiles PF01476: LysM domain, PF00069: Protein kinase domain   chr2:14226699-14228937 REVERSE   Aliases: F4P9.35, F4P9_35	5.7	5.3	0.4	1.2	100.0%	-4.3
5901	AT5G51300.3   similar to KH domain-containing quaking protein, putative [Arabidopsis thaliana] (TAIR:At1g09660.1); similar to related to branch point bridging protein (MSL5) [Neurospora crassa] (GB:CAD36971.1); contains InterPro domain KH domain (InterPro:IPR004087); contains InterPro domain Zn-finger, CCHC type (InterPro:IPR001878); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr5:20866213-20869556 REVERSE   Aliases: MWD22.25, MWD22_25	3.6	4.2	-0.6	-1.2	100.0%	-4.1
5902	AT5G13730.1   Symbol: SIGD   RNA polymerase sigma subunit SigD (sigD) / sigma-like factor (SIG4), identical to RNA polymerase sigma subunit SigD (Arabidopsis thaliana) GI:4972296, sigma-like factor (Arabidopsis thaliana) GI:3983260; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2   chr5:4428700-4430837 REVERSE   Aliases: MSH12.20, MSH12_20, SIG4, SIGMA LIKE FACTOR 4	4.8	4.2	0.6	1.2	100.0%	-3.9
5903	AT2G39770.1   Symbol: CYT1   GDP-mannose pyrophosphorylase (GMP1), identical to GDP-mannose pyrophosphorylase from Arabidopsis thaliana (GI:3598958); updated per Conklin PL et al, PNAS 1999, 96(7):4198-203   chr2:16595783-16598063 FORWARD   Aliases: CYTOKINESIS DEFECTIVE 1, EMB101, EMBRYO DEFECTIVE 101, GDP MANNOSE PYROPHOSPHORYLASE 1, GMP1, SENSITIVE TO OZONE 1, SOZ1, T5I7.7, T5I7_7, VITAMIN C DEFECTIVE 1, VTC1	8.1	7.4	0.7	1.2	100.0%	-4.3
5904	AT5G39520.1   expressed protein, predicted protein, Synechocystis sp., PIR:S77152   chr5:15840681-15842720 REVERSE   Aliases: MUL8.22, MUL8_22	3.0	3.2	-0.2	-1.2	100.0%	-4.8
5905	AT1G34065.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:12398696-12400861 REVERSE   Aliases: None	3.9	4.1	-0.3	-1.2	100.0%	-4.5
5906	AT1G23100.1   10 kDa chaperonin, putative, similar to 10 kDa chaperonin SP:P34893 from (Arabidopsis thaliana)   chr1:8195769-8196464 FORWARD   Aliases: T26J12.12, T26J12_12	5.4	5.9	-0.4	-1.2	100.0%	-3.9
5907	AT2G41220.1   Symbol: GLU2   glutamate synthase, chloroplast (GLU2) / ferredoxin-dependent glutamate synthase (Fd-GOGAT 2), identical to SP:Q9T0P4 Ferredoxin-dependent glutamate synthase 2, chloroplast precursor (EC 1.4.7.1) (Fd-GOGAT 2) {Arabidopsis thaliana}   chr2:17185012-17195829 FORWARD   Aliases: F13H10.23, F13H10_23, GLUTAMATE SYNTHASE PRECURSOR	8.9	8.5	0.4	1.2	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5908	AT3G23990.1   Symbol: HSP60   chaperonin (CPN60) (HSP60), identical to SWISS-PROT:P29197- chaperonin CPN60, mitochondrial precursor (HSP60) (Arabidopsis thaliana)   chr3:8668935-8672585 FORWARD   Aliases: F14O13.1	10.0	10.8	-0.7	-1.2	100.0%	-4.0
5909	AT5G04890.1   Symbol: RTM2   small heat shock-like protein (RTM2), similar to 17.9 kDa heat-shock protein (Helianthus annuus) GI:11990130; contains Pfam profile PF00011: Hsp20/alpha crystallin family; supporting cDNA gi:7407072:gb:AF208051.1:AF208051; identical to cDNA small heat shock-like protein (RTM2) GI:7407072, small heat shock-like protein (Arabidopsis thaliana) GI:7407073   chr5:1427174-1428455 FORWARD   Aliases: MUK11.22, MUK11_22, RESTRICTED TEV MOVEMENT 2	5.6	4.9	0.7	1.2	100.0%	-3.7
5910	AT2G35490.1   plastid-lipid associated protein PAP, putative, similar to plastid-lipid associated protein PAP3 (Brassica rapa) GI:14248552; contains Pfam profile PF04755: PAP_fibrillin   chr2:14919223-14920956 REVERSE   Aliases: T32F12.13, T32F12_13	8.5	8.0	0.5	1.2	100.0%	-4.0
5911	AT5G47435.2   formyltetrahydrofolate deformylase, putative, similar to formyltetrahydrofolate deformylase (strain PCC 6803- Synechocystis sp.) SWISS-PROT:Q55135   chr5:19258930-19261181 FORWARD   Aliases: None	11.2	10.8	0.3	1.2	100.0%	-4.6
5912	AT1G64020.1   serpin-related / serine protease inhibitor-related, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311   chr1:23755419-23755784 REVERSE   Aliases: F22C12.27, F22C12_27	2.2	2.3	-0.2	-1.2	100.0%	-5.0
5913	AT5G10530.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:3324979-3326934 REVERSE   Aliases: F12B17.120, F12B17_120	2.3	2.5	-0.2	-1.2	100.0%	-5.1
5914	AT5G22030.2   ubiquitin-specific protease 8, putative (UBP8), similar to ubiquitin-specific protease 8 partial sequence GI:11993469 (Arabidopsis thaliana)   chr5:7289706-7293597 REVERSE   Aliases: None	4.7	4.4	0.3	1.2	100.0%	-4.2
5915	AT3G18880.1   ribosomal protein S17 family protein, similar to 40S ribosomal protein S17 GB:Y08858 from (Nicotiana plumbaginifolia)   chr3:6509584-6510631 FORWARD   Aliases: MCB22.5	5.2	5.5	-0.3	-1.2	100.0%	-4.2
5916	AT5G46910.1   transcription factor jumonji (jnj) family protein, contains Pfam domains PF02375: jnjN domain and PF02373: jnjC domain   chr5:19065007-19068107 FORWARD   Aliases: MQD22.4, MQD22_4	4.2	4.8	-0.5	-1.2	100.0%	-4.1
5917	AT1G76260.1   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to retinoblastoma A associated protein; RbAp48 (GI:3309245) (Xenopus laevis)   chr1:28615206-28618838 FORWARD   Aliases: T23E18.19, T23E18_19	8.7	9.4	-0.7	-1.2	100.0%	-4.1
5918	AT3G06190.2   Symbol: ATBPM2	4.1	4.3	-0.3	-1.2	100.0%	-4.4
5919	AT3G12350.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr3:3931571-3933363 FORWARD   Aliases: T2E22.32	6.2	6.0	0.3	1.2	100.0%	-4.4
5920	AT1G74970.1   Symbol: RPS9   ribosomal protein S9 (RPS9), identical to ribosomal protein S9 (Arabidopsis thaliana) GI:5456946	5.6	6.2	-0.6	-1.2	100.0%	-3.7
5921	AT4G38690.1   1-phosphatidylinositol phosphodiesterase-related, contains weak similarity to 1-phosphatidylinositol phosphodiesterase precursor (EC 4.6.1.13) (Phosphatidylinositol diacylglycerol-lyase) (Phosphatidylinositol-specific phospholipase C) (PI-PLC). (Swiss-Prot:P34024) (Listeria monocytogenes)   chr4:18074469-18075759 REVERSE   Aliases: T9A14.2	3.1	2.9	0.2	1.2	100.0%	-4.7
5922	AT1G71720.1   S1 RNA-binding domain-containing protein, contains Pfam domain, PF00575: S1 RNA binding domain   chr1:26987406-26989652 FORWARD   Aliases: F14O23.10, F14O23_10	8.2	8.7	-0.5	-1.2	100.0%	-3.9
5923	AT4G15440.1   Symbol: HPL1   hydroperoxide lyase (HPL1), identical to hydroperoxide lyase GI:3822403 from (Arabidopsis thaliana)   chr4:8835494-8838675 FORWARD   Aliases: CYP74B2, DL3766W, FCAALL.125, HYDROPEROXIDE LYASE 1	3.5	3.2	0.3	1.2	100.0%	-4.3
5924	AT1G15470.1   transducin family protein / WD-40 repeat family protein, Strong similarity to gb AF096285 serine-threonine kinase receptor-associated protein from Mus musculus and contains 5 PF:00400 WD40, G-beta repeat domains. EST gb:F14050 comes from this gene   chr1:5315502-5317858 FORWARD   Aliases: F9L1.42, F9L1_42	7.1	7.6	-0.5	-1.2	100.0%	-4.4
5925	AT3G56630.1   Symbol: CYP94D2   cytochrome P450, putative, cytochrome P450 CYP94A1 - Vicia sativa, PIR:T08014	6.8	6.3	0.6	1.2	100.0%	-3.7
5926	AT5G54730.1   expressed protein   chr5:22251015-22254030 REVERSE   Aliases: K5F14.9, K5F14_9	6.3	6.7	-0.4	-1.2	100.0%	-4.1
5927	AT1G72350.1   MADS-box protein (AGL60), contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)   chr1:27242935-27243609 REVERSE   Aliases: T10D10.18, T10D10_18	2.8	2.6	0.2	1.2	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5928	AT4G35110.2   expressed protein   chr4:16712467-16714958 REVERSE   Aliases: T12J5.14	3.5	3.6	-0.2	-1.2	100.0%	-4.6
5929	AT2G31670.1   expressed protein, similar to NADH-ubiquinone oxidoreductase B16.6 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B16.6) (CI-B16.6) (Gene associated with retinoic-interferon-induced mortality 19 protein) (GRIM-19) (Cell death-regulatory protein GRIM-19) (Swiss-Prot:Q95KV7) (Bos taurus)   chr2:13479614-13480581 REVERSE   Aliases: T9H9.19, T9H9_19	7.4	8.0	-0.6	-1.2	100.0%	-4.2
5930	AT4G00230.1   Symbol: XSP1   subtilisin-like serine endopeptidase (XSP1), identical to subtilisin-type serine endopeptidase XSP1 GI:6708179 from (Arabidopsis thaliana)   chr4:93923-97449 FORWARD   Aliases: F6N15.3, F6N15_3, SUBTILISIN TYPE SERINE ENDOPEPTIDASE XSP1, XYLEM SERINE PEPTIDASE 1	4.1	3.6	0.5	1.2	100.0%	-4.0
5931	AT1G53920.1   GDSL-motif lipase/hydrolase family protein, similar to Anther-specific proline-rich proteins SP:P40603 SP:P40602 from {Arabidopsis thaliana}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr1:20141380-20143305 FORWARD   Aliases: T18A20.15, T18A20_15	3.6	3.8	-0.2	-1.2	100.0%	-4.5
5932	AT4G30220.1   small nuclear ribonucleoprotein F, putative / snRNP-F, putative / Sm protein F, putative, similar to SWISS-PROT:Q15356 small nuclear ribonucleoprotein F (snRNP-F, Sm protein F, Sm-F, SmF) (Mouse)   chr4:14802961-14804329 REVERSE   Aliases: F9N11.70, F9N11_70	8.1	8.6	-0.5	-1.2	100.0%	-3.8
5933	AT3G07960.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr3:2534893-2538342 FORWARD   Aliases: F17A17.30	4.3	4.7	-0.4	-1.2	100.0%	-4.2
5934	AT1G30080.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097948 from (Oryza sativa)   chr1:10550931-10553199 REVERSE   Aliases: T1P2.13, T1P2_13	5.8	5.4	0.3	1.2	100.0%	-4.0
5935	AT3G60910.1   expressed protein, low similarity to PIR:I46078 endothelin converting enzyme from Bos primigenius taurus	7.9	7.7	0.2	1.2	100.0%	-4.5
5936	AT3G06710.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g32670.1)   chr3:2118214-2120065 FORWARD   Aliases: T8E24.2	3.5	3.1	0.3	1.2	100.0%	-4.6
5937	AT1G57830.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:21423974-21424468 FORWARD   Aliases: F12K22.13, F12K22_13	2.5	2.7	-0.2	-1.2	100.0%	-4.7
5938	AT1G34770.2   MAGE-8 antigen-related, contains weak similarity to Swiss-Prot:P43361 melanoma-associated antigen 8 (MAGE-8 antigen) (Homo sapiens)   chr1:12746598-12748538 FORWARD   Aliases: F11O6.12	4.8	5.1	-0.3	-1.2	100.0%	-4.2
5939	AT3G13662.1   disease resistance-responsive protein-related / dirigent protein-related, similar to pathogenesis-related protein (Pisum sativum) gi:4585273:gb:AAD25355; similar to dirigent protein (Forsythia x intermedia) gi:6694695:gb:AAF25358   chr3:4467097-4467657 FORWARD   Aliases: MMM17.6	2.8	2.6	0.2	1.2	100.0%	-4.7
5940	AT2G27460.1   sec23/sec24 transport family protein, weak similarity to SP:P53992 Protein transport protein Sec24C (SEC24-related protein C) {Homo sapiens}; contains Pfam domains PF04811: Sec23/Sec24 trunk domain, PF04815: Sec23/Sec24 helical domain and PF04810: Sec23/Sec24 zinc finger   chr2:11747732-11752465 FORWARD   Aliases: F10A12.14, F10A12_14	4.5	4.8	-0.3	-1.2	100.0%	-4.6
5941	AT3G56300.1   tRNA synthetase class I (C) family protein, similar to cysteinyl-tRNA synthetase (Methanococcus maripaludis) GI:6599476; contains Pfam profile PF01406: tRNA synthetases class I (C)   chr3:20891148-20893345 FORWARD   Aliases: F18O21.260	4.2	4.5	-0.3	-1.2	100.0%	-4.2
5942	AT2G11370.1   hypothetical protein   chr2:4538787-4539393 FORWARD   Aliases: F3K12.11, F3K12_11	2.4	2.3	0.1	1.2	100.0%	-5.1
5943	AT5G11890.1   expressed protein   chr5:3831665-3832945 FORWARD   Aliases: F14F18.60, F14F18_60	3.5	4.0	-0.5	-1.2	100.0%	-4.1
5944	AT5G15850.1   Symbol: COL1   zinc finger protein CONSTANS-LIKE 1 (COL1), identical to Zinc finger protein CONSTANS-LIKE 1 SP:O50055 from (Arabidopsis thaliana)   chr5:5176094-5177900 REVERSE   Aliases: CONSTANS LIKE 1, F14F8.230, F14F8_230	4.2	3.9	0.3	1.2	100.0%	-4.3
5945	AT3G14330.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:4779695-4782459 REVERSE   Aliases: MLN21.12	3.2	3.5	-0.2	-1.2	100.0%	-4.5
5946	AT3G26100.2   regulator of chromosome condensation (RCC1) family protein, weak similarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	6.8	6.4	0.4	1.2	100.0%	-4.0
5947	AT5G01290.1   similar to mRNA capping enzyme family protein [Arabidopsis thaliana] (TAIR:At3g09100.1); similar to mRNA capping enzyme family protein [Arabidopsis thaliana] (TAIR:At3g09100.2); similar to mRNA capping enzyme family protein [Arabidopsis thaliana] (TAIR:At5g28210.1); similar to similar to ENSANGP00000009960 [Apis mellifera] (GB:XP_397436.1); contains InterPro domain mRNA capping enzyme (InterPro:IPR001339); contains InterPro domain Tyrosine specific protein phosphatase and dual specificity protein phosphatase (InterPro:IPR000387)   chr5:117306-121568 FORWARD   Aliases: T10O8.2	5.5	5.8	-0.3	-1.2	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5948	AT1G48630.1   guanine nucleotide-binding family protein / activated protein kinase C receptor, putative / RACK, putative, contains 7 WD-40 repeats (PF00400); very similar to guanine nucleotide-binding protein; activated protein kinase C receptor; RACK1 (GI:9294068) {Arabidopsis thaliana}; similar to WD-40 repeat auxin-dependent protein ARCA (SP:O24456) (Arabidopsis thaliana);   chr1:17985448-17986995 REVERSE   Aliases: F11I4.18, F11I4_18	10.5	11.1	-0.5	-1.2	100.0%	-4.2
5949	AT5G53070.1   ribosomal protein L9 family protein, contains similarity to ribosomal protein L9	4.3	4.8	-0.4	-1.2	100.0%	-3.9
5950	AT3G46750.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28770.1); similar to PREDICTED: similar to MATER protein isoform-H [Rattus norvegicus] (GB:XP_218237.3); similar to similar to ENSANGP00000017739 [Apis mellifera] (GB:XP_394403.1)   chr3:17230730-17232619 FORWARD   Aliases: T6H20.220	2.3	2.1	0.1	1.2	100.0%	-5.0
5951	AT3G24480.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	5.5	6.1	-0.6	-1.2	100.0%	-4.0
5952	AT3G46910.1   expressed protein   chr3:17289621-17290637 FORWARD   Aliases: T6H20.60	2.3	2.4	-0.1	-1.2	100.0%	-5.1
5953	AT5G26890.1   hypothetical protein   chr5:9460468-9460719 FORWARD   Aliases: F2P16.150, F2P16_150	3.2	2.8	0.4	1.2	100.0%	-4.2
5954	AT2G29120.1   Symbol: ATGLR2.7   similar to glutamate receptor family protein (GLR2.8) (GLUR9) [Arabidopsis thaliana] (TAIR:At2g29110.1); similar to glutamate receptor family protein (GLR2.1) (GLR3) [Arabidopsis thaliana] (TAIR:At5g27100.1); similar to glutamate receptor family protein (GLR2.3) [Arabidopsis thaliana] (TAIR:At2g24710.1); similar to glutamate receptor family protein (GLR2.9) [Arabidopsis thaliana] (TAIR:At2g29100.1); similar to glutamate receptor family protein (GLR2.2) [Arabidopsis thaliana] (TAIR:At2g24720.1); similar to Avr9/Cf-9 rapidly elicited protein 141 [Nicotiana tabacum] (GB:AAP03877.1); similar to GLR21_ARATH Glutamate receptor 2.1 precursor (Ligand-gated ion channel 2.1) (AtGLR3) (GB:O04660); similar to GLR25_ARATH Glutamate receptor 2.5 precursor (Ligand-gated ion channel 2.5) (GB:Q9LFN5); similar to GLR24_ARATH Glutamate receptor 2.4 precursor (Ligand-gated ion channel 2.4) (GB:O81776); similar to GLR26_ARATH Glutamate receptor 2.6 precursor (Ligand-gated ion channel 2.6) (GB:Q9LFN8); contains InterPro domain Extracellular ligand-binding receptor (InterPro:IPR001828); contains InterPro domain Ionotropic glutamate receptor (InterPro:IPR001320)	2.7	2.5	0.2	1.2	100.0%	-4.9
5955	AT5G62020.1   Symbol: AT HSF6A   heat shock factor protein, putative (HSF6) / heat shock transcription factor, putative (HTSF6), identical to heat shock transcription factor 6 (HSF6) SP: Q9SCW4 from (Arabidopsis thaliana) ;contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr5:24933315-24934869 FORWARD   Aliases: HSF6A, MTG10.7, MTG10_7	5.3	5.0	0.3	1.2	100.0%	-4.2
5956	AT4G24090.1   expressed protein   chr4:12512746-12514591 FORWARD   Aliases: T19F6.80, T19F6_80	5.5	5.1	0.3	1.2	100.0%	-4.1
5957	AT3G50310.1   Symbol: MAPKKK20   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:18659133-18660503 REVERSE   Aliases: F11C1.150	4.1	3.7	0.4	1.2	100.0%	-4.3
5958	AT2G47510.1   Symbol: FUM1   fumarate hydratase, putative / fumarase, putative, similar to SP:P55250 Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) {Rhizopus oryzae}; contains Pfam profile PF00206: Lyase   chr2:19505458-19509316 FORWARD   Aliases: FUMARASE 1, T30B22.19	8.7	9.4	-0.7	-1.2	100.0%	-3.9
5959	AT5G50950.2   fumarate hydratase, putative / fumarase, putative, similar to SP:P55250 Fumarate hydratase, mitochondrial precursor (EC 4.2.1.2) (Fumarase) {Rhizopus oryzae}; contains Pfam profile PF00206: Lyase   chr5:20746870-20751152 FORWARD   Aliases: K3K7.11, K3K7_11	8.7	9.4	-0.7	-1.2	100.0%	-3.9
5960	AT4G01370.1   Symbol: ATMPK4	9.1	9.6	-0.6	-1.2	100.0%	-4.2
5961	AT1G11240.1   expressed protein   chr1:3766754-3768294 REVERSE   Aliases: T28P6.24, T28P6_24	8.7	9.5	-0.8	-1.2	100.0%	-4.0
5962	AT1G06730.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr1:2067528-2070445 FORWARD   Aliases: F4H5.18, F4H5_18	5.2	4.9	0.3	1.2	100.0%	-4.1
5963	AT5G19930.1   integral membrane family protein, contains Pfam domain PF01940: Integral membrane protein   chr5:6737585-6739350 REVERSE   Aliases: F28I16.80, F28I16_80	7.2	6.6	0.5	1.2	100.0%	-4.1
5964	AT1G01290.1   Symbol: CNX3   molybdopterin biosynthesis CNX3 protein / molybdenum cofactor biosynthesis enzyme CNX3 (CNX3), identical to molybdopterin biosynthesis CNX3 protein SP:Q39056 from (Arabidopsis thaliana)   chr1:114286-115549 FORWARD   Aliases: COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 3, F6F3.9, F6F3_9	6.8	6.5	0.3	1.2	100.0%	-4.3
5965	AT1G48350.1   ribosomal protein L18 family protein, similar to ribosomal protein L18 GI:3980238 from (Thermotoga maritima)   chr1:17870876-17872010 FORWARD   Aliases: F11A17.10, F11A17_10	9.6	10.1	-0.5	-1.2	100.0%	-4.0
5966	AT1G06010.1   expressed protein   chr1:1822617-1823996 FORWARD   Aliases: T21E18.6, T21E18_6	6.1	6.6	-0.5	-1.2	100.0%	-4.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5967	AT3G26380.1   glycosyl hydrolase family protein 27 / alpha-galactosidase family protein / melibiase family protein, similar to alpha-galactosidase GI:10944326 from (Phanerochaete chrysosporium)   chr3:9661302-9664535 FORWARD   Aliases: F20C19.10	8.1	7.7	0.4	1.2	100.0%	-4.2
5968	AT1G08480.1   expressed protein   chr1:2684237-2685620 FORWARD   Aliases: T27G7.26	9.3	9.8	-0.5	-1.2	100.0%	-4.4
5969	AT3G62650.2   expressed protein, putative mitochondrial carrier protein At2g47490 - Arabidopsis thaliana, EMBL:AC002535   chr3:23179037-23180163 FORWARD   Aliases: F26K9.80	8.3	7.9	0.4	1.2	100.0%	-4.3
5970	AT5G56140.1   KH domain-containing protein   chr5:22742688-22745569 FORWARD   Aliases: MDA7.20, MDA7_20	4.3	3.8	0.5	1.2	100.0%	-4.0
5971	AT1G49760.1   Symbol: PAB8   polyadenylate-binding protein, putative / PABP, putative, similar to poly(A)-binding protein GB:AAF66825 GI:7673359 from (Nicotiana tabacum). Highly and ubiquitously expressed. Member of the class II PABP family.   chr1:18420148-18423715 FORWARD   Aliases: F14J22.3, F14J22_3, PAB8, POLY(A) BINDING PROTEIN 8	6.0	6.6	-0.6	-1.2	100.0%	-4.1
5972	AT1G69780.1   Symbol: ATHB13	3.9	4.2	-0.3	-1.2	100.0%	-4.3
5973	AT3G47370.3   similar to 40S ribosomal protein S20 (RPS20A) [Arabidopsis thaliana] (TAIR:At3g45030.1); similar to 40S ribosomal protein S20 (RPS20C) [Arabidopsis thaliana] (TAIR:At5g62300.1); similar to 40S subunit ribosomal protein [Oryza sativa (japonica cultivar-group)] (GB:XP_550614.1); contains InterPro domain Ribosomal protein S10, eukaryotic and archaeal form (InterPro:IPR005729); contains InterPro domain Ribosomal protein S10 (InterPro:IPR001848)   chr3:17464463-17465496 REVERSE   Aliases: T21L8.120	10.3	10.7	-0.4	-1.2	100.0%	-4.3
5974	AT1G65920.1   regulator of chromosome condensation (RCC1) family protein / zinc finger protein-related, contains Pfam profiles: regulator of chromosome condensation (RCC1), PF01363 FYVE zinc finger   chr1:24528765-24532957 REVERSE   Aliases: F12P19.9, F12P19_9	2.6	2.8	-0.2	-1.2	100.0%	-4.7
5975	AT5G22510.1   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr5:7474813-7477922 REVERSE   Aliases: MQJ16.5, MQJ16_5	6.5	6.0	0.5	1.2	100.0%	-4.0
5976	AT4G37650.1   Symbol: SHR   short-root transcription factor (SHR)   chr4:17691780-17693754 FORWARD   Aliases: F19F18.140, F19F18_140, SGR7, SHORT ROOT	5.1	5.5	-0.3	-1.2	100.0%	-4.2
5977	AT3G44320.1   Symbol: NIT3   nitrilase 3 (NIT3), identical to SP:P46010 Nitrilase 3 (EC 3.5.5.1) {Arabidopsis thaliana}   chr3:16004369-16006798 FORWARD   Aliases: NITRILASE 3, T10D17.110	6.5	7.0	-0.5	-1.2	100.0%	-4.3
5978	AT2G33290.1   Symbol: SUVH2   SET domain-containing protein (SUVH2), identical to SUVH2 (Arabidopsis thaliana) GI:13517745; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH2 (SUVH2) GI:13517744	4.0	4.3	-0.3	-1.2	100.0%	-4.4
5979	AT4G00720.1   shaggy-related protein kinase theta / ASK-theta (ASK8), identical to shaggy-related protein kinase theta (ASK-theta) (Arabidopsis thaliana) SWISS-PROT:Q96287   chr4:293641-297297 REVERSE   Aliases: F6N23.11, F6N23_11	6.7	6.0	0.7	1.2	100.0%	-4.1
5980	AT3G61840.1   expressed protein   chr3:22903456-22904244 FORWARD   Aliases: F21F14.10	2.5	2.4	0.1	1.2	100.0%	-5.1
5981	AT1G05500.1   C2 domain-containing protein, similar to Ca <sup>2+</sup> -dependent lipid-binding protein (CLB1) GI:2789434 from (Lycopersicon esculentum)   chr1:1625097-1628939 FORWARD   Aliases: T25N20.15	5.8	6.2	-0.4	-1.2	100.0%	-4.3
5982	AT3G01170.1   expressed protein   chr3:57675-58914 FORWARD   Aliases: T4P13.14, T4P13_14	5.2	5.1	0.2	1.2	100.0%	-4.6
5983	AT1G72740.1   DNA-binding family protein / histone H1/H5 family protein, similar to DNA-binding protein PcMYB1 (Petroselinum crispum) GI:2224897; contains Pfam profiles PF00538: linker histone H1 and H5 family, PF00249: Myb-like DNA-binding domain   chr1:27383956-27386586 REVERSE   Aliases: F28P22.7, F28P22_7	7.0	6.5	0.6	1.2	100.0%	-4.1
5984	AT3G55620.1   Symbol: EMB1624   eukaryotic translation initiation factor 6, putative / eIF-6, putative, similar to SP:O55135 Eukaryotic translation initiation factor 6 (eIF-6) (B4 integrin interactor) {Mus musculus}; contains Pfam profile PF01912: eIF-6 family   chr3:20645182-20647485 FORWARD   Aliases: EMB1624, EMBRYO DEFECTIVE 1624, F1I16.30	9.8	10.3	-0.5	-1.2	100.0%	-4.3
5985	AT5G32470.1   expressed protein   chr5:12102558-12105829 REVERSE   Aliases: F18O9.80, F18O9_80	6.0	6.4	-0.4	-1.2	100.0%	-4.1
5986	AT4G28230.1   expressed protein   chr4:13995793-13997313 REVERSE   Aliases: F26K10.110, F26K10_110	8.0	7.4	0.6	1.2	100.0%	-4.1
5987	AT2G43320.1   expressed protein   chr2:18003727-18007004 REVERSE   Aliases: F14B2.22	3.7	3.4	0.3	1.2	100.0%	-4.6
5988	AT1G27990.1   expressed protein   chr1:9752786-9753906 REVERSE   Aliases: F13K9.9, F13K9_9	3.7	3.4	0.3	1.2	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
5989	AT5G42470.1   expressed protein, low similarity to BRE alpha b isoform (Homo sapiens) GI:16326573   chr5:16999544-17002112 FORWARD   Aliases: MDH9.17, MDH9_17	7.6	7.2	0.4	1.2	100.0%	-4.0
5990	AT3G03470.1   Symbol: CYP89A9   cytochrome P450, putative, similar to cytochrome P450 89A2 GB:Q42602 (Arabidopsis thaliana)   chr3:824559-826444 REVERSE   Aliases: T21P5.11, T21P5_11	3.4	3.1	0.3	1.2	100.0%	-4.4
5991	AT4G33760.1   tRNA synthetase class II (D, K and N) family protein, similar to SP:P36419 Aspartyl-tRNA synthetase (EC 6.1.1.12) (Aspartate--tRNA ligase) (AspRS) {Thermus thermophilus}; contains Pfam profile PF00152: tRNA synthetases class II (D, K and N)	5.6	6.1	-0.4	-1.2	100.0%	-3.9
5992	AT3G63250.2   Symbol: ATHMT 2/HMT 2   homocysteine S-methyltransferase 2 (HMT-2), 99.7% identical to homocysteine S-methyltransferase AtHMT-2 (GI:6685163) (Arabidopsis thaliana)   chr3:23381313-23383591 REVERSE   Aliases: ATHMT 2, F16M2.100, HMT 2	10.1	9.6	0.4	1.2	100.0%	-4.0
5993	AT4G24220.1   Symbol: VEP1   expressed protein, protein induced upon wounding - Arabidopsis thaliana, PID:e257749   chr4:12564955-12567274 FORWARD   Aliases: AWI31, T22A6.50, T22A6_50, VEIN PATTERNING	7.8	7.3	0.5	1.2	100.0%	-4.2
5994	AT2G17080.1   hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr2:7440408-7441199 REVERSE   Aliases: F6P23.10, F6P23_10	2.9	2.7	0.2	1.2	100.0%	-4.6
5995	AT3G24515.1   ubiquitin-conjugating enzyme, putative, similar to Ubiquitin-conjugating enzyme E2 (Ubiquitin-protein ligase) (Ubiquitin carrier protein) from {Xenopus laevis} SP:P51669, {Schizosaccharomyces pombe} SP:P46595, {Caenorhabditis elegans} SP:P35129; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr3:8934479-8936286 REVERSE   Aliases: None	3.9	4.3	-0.4	-1.2	100.0%	-4.3
5996	AT1G62810.1   copper amine oxidase, putative, similar to copper amine oxidase (Cicer arietinum) gi:3819099:emb:CAA08855   chr1:23261391-23265631 REVERSE   Aliases: F23N19.18, F23N19_18	8.8	8.3	0.5	1.2	100.0%	-4.0
5997	AT5G51220.1   ubiquinol-cytochrome C chaperone family protein, contains Pfam PF03981: Ubiquinol-cytochrome C chaperone	7.6	8.1	-0.4	-1.2	100.0%	-4.2
5998	AT3G29100.1   Symbol: VTI13   vesicle transport v-SNARE 13 (VTI13) / vesicle soluble NSF attachment protein receptor 13, identical to identical to Vesicle transport v-SNARE 13 (SP:Q9LVP9) {Arabidopsis thaliana}; similar to v-snare AtVTI1a (GI:6690274) (GB:AAF24061) (Arabidopsis thaliana)   chr3:11077073-11078725 REVERSE   Aliases: ATVTI13, MXE2.7, VTI13	4.4	4.1	0.3	1.2	100.0%	-4.3
5999	AT4G31450.1   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:15255634-15258818 REVERSE   Aliases: F3L17.20, F3L17_20	5.0	4.7	0.4	1.2	100.0%	-4.0
6000	AT5G12420.1   expressed protein   chr5:4024315-4026742 REVERSE   Aliases: None	2.3	2.8	-0.5	-1.2	100.0%	-3.7
6001	AT5G55500.1   Symbol: AtXylT	5.6	5.3	0.3	1.2	100.0%	-4.3
6002	AT1G11330.1   S-locus lectin protein kinase family protein, contains Pfam domains, PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain, and PF01453: Lectin (probable mannose binding)   chr1:3810221-3813607 FORWARD   Aliases: T28P6.2, T28P6_2	8.7	9.2	-0.5	-1.2	100.0%	-3.8
6003	AT3G20310.1   Symbol: ATERF 7/ATERF7	6.3	5.7	0.6	1.2	100.0%	-4.1
6004	AT3G52340.3   Symbol: SPP2   similar to sucrose-phosphatase 1 (SPP1) [Arabidopsis thaliana] (TAIR:At2g35840.2); similar to sucrose-phosphatase 1 (SPP1) [Arabidopsis thaliana] (TAIR:At2g35840.1); similar to sucrose-6-phosphate phosphatase [Nicotiana tabacum] (GB:AAW32902.1); contains InterPro domain Sucrose-6F-phosphate phosphohydrolase, plant and cyanobacteria (InterPro:IPR006380); contains InterPro domain Sucrose-phosphate phosphatase (InterPro:IPR006378); contains InterPro domain HAD-superfamily hydrolase, subfamily IIB (InterPro:IPR006379)   chr3:19418001-19420311 FORWARD   Aliases: T25B15.110, sucrose phosphatase 2	5.4	5.7	-0.3	-1.2	100.0%	-4.6
6005	AT5G39830.2   DegP protease, putative, contains similarity to DegP protease precursor GI:2565436 from (Arabidopsis thaliana)   chr5:15960048-15963051 FORWARD   Aliases: K13H13.1, K13H13_1	3.8	4.0	-0.3	-1.2	100.0%	-4.5
6006	AT3G53130.1   Symbol: LUT1   cytochrome P450 family protein, similar to Cytochrome P450 97B2 (SP:048921) (Glycine max)   chr3:19703749-19708520 FORWARD   Aliases: CYP97C1, LUTEIN DEFICIENT 1, T4D2.60	4.7	5.0	-0.3	-1.2	100.0%	-4.3
6007	AT1G21550.1   calcium-binding protein, putative, contains similarity to calcium-binding protein GB:CAB63264 GI:6580549 from (Lotus japonicus)   chr1:7553090-7553865 REVERSE   Aliases: F24J8.15, F24J8_15	3.0	2.8	0.2	1.2	100.0%	-4.8
6008	AT3G19330.3   polyadenylate-binding protein-related / PABP-related, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana); similar to Polyadenylate-binding protein 2 (Poly(A)-binding protein 2) (PABP 2) (Swiss-Prot:P42731) (Arabidopsis thaliana)   chr3:6699329-6701261 FORWARD   Aliases: MLD14.6	2.8	2.9	-0.1	-1.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6009	AT5G64720.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At2g21740.1); similar to ECA1 protein [Hordeum vulgare] (GB:AAF23356.1)   chr5:25889572-25889943 REVERSE   Aliases: MVP7.4, MVP7_4	2.8	2.6	0.2	1.2	100.0%	-4.6
6010	AT1G75210.1   5' nucleotidase family protein, contains Pfam profile: PF05761 5' nucleotidase family   chr1:28227530-28232636 FORWARD   Aliases: F22H5.7, F22H5_7	7.5	7.9	-0.4	-1.2	100.0%	-4.0
6011	AT1G08660.2   glycosyl transferase family 29 protein / sialyltransferase family protein, contains Pfam profile: PF00777 sialyltransferase (Glycosyltransferase family 29)   chr1:2757046-2759767 REVERSE   Aliases: F22O13.14, F22O13_14	3.4	3.9	-0.5	-1.2	100.0%	-4.3
6012	AT3G27325.1   expressed protein   chr3:10097461-10103324 FORWARD   Aliases: K17E12.15	2.3	2.5	-0.1	-1.2	100.0%	-5.0
6013	AT4G08170.2   inositol 1,3,4-trisphosphate 5/6-kinase family protein, similar to inositol phosphate kinase (GI:27549256) (Zea mays); similar to inositol 1,3,4-trisphosphate 5/6-kinase (GI:3396079) (Arabidopsis thaliana)   chr4:5163396-5167176 REVERSE   Aliases: T12G13.10, T12G13_10	5.3	5.0	0.3	1.2	100.0%	-4.2
6014	AT1G50970.1   membrane trafficking VPS53 family protein, contains Pfam domain PF04100: Vps53-like, N-terminal   chr1:18899991-18903936 FORWARD   Aliases: F8A12.19, F8A12_19	2.7	2.5	0.2	1.2	100.0%	-4.9
6015	AT5G07620.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:2407402-2409067 REVERSE   Aliases: MBK20.5, MBK20_5	2.5	2.3	0.2	1.2	100.0%	-4.9
6016	AT1G32860.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097948 from (Oryza sativa)   chr1:11907089-11908908 REVERSE   Aliases: F9L11.6, F9L11_6	4.5	4.2	0.2	1.2	100.0%	-4.5
6017	AT2G07050.1   Symbol: CAS1   cycloartenol synthase (CAS1) / 2,3-epoxysqualene--cycloartenol cyclase / (S)-2,3-epoxysqualene mutase, identical to cycloartenol synthase (SP:P38605 : GI:452446) (PMID:7505443)	8.7	8.2	0.5	1.2	100.0%	-4.1
6018	AT1G47290.2   3-beta hydroxysteroid dehydrogenase/isomerase family protein, contains Pfam profile PF01073 3-beta hydroxysteroid dehydrogenase/isomerase domain; similar to NAD(P)-dependent steroid dehydrogenase from Homo sapiens (SP:Q15738), Mus musculus (SP:Q9R1J0)   chr1:17338294-17341713 FORWARD   Aliases: T3F24.9, T3F24_9	3.8	4.2	-0.4	-1.2	100.0%	-4.3
6019	AT5G22000.3   Symbol: CIC7E11   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:7277272-7280258 FORWARD   Aliases: CIC7E11, RHF2A, RING H2 FINGER PROTEIN RHF2A	7.9	7.5	0.3	1.2	100.0%	-4.3
6020	AT4G14990.1   expressed protein   chr4:8565618-8569810 REVERSE   Aliases: DL3535C, FCAALL.26	5.2	4.8	0.5	1.2	100.0%	-3.9
6021	AT1G47980.1   expressed protein   chr1:17695503-17697530 REVERSE   Aliases: T2J15.11, T2J15_11	3.6	3.9	-0.3	-1.2	100.0%	-4.2
6022	AT3G45620.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats; similar to PC326 protein (GI:200241) (PIR2:S37694) (Mus musculus);Human (H326) translated mRNA - Homo sapiens, EMBL:HS06631	7.2	7.7	-0.5	-1.2	100.0%	-3.9
6023	AT2G34860.1   chaperone protein dnaJ-related, contains Pfam PF00684 : DnaJ central domain (4 repeats); similar to Chaperone protein dnaJ (Heat shock protein 40) (SP:Q9UXR9) {Methanosarcina thermophila}   chr2:14715447-14717276 FORWARD   Aliases: F19I3.9, F19I3_9	7.4	7.0	0.4	1.2	100.0%	-4.1
6024	AT1G48940.1   plastocyanin-like domain-containing protein   chr1:18109476-18110090 REVERSE   Aliases: F27K7.4	2.5	2.3	0.1	1.2	100.0%	-5.0
6025	AT1G23490.1   Symbol: ATARF/ATARF1/ATARFA1A   Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct.   chr1:8336693-8338661 FORWARD   Aliases: ATARF, ATARF1, ATARFA1A, F28C11.12, F5O8.5, F5O8_5	9.8	9.3	0.5	1.2	100.0%	-4.3
6026	AT4G20050.1   Symbol: QRT3   expressed protein, C65DMY30S   chr4:10849792-10853356 REVERSE   Aliases: F18F4.150, F18F4_150, QUARTET 3	3.7	4.0	-0.3	-1.2	100.0%	-4.4
6027	AT1G65440.1   Symbol: GTB1   glycine-rich protein   chr1:24310330-24318236 REVERSE   Aliases: GLOBAL TRANSCRIPTION FACTOR GROUP B, T8F5.22, T8F5_22	7.8	7.4	0.4	1.2	100.0%	-4.3
6028	AT1G32730.1   expressed protein   chr1:11840890-11843237 FORWARD   Aliases: F6N18.11, F6N18_11	3.6	3.9	-0.3	-1.2	100.0%	-4.4
6029	AT4G27340.1   Met-10+ like family protein, ; contains Pfam profile PF02475: Met-10+ like-protein   chr4:13687202-13690376 REVERSE   Aliases: F27G19.9	5.0	5.4	-0.3	-1.2	100.0%	-4.2
6030	AT3G26810.1   transport inhibitor response protein, putative, E3 ubiquitin ligase SCF complex F-box subunit; similar to transport inhibitor response 1 GI:2352492 from (Arabidopsis thaliana)   chr3:9869082-9871877 FORWARD   Aliases: MDJ14.9	3.1	3.3	-0.3	-1.2	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6031	AT3G27320.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g14310.1); similar to putative esterase [Oryza sativa (japonica cultivar-group)] (GB:XP_469930.1)   chr3:10091302-10094028 FORWARD   Aliases: K17E12.14	3.6	3.8	-0.2	-1.2	100.0%	-4.6
6032	AT1G20580.1   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3, Sm-D3) (Mus musculus) SWISS-PROT:P43331   chr1:7128878-7130631 FORWARD   Aliases: F5M15.9, F5M15_9	9.4	9.0	0.4	1.2	100.0%	-4.2
6033	AT5G09740.1   histone acetyltransferase, putative, similar to histone acetyltransferase (Homo sapiens) gi:8317213:gb:AAF72665   chr5:3021981-3024726 REVERSE   Aliases: F17I14.70, F17I14_70	4.5	4.9	-0.4	-1.2	100.0%	-4.6
6034	AT3G11460.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:3608256-3610127 FORWARD   Aliases: F24K9.13	3.9	4.0	-0.2	-1.2	100.0%	-4.9
6035	AT4G16280.3   Symbol: FCA   flowering time control protein / FCA gamma (FCA), identical to SP:O04425 Flowering time control protein FCA {Arabidopsis thaliana}; four alternative splice variants, one splicing isoform contains a non-consensus CA donor splice site, based on cDNA: gi:2204090   chr4:9207179-9214428 REVERSE   Aliases: DL4180C, FCA, FCAALL.331, FLOWERING TIME CONTROL PROTEIN FCA ALPHA, BETA, DELTA AND GAMMA	3.3	3.5	-0.3	-1.2	100.0%	-4.3
6036	AT5G06290.1   2-cys peroxiredoxin, chloroplast, putative, very strong similarity to SP:Q96291 2-cys peroxiredoxin BAS1, chloroplast precursor {Arabidopsis thaliana}; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family   chr5:1919249-1921404 FORWARD   Aliases: MHF15.19, MHF15_19	9.3	9.9	-0.6	-1.2	100.0%	-3.7
6037	AT3G09880.1   Symbol: ATB' BETA   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'beta), identical to B' regulatory subunit of PP2A (Arabidopsis thaliana) GI:2160692; similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)   chr3:3029516-3032261 FORWARD   Aliases: F8A24.7	4.1	4.5	-0.3	-1.2	100.0%	-4.4
6038	AT1G02360.1   chitinase, putative, similar to chitinase precursor GI:5880845 from (Petroselinum crispum)   chr1:471990-473140 REVERSE   Aliases: T6A9.5, T6A9_5	4.6	5.6	-0.9	-1.2	100.0%	-3.8
6039	AT1G09180.1   Symbol: ATSAR1/ATSARA1A   GTP-binding protein, putative, strong similarity to SP:Q01474 GTP-binding protein SAR1B and SP:O04834 GTP-binding protein SAR1A (Arabidopsis thaliana)   chr1:2965025-2965974 FORWARD   Aliases: ATSAR1, ATSARA1A, T12M4.12, T12M4_12	4.7	4.4	0.3	1.2	100.0%	-4.5
6040	AT2G26110.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g26130.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81521.1)   chr2:11127984-11129137 FORWARD   Aliases: T19L18.8, T19L18_8	3.1	3.4	-0.3	-1.2	100.0%	-4.2
6041	AT5G37060.1   Symbol: ATCHX24   cation/hydrogen exchanger, putative (CHX24), similar to Na <sup>+</sup> /H <sup>+</sup> -exchanging protein NapA - Enterococcus hirae, PIR:A42111; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr5:14659971-14662644 REVERSE   Aliases: CHX24, MJG14.5, MJG14_5	3.5	3.4	0.2	1.2	100.0%	-4.8
6042	AT3G54650.1   F-box family protein (FBL17), contains similarity to F-box protein FBL2 GI:6010699 from (Rattus norvegicus)   chr3:20236764-20239899 REVERSE   Aliases: T5N23.10	4.0	4.4	-0.5	-1.2	100.0%	-4.3
6043	AT5G48580.1   Symbol: FKBP15 2   FK506-binding protein 2-2 (FKBP15-2) / immunophilin / peptidyl-prolyl cis-trans isomerase / rotamase, identical to SP:Q38936: FK506-binding protein 2-2 precursor (EC 5.2.1.8);   chr5:19713155-19714551 REVERSE   Aliases: IMMUNOPHILIN, K15N18.5, K15N18_5	8.0	8.5	-0.5	-1.2	100.0%	-4.0
6044	AT2G26000.2   similar to zinc finger (ubiquitin-hydrolase) domain-containing protein [Arabidopsis thaliana] (TAIR:At2g42160.1); similar to BRAP2-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464349.1); contains InterPro domain Zn-finger in ubiquitin thiolesterase (InterPro:IPR001607); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr2:11088380-11092406 FORWARD   Aliases: T19L18.19, T19L18_19	4.3	4.7	-0.4	-1.2	100.0%	-4.3
6045	AT1G67690.1   peptidase M3 family protein / thimet oligopeptidase family protein, similar to SP:P42676 Neurolysin, mitochondrial precursor (EC 3.4.24.16) (Mitochondrial oligopeptidase M) {Rattus norvegicus}; contains Pfam profile PF01432: Peptidase family M3   chr1:25372749-25377393 FORWARD   Aliases: F12A21.16	3.2	3.4	-0.2	-1.2	100.0%	-4.4
6046	AT3G09390.1   Symbol: MT2A   metallothionein protein, putative (MT2A), identical to Swiss-Prot:P25860 metallothionein-like protein 2A (MT-2A) (MT-K) (MT-1G) (Arabidopsis thaliana)   chr3:2889492-2890235 REVERSE   Aliases: ATMT 1, ATMT K, F3L24.28, METALLOTHIONEIN 2A, MT2	12.9	12.4	0.5	1.2	100.0%	-3.9
6047	AT1G60060.1   expressed protein   chr1:22142849-22145455 FORWARD   Aliases: T2K10.11, T2K10_11	2.6	2.4	0.2	1.2	100.0%	-5.1
6048	AT5G45780.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:18584173-18586852 REVERSE   Aliases: MRA19.22, MRA19_22	3.3	3.6	-0.3	-1.2	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6049	AT1G20810.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, identical to Probable FKBP-type peptidyl-prolyl cis-trans isomerase 1, chloroplast precursor (Ppiase) (Rotamase) (SP:Q9LM71)(Arabidopsis thaliana); similar to SP:P25138 FK506-binding protein (Peptidyl-prolyl cis-trans isomerase) (PPIase) (EC 5.2.1.8) (Rotamase) {Neisseria meningitidis}; contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr1:7232010-7233555 FORWARD   Aliases: F2D10.32, F2D10_32	4.5	4.3	0.3	1.2	100.0%	-4.3
6050	AT3G55005.1   Symbol: TON1B   tonneau 1b (TON1b), identical to tonneau 1b (TON1b) GI:11494366 from (Arabidopsis thaliana)   chr3:20394979-20397355 FORWARD   Aliases: TONNEAU 1B	4.3	4.5	-0.2	-1.2	100.0%	-4.4
6051	AT4G31860.2   protein phosphatase 2C, putative / PP2C, putative, protein phosphatase 2C, Schizosaccharomyces pombe, PIR2:S54297   chr4:15405953-15408997 REVERSE   Aliases: F11C18.60, F11C18_60	7.9	7.5	0.4	1.2	100.0%	-4.5
6052	AT5G66520.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:26569105-26570967 FORWARD   Aliases: K1F13.18, K1F13_18	2.7	2.9	-0.2	-1.2	100.0%	-4.8
6053	AT5G64610.1   histone acetyltransferase, putative, similar to histone acetyltransferase (Homo sapiens) gi:8317213:gb:AAF72665   chr5:25845386-25847750 REVERSE   Aliases: MUB3.13, MUB3_13	5.6	6.0	-0.4	-1.2	100.0%	-4.3
6054	AT2G46030.1   Symbol: UBC6   ubiquitin-conjugating enzyme 6 (UBC6), E2; identical to gi:431267, SP:P42750, PIR:S52661; contains a ubiquitin-conjugating enzymes active site (PDOC00163)   chr2:18938464-18940572 REVERSE   Aliases: T3F17.32, UBIQUITIN CONJUGATING ENZYME 6	5.7	5.1	0.6	1.2	100.0%	-4.2
6055	AT1G30130.2   expressed protein, similar to hypothetical protein GI:1469227 from (Brassica oleracea)   chr1:10587587-10589606 FORWARD   Aliases: T2H7.7, T2H7_7	5.1	5.6	-0.5	-1.2	100.0%	-4.0
6056	AT1G56070.1   Symbol: LOS1   elongation factor 2, putative / EF-2, putative, similar to ELONGATION FACTOR 2 GB:O14460 from (Schizosaccharomyces pombe)   chr1:20971595-20975407 REVERSE   Aliases: AT1G56075, AT1G56075.1, T6H22.13, T6H22.24, T6H22_13	11.1	11.5	-0.4	-1.2	100.0%	-4.6
6057	AT5G64250.2   2-nitropropane dioxygenase family / NPD family, contains Pfam profile PF03060: oxidoreductase, 2-nitropropane dioxygenase (NPD) family   chr5:25714450-25716438 REVERSE   Aliases: MSJ1.9, MSJ1_9	9.4	9.1	0.3	1.2	100.0%	-4.7
6058	AT3G46880.1   expressed protein, ; expression supported by MPSS   chr3:17276278-17277251 FORWARD   Aliases: T6H20.90	3.4	3.6	-0.2	-1.2	100.0%	-4.7
6059	AT5G60910.1   Symbol: AGL8   agamous-like MADS box protein AGL8 / FRUITFULL (AGL8), NAP1-1, Nicotiana tabacum, EMBL:AF009126; identical to SP:Q38876 Agamous-like MADS box protein AGL8 (Floral homeotic protein AGL8) (FRUITFULL){Arabidopsis thaliana} PMID:9502732, PMID:10648231; identical to cDNA agamous-like 8 (AGL8) GI:1004364   chr5:24519708-24523339 REVERSE   Aliases: AGAMOUS LIKE 8, AGL8, FRUITFULL, FUL, MSL3.30, MSL3_30	3.5	3.3	0.3	1.2	100.0%	-4.4
6060	AT1G32490.1   Symbol: EMB2733   RNA helicase, putative, similar to ATP-dependent RNA helicase #3 (Homo sapiens) GI:3107913; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr1:11742034-11749686 REVERSE   Aliases: EMB2733, EMBRYO DEFECTIVE 2733, F5D14.27, F5D14_27	3.5	3.8	-0.3	-1.2	100.0%	-4.4
6061	AT4G21880.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:11605117-11611220 FORWARD   Aliases: T8O5.90, T8O5_90	3.3	3.6	-0.3	-1.2	100.0%	-4.1
6062	AT1G77800.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr1:29258290-29265511 FORWARD   Aliases: T32E8.13, T32E8_13	6.2	5.8	0.3	1.2	100.0%	-4.2
6063	AT1G14230.1   nucleoside phosphatase family protein / GDA1/CD39 family protein, low similarity to SP:P49961 Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) {Homo sapiens}; contains Pfam profile PF01150: GDA1/CD39 (nucleoside phosphatase) family   chr1:4861262-4864089 FORWARD   Aliases: 7A19.33, 7A19_33, F7A19.33, F7A19_33	6.1	5.2	0.9	1.2	100.0%	-3.5
6064	AT1G14250.1   nucleoside phosphatase family protein / GDA1/CD39 family protein, low similarity to SP:P97687 Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) {Rattus norvegicus}; contains Pfam profile PF01150: GDA1/CD39 (nucleoside phosphatase) family	6.1	5.2	0.9	1.2	100.0%	-3.5
6065	AT1G11210.1   expressed protein, contains similarity to cotton fiber expressed protein 1 (Gossypium hirsutum) gi:3264828:gb:AAC33276   chr1:3755677-3756998 REVERSE   Aliases: T28P6.13, T28P6_13	4.4	3.8	0.6	1.2	100.0%	-4.1
6066	AT5G44820.1   expressed protein, similar to unknown protein (pir::T04881)   chr5:18112940-18114812 REVERSE   Aliases: K23L20.17, K23L20_17	2.6	2.7	-0.1	-1.2	100.0%	-5.2
6067	AT3G27230.1   expressed protein   chr3:10055166-10056928 FORWARD   Aliases: K17E12.5	7.4	7.9	-0.5	-1.2	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6068	AT1G10390.2   similar to nucleoporin family protein [Arabidopsis thaliana] (TAIR:At1g59660.1); similar to PREDICTED: nucleoporin 98 [Rattus norvegicus] (GB:XP_574504.1); contains InterPro domain Nucleoporin FG repeat (InterPro:IPR004325); contains InterPro domain Nucleoporin autopeptidase (InterPro:IPR007230)	5.7	5.2	0.5	1.2	100.0%	-4.1
6069	AT1G20410.1   expressed protein   chr1:7078889-7082537 REVERSE   Aliases: F5M15.23, F5M15_23	3.4	3.7	-0.3	-1.2	100.0%	-4.3
6070	AT5G08340.2   riboflavin biosynthesis protein-related, contains weak similarity to Riboflavin biosynthesis protein ribF. (Swiss-Prot:P08391) (Escherichia coli O157:H7)   chr5:2683838-2685998 FORWARD   Aliases: F8L15.70, F8L15_70	6.5	6.1	0.4	1.2	100.0%	-4.3
6071	AT1G19710.1   glycosyl transferase family 1 protein, contains Pfam profile: PF00534 glycosyl transferases group 1   chr1:6814828-6816707 FORWARD   Aliases: F14P1.19, F14P1_19	6.3	6.6	-0.3	-1.2	100.0%	-4.2
6072	AT1G66230.1   Symbol: MYB20   myb family transcription factor (MYB20), similar to myb-related transcription factor Gl:1430846 from (Lycopersicon esculentum); contains PFAM profile: Myb DNA binding domain PF00249   chr1:24680817-24682078 FORWARD   Aliases: MYB20, T6j19.5, T6j19_5	4.5	4.9	-0.4	-1.2	100.0%	-4.1
6073	AT1G67410.1   exostosin family protein, contains Pfam profile: PF03016	2.8	3.0	-0.2	-1.2	100.0%	-4.5
6074	AT5G40940.1   expressed protein   chr5:16423884-16425158 REVERSE   Aliases: MMG1.3, MMG1_3	2.3	2.2	0.1	1.2	100.0%	-5.2
6075	AT4G32810.1   Symbol: CCD8   Encodes a protein with similarity to carotenoid cleaving deoxygenases. Involved in the production of a graft transmissible signal to suppress axillary branching. Mutants have increased axillary branches. Expressed primarily in root apex.   chr4:15828232-15831481 FORWARD   Aliases: CAROTENOID CLEAVAGE DIOXYGENASE 8, MAX4, T16i18.20, T16i18_20	4.6	4.0	0.6	1.2	100.0%	-3.9
6076	AT1G05180.3   Symbol: AXR1   similar to auxin-resistance protein, putative [Arabidopsis thaliana] (TAIR:At2g32410.1); similar to putative ubiquitin-activating enzyme (alternative splicing product) [Oryza sativa (japonica cultivar-group)] (GB:XP_470133.1)   chr1:1498113-1501823 REVERSE   Aliases: AUXIN RESISTANT 1, AUXIN RESISTANT PROTEIN 1, YUP8H12.21, YUP8H12_21	9.5	9.8	-0.3	-1.2	100.0%	-4.9
6077	AT1G63200.1   hypothetical protein   chr1:23437295-23438265 REVERSE   Aliases: F16M19.10, F16M19_10	2.5	2.4	0.1	1.2	100.0%	-5.1
6078	AT4G22280.2   F-box family protein, contains Pfam profile PF00646: F-box domain   chr4:11776025-11778131 REVERSE   Aliases: T10i14.110, T10i14_110	3.3	3.1	0.2	1.2	100.0%	-4.6
6079	AT5G54860.1   integral membrane transporter family protein, contains 10 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS TIGR00788: folate/biopterin transporter; similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554) (Leishmania tarentolae)   chr5:22301855-22304432 FORWARD   Aliases: MBG8.12, MBG8_12	5.0	5.4	-0.4	-1.2	100.0%	-4.1
6080	AT4G14050.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:8103640-8105516 REVERSE   Aliases: DL3066C, FCAALL.80	2.6	2.8	-0.1	-1.2	100.0%	-4.9
6081	AT4G33905.1   peroxisomal membrane protein 22 kDa, putative, similar to 22 kDa peroxisomal membrane protein PMP22 (Mus musculus) gi:10954089:gb:AAG25724   chr4:16253820-16255617 REVERSE   Aliases: None	3.6	3.4	0.2	1.2	100.0%	-4.4
6082	AT5G51030.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short chain dehydrogenase/reductase SDR family   chr5:20765088-20766578 REVERSE   Aliases: K3K7.21, K3K7_21	2.8	2.6	0.2	1.2	100.0%	-4.7
6083	AT5G24420.1   glucosamine/galactosamine-6-phosphate isomerase-related, contains weak similarity to Swiss-Prot:O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) (Homo sapiens)   chr5:8336617-8337971 REVERSE   Aliases: K16H17.13, K16H17_13	2.5	2.4	0.2	1.2	100.0%	-4.9
6084	AT1G04140.2   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); similar to neural cell adhesion molecule 2, large isoform precursor gb:M76710 from Xenopus laevis, and beta transducin from S. cerevisiae gb:Q05946. ESTs gb:N65081 gb:Z30910, gb:Z34190, gb:Z34611, gb:R30101, gb:H36304, and gb:N65606 come from   chr1:1075544-1080629 REVERSE   Aliases: F20D22.9, F20D22_9	5.3	4.7	0.6	1.2	100.0%	-3.9
6085	AT5G41210.1   Symbol: ATGSTT1   glutathione S-transferase (GST10), identical to glutathione transferase AtGST 10 (Arabidopsis thaliana) GI:4049401   chr5:16509603-16511126 REVERSE   Aliases: GST10, MEE6.28, MEE6_28	9.0	9.5	-0.5	-1.2	100.0%	-4.2
6086	AT3G13670.1   protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain   chr3:4469229-4473696 FORWARD   Aliases: MMM17.17	6.1	6.9	-0.8	-1.1	100.0%	-4.3
6087	AT3G24770.1   Symbol: CLE41   CLE41, putative, CLAVATA/ESR-Related 41 (CLE41)	3.1	2.9	0.2	1.1	100.0%	-4.7
6088	ATCG00770.1   Symbol: RPS8   chloroplast 30S ribosomal protein S8   chrC:80068-80472 REVERSE   Aliases: RPS8	4.9	6.6	-1.6	-1.1	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6089	AT1G63970.2   Symbol: ISPF   2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase, putative, similar to 2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase Gl:7621712 from (Catharanthus roseus)   chr1:23742354-23743999 REVERSE   Aliases: 2C METHYL D ERYTHRITOL 2,4 CYCLODIPHOSPHATE SYNTHASE, T12P18.1, T12P18_1	7.6	7.0	0.6	1.1	100.0%	-3.9
6090	AT5G04270.1   zinc finger (DHHC type) family protein, low similarity to Golgi-specific DHHC zinc finger protein (Mus musculus) Gl:21728103; contains Pfam profile PF01529: DHHC zinc finger domain   chr5:1182719-1184719 REVERSE   Aliases: T19N18.6	4.0	4.3	-0.2	-1.1	100.0%	-4.5
6091	AT1G58030.1   Symbol: CAT2   amino acid permease family protein, similar to SP:P18581 Low-affinity cationic amino acid transporter-2 (CAT-2) (T-cell early activation protein) {Mus musculus}; contains Pfam profile PF00324: Amino acid permease   chr1:21467671-21472085 REVERSE   Aliases: CATIONIC AMINO ACID TRANSPORTER 2	7.5	7.1	0.4	1.1	100.0%	-4.5
6092	AT4G33950.1   Symbol: OST1   protein kinase, putative, similar to abscisic acid-activated protein kinase (Vicia faba) gi:6739629:gb:AAF27340; contains protein kinase domain, Pfam:PF00069   chr4:16272324-16274815 FORWARD   Aliases: F17I5.140, F17I5_140, OPEN STOMATA 1	5.3	4.8	0.6	1.1	100.0%	-4.2
6093	AT1G19680.1   expressed protein   chr1:6805450-6808126 FORWARD   Aliases: F14P1.21, F14P1_21	6.9	6.7	0.2	1.1	100.0%	-4.5
6094	AT1G05860.1   expressed protein   chr1:1769013-1771114 FORWARD   Aliases: T20M3.13, T20M3_13	3.6	3.8	-0.2	-1.1	100.0%	-4.8
6095	AT1G63610.2   expressed protein   chr1:23587190-23589386 REVERSE   Aliases: F2K11.3, F2K11_3	6.2	6.9	-0.6	-1.1	100.0%	-4.0
6096	AT1G64950.1   Symbol: CYP89A5   cytochrome P450, putative, similar to cytochrome P450 89A2 (CYPLXXXIX) (SP:Q42602) (Arabidopsis thaliana); similar to cytochrome P450 (Gl:438242) (Solanum melongena)   chr1:24131224-24133121 FORWARD   Aliases: F13O11.25, F13O11_25	10.4	9.9	0.5	1.1	100.0%	-5.1
6097	AT3G03670.1   peroxidase, putative, similar to peroxidase GB:CAA66966 (Arabidopsis thaliana)   chr3:901862-903384 REVERSE   Aliases: T12J13.5, T12J13_5	3.1	3.4	-0.3	-1.1	100.0%	-4.5
6098	AT5G56490.1   FAD-binding domain-containing protein, strong similarity to At1g32300, At2g46740, At2g46750, At2g46760; contains PF01565: FAD binding domain   chr5:22888689-22890670 FORWARD   Aliases: MCD7.26, MCD7_26	2.4	2.5	-0.1	-1.1	100.0%	-4.9
6099	AT3G51320.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:19060832-19062480 REVERSE   Aliases: F24M12.360	5.3	5.7	-0.3	-1.1	100.0%	-4.1
6100	AT4G22620.1   auxin-responsive family protein, auxin-induced protein 10A, Glycine max., PIR2:JQ1099   chr4:11907642-11908124 FORWARD   Aliases: T12H17.10	4.7	4.4	0.3	1.1	100.0%	-4.3
6101	AT2G25190.1   expressed protein   chr2:10741025-10742778 FORWARD   Aliases: F13D4.5	5.7	5.3	0.4	1.1	100.0%	-4.2
6102	AT5G10500.1   kinase interacting family protein, similar to kinase interacting protein 1 (Gl:13936326) (Petunia integrifolia)   chr5:3305332-3308110 FORWARD   Aliases: F12B17.150, F12B17_150	2.4	2.6	-0.2	-1.1	100.0%	-5.0
6103	AT1G60670.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g10820.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466887.1)   chr1:22347320-22351273 FORWARD   Aliases: F8A5.19, F8A5_19	3.2	3.0	0.2	1.1	100.0%	-4.8
6104	AT3G12180.1   cornichon family protein, contains Pfam profile: PF03311 cornichon protein   chr3:3883369-3884812 FORWARD   Aliases: F28J15.3	6.5	5.9	0.6	1.1	100.0%	-4.3
6105	AT1G74440.1   expressed protein, similar to YGL010w-like protein GB:AAC32136 (Picea mariana)   chr1:27980163-27984065 REVERSE   Aliases: F1M20.12, F1M20_12	4.8	4.5	0.3	1.1	100.0%	-4.3
6106	AT4G14180.1   expressed protein, ; expression supported by MPSS   chr4:8178325-8183510 FORWARD   Aliases: DL3130W, FCAALL.114	2.2	2.4	-0.1	-1.1	100.0%	-5.2
6107	AT2G30330.1   GCN5L1 family protein, similar to GCN5-like protein 1 (RT14 protein) (Swiss-Prot:P78537) (Homo sapiens)   chr2:12935844-12936814 REVERSE   Aliases: T9D9.14, T9D9_14	4.5	4.2	0.3	1.1	100.0%	-4.5
6108	AT3G10960.1   xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family   chr3:3424818-3427002 REVERSE   Aliases: F9F8.22	4.4	4.6	-0.2	-1.1	100.0%	-4.5
6109	AT3G16310.1   mitotic phosphoprotein N' end (MPPN) family protein, contains Pfam profile PF05172: MPPN (Mitotic PhosphoProtein N' end) (rrm-like) domain   chr3:5526424-5528606 REVERSE   Aliases: MYA6.11	8.9	8.4	0.5	1.1	100.0%	-4.2
6110	AT5G04140.2   Symbol: GLU1   glutamate synthase (GLU1) / ferredoxin-dependent glutamate synthase (Fd-GOGAT 1), identical to ferredoxin-dependent glutamate synthase precursor (Arabidopsis thaliana) Gl:3869251   chr5:1130032-1138439 FORWARD   Aliases: F21E1.60, F21E1_60, FERREDOXIN DEPENDENT GLUAMATE SYNTHASE 1, GLS1, GLUAMATE SYNTHASE 1, GLUTAMATE SYNTHASE	6.5	6.0	0.5	1.1	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6111	AT1G01440.1   extra-large G-protein-related, weak similarity to extra-large G-protein (AtXLG1) (GI:3201682) (Arabidopsis thaliana)   chr1:159935-162219 REVERSE   Aliases: F6F3.24, F6F3_24	3.6	3.4	0.2	1.1	100.0%	-4.5
6112	AT1G11390.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr1:3834459-3837498 REVERSE   Aliases: T23J18.5, T23J18_5	4.7	5.0	-0.2	-1.1	100.0%	-4.6
6113	ATMG00070.1   Symbol: NAD9   NADH dehydrogenase subunit 9   chrM:23663-24235 REVERSE   Aliases: NAD9	3.2	4.0	-0.7	-1.1	100.0%	-4.3
6114	AT4G22750.1   zinc finger (DHHC type) family protein, contains DHHC zinc finger domain PF01529	7.2	6.5	0.7	1.1	100.0%	-4.1
6115	AT1G20980.1   Symbol: SPL14   SPL1-Related2 protein (SPL1R2), strong similarity to SPL1-Related2 protein (Arabidopsis thaliana) GI:6006427; contains Pfam profile PF03110: SBP domain	6.1	6.4	-0.4	-1.1	100.0%	-4.1
6116	AT2G47070.1   Symbol: SPL1   squamosa promoter-binding protein-like 1 (SPL1), identical to squamosa promoter binding protein-like 1 (Arabidopsis thaliana) GI:5931655; contains Pfam profile PF03110: SBP domain   chr2:19343767-19347939 FORWARD   Aliases: F14M4.10, SQUAMOSA PROMOTER BINDING PROTEIN LIKE 1	5.2	5.0	0.2	1.1	100.0%	-4.6
6117	AT4G25080.3   magnesium-protoporphyrin O-methyltransferase, putative / magnesium-protoporphyrin IX methyltransferase, putative, similar to SP:Q55467 Magnesium-protoporphyrin O-methyltransferase (EC 2.1.1.1) (Magnesium-protoporphyrin IX methyltransferase) {Synechocystis sp.}   chr4:12876958-12878639 FORWARD   Aliases: F24A6.6, MGPIXMT	8.6	8.2	0.4	1.1	100.0%	-4.2
6118	AT1G43880.1   expressed protein, low similarity to protective antigen (Streptococcus pyogenes) GI:8996050, fibrinogen-binding protein (Streptococcus equi) GI:3093478   chr1:16630750-16632385 FORWARD   Aliases: F28H19.18, F28H19_18	2.6	2.5	0.1	1.1	100.0%	-5.2
6119	AT2G26540.1   uroporphyrinogen-III synthase family protein, contains Pfam PF02602: uroporphyrinogen-III synthase; weak similarity to Porphyrin biosynthesis protein HEMD)) (Uroporphyrinogen III methylase) (UROM); Uroporphyrinogen-III synthase (EC 4.2.1.75) (Swiss-Prot:Q59294) (Clostridium josui)   chr2:11294476-11297438 REVERSE   Aliases: T9J22.21, T9J22_21	5.5	5.2	0.3	1.1	100.0%	-4.2
6120	AT1G25450.1   very-long-chain fatty acid condensing enzyme, putative, nearly identical to fatty acid condensing enzyme CUT1 GI:5001734 from (Arabidopsis thaliana)   chr1:8938466-8940374 REVERSE   Aliases: F2J7.9, F2J7_9	2.8	3.0	-0.2	-1.1	100.0%	-4.8
6121	AT5G14770.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:4772884-4775700 REVERSE   Aliases: T9L3.70, T9L3_70	3.1	2.9	0.2	1.1	100.0%	-4.7
6122	AT1G35510.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator protein -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr1:13071143-13074927 FORWARD   Aliases: F15O4.45	3.9	3.6	0.2	1.1	100.0%	-4.5
6123	AT1G70910.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:26737817-26738302 FORWARD   Aliases: F15H11.25	3.1	3.3	-0.2	-1.1	100.0%	-5.0
6124	AT2G17972.1   expressed protein   chr2:7828667-7829403 FORWARD   Aliases: None	6.3	5.8	0.5	1.1	100.0%	-3.7
6125	AT5G05600.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase (Citrus unshiu)(gi:4126403), leucoanthocyanidin dioxygenase (Daucus carota)(gi:5924383); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr5:1672121-1674740 FORWARD   Aliases: MOP10.14, MOP10_14	4.7	4.1	0.6	1.1	100.0%	-3.9
6126	AT5G58500.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr5:23662761-23663309 REVERSE   Aliases: MQJ2.11, MQJ2_11	5.4	5.2	0.3	1.1	100.0%	-4.3
6127	AT2G42670.1   expressed protein   chr2:17778901-17781481 REVERSE   Aliases: F14N22.6, F14N22_6	4.5	4.2	0.3	1.1	100.0%	-4.3
6128	AT5G49700.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr5:20209825-20210655 FORWARD   Aliases: K2I5.6, K2I5_6	3.9	3.6	0.3	1.1	100.0%	-4.4
6129	AT5G50370.1   adenylate kinase, putative, similar to adenylate kinase (ATP-AMP transphosphorylase) (Arabidopsis thaliana) SWISS-PROT:O82514   chr5:20526385-20527926 REVERSE   Aliases: MXI22.8, MXI22_8	8.4	9.4	-1.0	-1.1	100.0%	-4.0
6130	AT5G14230.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:4593810-4595967 FORWARD   Aliases: F18O22.20, F18O22_20	4.1	4.4	-0.4	-1.1	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6131	AT2G01950.1   leucine-rich repeat transmembrane protein kinase, putative, similar to brassinosteroid insensitive protein   chr2:440635-444275 REVERSE   Aliases: F14H20.2, F14H20_2	4.3	4.8	-0.4	-1.1	100.0%	-4.2
6132	AT2G31250.1   glutamyl-tRNA reductase, putative, similar to HEMA2 (SP:P49294), HEMA1 (SP:P42804)   chr2:13326698-13328603 REVERSE   Aliases: F16D14.9, F16D14_9	4.1	4.5	-0.4	-1.1	100.0%	-4.3
6133	AT1G28130.2   Symbol: GH3.17	4.1	4.4	-0.3	-1.1	100.0%	-4.3
6134	AT4G14400.3   Symbol: ACD6   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr4:8294448-8298598 FORWARD   Aliases: ACCELERATED CELL DEATH 6, DL3240W, FCAALL.190	3.1	3.0	0.2	1.1	100.0%	-4.9
6135	AT5G17660.1   expressed protein, contains Pfam profile PF02390: Putative methyltransferase   chr5:5818550-5820866 REVERSE   Aliases: MVA3.1, MVA3_1	3.1	3.3	-0.2	-1.1	100.0%	-4.4
6136	AT1G63000.1   Symbol: NRS/ER	6.0	6.6	-0.6	-1.1	100.0%	-4.2
6137	AT2G40620.1   bZIP transcription factor family protein, identical to b-Zip DNA binding protein Gl:2246376 from (Arabidopsis thaliana); contains a bZIP transcription factor basic domain signature (PDOC00036)	3.2	3.0	0.2	1.1	100.0%	-4.6
6138	AT2G36360.2   similar to kelch repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g74150.1); similar to conjugation with cellular fusion-related protein, putative [Cryptococcus neoformans var. neoformans JEC21] (GB:AAW40898.1); contains InterPro domain Kelch repeat (InterPro:IPR006652)   chr2:15249983-15254694 REVERSE   Aliases: F2H17.3, F2H17_3	5.5	5.0	0.5	1.1	100.0%	-4.1
6139	AT1G76520.2   auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547   chr1:28720049-28722308 FORWARD   Aliases: F14G6.12, F14G6_12	9.0	8.2	0.8	1.1	100.0%	-3.9
6140	AT1G21500.1   expressed protein   chr1:7529871-7531014 REVERSE   Aliases: F24J8.11, F24J8_11	3.7	3.4	0.3	1.1	100.0%	-4.5
6141	AT1G51670.1   expressed protein   chr1:19160810-19162417 FORWARD   Aliases: F19C24.12, F19C24_12	3.0	2.8	0.2	1.1	100.0%	-4.7
6142	AT5G48400.2   Symbol: ATGLR1.2   glutamate receptor family protein (GLR1.2), plant glutamate receptor family, PMID:11379626   chr5:19633470-19636472 FORWARD   Aliases: GLR1.2, MJE7.3, MJE7_3	2.9	2.8	0.1	1.1	100.0%	-5.0
6143	AT5G01780.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to alkB protein - Escherichia coli, PIR:BVECKB, alkB (Caulobacter crescentus)(Gl:2055386); contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily   chr5:302362-304169 REVERSE   Aliases: T20L15.50, T20L15_50	6.2	5.6	0.6	1.1	100.0%	-4.1
6144	AT4G38510.4   similar to vacuolar ATP synthase subunit B / V-ATPase B subunit / vacuolar proton pump B subunit / V-ATPase 57 kDa subunit [Arabidopsis thaliana] (TAIR:At1g76030.1); similar to vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative [Arabidopsis thaliana] (TAIR:At1g20260.2); similar to vacuolar ATPase B subunit (GB:AAA81331.1); similar to H+-transporting two-sector ATPase (EC 3.6.3.14) chain B, vacuolar [imported] - Citrus unshiu (GB:T43789); similar to putative H+-transporting ATP synthase [Oryza sativa (japonica cultivar-group)] (GB:NP_916591.1); similar to vacuolar ATPase B subunit (GB:AAA81330.1); similar to VATB1_GOSHI Vacuolar ATP synthase subunit B isoform 1 (V-ATPase B subunit 1) (Vacuolar proton pump B subunit 1) (GB:Q43432); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, C-terminal (InterPro:IPR000793); contains InterPro domain ATP synthase V-type, B subunit (InterPro:IPR005723); contains InterPro domain H+-transporting two-sector ATPase, alpha subunit, C-terminal (InterPro:IPR000790); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, N-terminal (InterPro:IPR004100); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, central region (InterPro:IPR000194)	6.8	7.8	-0.9	-1.1	100.0%	-4.1
6145	AT2G46470.1   OXA1 protein, putative, similar to Oxa1 protein (Arabidopsis thaliana) Gl:10176922   chr2:19079385-19082195 FORWARD   Aliases: F11C10.16	5.0	5.4	-0.4	-1.1	100.0%	-4.0
6146	AT1G17040.1   transcription factor-related, contains Pfam profile: PF00017 Src homology domain 2; similar to transcription factor (Danio rerio) (Gl:3687402)   chr1:5824844-5828226 FORWARD   Aliases: F20D23.26, F20D23_26	4.3	4.6	-0.3	-1.1	100.0%	-4.4
6147	AT3G28700.1   expressed protein, contains Pfam PF02636: Uncharacterized ACR, COG1565   chr3:10760802-10763351 FORWARD   Aliases: MZN14.19	7.1	7.5	-0.4	-1.1	100.0%	-4.0
6148	AT3G53710.2   similar to arabidopsis pde1 suppressor 1 protein (ASP1) [Arabidopsis thaliana] (TAIR:At2g37550.1); similar to CG4237-PA [Drosophila melanogaster] (GB:NP_524040.2); similar to putative ARF1 GTPase activating protein [Drosophila melanogaster] (GB:AAB64300.1); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164)   chr3:19914291-19916494 REVERSE   Aliases: F5K20.10	7.1	6.9	0.2	1.1	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6149	AT3G19960.1   Symbol: ATATM   myosin (ATM), nearly identical to myosin (Arabidopsis thaliana) GI:6491702; similar to myosin GI:6491702 from (Arabidopsis thaliana) ;contains Pfam profiles: PF00063: myosin head (motor domain), PF00612: IQ calmodulin-binding motif; identical to cDNA myosin (ATM) GI:297068   chr3:6948782-6956972 FORWARD   Aliases: ATM1, MZE19.3	4.9	5.2	-0.3	-1.1	100.0%	-4.3
6150	AT1G35220.1   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAV43936.1)   chr1:12908892-12914780 FORWARD   Aliases: T9I1.1, T9I1_1	2.6	2.8	-0.2	-1.1	100.0%	-5.0
6151	AT4G07740.1   expressed protein   chr4:4539635-4540679 FORWARD   Aliases: T6L9.5, T6L9_5	2.3	2.5	-0.2	-1.1	100.0%	-4.6
6152	AT3G21620.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr3:7611051-7614048 REVERSE   Aliases: MIL23.19	2.5	2.7	-0.2	-1.1	100.0%	-4.7
6153	AT5G28010.1   Bet v I allergen family protein, similar to Csf-2 (Cucumis sativus)(GI:5762258)(J Am Soc Hortic Sci 124, 136-139 (1999)); contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr5:10024817-10025386 FORWARD   Aliases: F15F15.80, F15F15_80	2.3	2.2	0.2	1.1	100.0%	-5.0
6154	AT5G20820.1   auxin-responsive protein-related, similar to auxin-induced protein TGSAUR21 (GI:10185818) Tulipa gesneriana)   chr5:7046753-7047398 REVERSE   Aliases: T1M15.220, T1M15_220	4.0	4.7	-0.7	-1.1	100.0%	-3.6
6155	AT1G11610.1   Symbol: CYP71A18   cytochrome P450, putative, very strong similarity to cytochrome P450 (SP:Q9SAB6) (Arabidopsis thaliana); is a member of the PF:00067 Cytochrome P450 family   chr1:3907461-3909291 REVERSE   Aliases: F25C20.24, F25C20_24	2.3	2.5	-0.2	-1.1	100.0%	-5.2
6156	AT1G14470.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:4954075-4955697 FORWARD   Aliases: F14L17.25, F14L17_25	2.9	2.8	0.2	1.1	100.0%	-4.9
6157	AT4G01310.1   ribosomal protein L5 family protein, contains Pfam profiles PF00673: ribosomal L5P family C-terminus, PF00281: ribosomal protein L5   chr4:543970-545535 REVERSE   Aliases: F2N1.5, F2N1_5	6.5	7.3	-0.8	-1.1	100.0%	-3.9
6158	AT5G06750.1   protein phosphatase 2C family protein / PP2C family protein, similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain;   chr5:2086267-2088529 REVERSE   Aliases: MPH15.11, MPH15_11	8.0	8.4	-0.4	-1.1	100.0%	-4.3
6159	AT3G55850.2   Symbol: LAF3.1	4.4	4.7	-0.3	-1.1	100.0%	-4.2
6160	AT1G10680.1   P-glycoprotein, putative, similar to P-glycoprotein GI:4204793 from (Solanum tuberosum)   chr1:3538471-3543783 REVERSE   Aliases: F20B24.12, F20B24_12	3.0	2.8	0.2	1.1	100.0%	-4.7
6161	AT5G17190.1   expressed protein, similar to unknown protein (gb:AAF26109.1)   chr5:5652225-5652985 FORWARD   Aliases: MKP11.4, MKP11_4	9.8	9.1	0.7	1.1	100.0%	-4.4
6162	AT1G26340.1   Symbol: B5 #6   cytochrome b5, putative, similar to cytochrome b5 GB:BAA74839 GI:4240120 from (Arabidopsis thaliana)   chr1:9113887-9114958 FORWARD   Aliases: F28B23.1	4.6	4.4	0.2	1.1	100.0%	-4.9
6163	AT1G10460.1   Symbol: GLP7   germin-like protein (GLP7), identical to germin-like protein subfamily 1 member 1 (SP:P92998); similar to ESTs gb:T88481 and gb:A1099566	4.5	4.9	-0.4	-1.1	100.0%	-4.1
6164	AT1G24764.1   Symbol: ATMAP70 2   Member of the MAP70 protein family.	4.3	4.6	-0.3	-1.1	100.0%	-4.3
6165	AT1G58360.1   Symbol: AAP1   amino acid permease I (AAP1), identical to amino acid permease I GI:22641 from (Arabidopsis thaliana)   chr1:21680201-21684148 FORWARD   Aliases: F19C14.3, F19C14_3, NAT2, NEUTRAL AMINO ACID TRANSPORTER 2	9.0	7.8	1.2	1.1	100.0%	-4.0
6166	AT3G09700.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain; similar to a region of DNAJ domain-containing protein MCJ GB:AAD38506   chr3:2974886-2976282 REVERSE   Aliases: F11F8.29	6.4	6.7	-0.4	-1.1	100.0%	-4.1
6167	AT1G05690.1   TAZ zinc finger family protein / BTB/POZ domain-containing protein, contains Pfam PF00651 : BTB/POZ domain; contains Pfam PF02135 : TAZ zinc finger; similar to p300/CBP acetyltransferase-related protein (GI:12597461) (Arabidopsis thaliana); similar to Speckle-type POZ protein (SP:O43791) (Homo sapiens)   chr1:1707082-1709346 FORWARD   Aliases: F3F20.14, F3F20_14	4.4	4.1	0.3	1.1	100.0%	-4.2
6168	AT5G05870.1   Symbol: UGT76C1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:1767640-1769263 FORWARD   Aliases: K18J17.2, K18J17_2, UGT76C1	5.7	5.9	-0.2	-1.1	100.0%	-4.7
6169	AT2G47980.1   expressed protein   chr2:19638329-19644323 FORWARD   Aliases: T9J23.3	7.1	7.4	-0.3	-1.1	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6170	ATCG00650.1   Symbol: RPS18   chloroplast-encoded ribosomal protein S18   chrC:67917-68222 FORWARD   Aliases: RPS18	6.3	7.3	-0.9	-1.1	100.0%	-4.1
6171	AT5G15050.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr5:4871642-4873601 REVERSE   Aliases: F2G14.170, F2G14_170	5.4	5.8	-0.4	-1.1	100.0%	-4.2
6172	AT1G68850.1   peroxidase, putative, identical to peroxidase ATP23a GB:CAA70035 (Arabidopsis thaliana)   chr1:25887279-25888896 REVERSE   Aliases: T6L1.4, T6L1_4	2.9	3.2	-0.4	-1.1	100.0%	-4.0
6173	AT4G13260.1   flavin-containing monooxygenase / FMO (YUCCA2), identical to gi:16555354	4.6	4.9	-0.3	-1.1	100.0%	-4.2
6174	AT1G64110.2   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family   chr1:23800382-23805388 REVERSE   Aliases: F22C12.12, F22C12_12	11.2	10.7	0.4	1.1	100.0%	-4.3
6175	AT5G35160.1   endomembrane protein 70, putative, p76, Homo sapiens, EMBL:HSU81006   chr5:13432184-13434151 FORWARD   Aliases: T25C13.40, T25C13_40	6.3	6.8	-0.5	-1.1	100.0%	-4.3
6176	AT4G20150.1   expressed protein   chr4:10888309-10889606 REVERSE   Aliases: F1C12.70, F1C12_70	12.7	13.0	-0.2	-1.1	100.0%	-4.8
6177	AT1G42960.1   expressed protein localized to the inner membrane of the chloroplast.   chr1:16128235-16129727 FORWARD   Aliases: F13A11.2, F13A11_2	10.0	10.4	-0.4	-1.1	100.0%	-4.5
6178	AT5G25060.1   RNA recognition motif (RRM)-containing protein, KIAA0332 - Homo sapiens, EMBL:AB002330   chr5:8634077-8640220 REVERSE   Aliases: T11H3.70, T11H3_70	6.7	7.3	-0.6	-1.1	100.0%	-4.2
6179	AT1G72175.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:27161537-27163219 FORWARD   Aliases: None	6.3	6.0	0.3	1.1	100.0%	-4.3
6180	AT4G03200.1   expressed protein, contains Pfam PF03190: Protein of unknown function, DUF255   chr4:1408159-1412756 FORWARD   Aliases: F4C21.12, F4C21_12	7.8	7.4	0.4	1.1	100.0%	-4.3
6181	AT3G05350.1   similar to aminopeptidase P [Arabidopsis thaliana] (TAIR:At4g36760.1); similar to aminopeptidase-P [Aspergillus oryzae] (GB:BAD00702.1); contains InterPro domain Metallopeptidase family M24 (InterPro:IPR000994)   chr3:1526969-1530263 REVERSE   Aliases: T12H1.32, T12H1_32	5.9	5.6	0.3	1.1	100.0%	-4.4
6182	AT5G51620.2   expressed protein   chr5:20984324-20985253 FORWARD   Aliases: K17N15.17, K17N15_17	9.1	8.5	0.5	1.1	100.0%	-4.3
6183	AT5G55630.2   Symbol: KCO1   outward rectifying potassium channel (KCO1), identical to kco1 (Arabidopsis thaliana) gi:2230761:emb:CAA69158 of the 2 pore, 4 transmembrane (2P/4TM) K+ channel family, PMID:11500563   chr5:22548584-22550344 FORWARD   Aliases: MDF20.7, MDF20_7	4.1	4.4	-0.3	-1.1	100.0%	-4.2
6184	AT5G52310.1   Symbol: COR78   low-temperature-responsive protein 78 (LTI78) / desiccation-responsive protein 29A (RD29A)   chr5:21258075-21260839 FORWARD   Aliases: COLD REGULATED 78, K24M7.4, K24M7_4, LTI140, LTI78, RD29A, RESPONSIVE TO DESSICATION 29A	10.9	10.4	0.5	1.1	100.0%	-4.7
6185	AT2G21240.2   expressed protein   chr2:9108397-9110127 REVERSE   Aliases: F7O24.4, F7O24_4	7.8	7.4	0.4	1.1	100.0%	-4.2
6186	AT5G46410.1   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr5:18842330-18846448 FORWARD   Aliases: MPL12.21, MPL12_21	5.3	5.0	0.3	1.1	100.0%	-4.1
6187	AT5G22220.3   Symbol: E2F1   similar to E2F transcription factor-3 (E2F3) [Arabidopsis thaliana] (TAIR:At2g36010.1); similar to transcription factor (E2F) [Chenopodium rubrum] (GB:CAC17702.1); contains InterPro domain Transcription factor E2F/dimerisation partner (TDP) (InterPro:IPR003316)   chr5:7360538-7364457 FORWARD   Aliases: ATE2FB, E2F TRANSCRIPTION FACTOR 1 E2F1, E2FB, E2FB TRANSCRIPTION FACTOR	4.0	3.7	0.2	1.1	100.0%	-4.4
6188	NA	6.2	5.7	0.5	1.1	100.0%	-4.7
6189	AT5G56730.1   peptidase M16 family protein / insulinase family protein, contains Pfam domain, PF05193: Peptidase M16 inactive domain   chr5:22964132-22969802 REVERSE   Aliases: MIK19.18, MIK19_18	4.1	4.2	-0.2	-1.1	100.0%	-4.8
6190	AT1G11350.1   S-locus lectin protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108   chr1:3817591-3820805 REVERSE   Aliases: T23J18.2, T23J18_2	2.5	2.7	-0.1	-1.1	100.0%	-5.0
6191	AT1G10960.1   ferredoxin, chloroplast, putative, strong similarity to FERREDOXIN PRECURSOR GB:P16972 (SP:P16972) from (Arabidopsis thaliana)   chr1:3664386-3665039 FORWARD   Aliases: T19D16.12, T19D16_12	11.0	11.6	-0.6	-1.1	100.0%	-3.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6192	AT2G31750.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:13504310-13507763 FORWARD   Aliases: F20M17.21, F20M17_21	3.5	3.9	-0.4	-1.1	100.0%	-4.1
6193	AT5G53540.1   MSP1 protein, putative / intramitochondrial sorting protein, putative, similar to Swiss-Prot:P28737 MSP1 protein (TAT-binding homolog 4) (Saccharomyces cerevisiae); contains Pfam domain, PF00004: ATPase, AAA family   chr5:21766512-21768463 REVERSE   Aliases: MNC6.8, MNC6_8	8.6	8.9	-0.3	-1.1	100.0%	-4.4
6194	AT4G14760.1   M protein repeat-containing protein, contains Pfam profile: PF02370 M protein repeat   chr4:8475964-8481089 FORWARD   Aliases: DL3420W, FCAALL.305	5.8	6.3	-0.5	-1.1	100.0%	-4.1
6195	AT4G28240.1   wound-responsive protein-related, wound-induced protein - tomato (fragment), PIR2:S19773	8.2	7.8	0.4	1.1	100.0%	-4.4
6196	AT3G20960.1   Symbol: CYP705A33   cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	3.0	2.6	0.4	1.1	100.0%	-4.1
6197	AT3G01460.1   Symbol: MBD9   PHD finger family protein / methyl-CpG binding domain-containing protein, contains Pfam profiles PF00628: PHD-finger (2 copies), PF01429: Methyl-CpG binding domain   chr3:173323-182971 FORWARD   Aliases: T13O15.10, T13O15_10	4.4	4.7	-0.3	-1.1	100.0%	-4.5
6198	AT5G07260.1   homeobox protein-related, contains weak similarity to Homeobox protein FWA (Swiss-Prot:Q9FVI6) (Arabidopsis thaliana)   chr5:2277815-2280282 FORWARD   Aliases: T28J14.200, T28J14_200	3.1	3.2	-0.2	-1.1	100.0%	-4.9
6199	NA	2.8	2.7	0.1	1.1	100.0%	-5.1
6200	AT2G18910.1   hydroxyproline-rich glycoprotein family protein   chr2:8199790-8201420 REVERSE   Aliases: F19F24.21	6.6	6.1	0.5	1.1	100.0%	-4.1
6201	AT2G41630.1   Symbol: TFIIB   transcription initiation factor IIB-1 / general transcription factor TFIIB-1 (TFIIB1), identical to transcription initiation factor IIB-1 (TFIIB1) SP:P48512 from (Arabidopsis thaliana)   chr2:17362410-17364676 REVERSE   Aliases: T32G6.15, T32G6_15, TRANSCRIPTION FACTOR II B, TRANSCRIPTION FACTOR TFIIB	8.9	9.4	-0.6	-1.1	100.0%	-4.3
6202	AT3G50610.1   expressed protein   chr3:18790704-18791393 REVERSE   Aliases: T20E23.210	8.5	7.8	0.7	1.1	100.0%	-3.7
6203	AT4G37380.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:17572034-17573932 REVERSE   Aliases: F6G17.30, F6G17_30	6.0	6.4	-0.4	-1.1	100.0%	-4.1
6204	AT1G09660.2   KH domain-containing quaking protein, putative, similar to GB:AAC67357   chr1:3127783-3131049 REVERSE   Aliases: F21M12.5, F21M12_5	5.8	5.5	0.3	1.1	100.0%	-4.3
6205	AT3G33530.1   transducin family protein / WD-40 repeat family protein, similar to WD-repeat protein 11 (SP:Q9BZH6) {Homo sapiens}; contains Pfam PF00400: WD domain, G-beta repeat (4 copies, 3 weak):2763187:gb:T46504.1:T46504   chr3:14096340-14104656 FORWARD   Aliases: T4P3.9	5.2	5.5	-0.3	-1.1	100.0%	-4.3
6206	AT2G06210.2   Symbol: ELF8   phosphoprotein-related, low similarity to phosphoprotein from Mus musculus GI:1236239; contains Pfam profile PF00515 TPR Domain   chr2:2428900-2436684 REVERSE   Aliases: EARLY FLOWERING 8, F5K7.3, F5K7_3	5.3	6.0	-0.7	-1.1	100.0%	-4.3
6207	AT4G33000.2   Symbol: CBL10   calcineurin B-like protein 10 (CBL10), identical to calcineurin B-like protein 10 (Arabidopsis thaliana) GI:29150248   chr4:15924759-15926631 FORWARD   Aliases: ATCBL10, F26P21.120, F26P21_120	3.4	3.7	-0.3	-1.1	100.0%	-4.3
6208	AT3G15710.1   signal peptidase, putative, similar to SP:P13679 Microsomal signal peptidase 21 kDa subunit (EC 3.4.-.-) {Canis familiaris}; contains Pfam profile: PF00461 signal peptidase I   chr3:5323365-5324915 REVERSE   Aliases: MSJ11.11	8.1	8.5	-0.4	-1.1	100.0%	-4.3
6209	AT1G18910.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	3.6	4.1	-0.5	-1.1	100.0%	-3.9
6210	AT5G60300.2   lectin protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain and PF00139: Legume lectins beta domain   chr5:24281848-24284436 FORWARD   Aliases: F15L12.17, F15L12_17	6.1	5.7	0.4	1.1	100.0%	-4.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6211	AT5G10240.2   Symbol: ASN3   similar to asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) [Arabidopsis thaliana] (TAIR:At3g47340.3); similar to asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) [Arabidopsis thaliana] (TAIR:At3g47340.2); similar to asparagine synthetase 2 (ASN2) [Arabidopsis thaliana] (TAIR:At5g65010.1); similar to asparagine synthetase 1 (glutamine-hydrolyzing) / glutamine-dependent asparagine synthetase 1 (ASN1) [Arabidopsis thaliana] (TAIR:At3g47340.1); similar to asparagine synthetase 2 (ASN2) [Arabidopsis thaliana] (TAIR:At5g65010.2); similar to asparagine synthetase [Helianthus annuus] (GB:AAF02776.1); similar to glutamine-dependent asparagine synthetase 1 [Hordeum vulgare subsp. vulgare] (GB:AAK49456.1); similar to glutamine-dependent asparagine synthetase [Triticum aestivum] (GB:AAU89392.1); similar to putative asparagine synthetase [Pinus sylvestris] (GB:CAD43058.1); similar to asparagine synthetase [Striga hermonthica] (GB:AAM94340.1); contains InterPro domain Glutamine amidotransferase, class-II (InterPro:IPR000583); contains InterPro domain Asparagine synthase, glutamine-hydrolyzing (InterPro:IPR006426); contains InterPro domain Asparagine synthase (InterPro:IPR001962)	8.2	8.7	-0.5	-1.1	100.0%	-3.9
6212	AT2G34790.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr2:14680444-14684349 REVERSE   Aliases: F19I3.2, F19I3_2	3.9	4.3	-0.4	-1.1	100.0%	-4.3
6213	AT2G22090.2   UBP1 interacting protein 1a (UBA1a), nearly identical to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); based on cDNA of partial mRNA for UBP1 interacting protein 1a (uba1a) GI:19574235   chr2:9396080-9397586 REVERSE   Aliases: T16B14.6, T16B14_6	5.3	4.9	0.3	1.1	100.0%	-4.1
6214	AT4G02460.1   DNA mismatch repair protein, putative, similar to SP:P54278 PMS1 protein homolog 2 (DNA mismatch repair protein PMS2) {Homo sapiens}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF01119: DNA mismatch repair protein, C-terminal domain   chr4:1076136-1080667 REVERSE   Aliases: T14P8.6, T14P8_6	3.5	3.8	-0.2	-1.1	100.0%	-4.6
6215	AT4G02680.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr4:1181051-1184930 REVERSE   Aliases: T10P11.24, T10P11_24	7.9	8.5	-0.6	-1.1	100.0%	-4.1
6216	AT2G27310.1   F-box family protein, contains Pfam PF00646: F-box domain;; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr2:11690940-11692045 REVERSE   Aliases: F12K2.11, F12K2_11	5.8	5.2	0.6	1.1	100.0%	-4.0
6217	AT1G13180.1   Symbol: DIS1   actin-related protein 3 (ARP3), identical to actin-related protein 3 (ARP3) (Arabidopsis thaliana) GI:21427461; contains Pfam profile PF00022: Actin   chr1:4495025-4498466 FORWARD   Aliases: ACTIN RELATED PROTEIN 3, ARP3, ATARP3, DISTORTED TRICHOMES 1, F3F19.20, F3F19_20	5.4	5.7	-0.2	-1.1	100.0%	-4.5
6218	AT1G34570.1   expressed protein   chr1:12654918-12656464 REVERSE   Aliases: F12K21.27	3.8	3.2	0.6	1.1	100.0%	-3.9
6219	AT3G15750.1   expressed protein   chr3:5335232-5336483 FORWARD   Aliases: MSJ11.15	3.8	3.2	0.6	1.1	100.0%	-3.9
6220	AT5G11180.1   Symbol: ATGLR2.6   glutamate receptor family protein (GLR2.6), plant glutamate receptor family, PMID:11379626   chr5:3557262-3561576 REVERSE   Aliases: F2I11.70, F2I11_70, GLR2.6	2.6	2.4	0.1	1.1	100.0%	-5.0
6221	AT4G28450.1   transducin family protein / WD-40 repeat family protein, SOF1 (involved in rRNA processing) protein-yeast   chr4:14061465-14064679 REVERSE   Aliases: F2O09.130, F2O09_130	5.4	5.8	-0.4	-1.1	100.0%	-4.4
6222	AT5G16650.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P30725 Chaperone protein dnaJ Clostridium acetobutylicum; contains Pfam profile PF00226: Dnaj domain	7.2	7.5	-0.3	-1.1	100.0%	-4.3
6223	AT1G74110.1   Symbol: CYP78A10   cytochrome P450 family protein, similar to Cytochrome P450 78A4 (SP:O65012) Cytochrome P450 78A4 (Pinus radiata); similar to cytochrome P-450 GB:AAB37231 from (Phalaenopsis sp. SM9108)   chr1:27870328-27872029 REVERSE   Aliases: F2P9.2, F2P9_2	2.6	2.4	0.2	1.1	100.0%	-4.8
6224	AT2G04040.1   MATE efflux family protein, contains Pfam profile: PF01554 uncharacterized membrane protein family   chr2:1334515-1336485 REVERSE   Aliases: F3L12.13, F3L12_13	4.0	3.8	0.2	1.1	100.0%	-4.7
6225	AT1G32580.1   plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	5.9	6.4	-0.5	-1.1	100.0%	-4.0
6226	AT4G02250.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}, pistil-specific gene sts15 (Solanum tuberosum) GI:1616628; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.5	2.4	0.2	1.1	100.0%	-4.8
6227	AT5G44510.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:17946900-17951415 REVERSE   Aliases: MFC16.19, MFC16_19	3.3	3.5	-0.2	-1.1	100.0%	-4.6
6228	AT5G50160.1   ferric reductase-like transmembrane component family protein, contains Pfam profile PF01794: Ferric reductase like transmembrane component   chr5:20432997-20435930 FORWARD   Aliases: K6A12.2, K6A12_2	5.2	5.9	-0.7	-1.1	100.0%	-3.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6229	AT2G31500.1   Symbol: CPK24   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Arabidopsis thaliana) gi:836942:gb:AAA67655; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr2:13420841-13423613 FORWARD   Aliases: T28P16.1	3.0	2.8	0.2	1.1	100.0%	-5.0
6230	AT2G23740.1   similar to SET domain protein SDG117 [Zea mays] (GB:AAO32935.1); contains InterPro domain Nuclear protein Zn2+-binding (InterPro:IPR003606); contains InterPro domain Nuclear protein SET (InterPro:IPR001214); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087); contains InterPro domain Pre-SET (InterPro:IPR007728); contains InterPro domain SET-related region (InterPro:IPR003616)   chr2:10104639-10110478 FORWARD   Aliases: F27L4.8, F27L4_8	3.3	3.5	-0.2	-1.1	100.0%	-4.8
6231	AT1G07070.1   60S ribosomal protein L35a (RPL35aA), similar to ribosomal protein L35a GI:57118 from (Rattus norvegicus)   chr1:2168563-2169850 FORWARD   Aliases: F10K1.22, F10K1_22	8.6	9.1	-0.4	-1.1	100.0%	-4.1
6232	AT3G62930.1   glutaredoxin family protein, contains glutaredoxin domain, INTERPRO:IPR002109   chr3:23272513-23272821 REVERSE   Aliases: T20O10.30	3.2	3.0	0.2	1.1	100.0%	-4.7
6233	AT2G44840.1   Symbol: ATERF13   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr2:18502416-18503347 FORWARD   Aliases: ATERF13, T13E15.15	3.9	3.6	0.2	1.1	100.0%	-4.5
6234	AT1G74270.1   60S ribosomal protein L35a (RPL35aC), similar to ribosomal protein L33B GB:NP_014877 from (Saccharomyces cerevisiae)   chr1:27931917-27933158 REVERSE   Aliases: F1O17.6, F1O17_6	9.8	10.3	-0.5	-1.1	100.0%	-4.1
6235	AT5G65380.1   ripening-responsive protein, putative, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr5:26140215-26143665 REVERSE   Aliases: MNA5.11, MNA5_11	3.8	3.4	0.4	1.1	100.0%	-4.1
6236	AT3G15720.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Cucumis sativus) GI:6624205; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr3:5325297-5327544 REVERSE   Aliases: MSJ11.12	3.0	3.4	-0.4	-1.1	100.0%	-4.5
6237	AT5G64120.1   peroxidase, putative, identical to peroxidase (Arabidopsis thaliana) gi:1483222:emb:CAA67551   chr5:25676532-25678228 REVERSE   Aliases: MHJ24.10, MHJ24_10	2.9	3.7	-0.8	-1.1	100.0%	-4.0
6238	AT3G62060.1   pectinacylesterase family protein, similar to pectinacylesterase precursor GI:1431629 from (Vigna radiata); contains Pfam profile: PF03283 pectinacylesterase   chr3:22991031-22993919 FORWARD   Aliases: T17J13.20	4.8	5.3	-0.4	-1.1	100.0%	-4.1
6239	AT3G06810.1   acyl-CoA dehydrogenase-related, low similarity to acyl-CoA dehydrogenase (Acinetobacter sp. NCIMB9871) GI:14587418; contains Pfam profiles PF01636: Phosphotransferase enzyme family, PF00441: Acyl-CoA dehydrogenase C-terminal domain, PF02770: Acyl-CoA dehydrogenase middle domain   chr3:2146398-2150837 FORWARD   Aliases: AT3G06800, F3E22.5	4.4	4.7	-0.3	-1.1	100.0%	-4.4
6240	AT3G60410.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g25370.1); similar to P0519D04.26 [Oryza sativa (japonica cultivar-group)] (GB:NP_917004.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82551.1)   chr3:22342460-22344571 FORWARD   Aliases: T8B10.70	4.4	4.1	0.2	1.1	100.0%	-4.4
6241	AT1G03250.1   expressed protein   chr1:793353-795338 REVERSE   Aliases: F15K9.15, F15K9_15	5.5	5.1	0.4	1.1	100.0%	-4.2
6242	AT5G08200.1   peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	3.6	4.0	-0.4	-1.1	100.0%	-4.4
6243	AT5G06280.3   expressed protein, similar to unknown protein (pir::T08447)   chr5:1918282-1918897 REVERSE   Aliases: MHF15.20, MHF15_20	5.2	4.8	0.4	1.1	100.0%	-4.4
6244	AT2G16790.1   shikimate kinase family protein, similar to thermosensitive glucokinase from Escherichia coli (SP:P39208) (SP:P46859); contains Pfam profile PF01202: shikimate kinase   chr2:7291039-7292319 REVERSE   Aliases: T24I21.20, T24I21_20	7.2	6.7	0.6	1.1	100.0%	-4.2
6245	AT1G76200.1   expressed protein   chr1:28598144-28599636 FORWARD   Aliases: T23E18.30, T23E18_30	13.0	13.1	-0.1	-1.1	100.0%	-5.2
6246	AT4G10640.1   calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612   chr4:6571895-6574423 FORWARD   Aliases: T4F9.100, T4F9_100	4.3	3.9	0.4	1.1	100.0%	-4.2
6247	AT4G19430.1   expressed protein   chr4:10598456-10599155 REVERSE   Aliases: T5K18.210, T5K18_210	2.7	2.6	0.2	1.1	100.0%	-5.0
6248	AT1G65700.2   similar to small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative [Arabidopsis thaliana] (TAIR:At1g19120.1); similar to PREDICTED: similar to U6 snRNA-associated Sm-like protein LSm8 [Gallus gallus] (GB:XP_416009.1); contains InterPro domain Small nuclear ribonucleoprotein (Sm protein) (InterPro:IPR001163)   chr1:24437943-24439918 REVERSE   Aliases: F1E22.8, F1E22_8	9.2	9.6	-0.4	-1.1	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6249	AT2G15270.1   expressed protein   chr2:6644960-6646501 FORWARD   Aliases: F27O10.8, F27O10_8	7.4	8.2	-0.7	-1.1	100.0%	-4.1
6250	AT5G09380.1   DNA-directed RNA polymerase III RPC4 family protein, low similarity to SP:P25441 DNA-directed RNA polymerase III 47 kDa polypeptide (EC 2.7.7.6) (C53) (RNA polymerase C subunit 4) {Saccharomyces cerevisiae}; contains Pfam profile PF05132: RNA polymerase III RPC4   chr5:2911314-2913137 REVERSE   Aliases: T5E8.180, T5E8_180	4.7	4.5	0.2	1.1	100.0%	-4.4
6251	AT5G61820.1   expressed protein, MtN19, Medicago truncatula, EMBL:MTY15367   chr5:24851544-24853917 REVERSE   Aliases: MAC9.6, MAC9_6	10.3	10.0	0.3	1.1	100.0%	-4.5
6252	AT4G24680.1   expressed protein   chr4:12733435-12739747 FORWARD   Aliases: F22K18.120, F22K18_120	6.9	6.6	0.3	1.1	100.0%	-4.4
6253	AT2G43860.1   polygalacturonase, putative / pectinase, putative, similar to SP:P48979 Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) {Prunus persica}; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr2:18170022-18171505 REVERSE   Aliases: F18O19.3	3.5	3.2	0.3	1.1	100.0%	-4.5
6254	AT3G45480.1   zinc finger (C3HC4-type RING finger) family protein, contains a zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr3:16694189-16695577 REVERSE   Aliases: F9K21.60	3.0	3.1	-0.1	-1.1	100.0%	-5.2
6255	AT1G61520.2   Symbol: LHCA3*1   similar to chlorophyll A-B binding protein, putative (LHCA5) [Arabidopsis thaliana] (TAIR:At1g45474.1); similar to chlorophyll A-B binding protein, putative (LHCA5) [Arabidopsis thaliana] (TAIR:At1g45474.2); similar to probable chlorophyll a/b-binding protein type III precursor - garden pea chloroplast (GB:T06411); contains InterPro domain Chlorophyll A-B binding protein (InterPro:IPR001344)   chr1:22703738-22705048 FORWARD   Aliases: LHCA3*1, T25B24.12, T25B24_12	10.7	10.2	0.5	1.1	100.0%	-3.9
6256	AT2G01590.1   expressed protein   chr2:266648-267797 FORWARD   Aliases: F2I9.21, F2I9_21	3.4	3.7	-0.3	-1.1	100.0%	-4.6
6257	AT2G44950.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:18549369-18555666 REVERSE   Aliases: AT2G44960, T14P1.25, T14P1_25	4.9	4.7	0.2	1.1	100.0%	-4.7
6258	AT3G26710.1   expressed protein   chr3:9814763-9815987 FORWARD   Aliases: MLJ15.10	6.7	6.3	0.4	1.1	100.0%	-4.3
6259	AT1G02460.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:504673-507204 REVERSE   Aliases: T6A9.22	4.1	3.9	0.2	1.1	100.0%	-4.4
6260	AT1G74710.2   Symbol: ICS1   isochorismate synthase 1 (ICS1) / isochorismate mutase, identical to GI:17223087 and GB:AF078080; contains Pfam profile PF00425: chorismate binding enzyme; contains TIGRfam profile TIGR00543: isochorismate synthases; identical to cDNA isochorismate synthase 1 precursor (ICS1) nuclear gene for plastid product GI:17223086   chr1:28073957-28077779 FORWARD   Aliases: EDS16, F25A4.31, ISOCHORISMATE SYNTHASE, ISOCHORISMATE SYNTHASEI, SALICYLIC ACID INDUCTION DEFICIENT 2, SID2	3.5	3.8	-0.4	-1.1	100.0%	-4.1
6261	AT4G24470.2   Symbol: ZIM   zinc finger (GATA type) protein ZIM (ZIM), identical to zinc-finger protein expressed in Inflorescence Meristem, ZIM gi:8918533 from (Arabidopsis thaliana)   chr4:12645600-12647950 FORWARD   Aliases: T22A6.300, T22A6_300	10.2	9.7	0.5	1.1	100.0%	-4.3
6262	AT4G19640.1   Symbol: ARA7   Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB5A GI:1370178 from (Lotus japonicus)   chr4:10687258-10689621 REVERSE   Aliases: F24J7.190, F24J7_190	11.2	10.6	0.6	1.1	100.0%	-4.7
6263	AT1G12520.3   Symbol: CCS1   similar to superoxide dismutase (Cu-Zn), chloroplast (SODCP) / copper/zinc superoxide dismutase (CSD2) [Arabidopsis thaliana] (TAIR:At2g28190.1); similar to putative copper/zinc superoxide dismutase copper chaperone precursor [Lycopersicon esculentum] (GB:AAD12307.2); contains InterPro domain Copper/Zinc superoxide dismutase (InterPro:IPR001424)   chr1:4267104-4268884 REVERSE   Aliases: ATCCS, COPPER/ZINC SUPEROXIDE DISMUTASE COPPER CHAPERONE, F5O11.26, F5O11_26	9.0	9.5	-0.5	-1.1	100.0%	-4.4
6264	AT1G13910.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0A (Lycopersicon esculentum) gi:3894385:gb:AAC78592	4.3	4.0	0.3	1.1	100.0%	-4.1
6265	AT1G06500.2   expressed protein   chr1:1989485-1990727 FORWARD   Aliases: F12K11.25, F12K11_25	7.6	7.2	0.5	1.1	100.0%	-4.1
6266	AT4G38220.2   aminoacylase, putative / N-acyl-L-amino-acid amidohydrolase, putative, similar to aminoacylase-1 (N-acyl-L-amino-acid amidohydrolase, ACY-1)(Homo sapiens) SWISS-PROT:Q03154   chr4:17925174-17927091 FORWARD   Aliases: F20D10.340, F20D10_340	9.5	9.2	0.4	1.1	100.0%	-4.4
6267	AT5G10730.1   expressed protein   chr5:3390615-3393107 REVERSE   Aliases: MAJ23.90, MAJ23_90	8.4	8.9	-0.5	-1.1	100.0%	-4.1
6268	AT2G31980.1   cysteine proteinase inhibitor-related, contains similarity to extracellular insoluble cystatin GI:2204077 from (Daucus carota)   chr2:13616174-13616979 REVERSE   Aliases: F22D22.27, F22D22_27	4.2	4.5	-0.3	-1.1	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6269	AT5G09820.2   similar to plastid-lipid associated protein PAP / fibrillin family protein [Arabidopsis thaliana] (TAIR:At3g26070.1); similar to fibrillin [Thermosynechococcus elongatus BP-1] (GB:NP_681209.1); contains InterPro domain PAP fibrillin (InterPro:IPR006843)   chr5:3055892-3057445 REVERSE   Aliases: MYH9.3, MYH9_3	3.7	4.0	-0.3	-1.1	100.0%	-4.5
6270	AT1G05380.1   PHD finger transcription factor, putative   chr1:1578784-1582613 FORWARD   Aliases: T25N20.3, T25N20_3	5.5	5.1	0.4	1.1	100.0%	-4.3
6271	AT5G40640.1   expressed protein   chr5:16294270-16297652 FORWARD   Aliases: MNF13.19, MNF13_19	3.9	4.1	-0.2	-1.1	100.0%	-4.5
6272	AT1G32070.2   GCN5-related N-acetyltransferase (GNAT) family protein / nuclear shuttle interacting protein (NSI), very low similarity to SP:P09453 Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) {Escherichia coli}; contains Pfam profile PF00583: acetyltransferase, GNAT family; PMID 12837950; identical to cDNA nuclear shuttle interacting protein (NSI) GI: 30790420   chr1:11534664-11536318 REVERSE   Aliases: T12O21.3, T12O21_3	7.4	7.1	0.3	1.1	100.0%	-4.4
6273	AT1G76850.1   expressed protein   chr1:28852845-28859393 FORWARD   Aliases: F7O12.2, F7O12_2	4.1	4.6	-0.5	-1.1	100.0%	-4.3
6274	AT3G57710.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:21396936-21398376 REVERSE   Aliases: F15B8.100	4.2	4.4	-0.2	-1.1	100.0%	-4.6
6275	AT4G03230.1   S-locus lectin protein kinase family protein, contains Pfam domins, PF00069: Protein kinase domain, PF00954: S-locus glycoprotein family and PF01453: Lectin (probable mannose binding)   chr4:1419278-1422828 REVERSE   Aliases: F4C21.16, F4C21_16	5.9	6.6	-0.6	-1.1	100.0%	-4.3
6276	AT1G68790.1   expressed protein   chr1:25838372-25842982 REVERSE   Aliases: F14K14.10, F14K14_10	9.1	10.0	-0.8	-1.1	100.0%	-4.2
6277	AT2G01580.1   expressed protein, and genefinder   chr2:265043-265904 REVERSE   Aliases: F2I9.20, F2I9_20	4.7	5.3	-0.6	-1.1	100.0%	-4.2
6278	AT4G25990.2   Symbol: CIL   expressed protein	2.6	2.5	0.1	1.1	100.0%	-5.0
6279	AT4G16610.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr4:9354343-9355309 REVERSE   Aliases: DL4330C, FCAALL.418	3.6	3.8	-0.3	-1.1	100.0%	-4.3
6280	AT1G22050.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr1:7771659-7773640 FORWARD   Aliases: F2E2.12, F2E2_12	8.6	8.0	0.5	1.1	100.0%	-4.3
6281	AT1G19240.1   expressed protein   chr1:6649089-6650411 REVERSE   Aliases: T29M8.11, T29M8_11	8.5	8.1	0.4	1.1	100.0%	-4.1
6282	AT3G59100.1   Symbol: ATGSL11   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr3:21854384-21864837 FORWARD   Aliases: F17J16.150, GLUCAN SYNTHASE LIKE 11, GSL11	6.1	5.8	0.3	1.1	100.0%	-4.5
6283	AT1G79950.1   helicase-related, similar to BRCA1-binding helicase-like protein BACH1 (GI:13661819) Homo sapiens.; contains similarity to helicase-like protein NHL GI:6969265 from (Homo sapiens)   chr1:30078473-30084430 FORWARD   Aliases: F18B13.3, F18B13_3	7.1	7.8	-0.7	-1.1	100.0%	-4.4
6284	AT3G16530.1   legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain   chr3:5624383-5625476 REVERSE   Aliases: MDC8.19	3.1	3.4	-0.2	-1.1	100.0%	-4.3
6285	AT4G04870.1   CDP-alcohol phosphatidyltransferase family protein, similar to SP:Q07560 Cardiolipin synthetase (EC 2.7.8.-) {Saccharomyces cerevisiae; contains Pfam profile PF01066: CDP-alcohol phosphatidyltransferase   chr4:2461211-2464141 REVERSE   Aliases: T4B21.19, T4B21_19	8.3	8.7	-0.4	-1.1	100.0%	-4.1
6286	AT3G54890.3   Symbol: LHCA1   chlorophyll A-B binding protein / LHCI type I (CAB), identical to chlorophyll A/B-binding protein (Arabidopsis thaliana) GI:16207; contains Pfam profile: PF00504 chlorophyll A-B binding protein   chr3:20350482-20351968 REVERSE   Aliases: F28P10.130, F28P10_130, LHCA1	11.7	11.3	0.4	1.1	100.0%	-3.9
6287	AT4G19380.1   alcohol oxidase-related, similar to long chain fatty alcohol oxidase from Candida cloacae (GI:6983581), Candida tropicalis (GI:6983594)   chr4:10568376-10572423 REVERSE   Aliases: T5K18.160, T5K18_160	2.7	2.5	0.2	1.1	100.0%	-4.7
6288	AT5G14080.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:4543137-4545258 REVERSE   Aliases: MUA22.8, MUA22_8	5.2	5.5	-0.3	-1.1	100.0%	-4.5
6289	AT5G11820.1   expressed protein, self-incompatibility protein S3 precursor, Papaver rhoeas cv., PIR:S69186   chr5:3810650-3811177 REVERSE   Aliases: F14F18.2	2.0	1.9	0.1	1.1	100.0%	-5.2
6290	AT1G47970.1   expressed protein   chr1:17690940-17692485 FORWARD   Aliases: T2J15.12, T2J15_12	7.9	7.5	0.4	1.1	100.0%	-4.6
6291	AT1G13940.1   expressed protein   chr1:4762700-4766746 REVERSE   Aliases: F16A14.15	4.6	4.9	-0.3	-1.1	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6292	AT4G00350.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 ( <i>Lycopersicon esculentum</i> ) GI:12231296; contains Pfam profile PF01554 Uncharacterized membrane protein family   chr4:151919-154130 FORWARD   Aliases: A_IG005I10.20, A_IG005I10_20, F5I10.20, F5I10_20	2.6	2.4	0.2	1.1	100.0%	-4.8
6293	AT3G10010.1   HhH-GPD base excision DNA repair family protein, similar to DEMETER protein ( <i>Arabidopsis thaliana</i> ) GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein   chr3:3081819-3088200 REVERSE   Aliases: T22K18.18	2.7	2.9	-0.2	-1.1	100.0%	-4.6
6294	AT3G46130.2   Symbol: MYB111	7.6	7.1	0.4	1.1	100.0%	-4.1
6295	AT4G05080.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.3	2.4	-0.1	-1.1	100.0%	-5.1
6296	AT2G30790.1   photosystem II oxygen-evolving complex 23, putative, expression not detected; similar to SP:O49344 (GI:28800560 (OEC23) <i>Arabidopsis</i> ; Non-identical EST and protein matches suggested a possible frameshift in exon 1 (a 4 base deletion between 73745 and 73746) and a different start for exon 2 (base 73645).   chr2:13126124-13127167 REVERSE   Aliases: T11J7.18, T11J7_18	3.4	3.2	0.2	1.1	100.0%	-4.5
6297	AT5G53960.1   expressed protein   chr5:21924951-21925678 FORWARD   Aliases: K19P17.13, K19P17_13	2.2	2.1	0.1	1.1	100.0%	-5.5
6298	AT3G21110.2   Symbol: PUR7   similar to SAICAR synthetase [ <i>Nicotiana tabacum</i> ] (GB:AAR06292.1); contains InterPro domain SAICAR synthetase (InterPro:IPR001636)   chr3:7402141-7405614 REVERSE   Aliases: 5' PHOSPHORIBOSYL 4 (N SUCCINOCARBOXAMIDE) 5 AMINOIMIDAZOLE SYNTHETASE, MSA6.26, PURC, SAICAR SYNTHETASE	8.8	9.2	-0.4	-1.1	100.0%	-4.0
6299	AT1G77690.1   amino acid permease, putative, similar to AUX1 (regulator of root gravitropism, putative permease) GI:1531758 GB:CAA67308 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:29205835-29208234 REVERSE   Aliases: T32E8.2, T32E8_2	5.4	5.9	-0.5	-1.1	100.0%	-4.3
6300	ATCG00020.1   Symbol: PSBA   Encodes chlorophyll binding protein D1, a part of the photosystem II reaction center core   chrC:383-1444 REVERSE   Aliases: PSBA	12.0	11.0	1.1	1.1	100.0%	-3.9
6301	AT2G29660.1   zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	6.4	6.1	0.3	1.1	100.0%	-4.4
6302	AT1G71750.1   phosphoribosyltransferase family protein, similar to SP:Q02522 Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8) (HGPRT) (HGPRTase) { <i>Lactococcus lactis</i> }; contains Pfam profile PF00156: Phosphoribosyl transferase domain   chr1:26991465-26992822 REVERSE   Aliases: F14O23.13, F14O23_13	5.4	5.8	-0.4	-1.1	100.0%	-4.3
6303	AT1G15810.1   ribosomal protein S15 family protein, contains similarity to ribosomal protein S15   chr1:5444413-5447229 FORWARD   Aliases: F7H2.15, F7H2_15	5.9	6.5	-0.6	-1.1	100.0%	-4.2
6304	AT5G02620.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr5:589525-591675 FORWARD   Aliases: T22P11.210, T22P11_210	4.5	4.3	0.2	1.1	100.0%	-4.3
6305	AT5G49480.1   Symbol: ATPC1   sodium-inducible calcium-binding protein (ACP1) / sodium-responsive calcium-binding protein (ACP1), identical to NaCl-inducible Ca <sup>2+</sup> -binding protein GI:2352828 from ( <i>Arabidopsis thaliana</i> )   chr5:20087969-20088864 FORWARD   Aliases: ACP1, K6M13.2, K6M13_2	8.2	7.8	0.4	1.1	100.0%	-4.2
6306	AT2G34780.1   Symbol: EMB1611   expressed protein   chr2:14675732-14680686 FORWARD   Aliases: EMB1611, EMBRYO DEFECTIVE 1611, F19I3.1, F19I3_1	4.7	4.9	-0.3	-1.1	100.0%	-4.5
6307	AT1G77670.1   aminotransferase class I and II family protein, similar to kynurenine aminotransferase /glutamine transaminase K GI:1030066 ( <i>Rattus norvegicus</i> )   chr1:29193795-29195869 REVERSE   Aliases: T5M16.26, T5M16_26	8.2	8.9	-0.7	-1.1	100.0%	-3.8
6308	AT3G56480.1   myosin heavy chain-related, contains weak similarity to Myosin heavy chain, cardiac muscle alpha isoform (MyHC-alpha) (Alpha isomyosin) (Fragment) (Swiss-Prot:P04460) ( <i>Oryctolagus cuniculus</i> )   chr3:20947077-20950609 REVERSE   Aliases: T5P19.130	2.3	2.5	-0.2	-1.1	100.0%	-4.9
6309	AT1G16180.1   TMS membrane family protein / tumour differentially expressed (TDE) family protein, contains Pfam domain, PF03348: TMS membrane protein/tumour differentially expressed protein (TDE)   chr1:5540899-5542896 FORWARD   Aliases: T24D18.26, T24D18_26	9.7	9.1	0.7	1.1	100.0%	-4.5
6310	AT3G18420.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile: PF00515 tetratricopeptide repeat domain (TPR domain)   chr3:6324639-6325799 REVERSE   Aliases: MYF24.14	7.1	7.7	-0.6	-1.1	100.0%	-4.0
6311	AT1G22720.1   wall-associated kinase, putative, contains similarity to serine/threonine kinase gb:Y12531 from <i>Brassica oleracea</i>   chr1:8044221-8045654 REVERSE   Aliases: T22J18.11, T22J18_11	3.1	3.0	0.2	1.1	100.0%	-4.9
6312	AT3G28890.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0B ( <i>Lycopersicon esculentum</i> ) gi:3894387:gb:AAC78593	2.8	2.7	0.1	1.1	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6313	AT5G44630.1   Encodes a sesquiterpene synthase involved in generating all of the group B sesquiterpenes found in the Arabidopsis floral volatile blend. Strongly expressed in intrafloral nectaries.   chr5:18020507-18022843 FORWARD   Aliases: K15C23.7, K15C23_7	3.0	2.7	0.2	1.1	100.0%	-4.7
6314	AT1G67830.1   GDSL-motif lipase/hydrolase family protein, similar to early nodulin ENOD8 (Medicago sativa) GI:304037, elicitor-induced glycoprotein iEP4 (Daucus carota) GI:1911765, lanatoside 15'-O-acetylerase (Digitalis lanata) GI:3688284; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr1:25434992-25436635 REVERSE   Aliases: F12A21.4, F12A21_4	5.5	5.8	-0.3	-1.1	100.0%	-4.1
6315	AT4G11240.1   Symbol: TOPP7   serine/threonine protein phosphatase PP1 isozyme 6 (PP1BG) (TOPP6), identical to SP:P48486 Serine/threonine protein phosphatase PP1 isozyme 6 (EC 3.1.3.16) {Arabidopsis thaliana}   chr4:6847115-6849237 FORWARD   Aliases: F8L21.30, F8L21_30	5.1	5.6	-0.5	-1.1	100.0%	-4.1
6316	AT3G47540.1   chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus)   chr3:17532014-17533254 FORWARD   Aliases: F1P2.90	6.1	6.4	-0.4	-1.1	100.0%	-4.5
6317	AT2G40690.1   Symbol: SFD1   NAD-dependent glycerol-3-phosphate dehydrogenase family protein, low similarity to SP:Q26756 Glycerol-3-phosphate dehydrogenase (NAD+), glycosomal (EC 1.1.1.8) {Trypanosoma brucei rhodesiense}; contains Pfam profile PF01210: NAD-dependent glycerol-3-phosphate dehydrogenase   chr2:16981107-16983517 FORWARD   Aliases: SUPPRESSOR OF FATTY ACID DESATURASE DEFICIENCY 1, T7D17.13, T7D17_13	3.4	3.7	-0.3	-1.1	100.0%	-4.4
6318	ATCG00700.1   Symbol: PSBN   PSII low MW protein   chrC:74249-74380 REVERSE   Aliases: PSBN	3.7	3.3	0.4	1.1	100.0%	-4.3
6319	AT5G09640.1   Symbol: SNG2   sinapoylglucose:choline sinapoyltransferase (SNG2), GC donor splice site at exon 11 and 13; TA donor splice site at exon 10; similar to serine carboxypeptidase I precursor (SP:P37890) (Oryza sativa); wound-inducible carboxypeptidase, Lycopersicon esculentum, EMBL:AF242849; contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:choline sinapoyltransferase (SNG2) GI:15418806   chr5:2988315-2991157 FORWARD   Aliases: F17114.170, F17114_170, SCPL19, SINAPOYLGLUCOSE ACCUMULATOR 2	3.2	3.3	-0.2	-1.1	100.0%	-4.8
6320	AT4G29735.1   expressed protein, contains Pfam domain PF05251: Uncharacterised protein family (UPF0197)   chr4:14562645-14564384 REVERSE   Aliases: None	10.9	10.4	0.5	1.1	100.0%	-4.3
6321	AT1G29940.1   Symbol: NRPA2   similar to DNA-directed RNA polymerase, putative [Arabidopsis thaliana] (TAIR:At5g45140.1); similar to hypothetical protein UM01133.1 [Ustilago maydis 521] (GB:EAK81692.1); similar to unnamed protein product [Debaryomyces hansenii CBS767] (GB:CAG89744.1); similar to SPBP23A10.07 [Schizosaccharomyces pombe] (GB:CAB66435.1); similar to hypothetical protein CaO19.7062 [Candida albicans SC5314] (GB:EAL01509.1); similar to putative DNA-directed RNA polymerase I subunit, 5'-partial [Oryza sativa (japonica cultivar-group)] (GB:AAM92814.1); contains InterPro domain RNA polymerase Rpb2, domain 3 (InterPro:IPR007645); contains InterPro domain RNA polymerase Rpb2, domain 7 (InterPro:IPR007641); contains InterPro domain RNA polymerase beta subunit (InterPro:IPR007644); contains InterPro domain RNA polymerase Rpb2, domain 2 (InterPro:IPR007642); contains InterPro domain RNA polymerase Rpb2, domain 6 (InterPro:IPR007120); contains InterPro domain RNA polymerase, beta subunit (InterPro:IPR007121)   chr1:10479170-10486803 REVERSE   Aliases: F1N18.2	7.2	7.7	-0.5	-1.1	100.0%	-4.0
6322	AT3G08980.1   signal peptidase I family protein, similar to SP:P46972 Mitochondrial inner membrane protease subunit 2 (EC 3.4.99.-) {Saccharomyces cerevisiae}; contains Pfam profile PF00461: Signal peptidase I   chr3:2740813-2742690 FORWARD   Aliases: T16O11.6	4.6	5.0	-0.4	-1.1	100.0%	-4.0
6323	AT5G07950.1   expressed protein, ferredoxin (2Fe-2S), Arabidopsis thaliana, PIR:B71412	4.2	4.0	0.2	1.1	100.0%	-4.6
6324	AT3G63220.2   kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	5.6	5.3	0.3	1.1	100.0%	-4.3
6325	AT3G18210.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily   chr3:6237936-6240611 REVERSE   Aliases: MRC8.21	5.9	6.4	-0.5	-1.1	100.0%	-3.9
6326	AT4G16040.1   hypothetical protein   chr4:9087194-9087466 REVERSE   Aliases: DL4060C, FCAALL.265	2.1	2.1	0.1	1.1	100.0%	-5.6
6327	AT2G42750.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to GFA2 (Arabidopsis thaliana) GI:21429604; contains Pfam profile PF00226: DnaJ domain   chr2:17800384-17802757 FORWARD   Aliases: F7D19.25, F7D19_25	5.5	5.1	0.4	1.1	100.0%	-4.1
6328	AT5G16550.1   expressed protein   chr5:5405468-5406887 FORWARD   Aliases: MQK4.30, MQK4_30	6.3	5.8	0.6	1.1	100.0%	-4.3
6329	AT5G44290.3   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g03740.1); similar to putative CRK1 protein [Oryza sativa (japonica cultivar-group)] (GB:XP_479750.1); similar to putative CRK1 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD89473.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:17857651-17860824 REVERSE   Aliases: K9L2.5, K9L2_5	5.4	5.0	0.4	1.1	100.0%	-4.1
6330	AT5G49940.1   Symbol: NFU2   nitrogen fixation NifU-like family protein, similar to Nitrogen fixation protein nifU (SP:Q43885) {Anabaena azollae}; contains Pfam profile: PF01106 NifU-like domain   chr5:20332639-20334626 FORWARD   Aliases: ATCNFU2, K9P8.16	7.7	7.3	0.3	1.1	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6331	AT4G23330.1   eukaryotic translation initiation factor-related, contains weak similarity to Swiss-Prot:Q9LD55 eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (Eukaryotic translation initiation factor 3 large subunit) (eIF3a) (p114) (Arabidopsis thaliana)   chr4:12192146-12194620 FORWARD   Aliases: F16G20.30	3.6	3.3	0.3	1.1	100.0%	-4.2
6332	AT1G54570.1   esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379   chr1:20384145-20388688 REVERSE   Aliases: T22H22.2, T22H22_2	7.2	6.9	0.3	1.1	100.0%	-4.2
6333	AT1G73920.2   lipase family protein, similar to lipase GB:CAA74737 (SP:O46108) from (Drosophila melanogaster)   chr1:27794537-27798575 FORWARD   Aliases: F2P9.21, F2P9_21	5.8	6.3	-0.4	-1.1	100.0%	-4.0
6334	AT3G29320.1   glucan phosphorylase, putative, similar to alpha-glucan phosphorylase, L isozyme 1 precursor GB:P04045 from (Solanum tuberosum) (J. Biochem. 106 (4), 691-695 (1989))   chr3:11254059-11259051 FORWARD   Aliases: MUO10.17	9.1	9.6	-0.5	-1.1	100.0%	-4.0
6335	AT3G13480.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g55475.1); similar to P0415C01.14 [Oryza sativa (japonica cultivar-group)] (GB:NP_917459.1)	7.5	6.9	0.6	1.1	100.0%	-4.4
6336	AT1G61700.1   DNA-directed RNA polymerase II, putative (RPB10), identical to SP:Q9SYA6 DNA-directed RNA polymerase II 8.2 kDa polypeptide (EC 2.7.7.6) (RPB10) (RP10) (ABC10) {Arabidopsis thaliana}; very strong similarity to SP:Q39290 DNA-directed RNA polymerase II 8.2 kDa polypeptide {Brassica napus}; contains Pfam profile: PF01194 RNA polymerases N / 8 kDa subunit   chr1:22790770-22791777 FORWARD   Aliases: T13M11.6, T13M11_6	2.9	2.7	0.1	1.1	100.0%	-4.9
6337	AT2G37410.2   Symbol: ATTIM17 2   mitochondrial import inner membrane translocase (TIM17), nearly identical to SP:Q9SP35 Mitochondrial import inner membrane translocase subunit TIM17 {Arabidopsis thaliana}	10.5	9.8	0.7	1.1	100.0%	-4.3
6338	AT5G16930.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family   chr5:5568396-5571958 FORWARD   Aliases: F2K13.80, F2K13_80	3.0	3.2	-0.2	-1.1	100.0%	-4.7
6339	AT1G70570.1   anthranilate phosphoribosyltransferase, putative, similar to anthranilate phosphoribosyltransferase (EC 2.4.2.18) SP:O66576 from (Aquifex aeolicus)   chr1:26612290-26615947 FORWARD   Aliases: F24J13.14, F24J13_14	7.0	6.6	0.4	1.1	100.0%	-4.3
6340	AT4G15770.1   60S ribosome subunit biogenesis protein, putative, contains similarity to 60S ribosome subunit biogenesis protein NIP7 (Swiss-Prot:Q08962) (Saccharomyces cerevisiae)   chr4:8978009-8978877 FORWARD   Aliases: DL3925W, FCAALL.377	8.9	9.1	-0.2	-1.1	100.0%	-4.7
6341	AT3G61760.1   dynamin-like protein B (DL1B), identical to dynamin-like protein B (Arabidopsis thaliana) GI:27543504; strong similarity to GTP-binding protein (Arabidopsis thaliana) GI:807577, phragmoplastin SDL5A (Glycine max) GI:1218004; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain   chr3:22871489-22875128 REVERSE   Aliases: ADL1B, F21F14.15	4.2	4.5	-0.3	-1.1	100.0%	-4.4
6342	AT4G01810.1   protein transport protein-related, related to Sec23 protein (Homo sapiens) gi:1296664:emb:CAA65774   chr4:776488-780331 REVERSE   Aliases: T7B11.7, T7B11_7	3.8	4.3	-0.4	-1.1	100.0%	-4.2
6343	AT2G37390.1   heavy-metal-associated domain-containing protein, contains Pfam PF00403: Heavy-metal-associated domain; similar to copper homeostasis factor (CCH) (ATX1) (GB:U88711) (TIGR_Ath1:At3g56240) (Arabidopsis thaliana)   chr2:15701299-15702904 FORWARD   Aliases: F3G5.18, F3G5_18	3.0	2.8	0.2	1.1	100.0%	-4.8
6344	AT5G20640.1   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr5:6984381-6985207 FORWARD   Aliases: T1M15.40, T1M15_40	5.9	5.5	0.4	1.1	100.0%	-4.4
6345	AT3G27310.1   Symbol: PUX1   expressed protein   chr3:10088438-10090338 REVERSE   Aliases: K17E12.13, PLANT UBX DOMAIN CONTAINING PROTEIN 1	7.0	6.7	0.3	1.1	100.0%	-4.4
6346	AT3G59060.4   Symbol: PIL6   similar to phytochrome-interacting factor 4 (PIF4) / basic helix-loop-helix protein 9 (bHLH9) / short under red-light 2 (SRL2) [Arabidopsis thaliana] (TAIR:At2g43010.1); similar to BP-5 protein [Oryza sativa] (GB:CAD32238.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr3:21838955-21841484 REVERSE   Aliases: F17J16.110, PHYTOCHROME INTERACTING FACTOR 3 LIKE 6, PHYTOCHROME INTERACTING FACTOR 5, PIF5	2.9	2.7	0.2	1.1	100.0%	-4.9
6347	AT3G53580.1   diaminopimelate epimerase family protein, contains Pfam profile PF01678: Diaminopimelate epimerase   chr3:19875742-19878112 FORWARD   Aliases: F4P12.280	10.7	11.0	-0.2	-1.1	100.0%	-4.5
6348	AT4G36760.2   Symbol: ATAPP1	6.9	7.5	-0.6	-1.1	100.0%	-4.3
6349	AT3G63000.1   NPL4 family protein, contains Pfam domain, PF05021: NPL4 family   chr3:23294584-23296515 FORWARD   Aliases: T20O10.100	9.1	9.4	-0.3	-1.1	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6350	AT5G25280.2   serine-rich protein-related, contains some similarity to serine-rich proteins   chr5:8773795-8776003 FORWARD   Aliases: F18G18.20, F18G18_20	5.6	5.0	0.6	1.1	100.0%	-3.9
6351	AT5G54840.2   GTP-binding family protein, similar to SP:P87027 Septum-promoting GTP-binding protein 1 (GTPase spg1)(Sid3 protein) {Schizosaccharomyces pombe}   chr5:22293856-22295643 REVERSE   Aliases: MBG8.10, MBG8_10	7.0	6.5	0.5	1.1	100.0%	-4.4
6352	AT1G76820.1   expressed protein   chr1:28842467-28843745 FORWARD   Aliases: F28O16.19, F28O16_19	8.3	7.5	0.7	1.1	100.0%	-3.9
6353	AT4G24880.1   expressed protein   chr4:12808530-12811383 FORWARD   Aliases: F13M23.20, F13M23_20	6.0	5.7	0.3	1.1	100.0%	-4.2
6354	AT2G30650.1   3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative, strong similarity to gi:8572760; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein   chr2:13060854-13063457 REVERSE   Aliases: T11J7.4, T11J7_4	2.4	2.2	0.1	1.1	100.0%	-5.2
6355	AT2G28610.1   Symbol: PRS   homeobox-leucine zipper transcription factor (PRESSED FLOWER), identical to PRESSED FLOWER (GP:17907768) {Arabidopsis thaliana}   chr2:12269090-12270492 FORWARD   Aliases: PRESSED FLOWER, T8O18.10, T8O18_10	2.5	2.7	-0.2	-1.1	100.0%	-4.8
6356	AT1G43560.1   thioredoxin family protein, contains Pfam profile: PF00085 Thioredoxin; similar to thioredoxin GI:142153 from (Synechococcus PCC6301)   chr1:16400539-16402318 REVERSE   Aliases: AT1G43565, T10P12.4, T10P12_4	6.2	6.8	-0.6	-1.1	100.0%	-3.8
6357	AT5G11680.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr5:3758859-3760848 FORWARD   Aliases: T22P22.70, T22P22_70	9.4	9.1	0.3	1.1	100.0%	-4.4
6358	AT3G30180.1   Symbol: BR6OX2/CYP85A2	2.9	3.1	-0.2	-1.1	100.0%	-4.6
6359	AT4G24520.1   Symbol: ATR1   NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative, similar to NADPH-ferrihemoprotein reductase NADPH-cytochrome P450 oxydo-reductase isoform 1 (Populus balsamifera subsp. trichocarpa x Populus deltoides) GI:13183562, SP:P37116 NADPH-cytochrome P450 reductase (EC 1.6.2.4) (CPR) (Vigna radiata) {Phaseolus aureus}   chr4:12662851-12667165 REVERSE   Aliases: AR1, ARABIDOPSIS CYTOCHROME REDUCTASE, ARABIDOPSIS P450 REDUCTASE 1, F22K18.280, F22K18_280	5.7	6.2	-0.5	-1.1	100.0%	-4.0
6360	AT1G06390.2   Symbol: GSK1   shaggy-related protein kinase iota / ASK-iota (ASK9) (GSK1), identical to shaggy-related protein kinase iota (ASK-iota) (Arabidopsis thaliana) SWISS-PROT:Q39012	4.4	5.0	-0.6	-1.1	100.0%	-4.3
6361	AT5G08040.1   expressed protein   chr5:2577203-2578120 REVERSE   Aliases: T22D6.2	10.0	10.5	-0.5	-1.1	100.0%	-4.3
6362	AT1G07260.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:2227593-2229318 REVERSE   Aliases: F10K1.3, F10K1_3	4.9	5.2	-0.3	-1.1	100.0%	-4.3
6363	AT5G17830.1   expressed protein, contains Pfam domain, PF04515: Protein of unknown function, DUF580   chr5:5893384-5895369 FORWARD   Aliases: MVA3.19, MVA3_19	2.2	2.4	-0.1	-1.1	100.0%	-5.0
6364	AT5G67370.1   expressed protein, similar to unknown protein (gb:AAC18972.1)   chr5:26894794-26896768 REVERSE   Aliases: K8K14.9, K8K14_9	7.8	7.5	0.3	1.1	100.0%	-4.4
6365	AT3G11520.1   Symbol: CYCB1;3   cyclin, putative (CYC2), similar to cyclin (Arabidopsis thaliana) GI:1360646; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain; identical to cDNA cyclin box (cyc2) partial cds GI:456019   chr3:3625330-3627236 REVERSE   Aliases: CYC2, CYCLIN B1;3, F24K9.20	3.3	3.8	-0.5	-1.1	100.0%	-4.2
6366	NA	11.1	10.9	0.2	1.1	100.0%	-4.7
6367	AT2G20560.1   DNAJ heat shock family protein, SP:Q9UDY4 DnaJ homolog subfamily B member 4 (Heat shock 40 kDa protein 1 homolog) {Homo sapiens}; contains Pfam profile PF00226: DnaJ domain   chr2:8855211-8857051 REVERSE   Aliases: T13C7.15, T13C7_15	8.0	7.4	0.6	1.1	100.0%	-3.9
6368	AT5G37050.1   expressed protein, hypothetical protein T28J14.60 - Arabidopsis thaliana, PIR:T48483   chr5:14657740-14658651 REVERSE   Aliases: MJG14.3	2.4	2.3	0.1	1.1	100.0%	-5.2
6369	AT5G28920.1   expressed protein   chr5:10940039-10943382 REVERSE   Aliases: F7P1.1	4.7	4.3	0.4	1.1	100.0%	-4.1
6370	AT3G19860.2   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At4g36060.1); similar to putative amelogenin precursor [Oryza sativa] (GB:XP_470739.1); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr3:6903839-6906127 FORWARD   Aliases: MPN9.10	6.1	5.6	0.5	1.1	100.0%	-4.2
6371	AT4G13140.1   expressed protein   chr4:7650322-7651141 REVERSE   Aliases: F17N18.30, F17N18_30	8.6	8.1	0.4	1.1	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6372	AT4G32260.1   ATP synthase family, contains Pfam profile: PF00430 ATP synthase B/B' CF(0); identical to cDNA chloroplast ATP synthase beta chain precursor (atpG) GI:5730140   chr4:15573643-15574743 REVERSE   Aliases: F10M6.100, F10M6_100	7.9	7.0	0.9	1.1	100.0%	-3.9
6373	AT1G14910.1   epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Chain A, Calm-N N-Terminal Domain Of Clathrin Assembly Lymphoid Myeloid Leukaemia Protein, Pi(4,5)p2 Complex (GP:13399999) {Homo sapiens}   chr1:5139707-5143680 REVERSE   Aliases: F10B6.32, F10B6_32	5.8	5.4	0.4	1.1	100.0%	-4.2
6374	AT5G02370.1   kinesin motor protein-related, kinesin, <i>Xenopus laevis</i> , EMBL:XLA249840   chr5:503406-506922 FORWARD   Aliases: T1E22.130, T1E22_130	4.5	4.9	-0.4	-1.1	100.0%	-4.3
6375	AT4G11220.1   reticulon family protein (RTNLB2), similar to SP:Q64548 Reticulon 1 (Neuroendocrine-specific protein) { <i>Rattus norvegicus</i> }; contains Pfam profile PF02453: Reticulon   chr4:6837946-6839791 REVERSE   Aliases: F8L21.10, F8L21_10	9.0	8.6	0.5	1.1	100.0%	-4.4
6376	AT3G48720.1   transferase family protein, similar to hypersensitivity-related hsr201 protein - <i>Nicotiana tabacum</i> , PIR2:T03274; contains Pfam transferase family domain PF00248   chr3:18057308-18060437 FORWARD   Aliases: T8P19.230	3.3	3.1	0.2	1.1	100.0%	-4.6
6377	AT4G19710.2   bifunctional aspartate kinase/homoserine dehydrogenase, putative / AK-HSDH, putative, similar to gb:X71364 (PIR:S46497) aspartate kinase / homoserine dehydrogenase from <i>Arabidopsis thaliana</i>   chr4:10724865-10729681 FORWARD   Aliases: T16H5.70, T16H5_70	8.6	9.1	-0.6	-1.1	100.0%	-3.9
6378	AT4G35130.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:16721089-16723503 REVERSE   Aliases: T12J5.8	3.7	3.9	-0.2	-1.1	100.0%	-4.9
6379	AT4G01110.1   expressed protein, similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g46300.1); similar to hypothetical protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:BAD72426.1)   chr4:479501-481160 REVERSE   Aliases: F2N1.3, F2N1_3	3.4	3.1	0.3	1.1	100.0%	-4.3
6380	AT3G55590.1   GDP-mannose pyrophosphorylase, putative, strong similarity to GDP-mannose pyrophosphorylase from <i>Arabidopsis thaliana</i> (GI:3598958), <i>Pichia angusta</i> (GI:7331158); contains Pfam profile PF00483 Nucleotidyl transferase   chr3:20628458-20629860 FORWARD   Aliases: F1I16.2	3.2	3.0	0.2	1.1	100.0%	-4.6
6381	AT1G15720.1   Symbol: TRFL5   myb family transcription factor, contains Pfam PF00249: Myb-like DNA-binding domain   chr1:5406020-5407481 FORWARD   Aliases: F7H2.6, F7H2_6, TRF LIKE 5	3.9	4.2	-0.3	-1.1	100.0%	-4.5
6382	AT2G38970.1   zinc finger (C3HC4-type RING finger) family protein, very low similarity to SP:P97280 Inter-alpha-trypsin inhibitor heavy chain H3 precursor { <i>Mesocricetus auratus</i> }; contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF00092: von Willebrand factor type A domain	5.3	5.0	0.3	1.1	100.0%	-4.2
6383	AT3G51690.1   expressed protein, low similarity to SP:P07271 DNA repair and recombination protein PIF1, mitochondrial precursor { <i>Saccharomyces cerevisiae</i> }   chr3:19187416-19189086 REVERSE   Aliases: T18N14.70	2.2	2.1	0.1	1.1	100.0%	-5.5
6384	AT1G11020.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:3676691-3678524 FORWARD   Aliases: T19D16.25, T19D16_25	6.5	6.1	0.4	1.1	100.0%	-4.4
6385	AT3G09640.2   Symbol: APX2   similar to L-ascorbate peroxidase 1, cytosolic (APX1) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g07890.2); similar to L-ascorbate peroxidase 1, cytosolic (APX1) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g07890.3); similar to L-ascorbate peroxidase 1, cytosolic (APX1) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g07890.1); similar to cytosolic ascorbate peroxidase [ <i>Fragaria x ananassa</i> ] (GB:AAB94574.1); similar to cytosolic ascorbate peroxidase [ <i>Vigna unguiculata</i> ] (GB:AAB03844.1); similar to cytosolic ascorbate peroxidase 2 [ <i>Glycine max</i> ] (GB:BAC92740.1); contains InterPro domain Haem peroxidase (InterPro:IPR002016); contains InterPro domain Fungal lignin peroxidase (InterPro:IPR001621); contains InterPro domain Plant ascorbate peroxidase (InterPro:IPR002207)   chr3:2956161-2958332 FORWARD   Aliases: APX1B, ASCORBATE PEROXIDASE 2, CS2, F11F8.23	3.2	3.1	0.2	1.1	100.0%	-4.8
6386	AT2G01430.1   homeobox-leucine zipper protein 17 (HB-17) / HD-ZIP transcription factor 17, identical to (GI:18857716) homeodomain-leucine zipper protein ATHB-17 (GI:18857716) ( <i>Arabidopsis thaliana</i> )   chr2:187797-190368 REVERSE   Aliases: F2I9.5, F2I9_5	2.6	2.8	-0.2	-1.1	100.0%	-4.8
6387	AT1G12710.1   Symbol: ATPP2 A12   F-box family protein / SKP1 interacting partner 3-related, contains Pfam profile PF00646: F-box domain   chr1:4326737-4328479 REVERSE   Aliases: ATPP2 A12, T12C24.23, T12C24_23	3.8	3.7	0.2	1.1	100.0%	-4.8
6388	AT1G54030.1   GDSL-motif lipase, putative, similar to myrosinase-associated proteins GI:1769968, GI:1769970, GI:1216391, GI:1216389 from ( <i>Brassica napus</i> ); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr1:20171302-20173268 FORWARD   Aliases: F15I1.11, F15I1_11	7.4	8.2	-0.8	-1.1	100.0%	-4.2
6389	AT1G72410.1   COP1-interacting protein-related, similar to COP1-Interacting Protein1 7 (CIP7) ( <i>Arabidopsis thaliana</i> ) GI:3327870   chr1:27255358-27259908 REVERSE   Aliases: T10D10.12, T10D10_12	3.5	3.6	-0.1	-1.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6390	AT5G22750.1   Symbol: RAD5   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to SP:P36607 DNA repair protein rad8 {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:7565040-7571086 REVERSE   Aliases: MDJ22.17, MDJ22_17	3.5	3.7	-0.2	-1.1	100.0%	-4.8
6391	AT3G21500.2   1-deoxy-D-xylulose 5-phosphate synthase, putative / 1-deoxyxylulose-5-phosphate synthase, putative / DXP-synthase, putative, strong similarity to 1-D-deoxyxylulose 5-phosphate synthase (Lycopersicon esculentum) GI:5059160, DEF (deficient in photosynthesis) protein (Arabidopsis thaliana) GI:1399261; ; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain   chr3:7573643-7576579 REVERSE   Aliases: MIL23.4	3.8	3.5	0.3	1.1	100.0%	-4.4
6392	AT1G17130.1   cell cycle control protein-related, contains similarity to Swiss-Prot:Q9P7C5 cell cycle control protein cwf16 (Schizosaccharomyces pombe)   chr1:5854141-5856968 FORWARD   Aliases: F20D23.18, F20D23_18	6.6	7.1	-0.6	-1.1	100.0%	-4.0
6393	AT5G47770.1   Symbol: FPS1   farnesyl pyrophosphate synthetase 1, mitochondrial (FPS1) / FPP synthetase 1 / farnesyl diphosphate synthase 1, identical to SP:Q09152 Farnesyl pyrophosphate synthetase 1, mitochondrial precursor (FPP synthetase 1) (FPS 1) (Farnesyl diphosphate synthetase 1) (Includes: Dimethylallyltransferase (EC 2.5.1.1); Geranyltranstransferase (EC 2.5.1.10)) {Arabidopsis thaliana}   chr5:19362399-19364855 FORWARD   Aliases: FARNESYL DIPHOSPHATE SYNTHASE 1, MCA23.9, MCA23_9	6.5	7.0	-0.5	-1.1	100.0%	-4.4
6394	AT1G65860.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase FMO3 (dimethylaniline monooxygenase (N-oxide forming) 3) GI:349533 (SP:P32417) from Oryctolagus cuniculus, (SP:P97501) from Mus musculus; contains Pfam profile PF00743 Flavin-binding monooxygenase-like domain   chr1:24502729-24506408 REVERSE   Aliases: F12P19.2, F12P19_2	3.1	3.3	-0.2	-1.1	100.0%	-4.9
6395	AT1G44160.1   DNAJ chaperone C-terminal domain-containing protein, contains Pfam profile PF01556: DnaJ C terminal region   chr1:16797269-16798856 FORWARD   Aliases: T7O23.16, T7O23_16	3.0	3.6	-0.6	-1.1	100.0%	-3.7
6396	AT3G02470.2   Symbol: SAMDC   similar to adenosylmethionine decarboxylase family protein [Arabidopsis thaliana] (TAIR:At5g15950.1); similar to S-adenosyl-L-methionine decarboxylase [Brassica juncea] (GB:AAF20160.1); contains InterPro domain S-adenosylmethionine decarboxylase (InterPro:IPR001985)   chr3:509428-511583 FORWARD   Aliases: ADOMETDC, F16B3.10, F16B3_10, S ADENOSYLMETHIONINE DECARBOXYLASE	11.7	11.9	-0.3	-1.1	100.0%	-5.0
6397	NA	8.1	7.5	0.5	1.1	100.0%	-4.5
6398	AT2G43930.1   protein kinase family protein, contains similarity to NPK1-related protein kinase 2 GI:2342425 from (Arabidopsis thaliana)   chr2:18200227-18202658 FORWARD   Aliases: F6E13.6	5.7	5.5	0.2	1.1	100.0%	-4.4
6399	AT3G48880.2   F-box family protein, N7 protein - Medicago truncatula, EMBL:CAA76808 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr3:18137897-18140157 FORWARD   Aliases: T21J18.150	5.2	4.9	0.4	1.1	100.0%	-4.3
6400	AT3G07870.1   F-box family protein, contains F-box domain Pfam:PF00646	5.7	5.5	0.2	1.1	100.0%	-4.5
6401	AT4G12420.1   Symbol: SKU5   multi-copper oxidase, putative (SKU5), identical to multi-copper oxidase-related protein (SKU5)(GI:18158154) (Arabidopsis thaliana); similar to pollen-specific protein precursor - common tobacco, PIR2:S22495; contains Pfam profile: PF00394 Multicopper oxidase   chr4:7349938-7353020 REVERSE   Aliases: T1P17.10, T1P17_10	5.8	6.3	-0.5	-1.1	100.0%	-4.1
6402	AT3G08890.2   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr3:2706642-2708753 FORWARD   Aliases: T16O11.17	4.5	4.3	0.3	1.1	100.0%	-4.5
6403	AT2G19800.1   Symbol: MIOX2   expressed protein, similar to myo-inositol oxygenase (Sus scrofa) gi:17432544:gb:AAL39076   chr2:8537986-8540533 REVERSE   Aliases: F6F22.17, F6F22_17, MYO INOSITOL OXYGENASE 2	9.7	9.0	0.7	1.1	100.0%	-3.9
6404	AT1G50120.1   expressed protein   chr1:18565497-18569804 FORWARD   Aliases: F2J10.3, F2J10_3	7.0	7.5	-0.5	-1.1	100.0%	-4.2
6405	AT1G25320.1   leucine-rich repeat transmembrane protein kinase, putative, similar to putative receptor-like protein kinase GI:4262228 from (Arabidopsis thaliana)   chr1:8877844-8880297 FORWARD   Aliases: F4F7.29, F4F7_29	5.2	5.5	-0.3	-1.1	100.0%	-4.6
6406	AT4G10620.1   expressed protein   chr4:6564275-6566500 FORWARD   Aliases: T4F9.80, T4F9_80	6.7	7.1	-0.3	-1.1	100.0%	-4.2
6407	AT5G46520.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18884953-18889533 FORWARD   Aliases: K11I1.11, K11I1_11	2.8	3.3	-0.6	-1.1	100.0%	-3.9
6408	AT5G52500.1   expressed protein, strong similarity to unknown protein (emb:CAB68146.1)	2.6	2.8	-0.2	-1.1	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6409	AT1G22140.2   expressed protein   chr1:7814830-7815620 REVERSE   Aliases: F2E2.21, F2E2_21	9.3	8.9	0.4	1.1	100.0%	-4.2
6410	AT5G06740.1   lectin protein kinase family protein, contains Legume lectins beta-chain signature, PROSITE:PS00307 and Serine/Threonine protein kinases active-site signature, PROSITE:PS00108   chr5:2084095-2086053 FORWARD   Aliases: MPH15.10, MPH15_10	4.1	4.4	-0.3	-1.1	100.0%	-4.3
6411	AT1G65820.1   microsomal glutathione s-transferase, putative, similar to MGST3_HUMAN SP:O14880	10.7	10.3	0.4	1.1	100.0%	-5.0
6412	AT3G04750.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:1301397-1303382 REVERSE   Aliases: F7O18.24, F7O18_24	4.3	4.0	0.3	1.1	100.0%	-4.6
6413	AT4G25570.1   Symbol: ACYB 2	8.9	7.7	1.2	1.1	100.0%	-4.0
6414	AT4G27110.1   phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region   chr4:13599242-13601527 REVERSE   Aliases: T24A18.60, T24A18_60	2.8	3.0	-0.2	-1.1	100.0%	-4.8
6415	AT5G56360.1   calmodulin-binding protein, similar to alpha glucosidase II beta subunit from GI:2104691 (Mus musculus)   chr5:22840528-22845223 REVERSE   Aliases: MCD7.9, MCD7_9	8.8	9.2	-0.4	-1.1	100.0%	-4.4
6416	AT3G56200.1   amino acid transporter family protein, low similarity to N system amino acids transporter NAT-1 (Mus musculus) GI:7406950; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II   chr3:20861023-20863001 FORWARD   Aliases: F18O21.160	6.1	5.6	0.5	1.1	100.0%	-4.1
6417	AT4G26890.1   Symbol: MAPKKK16   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:13511845-13513412 FORWARD   Aliases: F10M23.230, F10M23_230	3.9	3.5	0.4	1.1	100.0%	-4.1
6418	AT1G75910.1   Symbol: EXL4   family II extracellular lipase 4 (EXL4), EXL4 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 (Arabidopsis thaliana (Mouse-ear cress))   chr1:28505098-28506937 FORWARD   Aliases: T4O12.250, T4O12_250	2.7	2.9	-0.2	-1.1	100.0%	-4.8
6419	AT4G20090.1   Symbol: EMB1025   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:10868410-10870392 REVERSE   Aliases: EMB1025, EMBRYO DEFECTIVE 1025, F18F4.190, F18F4_190	3.7	3.8	-0.1	-1.1	100.0%	-4.9
6420	AT1G80720.1   mitochondrial glycoprotein family protein / MAM33 family protein, similar to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein   chr1:30341030-30342450 FORWARD   Aliases: F23A5.7, F23A5_7	3.5	3.8	-0.3	-1.1	100.0%	-4.3
6421	AT3G02970.1   phosphate-responsive 1 family protein, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr3:669110-670502 REVERSE   Aliases: F13E7.8, F13E7_8	1.9	2.0	-0.1	-1.1	100.0%	-5.3
6422	AT3G22440.1   hydroxyproline-rich glycoprotein family protein, identical to hydroxyproline-rich glycoprotein (Arabidopsis thaliana) gi:9293881:dbj:BAB01784   chr3:7959761-7962207 FORWARD   Aliases: MCB17.3	6.1	6.6	-0.6	-1.1	100.0%	-4.1
6423	AT1G58430.1   Symbol: RXF26   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr1:21715230-21716768 REVERSE   Aliases: F9K23.4, F9K23_4, RXF26	2.5	2.7	-0.1	-1.1	100.0%	-5.2
6424	AT4G31420.2   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr4:15245822-15247930 REVERSE   Aliases: F3L17.9	8.6	8.3	0.3	1.1	100.0%	-4.5
6425	AT1G55260.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr1:20618418-20620034 FORWARD   Aliases: F7A10.16, F7A10_16	2.6	2.8	-0.2	-1.1	100.0%	-5.1
6426	AT5G53580.1   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr5:21782305-21784210 REVERSE   Aliases: MNC6.12, MNC6_12	9.7	9.3	0.4	1.1	100.0%	-4.0
6427	AT5G60520.1   late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (Picea glauca) GI:1350543   chr5:24349013-24350173 REVERSE   Aliases: MUF9.15, MUF9_15	3.4	3.2	0.2	1.1	100.0%	-4.8
6428	AT4G01880.1   expressed protein, contains Pfam PF05206: Protein of unknown function (DUF715)   chr4:810699-812925 REVERSE   Aliases: T7B11.14, T7B11_14	3.8	4.2	-0.3	-1.1	100.0%	-4.2
6429	AT3G54660.1   Symbol: GR   glutathione reductase, chloroplast, nearly identical to SP:P42770 Glutathione reductase, chloroplast precursor (EC 1.8.1.7) (GR) (GRASE) {Arabidopsis thaliana}; identical to cDNA glutathione reductase GI:451197   chr3:20240723-20244160 REVERSE   Aliases: EMB2360, EMBRYO DEFECTIVE 2360, GLUTATHIONE REDUCTASE, T5N23.20	7.7	7.1	0.6	1.1	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6430	AT5G02040.2   prenylated rab acceptor (PRA1) family protein, contains Pfam PF03208: PRA1 family protein   chr5:400896-402873 FORWARD   Aliases: T7H20.90, T7H20_90	4.5	4.1	0.4	1.1	100.0%	-4.2
6431	AT1G24150.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr1:8549507-8551982 FORWARD   Aliases: F3I6.8, F3I6_8	2.9	3.7	-0.8	-1.1	100.0%	-4.3
6432	AT3G59760.3   Symbol: OASC   cysteine synthase, mitochondrial, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to SP:Q43725 Cysteine synthase, mitochondrial precursor (EC 4.2.99.8) (O- acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}   chr3:22083451-22086393 REVERSE   Aliases: ATCS C, CSASE C, F24G16.30	10.1	10.8	-0.7	-1.1	100.0%	-4.1
6433	AT1G10930.1   Symbol: ATSGS1	3.1	3.4	-0.3	-1.1	100.0%	-4.3
6434	AT3G45100.2   Symbol: SETH2   N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein, putative, similar to PIG-A from Mus musculus (gi:577723), Homo sapiens (SP:P37287); contains Pfam glycosyl transferase, group 1 family protein domain PF00534   chr3:16515445-16517988 FORWARD   Aliases: T14D3.40	8.0	7.6	0.4	1.1	100.0%	-4.1
6435	AT2G20160.1   Symbol: MEO   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At17), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1b GI:3068809, UIP2 GI:3719211 from (Arabidopsis thaliana)   chr2:8706753-8707205 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 17, ASK17, MEIDOS, T2G17.4, T2G17_4	3.3	3.1	0.2	1.1	100.0%	-4.6
6436	AT5G16800.2   GCN5-related N-acetyltransferase (GNAT) family protein, very low similarity to SP:P39909 Spermine/spermidine acetyltransferase (EC 2.3.1.57) {Bacillus subtilis}; contains Pfam profile PF00583: acetyltransferase, GNAT family   chr5:5524317-5526566 REVERSE   Aliases: F5E19.140, F5E19_140	6.8	6.3	0.4	1.1	100.0%	-4.2
6437	AT2G42360.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:17647876-17648866 FORWARD   Aliases: MHK10.8, MHK10_8	2.3	2.5	-0.2	-1.1	100.0%	-4.8
6438	AT1G50500.1   membrane trafficking VPS53 family protein, contains Pfam domain PF04100: Vps53-like, N-terminal   chr1:18711655-18719645 REVERSE   Aliases: F11F12.15	4.4	4.8	-0.3	-1.1	100.0%	-4.6
6439	AT5G58080.1   Symbol: ARR18   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain   chr5:23519011-23521227 REVERSE   Aliases: ARABIDOPSIS RESPONSE REGULATOR 18, K21L19.7, K21L19_7	2.6	2.4	0.2	1.1	100.0%	-4.9
6440	AT4G23950.1   expressed protein, ; expression supported by MPSS   chr4:12442563-12444340 FORWARD   Aliases: T32A16.120, T32A16_120	4.3	4.6	-0.3	-1.1	100.0%	-4.4
6441	AT5G08130.1   Symbol: BIM1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.5	6.1	-0.6	-1.1	100.0%	-4.3
6442	AT1G04645.1   self-incompatibility protein-related, similar to S3 self-incompatibility protein (Papaver rhoeas) GI:1107841   chr1:1293769-1294262 REVERSE   Aliases: None	2.6	2.8	-0.1	-1.1	100.0%	-5.1
6443	AT5G62950.1   expressed protein   chr5:25279458-25281047 REVERSE   Aliases: MQB2.27, MQB2_27	5.9	5.6	0.3	1.1	100.0%	-4.2
6444	AT4G14920.1   PHD finger transcription factor, putative   chr4:8531153-8535838 REVERSE   Aliases: DL3500C, FCAALL.143	4.4	4.7	-0.2	-1.1	100.0%	-4.4
6445	AT2G26550.1   Symbol: HO2   heme oxygenase 2 (HO2), similar to heme oxygenase 2 (Arabidopsis thaliana) gi:4530595:gb:AAD22109	5.0	4.8	0.2	1.1	100.0%	-4.5
6446	AT1G26250.1   proline-rich extensin, putative, similar to extensin gi:1165322:gb:AAB53156; contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:9083825-9085451 FORWARD   Aliases: F28B23.9, F28B23_9	3.3	3.8	-0.5	-1.1	100.0%	-4.2
6447	AT5G02210.1   expressed protein, ; expression supported by MPSS   chr5:439251-439872 REVERSE   Aliases: T7H20.260, T7H20_260	4.5	4.0	0.5	1.1	100.0%	-4.0
6448	AT3G46390.1   expressed protein   chr3:17082240-17082668 REVERSE   Aliases: F18L15.110	2.2	2.4	-0.2	-1.1	100.0%	-4.9
6449	AT1G05385.1   photosystem II 11 kDa protein-related, similar to Photosystem II 11 kDa protein precursor (SP:P74367)(strain PCC 6803) {Synechocystis sp.}   chr1:1582673-1583717 REVERSE   Aliases: None	5.1	5.3	-0.3	-1.1	100.0%	-4.3
6450	AT1G23410.1   ubiquitin extension protein, putative / 40S ribosomal protein S27A (RPS27aA), strong similarity to ubiquitin extension protein (UBQ5) GB:AAA32906 GI:166934 from (Arabidopsis thaliana)   chr1:8314913-8315520 FORWARD   Aliases: F26F24.28, F26F24_28	7.7	8.2	-0.5	-1.1	100.0%	-3.8
6451	AT3G47780.1   Symbol: ATATH6	6.2	6.5	-0.4	-1.1	100.0%	-4.1
6452	AT2G02040.1   Symbol: ATPTR2 B   peptide transporter (PTR2-B) / oligopeptide transporter 1-1, putative (OPT1-1), identical to peptide transporter PTR2-B SP:P46032 from (Arabidopsis thaliana); contains Pfam profile: PF00854 POT family; identical to cDNA NT1 GI:510237   chr2:487422-489830 FORWARD   Aliases: F14H20.11, F14H20_11, HISTIDINE TRANSPORT PROTEIN, NITRATE TRANSPORTER 1, NTR1, PTR2 B	8.1	7.3	0.8	1.1	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6453	AT1G02000.1   Symbol: GAE2   NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from <i>Vibrio vulnificus</i> GI:3093975 (PID:g3093975), WbnF ( <i>Escherichia coli</i> ) GI:5739472, CAPI protein { <i>Staphylococcus aureus</i> } SP:P39858; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	5.9	5.5	0.3	1.1	100.0%	-4.5
6454	AT1G53420.1   serine/threonine protein kinase-related, contains 1 predicted transmembrane domain; low similarity to receptor-like serine/threonine kinase ( <i>Arabidopsis thaliana</i> ) GI:2465923   chr1:19930294-19935162 REVERSE   Aliases: F12M16.30	2.4	2.3	0.1	1.1	100.0%	-5.5
6455	AT4G13180.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain type dehydrogenase/reductase SP:Q08632 ( <i>Picea abies</i> )   chr4:7657192-7658193 REVERSE   Aliases: F17N18.70, F17N18_70	10.7	9.5	1.2	1.1	100.0%	-3.9
6456	AT5G16080.1   expressed protein, similar to PrMC3 ( <i>Pinus radiata</i> ) GI:5487873   chr5:5252318-5253621 REVERSE   Aliases: F1N13.220, F1N13_220	3.3	3.7	-0.4	-1.1	100.0%	-4.2
6457	AT1G16670.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; similar to receptor-like serine/threonine kinase GI:2465923 from ( <i>Arabidopsis thaliana</i> )   chr1:5697332-5699762 FORWARD   Aliases: F19K19.4, F19K19_4	6.1	5.8	0.3	1.1	100.0%	-4.3
6458	AT1G64050.1   expressed protein   chr1:23766030-23769696 FORWARD   Aliases: F22C12.19, F22C12_19	2.9	3.3	-0.4	-1.1	100.0%	-4.5
6459	AT1G73490.1   RNA recognition motif (RRM)-containing protein, contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain   chr1:27636927-27638593 REVERSE   Aliases: T9L24.49, T9L24_49	7.2	6.9	0.3	1.1	100.0%	-4.6
6460	AT4G34400.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr4:16445327-16447600 FORWARD   Aliases: F10M10.170, F10M10_170	3.1	2.9	0.2	1.1	100.0%	-4.7
6461	AT3G09180.1   expressed protein   chr3:2819123-2821430 FORWARD   Aliases: MZB10.22	5.8	5.5	0.3	1.1	100.0%	-4.2
6462	AT5G23530.1   expressed protein, contains similarity to PrMC3 ( <i>Pinus radiata</i> ) GI:5487873   chr5:7932969-7934439 REVERSE   Aliases: MQM1.21, MQM1_21	3.0	3.3	-0.3	-1.1	100.0%	-4.1
6463	AT1G22070.1   Symbol: TGA3   bZIP family transcription factor (TGA3), identical to transcription factor GI:304113 from ( <i>Arabidopsis thaliana</i> )	7.1	6.7	0.3	1.1	100.0%	-4.5
6464	AT1G77850.1   Symbol: ARF17   transcriptional factor B3 family protein, similar to auxin response factor 10 GI:6165644 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF02362: B3 DNA binding domain   chr1:29277207-29280313 FORWARD   Aliases: ARF17, AUXIN RESPONSE FACTOR 17, F28K19.6, F28K19_6	3.5	3.2	0.3	1.1	100.0%	-4.4
6465	AT1G16190.1   DNA repair protein RAD23, putative, similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II GI:1914685 from ( <i>Daucus carota</i> )	3.0	3.3	-0.3	-1.1	100.0%	-4.6
6466	AT3G58540.1   expressed protein   chr3:21659570-21660364 FORWARD   Aliases: F14P22.130	4.9	4.6	0.4	1.1	100.0%	-4.3
6467	AT2G22480.1   phosphofructokinase family protein, similar to phosphofructokinase ( <i>Amycolatopsis methanolica</i> ) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase   chr2:9552656-9555643 FORWARD   Aliases: F14M13.12, F14M13_12	8.8	9.4	-0.6	-1.1	100.0%	-4.2
6468	AT5G23440.1   ferredoxin-thioredoxin reductase, putative, similar to ferredoxin-thioredoxin reductase, variable chain (FTR-V, Ferredoxin-thioredoxin reductase subunit A, FTR-A) ( <i>Zea mays</i> ) SWISS-PROT:P80680	4.6	4.3	0.3	1.1	100.0%	-4.4
6469	AT1G01130.1   expressed protein, ; expression supported by MPSS   chr1:61963-63811 REVERSE   Aliases: F6F3.33	4.3	3.9	0.4	1.1	100.0%	-4.1
6470	AT5G58190.2   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr5:23563599-23566775 FORWARD   Aliases: MCK7.6, MCK7_6	5.7	6.2	-0.5	-1.1	100.0%	-4.2
6471	AT5G16120.1   hydrolase, alpha/beta fold family protein, similar to monoglyceride lipase from ( <i>Homo sapiens</i> ) GI:14594904, ( <i>Mus musculus</i> ) GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:5265957-5267982 FORWARD   Aliases: T21H19.40, T21H19_40	7.8	7.6	0.3	1.1	100.0%	-4.4
6472	AT4G11690.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:7056248-7057948 FORWARD   Aliases: T5C23.120, T5C23_120	2.9	3.2	-0.2	-1.1	100.0%	-4.8
6473	AT1G21350.3   expressed protein   chr1:7476930-7479021 REVERSE   Aliases: F24J8.1, F24J8_1	4.2	4.5	-0.3	-1.1	100.0%	-4.2
6474	AT2G41380.1   embryo-abundant protein-related, similar to embryo-abundant protein ( <i>Picea glauca</i> ) GI:1350531   chr2:17259019-17260135 FORWARD   Aliases: F13H10.7, F13H10_7	3.8	3.6	0.2	1.1	100.0%	-4.6
6475	AT4G35940.1   expressed protein   chr4:17021675-17023767 FORWARD   Aliases: T19K4.70	6.1	5.8	0.4	1.1	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6476	AT1G11700.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr1:3945737-3946613 FORWARD   Aliases: F25C20.15, F25C20_15	4.6	4.2	0.3	1.1	100.0%	-4.5
6477	AT4G03210.2   Symbol: XTH9   similar to xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXGT-A4) [Arabidopsis thaliana] (TAIR:At5g13870.1); similar to sadtomato protein [Capsicum annuum] (GB:AAS77347.1); contains InterPro domain Glycoside hydrolase, family 16 (InterPro:IPR000757); contains InterPro domain Beta-glucanase (InterPro:IPR008264)   chr4:1415953-1417352 FORWARD   Aliases: F4C21.14, F4C21_14, XYLOGLUCAN ENDOTRANGLUCOSYLASE/HYDROLASE 9	10.2	9.8	0.4	1.1	100.0%	-4.2
6478	AT3G60190.1   Symbol: ADL4   dynamin-like protein E (DL1E), nearly identical to dynamin-like protein E (Arabidopsis thaliana) GI:19423872; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain   chr3:22255144-22258773 REVERSE   Aliases: ADL1E, ADL4, ADLP2, DYNAMIN LIKE PROTEIN 4, F27H5.4	6.9	7.2	-0.3	-1.1	100.0%	-4.5
6479	AT5G20940.1   glycosyl hydrolase family 3 protein, beta-glucosidase, common nasturtium, PIR:T10521   chr5:7103929-7106703 REVERSE   Aliases: F22D1.110, F22D1_110	3.8	3.6	0.2	1.1	100.0%	-4.6
6480	AT3G47910.1   expressed protein, low similarity to nonmuscle myosin heavy chain (NMHC) (Homo sapiens) GI:189036; contains Pfam profiles PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr3:17687622-17692715 REVERSE   Aliases: T17F15.220	2.3	2.4	-0.1	-1.1	100.0%	-5.4
6481	AT5G58430.1   exocyst subunit EXO70 family protein, leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495; contains Pfam domain PF03081: Exo70 exocyst complex subunit; similar to rexo70 (GI:2827160) {Rattus norvegicus}   chr5:23638409-23640670 REVERSE   Aliases: MQJ2.2, MQJ2_2	6.9	7.8	-1.0	-1.1	100.0%	-4.3
6482	AT1G30900.1   vacuolar sorting receptor, putative, similar to BP-80 vacuolar sorting receptor (Pisum sativum) GI:1737222   chr1:10997256-11000524 FORWARD   Aliases: F17F8.23	5.9	5.3	0.5	1.1	100.0%	-4.0
6483	AT3G26750.1   expressed protein   chr3:9841247-9843316 REVERSE   Aliases: MDJ14.3	3.7	4.0	-0.3	-1.1	100.0%	-4.6
6484	AT3G59640.1   glycine-rich protein   chr3:22039758-22041422 FORWARD   Aliases: T16L24.190	6.0	5.8	0.2	1.1	100.0%	-4.7
6485	AT1G78950.1   beta-amyrin synthase, putative, similar to beta-Amyrin Synthase GI:3688600 from (Panax ginseng) and GI:8918271 from (Pisum sativum)   chr1:29689330-29693566 REVERSE   Aliases: YUP8H12R.44, YUP8H12R_44	4.5	4.2	0.3	1.1	100.0%	-4.3
6486	AT2G22270.1   expressed protein   chr2:9470774-9472547 FORWARD   Aliases: T26C19.7, T26C19_7	4.0	3.7	0.3	1.1	100.0%	-4.4
6487	AT5G14570.2   Symbol: ATNRT2.7   transporter, putative, similar to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362; contains Pfam profile PF00083: Sugar (and other) transporter   chr5:4695189-4697081 REVERSE   Aliases: T15N1.60, T15N1_60	6.0	5.5	0.4	1.1	100.0%	-4.1
6488	AT4G30340.1   diacylglycerol kinase family protein, contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain   chr4:14838315-14841073 REVERSE   Aliases: F17I23.320, F17I23_320	2.3	2.4	-0.1	-1.1	100.0%	-5.2
6489	AT5G63970.2   similar to copine-related [Arabidopsis thaliana] (TAIR:At3g01650.1); similar to P0401G10.23 [Oryza sativa (japonica cultivar-group)] (GB:NP_914244.1); contains InterPro domain von Willebrand factor, type A (InterPro:IPR002035)   chr5:25623997-25626213 REVERSE   Aliases: MBM17.7, MBM17_7	8.7	8.5	0.2	1.1	100.0%	-4.7
6490	AT2G35810.1   expressed protein   chr2:15056229-15057324 FORWARD   Aliases: F11F19.28, F11F19_28	10.1	10.8	-0.8	-1.1	100.0%	-4.0
6491	AT2G46770.1   Symbol: ANAC043/EMB2301   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr2:19227797-19229986 REVERSE   Aliases: ANAC043, EMB2301, EMBRYO DEFECTIVE 2301, F19D11.5	1.9	2.0	-0.1	-1.1	100.0%	-5.4
6492	AT1G47470.1   hypothetical protein   chr1:17417051-17417521 REVERSE   Aliases: F16N3.31, F16N3_31	2.4	2.5	-0.1	-1.1	100.0%	-5.3
6493	AT1G80450.1   VQ motif-containing protein, contains PF05678: VQ motif   chr1:30248847-30249580 REVERSE   Aliases: T21F11.22, T21F11_22	1.9	2.0	-0.2	-1.1	100.0%	-5.3
6494	AT1G18270.1   ketose-bisphosphate aldolase class-II family protein, low similarity to KbaY (tagatose-1,6-bisphosphate aldolase) (Escherichia coli) GI:8895753; contains Pfam profile PF01116: Fructose-bisphosphate aldolase class-II   chr1:6283405-6293821 REVERSE   Aliases: T10O22.24, T10O22_24	8.1	7.7	0.4	1.1	100.0%	-4.0
6495	AT2G32810.1   Symbol: BGAL9   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase GI:7939617 from (Lycopersicon esculentum)   chr2:13925214-13932408 REVERSE   Aliases: F24L7.5, F24L7_5	6.7	7.2	-0.4	-1.1	100.0%	-4.5
6496	AT4G29770.1   expressed protein   chr4:14575846-14577645 FORWARD   Aliases: F27B13.10, F27B13_10	6.2	6.9	-0.6	-1.1	100.0%	-3.6
6497	AT1G06510.1   expressed protein   chr1:1992384-1993839 FORWARD   Aliases: F12K11.16, F12K11_16	4.6	4.3	0.3	1.1	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6498	AT3G50780.1   expressed protein   chr3:18886380-18888505 REVERSE   Aliases: F18B3.60	4.7	4.9	-0.3	-1.1	100.0%	-4.3
6499	AT1G13140.1   Symbol: CYP86C3   cytochrome P450 family protein, similar to Cytochrome P450 86A2 (SP:O23066) (Arabidopsis thaliana); contains Pfam PF:00067 Cytochrome P450 family   chr1:4478489-4480268 REVERSE   Aliases: F3F19.16, F3F19_16	2.9	3.2	-0.3	-1.1	100.0%	-4.6
6500	AT4G09980.1   Symbol: EMB1691   methyltransferase MT-A70 family protein, low similarity to SP:P25583 Karyogamy protein KAR4 {Saccharomyces cerevisiae}, (N6-adenosine)-methyltransferase (Mus musculus) GI:10179948; contains Pfam profile PF05063: MT-A70 (S-adenosylmethionine-binding subunit of human mRNA:m6A methyl-transferase (MTase))   chr4:6247732-6252285 REVERSE   Aliases: EMB1691, EMBRYO DEFECTIVE 1691, T5L19.110, T5L19_110	2.7	2.5	0.1	1.1	100.0%	-5.0
6501	AT1G48760.3   similar to gamma-adaptin, putative [Arabidopsis thaliana] (TAIR:At1g60070.1); similar to AP3D1 protein [Homo sapiens] (GB:AAH05142.1); contains InterPro domain Adaptin, N-terminal (InterPro:IPR002553)	3.9	4.3	-0.4	-1.1	100.0%	-4.3
6502	AT2G20850.1   similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At4g03390.1); similar to putative leucine-rich repeat transmembrane protein kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_464408.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr2:8982429-8986460 REVERSE   Aliases: F5H14.18, F5H14_18	3.3	3.5	-0.2	-1.1	100.0%	-4.6
6503	AT1G28210.2   Symbol: ATJ1   DNAJ heat shock protein, putative, strong similarity to mitochondrial DnaJ protein (AtJ1) GI:564030 from (Arabidopsis thaliana); contains Pfam profiles PF00226: DnaJ domain, PF01556: DnaJ C terminal region, PF00684: DnaJ central domain (4 repeats); identical to cDNA DnaJ homolog AtJ1 (atj) GI:564029   chr1:9854533-9860145 FORWARD   Aliases: ATJ, F3H9.13, F3H9_13	5.5	6.1	-0.5	-1.1	100.0%	-4.2
6504	AT3G53480.1   ABC transporter family protein, PDR5-like ABC transporter, Spirodela polyrrhiza, EMBL:Z70524   chr3:19836285-19842755 FORWARD   Aliases: F4P12.180	3.2	3.6	-0.3	-1.1	100.0%	-4.4
6505	AT5G37630.1   Symbol: EMB2656   chromosome condensation family protein, contains pfam profile: PF04154 chromosome condensation protein 3, C-terminal region   chr5:14964637-14969995 FORWARD   Aliases: EMB2656, EMBRYO DEFECTIVE 2217, EMBRYO DEFECTIVE 2656, K12B20.9, K12B20_9	3.7	4.0	-0.3	-1.1	100.0%	-4.3
6506	AT3G55360.1   Symbol: CER10/ECR   Enoyl-CoA reductase (ECA) is involved in all very long chain fatty acids (VLCFA) elongation reactions that are required for cuticular wax, storage lipid and sphingolipid metabolism. The protein is located in the ER, but in contrast to its yeast homolog TSC13 is not particularly enriched in the nuclear envelope-vacuole junction. Mutants in this gene show abnormal organ morphology and stem glossiness. Cells in all tissues are only about 1/3 of the size of wild type cells. The morphological changes are most likely to result from the reduction in the VLCFA content of sphingolipids. Mutants also show abnormalities in the endocytic membrane organization and transport.   chr3:20531907-20533963 REVERSE   Aliases: CER10, ECR, T22E16.20	4.4	5.0	-0.6	-1.1	100.0%	-4.2
6507	AT4G00550.1   Symbol: DGD2   UDP-galactose:MGDG galactosyltransferase 2 / digalactosyldiacylglycerol synthase 2 (DGD2), identical to digalactosyldiacylglycerol synthase (DGD2) GI:18141112 (Arabidopsis thaliana)   chr4:237967-240500 REVERSE   Aliases: F6N23.24, F6N23_24	5.3	5.0	0.2	1.1	100.0%	-4.5
6508	AT3G49310.1   expressed protein, contains PF05631: Protein of unknown function (DUF791)   chr3:18295849-18299037 REVERSE   Aliases: F2K15.170	4.4	4.1	0.3	1.1	100.0%	-4.6
6509	AT4G21270.1   Symbol: ATK1   kinesin-like protein A (KATA)   chr4:11329373-11334145 REVERSE   Aliases: ARABIDOPSIS THALIANA KINESIN 1, F7J7.210, F7J7_210, KATA, KATAP, KINESIN LIKE PROTEIN A	2.7	2.8	-0.2	-1.1	100.0%	-4.8
6510	AT2G17840.1   Symbol: ERD7   senescence/dehydration-associated protein-related (ERD7), similar to senescence-associated protein 12 (Hemerocallis hybrid cultivar) gi:3551958:gb:AAC34857; strong similarity to early-responsive to dehydration stress ERD7 protein (Arabidopsis thaliana) gi:15320412:dbj:BA63916; identical to cDNA ERD7 partial cds GI:15320411   chr2:7762687-7764934 REVERSE   Aliases: EARLY RESPONSIVE TO DEHYDRATION 7, T13L16.14, T13L16_14	8.3	7.7	0.6	1.1	100.0%	-4.2
6511	AT2G45500.1   similar to spastin ATPase, putative [Arabidopsis thaliana] (TAIR:At3g27120.1); similar to Tobacco mosaic virus helicase domain-binding protein [Nicotiana tabacum] (GB:AAL25088.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr2:18756872-18759277 REVERSE   Aliases: F17K2.3	4.5	4.1	0.4	1.1	100.0%	-4.2
6512	AT1G49570.1   peroxidase, putative, identical to peroxidase ATP5a (Arabidopsis thaliana) gi:1546702:emb:CAA67341; similar to peroxidase SWISS-PROT:P80679 from (Armoracia rusticana)   chr1:18350704-18352619 FORWARD   Aliases: F14J22.19, F14J22_19	3.3	2.8	0.6	1.1	100.0%	-4.3
6513	AT5G59290.1   Symbol: UXS3   UDP-glucuronic acid decarboxylase (UXS3), identical to UDP-glucuronic acid decarboxylase (Arabidopsis thaliana) GI:14595666; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family; identical to cDNA	7.7	8.4	-0.7	-1.1	100.0%	-4.3
6514	AT4G18920.1   expressed protein   chr4:10368766-10370223 FORWARD   Aliases: F13C5.90, F13C5_90	3.4	3.7	-0.3	-1.1	100.0%	-4.5
6515	AT1G41830.1   Symbol: SKS6   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr1:15606058-15610302 REVERSE   Aliases: F5A13.5, F5A13_5, SKS6	8.5	9.1	-0.6	-1.1	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6516	AT3G11800.1   expressed protein   chr3:3726114-3727734 FORWARD   Aliases: F26K24.9	8.3	7.7	0.6	1.1	100.0%	-4.4
6517	AT1G28240.1   expressed protein   chr1:9868303-9872198 REVERSE   Aliases: F3H9.11, F3H9_11	4.2	3.9	0.3	1.1	100.0%	-4.7
6518	AT2G30620.1   histone H1.2, nearly identical to SP:P26569 Histone H1.2 {Arabidopsis thaliana}   chr2:13052008-13053588 FORWARD   Aliases: T6B20.3, T6B20_3	10.0	10.3	-0.3	-1.1	100.0%	-4.4
6519	AT5G17230.2   Symbol: PSY   similar to phytoene synthase [Capsicum annuum] (GB:CAA48155.1); contains InterPro domain Squalene/phytoene synthase (InterPro:IPR002060)   chr5:5659551-5662467 REVERSE   Aliases: MKP11.25, MKP11_25, PHYTOENE SYNTHASE	6.3	5.7	0.5	1.1	100.0%	-4.5
6520	AT4G25840.1   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:Q08623 GS1 protein {Homo sapiens}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	4.9	5.1	-0.3	-1.1	100.0%	-4.5
6521	AT1G15740.1   leucine-rich repeat family protein   chr1:5410929-5415297 FORWARD   Aliases: F7H2.8, F7H2_8	7.0	6.3	0.7	1.1	100.0%	-4.2
6522	AT1G13810.1   expressed protein, ; expression supported by MPSS   chr1:4734085-4735161 FORWARD   Aliases: F16A14.30, F16A14_30	5.7	6.1	-0.4	-1.1	100.0%	-4.0
6523	AT2G46510.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	4.1	3.8	0.3	1.1	100.0%	-4.6
6524	AT4G17310.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g47455.3)   chr4:9685190-9686940 REVERSE   Aliases: DL4690C, FCAALL.398	4.7	4.4	0.3	1.1	100.0%	-4.4
6525	AT2G40970.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:17104628-17105773 REVERSE   Aliases: T20B5.17, T20B5_17	7.1	6.7	0.4	1.1	100.0%	-4.3
6526	AT1G58300.1   heme oxygenase, putative, similar to heme oxygenase 4 GI:14485565 from (Arabidopsis thaliana)   chr1:21631677-21633661 REVERSE   Aliases: F19C14.8, F19C14_8	2.7	2.6	0.2	1.1	100.0%	-4.9
6527	AT1G39350.1   expressed protein   chr1:14610274-14611094 REVERSE   Aliases: F12G6.5	3.2	3.4	-0.2	-1.1	100.0%	-4.9
6528	AT3G21810.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr3:7684437-7688623 FORWARD   Aliases: MSD21.12	4.7	4.2	0.5	1.1	100.0%	-4.3
6529	AT4G14670.1   heat shock protein 101, putative / HSP101, putative, similar to heat shock protein 101 GI:6715468 GB:AAF26423 from (Arabidopsis thaliana)   chr4:8410049-8412552 FORWARD   Aliases: DL3375W, FCAALL.285	2.8	2.6	0.2	1.1	100.0%	-4.8
6530	AT5G63150.1   expressed protein   chr5:25347426-25348070 FORWARD   Aliases: MDC12.12, MDC12_12	5.2	5.7	-0.4	-1.1	100.0%	-4.2
6531	AT5G28080.2   Symbol: WNK9   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g04910.1); similar to mitogen activated protein kinase kinase [Oryza sativa] (GB:AAC32599.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:10090074-10092406 REVERSE   Aliases: T24G3.10, T24G3_10	4.0	3.7	0.3	1.1	100.0%	-4.5
6532	AT5G19320.1   Symbol: RANGAP2   RAN GTPase activating protein 2 (RanGAP2), identical to RAN GTPase activating protein 2 GI:6708468 from (Arabidopsis thaliana)   chr5:6505112-6507410 REVERSE   Aliases: RAN GTPASE ACTIVATING PROTEIN 2	4.6	5.0	-0.4	-1.1	100.0%	-4.3
6533	AT2G32520.1   diene lactone hydrolase family protein, low similarity to diene lactone hydrolase (Pseudomonas resinovorans) GI:13094163; contains Pfam profile PF01738: Diene lactone hydrolase family   chr2:13812596-13814613 REVERSE   Aliases: T26B15.8, T26B15_8	11.1	11.5	-0.4	-1.1	100.0%	-4.6
6534	AT2G14570.1   SWIM zinc finger family protein   chr2:6228862-6230999 REVERSE   Aliases: T13P21.5, T13P21_5	4.3	4.4	-0.2	-1.1	100.0%	-4.7
6535	AT1G28070.1   expressed protein, ; expression supported by MPSS   chr1:9783069-9783851 FORWARD   Aliases: F13K9.17, F13K9_17	5.9	5.5	0.4	1.1	100.0%	-4.3
6536	AT5G03900.2   expressed protein, predicted protein, Synechocystis sp., PIR:S74969   chr5:1048294-1052385 FORWARD   Aliases: F8F6.110	3.8	3.6	0.2	1.1	100.0%	-4.7
6537	AT5G24860.1   Symbol: FPF1   expressed protein   chr5:8541781-8542452 FORWARD   Aliases: F6A4.70, F6A4_70, FLOWERING PROMOTING FACTOR 1, FPF	3.2	3.0	0.1	1.1	100.0%	-4.9
6538	AT3G07510.1   expressed protein   chr3:2393697-2394681 REVERSE   Aliases: F21O3.22	5.5	5.7	-0.2	-1.1	100.0%	-4.5
6539	AT1G01170.2   similar to stress-related ozone-induced protein (OZ11) / stress-related ozone-responsive protein [Arabidopsis thaliana] (TAIR:At4g00860.1); similar to ozone-responsive stress-related protein-like [Oryza sativa (japonica cultivar-group)] (GB:NP_910318.1)   chr1:73824-74731 REVERSE   Aliases: F6F3.32	8.7	8.2	0.4	1.1	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6540	AT1G02980.1   Symbol: CUL2   cullin family protein, similar to cullin 1 (Homo sapiens) GI:3139077; contains Pfam profile PF00888: Cullin family   chr1:677869-681212 FORWARD   Aliases: ATCUL2, F22D16.2, F22D16_2	2.8	3.0	-0.2	-1.1	100.0%	-5.0
6541	AT5G27680.1   DEAD/DEAH box helicase, putative, similar to WRN (Werner syndrome) protein - Mus musculus, EMBL:AF241636; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF00627: UBA/TS-N domain   chr5:9793793-9798647 REVERSE   Aliases: T1G16.10, T1G16_10	2.5	2.7	-0.2	-1.1	100.0%	-5.0
6542	AT1G29070.1   ribosomal protein L34 family protein, similar to plastid ribosomal protein L34 precursor GB:AAF64157 GI:7578860 from (Spinacia oleracea)	6.8	7.3	-0.5	-1.1	100.0%	-3.9
6543	AT5G67570.1   Symbol: EMB1408   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:26969551-26972073 FORWARD   Aliases: EMB1408, EMBRYO DEFECTIVE 1408, K9I9.14, K9I9_14	3.0	2.8	0.2	1.1	100.0%	-4.9
6544	AT3G44210.1   hypothetical protein   chr3:15927257-15928319 FORWARD   Aliases: F26G5.160	2.3	2.4	-0.1	-1.1	100.0%	-5.4
6545	AT4G04960.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr4:2533054-2535356 FORWARD   Aliases: T32N4.9, T32N4_9	5.2	4.9	0.4	1.1	100.0%	-4.3
6546	AT1G67950.4   RNA recognition motif (RRM)-containing protein   chr1:25482030-25483839 REVERSE   Aliases: T23K23.20, T23K23_20	5.5	5.9	-0.4	-1.1	100.0%	-4.1
6547	AT3G47450.2   expressed protein   chr3:17494053-17497332 REVERSE   Aliases: T21L8.200	5.2	5.7	-0.5	-1.1	100.0%	-3.9
6548	AT2G26240.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)   chr2:11174335-11175535 REVERSE   Aliases: T1D16.12, T1D16_12	9.3	9.1	0.2	1.1	100.0%	-4.4
6549	AT4G37870.2   similar to phosphoenolpyruvate carboxykinase (ATP), putative / PEP carboxykinase, putative / PEPCK, putative [Arabidopsis thaliana] (TAIR:At5g65690.1); similar to phosphoenolpyruvate carboxykinase [Flaveria pringlei] (GB:BAB43909.1); similar to phosphoenolpyruvate carboxykinase [Zoyisia japonica] (GB:BAD88616.1); similar to phosphoenolpyruvate carboxykinase [Flaveria trinervia] (GB:BAB43907.1); similar to PEPCK [Cucumis sativus] (GB:AAM00814.1); similar to phosphoenolpyruvate carboxykinase [Lycopersicon esculentum] (GB:AAG01894.2); contains InterPro domain Phosphoenolpyruvate carboxykinase (ATP) (InterPro:IPR001272); contains InterPro domain Phosphoenolpyruvate carboxykinase, N-terminal (InterPro:IPR008210)   chr4:17802688-17806533 REVERSE   Aliases: T28I19.150, T28I19_150	11.3	12.1	-0.8	-1.1	100.0%	-4.2
6550	AT3G52910.1   Symbol: AtGRF4	7.3	7.9	-0.6	-1.1	100.0%	-3.7
6551	AT5G02050.1   mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	7.6	8.2	-0.6	-1.1	100.0%	-3.8
6552	AT5G65580.1   expressed protein   chr5:26224880-26225188 FORWARD   Aliases: K21L13.9, K21L13_9	2.5	2.4	0.1	1.1	100.0%	-5.3
6553	ATCG00470.1   Symbol: ATPE   ATPase epsilon subunit   chrC:52265-52663 REVERSE   Aliases: ATPE	13.3	13.5	-0.2	-1.1	100.0%	-4.9
6554	AT5G21130.1   expressed protein   chr5:7185971-7186816 FORWARD   Aliases: T10F18.160, T10F18_160	3.1	2.9	0.2	1.1	100.0%	-4.7
6555	AT1G19170.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, low similarity to SP:P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28   chr1:6616634-6618977 FORWARD   Aliases: T29M8.4, T29M8_4	5.9	6.2	-0.3	-1.1	100.0%	-4.6
6556	AT1G73850.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g20260.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483358.1)   chr1:27771557-27774118 FORWARD   Aliases: F2P9.28, F2P9_28	3.7	3.5	0.3	1.1	100.0%	-4.5
6557	AT1G17615.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:6059434-6060660 FORWARD   Aliases: F1L3.31, F1L3_31	2.4	2.5	-0.1	-1.1	100.0%	-5.4
6558	AT1G78790.1   expressed protein   chr1:29628422-29629935 REVERSE   Aliases: F9K20.17, F9K20_17	7.1	6.7	0.4	1.1	100.0%	-3.9
6559	AT5G58380.1   Symbol: CIPK10	8.3	8.9	-0.6	-1.1	100.0%	-4.4
6560	AT4G05200.1   protein kinase family protein, contains Prosite:PS00108: Serine/Threonine protein kinases active-site signature   chr4:2679721-2682307 REVERSE   Aliases: C17L7.120, C17L7_120	2.7	3.1	-0.3	-1.1	100.0%	-4.1
6561	AT1G52410.2   caldesmon-related, weak similarity to Caldesmon (CDM) (Swiss-Prot:P12957) (Gallus gallus)   chr1:19524403-19529293 FORWARD   Aliases: F19K6.14, F19K6_14	2.2	2.3	-0.1	-1.1	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6562	AT1G54210.1   autophagy 12a (APG12a), identical to autophagy 12a (Arabidopsis thaliana) GI:19912169   chr1:20244912-20246230 FORWARD   Aliases: F20D21.38, F20D21_38	5.2	4.9	0.3	1.1	100.0%	-4.3
6563	AT5G40090.1   disease resistance protein-related, contains Pfam domain, PF00931: NB-ARC domain, a novel signalling motif found in plant resistance gene products   chr5:16059147-16060680 REVERSE   Aliases: MUD12.70, MUD12_70	2.8	2.6	0.2	1.1	100.0%	-4.5
6564	AT3G11160.1   expressed protein   chr3:3496073-3497169 REVERSE   Aliases: F11B9.9	3.7	3.4	0.3	1.1	100.0%	-4.3
6565	AT5G47940.1   expressed protein   chr5:19426468-19429119 REVERSE   Aliases: K16F13.3, K16F13_3	4.2	4.5	-0.3	-1.1	100.0%	-4.3
6566	AT3G22760.1   Symbol: SOL1   CXC domain containing TSO1-like protein 1 (SOL1), identical to CXC domain containing TSO1-like protein 1 (SOL1) (Arabidopsis thaliana) GI:7767427; contains Pfam profile PF03638: Tesmin/TSO1-like CXC domain; supporting cDNA gi:7767426:gb:AF205142.1:AF205142	3.5	3.7	-0.3	-1.1	100.0%	-4.5
6567	AT1G61870.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:22868669-22870280 REVERSE   Aliases: F8K4.8, F8K4_8	6.8	7.4	-0.6	-1.1	100.0%	-4.0
6568	AT5G43530.1   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to SP:P36607 DNA repair protein rad8 {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:17506555-17512058 FORWARD   Aliases: K9D7.2, K9D7_2	2.8	3.0	-0.2	-1.1	100.0%	-4.6
6569	AT4G38580.1   Symbol: ATFP6   heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related, low similarity to copper homeostasis factor (PMID:9701579)(GI:3168840); nearly identical to farnesylated protein TFP6 (GI:4097553); contains Heavy-metal-associated domain PF00403   chr4:18034445-18035879 FORWARD   Aliases: F20M13.140, F20M13_140, FARNESYLATED PROTEIN 6	7.7	7.0	0.7	1.1	100.0%	-4.1
6570	AT2G23140.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr2:9852933-9855842 REVERSE   Aliases: T20D16.23, T20D16_23	3.5	3.7	-0.2	-1.1	100.0%	-4.8
6571	AT2G39840.1   Symbol: TOPP4   serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) / phosphoprotein phosphatase 1, identical to SP:P48484 Serine/threonine protein phosphatase PP1 isozyme 4 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GI:166801 (Arabidopsis thaliana); contains a Ser/Thr protein phosphatase signature (PDOC00115); contains a metallo-phosphoesterase motif (QDOC50185)   chr2:16634336-16636367 FORWARD   Aliases: None	5.2	4.8	0.4	1.1	100.0%	-4.5
6572	AT3G14860.2   NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	5.2	5.5	-0.4	-1.1	100.0%	-4.5
6573	AT3G27930.1   expressed protein   chr3:10370536-10373673 REVERSE   Aliases: K24A2.1	6.6	6.4	0.2	1.1	100.0%	-4.4
6574	AT5G63390.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter-related protein' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.; expression supported by MPSS   chr5:25407738-25409817 REVERSE   Aliases: MLE2.2, MLE2_2	3.3	3.1	0.2	1.1	100.0%	-4.6
6575	AT4G14240.2   similar to CBS domain-containing protein-related [Arabidopsis thaliana] (TAIR:At4g14230.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAT07635.1); contains InterPro domain CBS (InterPro:IPR002550)   chr4:8204342-8207340 REVERSE   Aliases: DL3160C, FCAALL.149	4.5	4.2	0.3	1.1	100.0%	-4.4
6576	AT1G56430.1   nicotianamine synthase, putative, similar to nicotianamine synthase (Lycopersicon esculentum)(GI:4753801), nicotianamine synthase 2 (Hordeum vulgare)(GI:4894912)   chr1:21140609-21141752 FORWARD   Aliases: F13N6.10, F13N6_10	4.8	4.5	0.4	1.1	100.0%	-4.0
6577	AT3G23670.2   similar to phragmoplast-associated kinesin-related protein (PAKRP1) [Arabidopsis thaliana] (TAIR:At4g14150.1); similar to OSJNBa0038P21.12 [Oryza sativa (japonica cultivar-group)] (GB:CAE05519.1); contains InterPro domain Kinesin, motor region (InterPro:IPR001752)	4.5	4.9	-0.4	-1.1	100.0%	-4.3
6578	AT1G66250.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis)	5.0	5.3	-0.4	-1.1	100.0%	-4.1
6579	AT3G11640.1   expressed protein   chr3:3674505-3675204 FORWARD   Aliases: T19F11.4	4.0	3.7	0.4	1.1	100.0%	-4.5
6580	AT1G22700.2   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain; ESTs gb:T43026, gb:R64902, gb:Z18169 and gb:N37374 come from this gene   chr1:8028181-8029956 REVERSE   Aliases: T22J18.13, T22J18_13	5.2	4.8	0.4	1.1	100.0%	-4.4
6581	AT4G04880.1   adenosine/AMP deaminase family protein, low similarity to SP:P03958 Adenosine deaminase (EC 3.5.4.4) (Adenosine aminohydrolase) {Mus musculus}; contains Pfam profile PF00962: Adenosine/AMP deaminase   chr4:2464892-2467164 REVERSE   Aliases: T4B21.20, T4B21_20	4.6	5.0	-0.4	-1.1	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6582	AT4G23710.1   vacuolar ATP synthase subunit G 2 (VATG2) / V-ATPase G subunit 2 (VAG2) / vacuolar proton pump G subunit 2, identical to Swiss-Prot:O82629 vacuolar ATP synthase subunit G 2 (V-ATPase G subunit 2, Vacuolar proton pump G subunit 2) (Arabidopsis thaliana)   chr4:12350099-12351634 FORWARD   Aliases: F9D16.180, F9D16_180	8.4	7.9	0.6	1.1	100.0%	-4.2
6583	AT3G61590.1   F-box family protein, contains weak hit to Pfam PF00646: F-box domain; stamina pistilloidia (Stp) - Pisum sativum, EMBL:AF004843	4.6	4.8	-0.2	-1.1	100.0%	-4.5
6584	AT5G23150.1   Symbol: HUA2   PWWP domain-containing protein, identical to cDNA putative transcription factor (HUA2) GI:4868119; contains Pfam profile	3.9	3.7	0.2	1.1	100.0%	-4.6
6585	AT1G31130.1   expressed protein   chr1:11114682-11116176 REVERSE   Aliases: F28K20.6, F28K20_6	6.2	5.6	0.6	1.1	100.0%	-4.1
6586	AT5G57680.1   expressed protein   chr5:23379971-23380920 REVERSE   Aliases: MRI1.3, MRI1_3	2.5	2.4	0.2	1.1	100.0%	-5.0
6587	AT3G17830.1   DNAJ heat shock family protein, similar to SP:P35514 Chaperone protein dnaJ {Lactococcus lactis}; contains Pfam profiles PF00226: DnaJ domain, PF01556: DnaJ C terminal region, PF00684: DnaJ central domain (4 repeats)	3.6	3.9	-0.3	-1.1	100.0%	-4.2
6588	AT3G09070.1   glycine-rich protein, similar to hypothetical protein GB:AAD32765 (Arabidopsis thaliana)	4.5	4.7	-0.2	-1.1	100.0%	-4.6
6589	AT2G31070.1   TCP family transcription factor, putative, similar to TCP1 protein (GI:20269127) {Lupinus albus} and cycloidea (GI:12002867) (Lycopersicon esculentum)   chr2:13227555-13229686 REVERSE   Aliases: T16B12.12, T16B12_12	3.1	2.9	0.2	1.1	100.0%	-5.0
6590	AT5G56260.1   dimethylmenaquinone methyltransferase family protein, similar to bacterial S-adenosylmethionine:2-demethylmenaquinone methyltransferases; contains Pfam profile PF03737: Dimethylmenaquinone methyltransferase   chr5:22792551-22794437 REVERSE   Aliases: K24C1.7, K24C1_7	7.8	7.4	0.4	1.1	100.0%	-4.3
6591	AT3G14440.1   Symbol: NCED3   9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, similar to 9-cis-epoxycarotenoid dioxygenase GB:AAF26356 (GI:6715257)(Phaseolus vulgaris)   chr3:4831295-4833606 REVERSE   Aliases: 9 CIS EPOXYCAROTENOID DIOXYGENASE, ATNCED3, MOA2.4, NINE CIS EPOXYCAROTENOID DIOXYGENASE3, STO1	2.4	2.3	0.1	1.1	100.0%	-5.2
6592	AT1G14380.3   similar to calmodulin-binding family protein [Arabidopsis thaliana] (TAIR:At2g02790.1); similar to 'unknown protein, contains IQ calmodulin-binding motif' [Oryza sativa (japonica cultivar-group)] (GB:XP_475770.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048)	5.8	5.5	0.3	1.1	100.0%	-4.5
6593	AT5G09870.1   Symbol: CESA5   cellulose synthase, catalytic subunit, putative, similar to gi:2827141 cellulose synthase catalytic subunit (Ath-A), Arabidopsis thaliana   chr5:3073357-3077975 FORWARD   Aliases: CELLULASE SYNTHASE 5, MYH9.8, MYH9_8	6.1	5.9	0.2	1.1	100.0%	-4.4
6594	AT1G22410.1   2-dehydro-3-deoxyphosphoheptonate aldolase, putative / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase, putative / DAHP synthetase, putative, similar to 3-deoxy-D-arabino-heptulosonate 7-phosphate GI:170224 from (Nicotiana tabacum), SP:P21357 from Solanum tuberosum; contains Pfam Class-II DAHP synthetase family domain PF01474   chr1:7912043-7914992 FORWARD   Aliases: F12K8.24, F12K8_24	11.0	11.4	-0.5	-1.1	100.0%	-5.0
6595	AT3G52110.1   expressed protein   chr3:19334761-19336629 REVERSE   Aliases: F4F15.220	3.5	3.8	-0.2	-1.1	100.0%	-4.8
6596	AT4G26380.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.7	3.4	0.3	1.1	100.0%	-4.2
6597	AT1G03860.3   Symbol: ATPHB2	7.7	8.5	-0.8	-1.1	100.0%	-4.1
6598	AT4G12530.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:7428024-7428560 REVERSE   Aliases: T1P17.120, T1P17_120	2.7	2.5	0.2	1.1	100.0%	-5.0
6599	AT1G04690.1   Symbol: KAB1   potassium channel protein, putative, nearly identical to K+ channel protein (Arabidopsis thaliana) GI:1063415; contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family	8.8	9.4	-0.6	-1.1	100.0%	-4.6
6600	AT4G05400.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g21140.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73259.1)   chr4:2741157-2743306 FORWARD   Aliases: C6L9.80, C6L9_80	6.7	7.3	-0.6	-1.1	100.0%	-4.1
6601	AT5G18610.1   protein kinase family protein, contains eukaryotic protein kinase domain, PROSITE:PS00107   chr5:6192738-6195373 FORWARD   Aliases: T28N17.90, T28N17_90	2.8	2.6	0.2	1.1	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6602	AT4G14360.2   similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At5g14430.2); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At5g14430.1); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At3g23300.1); similar to dehydration-responsive protein-related [Arabidopsis thaliana] (TAIR:At1g04430.1); similar to dehydration-responsive protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD46056.1); contains InterPro domain Putative methyltransferase DUF248 (InterPro:IPR004159)   chr4:8267285-8270989 REVERSE   Aliases: DL3220C, FCAALL.222	6.7	7.4	-0.7	-1.1	100.0%	-4.2
6603	ATMG00130.1   Symbol: ORF121A   hypothetical protein   chrM:34190-34555 FORWARD   Aliases: ORF121A	2.1	2.2	-0.1	-1.1	100.0%	-5.3
6604	AT5G49060.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QYI4 DnaJ homolog subfamily B member 12 {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr5:19903724-19905576 FORWARD   Aliases: K20J1.3, K20J1_3	3.2	3.0	0.2	1.1	100.0%	-4.8
6605	AT4G32040.1   Symbol: KNAT5   homeobox protein knotted-1 like 5 (KNAT5) / homeodomain containing protein 1 (H1), identical to homeobox protein knotted-1 like 5 (KNAT5) SP:P48002 from (Arabidopsis thaliana)	5.2	4.7	0.5	1.1	100.0%	-4.0
6606	AT4G22756.1   Symbol: SMO1 2	5.9	6.7	-0.8	-1.1	100.0%	-4.3
6607	AT1G69670.1   Symbol: ATCUL3B/CUL3B   cullin, putative, contains similarity to Cullin homolog 3 (CUL-3) SP:Q13618, GI:3639052 from (Homo sapiens); contains Pfam profile PF00888: Cullin family. Interacts with members of AtBPM family and RBX1 suggesting it is part of an E3 ligase complex involved in RUB modification.   chr1:26205694-26207639 REVERSE   Aliases: ATCUL3B, CUL3B, T6C23.13, T6C23_13	3.9	4.3	-0.5	-1.1	100.0%	-4.4
6608	AT2G46270.2   Symbol: GBF3   G-box binding factor 3 (GBF3), identical to G-box binding factor 3 (GBF3) SP:P42776 from (Arabidopsis thaliana); contains Pfam profile: PF00170 bZIP transcription factor   chr2:19007264-19010476 FORWARD   Aliases: BZIP TRANSCRIPTION FACTOR, G BOX BINDING FACTOR 3, T3F17.8	5.5	5.0	0.5	1.1	100.0%	-4.2
6609	AT1G32500.1   Symbol: ATNAP6	7.5	8.0	-0.5	-1.1	100.0%	-4.2
6610	AT1G01640.2   speckle-type POZ protein-related, contains Pfam profile:PF00651 BTB/POZ domain; similar to Speckle-type POZ protein (SP:O43791) (Homo sapiens)   chr1:230994-232313 REVERSE   Aliases: T1N6.2, T1N6_2	7.7	6.9	0.8	1.1	100.0%	-4.1
6611	AT5G63520.1   expressed protein, contains InterPro domain Cyclin-like F-box (InterPro:IPR001810)   chr5:25443403-25446338 REVERSE   Aliases: MLE2.15, MLE2_15	5.5	6.0	-0.5	-1.1	100.0%	-4.3
6612	AT3G06010.1   homeotic gene regulator, putative, similar to SP:P25439 Homeotic gene regulator (Brahma protein) {Drosophila melanogaster}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain	3.6	4.5	-0.9	-1.1	100.0%	-4.3
6613	AT2G21300.2   similar to kinesin motor family protein [Arabidopsis thaliana] (TAIR:At4g38950.1); similar to kinesin heavy chain [Zea mays] (GB:AAK91812.1); similar to putative kinesin heavy chain [Oryza sativa (japonica cultivar-group)] (GB:XP_467026.1); similar to OSJNBa0091D06.23 [Oryza sativa (japonica cultivar-group)] (GB:XP_473345.1); similar to putative kinesin heavy chain [Oryza sativa (japonica cultivar-group)] (GB:BAD46370.1); similar to kinesin heavy chain [Zea mays] (GB:AAK91822.1); contains InterPro domain Kinesin, motor region (InterPro:IPR001752)	2.3	2.5	-0.2	-1.1	100.0%	-4.9
6614	AT5G61060.1   histone deacetylase family protein, similar to SP:Q9UBN7 Histone deacetylase 6 (HD6) {Homo sapiens}; contains Pfam profile PF00850: Histone deacetylase family   chr5:24584017-24588292 REVERSE   Aliases: MAF19.7, MAF19_7	4.7	5.2	-0.4	-1.1	100.0%	-4.1
6615	ATMG00060.1   Symbol: NAD5C   Mitochondrial NADH dehydrogenase subunit 5. The gene is trans-spliced from the three different pre-cursors, NAD5a, NAD5b and NAD5c.   chrM:20571-22086 REVERSE   Aliases: NAD5, NAD5.3, NAD5C	3.5	3.9	-0.4	-1.1	100.0%	-4.4
6616	AT1G62660.1   beta-fructosidase (BFRUCT3) / beta-fructofuranosidase / invertase, vacuolar, identical to beta-fructosidase GB:CAA67560 GI:1429209 (Arabidopsis thaliana); supported by full-length cDNA GI:14517549; identical to cDNA	2.7	3.2	-0.5	-1.1	100.0%	-4.2
6617	AT5G67010.1   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr5:26766284-26766842 REVERSE   Aliases: K8A10.8, K8A10_8	2.7	2.5	0.1	1.1	100.0%	-5.0
6618	AT3G06890.1   expressed protein   chr3:2176862-2177592 FORWARD   Aliases: F17A9.4	5.2	4.8	0.4	1.1	100.0%	-4.3
6619	AT5G49250.1   expressed protein   chr5:19982569-19983171 FORWARD   Aliases: K21P3.13, K21P3_13	2.8	2.6	0.2	1.1	100.0%	-4.6
6620	AT5G07400.1   forkhead-associated domain-containing protein / FHA domain-containing protein   chr5:2340643-2345453 FORWARD   Aliases: T2I1.110, T2I1_110	4.3	4.6	-0.3	-1.1	100.0%	-4.6
6621	AT3G48020.1   expressed protein   chr3:17735578-17735985 FORWARD   Aliases: T17F15.110	4.4	4.1	0.4	1.1	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6622	AT3G50760.1   similar to glycosyl transferase family 8 protein [Arabidopsis thaliana] (TAIR:At1g19300.1); similar to putative Avr9/Cf-9 rapidly elicited protein 231 [Oryza sativa (japonica cultivar-group)] (GB:BAD45664.1); contains InterPro domain Glycosyl transferase, family 8 (InterPro:IPR002495)   chr3:18879055-18880365 FORWARD   Aliases: F18B3.40	3.2	3.6	-0.4	-1.1	100.0%	-4.0
6623	AT4G29550.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr4:14502218-14503853 FORWARD   Aliases: T16L4.60, T16L4_60	2.7	2.9	-0.2	-1.1	100.0%	-4.9
6624	AT1G35470.2   SPLa/Ryanodine receptor (SPRY) domain-containing protein, similar to RanBPM (Homo sapiens) GI:15080674; contains Pfam profile PF00622: SPRY domain   chr1:13051436-13054965 REVERSE   Aliases: F12A4.1, F12A4_1	5.0	5.2	-0.3	-1.1	100.0%	-4.3
6625	AT1G44170.2   Symbol: ALDH3H1   aldehyde dehydrogenase, putative (ALDH), similar to aldehyde dehydrogenase ALDH (Craterostigma plantagineum) gi:17065918:emb:CAC84900	6.2	6.8	-0.6	-1.1	100.0%	-4.1
6626	AT1G54160.1   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr1:20221003-20223028 REVERSE   Aliases: F15I1.26, F15I1_26	6.9	6.4	0.5	1.1	100.0%	-3.8
6627	AT1G14300.1   expressed protein, contains Pfam PF04063: Domain of unknown function (DUF383) and PF04064: Domain of unknown function (DUF384)   chr1:4882371-4884780 REVERSE   Aliases: F14L17.6, F14L17_6	6.0	6.3	-0.3	-1.1	100.0%	-4.4
6628	AT4G34430.4   Symbol: ATSWI3C   DNA-binding family protein, contains Pfam domains PF04433: SWIRM domain, PF00249: Myb-like DNA-binding domain and PF00569: Zinc finger, ZZ type   chr4:16460924-16465327 FORWARD   Aliases: CHB03, CHB3, CHROMATIN REMODELING COMPLEX SUBUNIT B, F10M10.200, F10M10_200	3.3	3.1	0.1	1.1	100.0%	-4.9
6629	AT4G04640.1   Symbol: ATPC1   ATP synthase gamma chain 1, chloroplast (ATPC1), identical to SP:Q01908 ATP synthase gamma chain 1, chloroplast precursor (EC 3.6.3.14) {Arabidopsis thaliana}   chr4:2350496-2352016 REVERSE   Aliases: T19J18.4, T19J18_4	9.4	8.9	0.5	1.1	100.0%	-4.1
6630	AT1G26220.1   GCN5-related N-acetyltransferase (GNAT) family protein, low similarity to SP:P09453 Ribosomal-protein-alanine acetyltransferase (EC 2.3.1.128) {Escherichia coli}; contains Pfam profile PF00583: acetyltransferase, GNAT family	3.2	3.0	0.2	1.1	100.0%	-4.6
6631	AT4G18430.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	2.8	3.2	-0.4	-1.1	100.0%	-3.9
6632	AT3G20190.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor kinase GB:AAA33715 (Petunia integrifolia)   chr3:7044950-7047396 FORWARD   Aliases: MAL21.23	3.1	3.3	-0.2	-1.1	100.0%	-4.9
6633	AT1G33050.2   expressed protein   chr1:11968897-11971001 REVERSE   Aliases: T9L6.12, T9L6_12	5.7	5.2	0.4	1.1	100.0%	-4.2
6634	AT1G23090.1   Symbol: AST91   sulfate transporter, putative, similar to sulfate transporter (Arabidopsis thaliana) GI:2285885; contains Pfam profiles PF00916: Sulfate transporter family, PF01740: STAS domain   chr1:8184941-8189020 REVERSE   Aliases: SULFATE TRANSPORTER, SULFATE TRANSPORTER 91, SULTR3;3, T26J12.13, T26J12_13	4.2	4.5	-0.3	-1.1	100.0%	-4.4
6635	AT5G58800.2   similar to quinone reductase family protein [Arabidopsis thaliana] (TAIR:At4g27270.1); similar to unknown [Prunus armeniaca] (GB:AAD38143.1); contains InterPro domain Flavodoxin/nitric oxide synthase (InterPro:IPR008254)   chr5:23763109-23764499 REVERSE   Aliases: MZN1.27, MZN1_27	8.4	8.0	0.4	1.1	100.0%	-4.3
6636	AT3G05970.1   Symbol: LACS6   long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase (LACS6), strong similarity to AMP-binding protein (MF39P) gi:1617274 from Brassica napus, similar to putative long-chain-fatty-acid--CoA ligase (brain isozyme) GB:P33124 (Rattus norvegicus); contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA AtLACS6 for long-chain acyl-CoA synthetase GI:22531705   chr3:1786324-1791808 REVERSE   Aliases: F2O10.7, F2O10_7, LONG CHAIN ACYL COA SYNTHETASE 6	9.7	9.5	0.2	1.1	100.0%	-4.7
6637	AT1G18340.1   basal transcription factor complex subunit-related, similar to TFIIH basal transcription factor complex p34 subunit (Basic transcription factor 2 34 kDa subunit) (BTF2-p34) (General transcription factor IIH polypeptide 3) (SP:Q8VD76) {Mus musculus}; contains Pfam PF03850: Transcription factor Tfb4   chr1:6311476-6313924 REVERSE   Aliases: F15H18.15, F15H18_15	5.7	5.9	-0.2	-1.1	100.0%	-4.5
6638	AT5G57570.1   expressed protein   chr5:23331010-23331420 REVERSE   Aliases: MUA2.15, MUA2_15	3.6	3.3	0.3	1.1	100.0%	-4.6
6639	AT5G19920.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); related to TipD protein (SP:O15736, PIR:T08602) (Dictyostelium discoideum); related to WD-repeat protein RBAP1 (GI:9716495) (Zea mays)   chr5:6733218-6737375 REVERSE   Aliases: F28I16.70, F28I16_70	3.2	3.5	-0.3	-1.1	100.0%	-4.5
6640	AT3G17470.1   RelA/SpoT domain-containing protein / calcium-binding EF-hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain, Pfam profile PF04607: Region found in RelA / SpoT proteins   chr3:5979840-5982121 FORWARD   Aliases: MKP6.2	5.4	5.6	-0.2	-1.1	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6641	AT1G52680.1   late embryogenesis abundant protein-related / LEA protein-related, low similarity to late embryogenesis abundant proteins from (Brassica napus) SP:P13934, (Cicer arietinum) GI:2909420   chr1:19621811-19622680 REVERSE   Aliases: F6D8.10, F6D8_10	2.5	2.4	0.1	1.1	100.0%	-5.1
6642	AT5G62150.1   peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain	5.3	4.9	0.4	1.1	100.0%	-4.0
6643	AT5G06940.1   leucine-rich repeat family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr5:2148079-2150772 REVERSE   Aliases: MOJ9.11, MOJ9_11	2.6	2.5	0.1	1.1	100.0%	-5.0
6644	AT4G26070.3   Symbol: MEK1   mitogen-activated protein kinase kinase (MAPKK) (MKK1) (MEK1), identical to MEK1 (Arabidopsis thaliana) gi:2196704:gb:AAB97145; mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167   chr4:13217658-13219942 FORWARD   Aliases: ATMEK1, F20B18.180, F20B18_180, MITOGEN ACTIVATED PROTEIN KINASE KINASE, MKK1, NMAPKK	5.9	6.1	-0.3	-1.1	100.0%	-4.5
6645	AT4G24530.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'PsRT17-1 like protein' based on similarity to PsRT17-1 (GP:1778376) (Pisum sativum) which was based upon similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr4:12667368-12670023 REVERSE   Aliases: F22K18.270, F22K18_270	6.0	5.7	0.3	1.1	100.0%	-4.3
6646	AT1G07380.1   ceramidase family protein, contains similarity to mitochondrial ceramidase (Homo sapiens) gi:9246993:gb:AAF86240	5.6	5.3	0.3	1.1	100.0%	-4.2
6647	AT1G80920.1   Symbol: J8   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q05646 Chaperone protein dnaJ Erysipelothrix rhusiopathiae, SP:P45555 Chaperone protein dnaJ (HSP40) Staphylococcus aureus; contains Pfam profile PF00226 DnaJ domain   chr1:30408536-30409577 REVERSE   Aliases: F23A5.28, F23A5_28, J8	6.9	6.5	0.4	1.1	100.0%	-4.0
6648	AT1G27620.1   transferase family protein, similar to hypersensitivity-related gene product HSR201 - Nicotiana tabacum, EMBL:X95343; contains Pfam transferase family domain PF00248   chr1:9608406-9610529 FORWARD   Aliases: T22C5.6	3.9	4.3	-0.4	-1.1	100.0%	-4.1
6649	AT3G02555.1   expressed protein   chr3:539712-541510 REVERSE   Aliases: None	4.5	4.3	0.2	1.1	100.0%	-4.5
6650	AT2G36900.1   Symbol: MEMB11	8.2	8.0	0.2	1.1	100.0%	-4.7
6651	AT3G58660.1   60S ribosomal protein-related, contains weak similarity to 60S ribosomal protein L10A (CSA-19) (NEDD-6) (Swiss-Prot:P53026) (Mus musculus)   chr3:21712511-21714091 FORWARD   Aliases: T20N10.10	6.9	7.8	-0.9	-1.1	100.0%	-4.2
6652	AT1G35500.1   expressed protein   chr1:13066065-13066574 FORWARD   Aliases: F12A4.10, F12A4_10	3.4	3.2	0.2	1.1	100.0%	-4.7
6653	AT1G52060.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	4.1	3.8	0.3	1.1	100.0%	-4.4
6654	AT3G10810.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)   chr3:3381853-3384510 REVERSE   Aliases: T7M13.11	5.5	5.8	-0.3	-1.1	100.0%	-4.7
6655	AT5G25220.2   Symbol: KNAT3   similar to homeobox protein knotted-1 like 4 (KNAT4) [Arabidopsis thaliana] (TAIR:At5g11060.1); similar to homeobox protein NTH23 - common tobacco (GB:T02220); contains InterPro domain Homeobox (InterPro:IPR001356); contains InterPro domain KNOX1 domain (InterPro:IPR005540); contains InterPro domain ELK domain (InterPro:IPR005539); contains InterPro domain KNOX2 domain (InterPro:IPR005541); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr5:8736077-8738587 FORWARD   Aliases: F21J6.18, F21J6_18, KNAT3 HOMEBOX PROTEIN, KNOTTED1 LIKE HOMEBOX GENE 3	6.7	6.2	0.4	1.1	100.0%	-4.3
6656	AT4G11100.1   expressed protein   chr4:6768611-6770180 FORWARD   Aliases: T22B4.80, T22B4_80	3.3	3.5	-0.2	-1.1	100.0%	-4.6
6657	AT1G47210.2   Symbol: CYCA3;2   cyclin family protein, similar to A-type cyclin (Catharanthus roseus) GI:2190259; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr1:17303396-17305306 FORWARD   Aliases: CYCA3;2, Cyclin A3;2, F8G22.8, F8G22_8	3.8	4.1	-0.3	-1.1	100.0%	-4.5
6658	AT2G35060.2   Symbol: KUP11   similar to potassium transporter family protein [Arabidopsis thaliana] (TAIR:At1g31120.1); similar to potassium transporter (KUP1) [Arabidopsis thaliana] (TAIR:At2g30070.1); similar to potassium transporter family protein [Arabidopsis thaliana] (TAIR:At1g60160.1); similar to potassium transporter family protein [Arabidopsis thaliana] (TAIR:At4g19960.1); similar to potassium transporter (KUP3) [Arabidopsis thaliana] (TAIR:At3g02050.1); similar to putative potassium transporter [Oryza sativa (japonica cultivar-group)] (GB:CAD21002.1); similar to OSJNBa0070C17.23 [Oryza sativa (japonica cultivar-group)] (GB:XP_473875.1); similar to putative potassium transporter [Oryza sativa (japonica cultivar-group)] (GB:BAD46101.1); similar to POT9_ARATH Putative potassium transporter 9 (AtPOT9) (GB:O49423); similar to putative potassium transporter [Oryza sativa (japonica cultivar-group)] (GB:XP_479449.1); contains InterPro domain K+ potassium transporter (InterPro:IPR003855)   chr2:14782142-14785949 REVERSE   Aliases: F19I3.29, F19I3_29	4.3	4.1	0.2	1.1	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6659	AT5G40760.1   Symbol: G6PD6   Encodes a cytosolic glucose-6-phosphate dehydrogenase that is insensitive to reduction by DTT and whose mRNA is expressed ubiquitously.	9.0	9.6	-0.7	-1.1	100.0%	-4.3
6660	AT4G05060.1   vesicle-associated membrane family protein / VAMP family protein, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia)   chr4:2590063-2592161 REVERSE   Aliases: C17L7.8	4.6	4.4	0.3	1.1	100.0%	-4.6
6661	AT3G01930.2   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr3:319068-321565 REVERSE   Aliases: F28J7.26	4.8	4.4	0.5	1.1	100.0%	-4.4
6662	AT2G01090.1   ubiquinol-cytochrome C reductase complex 7.8 kDa protein, putative / mitochondrial hinge protein, putative, similar to SP:P48504 Ubiquinol-cytochrome C reductase complex 7.8 kDa protein (EC 1.10.2.2) (Mitochondrial hinge protein) (CR7) {Solanum tuberosum}; contains Pfam profile PF02320: Ubiquinol-cytochrome C reductase hinge protein   chr2:80014-81200 FORWARD   Aliases: F23H14.6, F23H14_6	9.8	9.3	0.4	1.1	100.0%	-4.2
6663	AT3G63130.1   Symbol: RANGAP1   RAN GTPase activating protein 1 (RanGAP1), contains Pfam PF00560: Leucine Rich Repeat domains; identical to RAN GTPase activating protein 1 (GI:6708466)(Arabidopsis thaliana)   chr3:23335596-23337888 FORWARD   Aliases: RAN GTPASE ACTIVATING PROTEIN 1, T20O10.230	3.6	3.8	-0.3	-1.1	100.0%	-4.5
6664	AT2G21220.1   auxin-responsive protein, putative, similar to auxin-induced protein TGSUR22 (GI:10185820) (Tulipa gesneriana)   chr2:9096407-9096894 FORWARD   Aliases: F7O24.6, F7O24_6	2.4	2.5	-0.1	-1.1	100.0%	-5.1
6665	AT1G14310.1   haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	7.7	8.0	-0.3	-1.1	100.0%	-4.3
6666	AT1G62740.1   stress-inducible protein, putative, similar to sti (stress inducible protein) (Glycine max) GI:872116; contains Pfam profile PF00515 TPR Domain   chr1:23234626-23237449 FORWARD   Aliases: F23N19.10, F23N19_10	8.3	8.7	-0.4	-1.1	100.0%	-4.3
6667	AT2G44530.1   ribose-phosphate pyrophosphokinase, putative / phosphoribosyl diphosphate synthetase, putative, very strong similarity to phosphoribosyl pyrophosphate synthase (Spinacia oleracea) GI:4902849; contains Pfam profile PF00156: Phosphoribosyl transferase domain	5.3	5.0	0.3	1.1	100.0%	-4.4
6668	AT1G71850.1   expressed protein, ; expression supported by MPSS   chr1:27028537-27029949 REVERSE   Aliases: F14O23.23, F14O23_23	4.8	5.1	-0.3	-1.1	100.0%	-4.2
6669	AT1G28100.3   expressed protein   chr1:9801069-9804413 FORWARD   Aliases: F13K9.27, F13K9_27	8.1	8.5	-0.4	-1.1	100.0%	-4.3
6670	AT2G37020.1   translin family protein, similar to SP:Q62348 Translin {Mus musculus}; contains Pfam profile PF01997: Translin family   chr2:15553609-15556116 FORWARD   Aliases: T1J8.20, T1J8_20	5.7	6.3	-0.5	-1.1	100.0%	-4.1
6671	AT1G33440.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:12127454-12130369 REVERSE   Aliases: F10C21.11, F10C21_11	3.1	2.9	0.2	1.1	100.0%	-4.6
6672	AT1G64640.1   plastocyanin-like domain-containing protein, contains InterPro:IPR003245 plastocyanin-like domain   chr1:24025387-24026820 REVERSE   Aliases: F1N19.21, F1N19_21	2.7	2.9	-0.1	-1.1	100.0%	-5.2
6673	AT2G04220.1   expressed protein   chr2:1445398-1446321 FORWARD   Aliases: T23O15.16	2.4	2.3	0.1	1.1	100.0%	-5.2
6674	AT4G39420.1   expressed protein, ; expression supported by MPSS   chr4:18339725-18342147 FORWARD   Aliases: F23K16.50, F23K16_50	3.0	2.9	0.1	1.1	100.0%	-5.0
6675	AT1G15350.3   expressed protein   chr1:5278286-5279860 REVERSE   Aliases: F9L1.29, F9L1_29	5.6	5.2	0.5	1.1	100.0%	-4.2
6676	AT1G55280.1   expressed protein   chr1:20626627-20628297 REVERSE   Aliases: F7A10.4, F7A10_4	3.3	3.0	0.3	1.1	100.0%	-4.4
6677	AT5G03720.1   Symbol: AT HSFA3   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr5:971912-973682 REVERSE   Aliases: F17C15.140, F17C15_140, HSFA3	6.2	5.7	0.5	1.1	100.0%	-4.1
6678	AT2G45470.1   Symbol: FLA8   fasciclin-like arabinogalactan-protein (FLA8)   chr2:18749614-18751185 REVERSE   Aliases: F4L23.2	4.4	5.2	-0.8	-1.1	100.0%	-4.2
6679	AT5G15200.1   40S ribosomal protein S9 (RPS9B), 40S ribosomal protein S9, Chlamydomonas sp., EMBL:AU066528   chr5:4934886-4936384 REVERSE   Aliases: F8M21.90, F8M21_90	11.4	11.7	-0.3	-1.1	100.0%	-4.5
6680	AT5G07320.1   mitochondrial substrate carrier family protein, similar to peroxisomal Ca-dependent solute carrier (Oryctolagus cuniculus) GI:2352427 (mitochondrial carrier superfamily); contains INTERPRO:IPR001993 Mitochondrial substrate carrier family, INTERPRO:IPR002048 calcium-binding EF-hand domain	6.1	6.6	-0.4	-1.1	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6681	AT1G77960.1   similar to octicosapeptide/Phox/Bem1p (PB1) domain-containing protein [Arabidopsis thaliana] (TAIR:At5g09620.1); similar to hypothetical protein DDB0216723 [Dictyostelium discoideum] (GB:EAL72846.1); contains domain HIS_RICH (PS50316); contains domain GLN_RICH (PS50322)   chr1:29315359-29317867 REVERSE   Aliases: F28K19.17, F28K19_17	2.7	2.8	-0.1	-1.1	100.0%	-5.3
6682	AT5G61530.2   small G protein family protein / RhoGAP family protein, contains Pfam domain, PF00620: RhoGAP domain   chr5:24759311-24761985 FORWARD   Aliases: K11J9.10, K11J9_10	8.2	7.7	0.5	1.1	100.0%	-4.3
6683	AT1G70580.4   Symbol: AOAT2   similar to glutamate:glyoxylate aminotransferase 1 (GGT1) [Arabidopsis thaliana] (TAIR:At1g23310.1); similar to alanine aminotransferase [Oryza sativa (indica cultivar-group)] (GB:AAO84040.1); contains InterPro domain Aminotransferase, class I and II (InterPro:IPR004839); contains InterPro domain 1-aminocyclopropane-1-carboxylate synthase (InterPro:IPR001176)   chr1:26616525-26619732 FORWARD   Aliases: ALANINE 2 OXOGLUTARATE AMINOTRANSFERASE 2, F5A18.24, F5A18_24, GGT2, GLUTAMATE:GLYOXYLATE AMINOTRANSFERASE 2	7.3	7.9	-0.6	-1.1	100.0%	-4.1
6684	AT1G25350.1   glutamine-tRNA ligase, putative / glutaminyl-tRNA synthetase, putative / GlnRS, putative, similar to tRNA-glutamine synthetase GI:2995454 from (Lupinus luteus)   chr1:8889097-8894245 REVERSE   Aliases: F4F7.26, F4F7_26	7.2	7.6	-0.4	-1.1	100.0%	-4.8
6685	AT2G38800.1   calmodulin-binding protein-related, contains similarity to potato calmodulin-binding protein PCBP GI:17933110 from (Solanum tuberosum)   chr2:16224077-16226237 FORWARD   Aliases: F13I13.3, F13I13_3	8.4	8.0	0.4	1.1	100.0%	-4.2
6686	AT2G33440.1   splicing factor family protein, similar to Splicing factor U2AF 65 kDa subunit (U2 snRNP auxiliary factor large subunit) {Homo sapiens} SP:P26368, {Mus musculus} SP:P26369; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:14177716-14180513 FORWARD   Aliases: F4P9.21, F4P9_21	3.9	4.1	-0.2	-1.1	100.0%	-4.7
6687	AT1G55810.3   uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative, similar to SP:O65583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Arabidopsis thaliana}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family   chr1:20864294-20867932 FORWARD   Aliases: F20N2.21, F20N2_21	5.1	5.4	-0.3	-1.1	100.0%	-4.7
6688	AT5G05900.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:1774514-1776382 FORWARD   Aliases: K18J17.5, K18J17_5	3.2	3.4	-0.2	-1.1	100.0%	-4.5
6689	AT4G33150.2   Symbol: LKR   lysine-ketoglutarate reductase/saccharopine dehydrogenase bifunctional enzyme, identical to lysine-ketoglutarate reductase/saccharopine dehydrogenase GI:2052508 from (Arabidopsis thaliana)   chr4:15985201-15991541 REVERSE   Aliases: F4I10.80, F4I10_80, LYSINE KETOGLUTARATE REDUCTASE/SACCHAROPINE DEHYDROGENASE, SACCHAROPINE DEHYDROGENASE	7.7	7.3	0.4	1.1	100.0%	-4.4
6690	AT3G29180.1   expressed protein   chr3:11149452-11152797 FORWARD   Aliases: MUO22.2	8.6	8.9	-0.3	-1.1	100.0%	-4.5
6691	AT1G28150.1   expressed protein   chr1:9834930-9835886 REVERSE   Aliases: F13K9.24	7.7	7.3	0.3	1.1	100.0%	-4.3
6692	AT2G16365.2   F-box family protein, contains Pfam:PF00646 F-box domain	5.9	5.5	0.4	1.1	100.0%	-4.2
6693	AT1G47400.1   expressed protein   chr1:17388157-17388626 FORWARD   Aliases: T3F24.21, T3F24_21	3.9	4.3	-0.3	-1.1	100.0%	-4.3
6694	AT5G02770.1   expressed protein   chr5:627117-629253 REVERSE   Aliases: F9G14.80, F9G14_80	4.2	3.9	0.4	1.1	100.0%	-4.4
6695	AT3G16910.1   Symbol: AAE7/ACN1   Encodes a peroxisomal protein with acetyl-CoA synthetase activity that is responsible for the activation of acetate for entry into the glyoxylate cycle.   chr3:5773061-5775507 REVERSE   Aliases: AAE7, AC NON UTILIZING 1, ACN1, ACYL ACTIVATING ENZYME 7, K14A17.23	8.5	7.8	0.7	1.1	100.0%	-4.1
6696	AT4G33440.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to SP:P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28   chr4:16091943-16094961 FORWARD   Aliases: F17M5.200, F17M5_200	4.8	5.2	-0.4	-1.1	100.0%	-4.3
6697	AT2G40700.1   DEAD/DEAH box helicase, putative (RH17), identical to GB:CAA09207, contains a DEAD/DEAH box family ATP-dependent helicase signature; identical to cDNA DEAD box RNA helicase, RH17 GI:3776008   chr2:16983861-16986636 FORWARD   Aliases: T7D17.12, T7D17_12	3.8	4.1	-0.3	-1.1	100.0%	-4.4
6698	AT1G24490.1   Symbol: ARTEMIS   60 kDa inner membrane family protein, similar to chloroplast membrane protein (ALBINO3) (GI:3927828) (Arabidopsis thaliana)   chr1:8678846-8685262 FORWARD   Aliases: ARABIDOPSIS THALIANA ENVELOPE MEMBRANE INTEGRASE, F21J9.16	5.9	6.3	-0.4	-1.1	100.0%	-4.3
6699	AT3G24030.1   hydroxyethylthiazole kinase family protein, contains Pfam profile: PF02110 hydroxyethylthiazole kinase family   chr3:8679196-8680819 REVERSE   Aliases: F14O13.24	8.0	7.6	0.4	1.1	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6700	AT1G64140.1   expressed protein, similar to putative disease resistance protein GB:CAB40943 GI:4586107 from ( <i>Arabidopsis thaliana</i> ); weak similarity to Loricrin (Swiss-Prot:P23490) ( <i>Homo sapiens</i> )   chr1:23807456-23810822 REVERSE   Aliases: F22C12.10, F22C12_10	7.1	6.5	0.5	1.1	100.0%	-4.1
6701	AT4G05150.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, various predicted proteins contains Pfam profile PF00564: PB1 domain	5.8	5.3	0.5	1.1	100.0%	-4.1
6702	AT5G46400.1   expressed protein   chr5:18837259-18841877 FORWARD   Aliases: MPL12.20, MPL12_20	3.2	3.3	-0.1	-1.1	100.0%	-4.9
6703	AT3G05410.1   expressed protein   chr3:1554779-1555405 FORWARD   Aliases: F22F7.15, F22F7_15	3.2	3.0	0.2	1.1	100.0%	-4.6
6704	AT4G09160.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to polyphosphoinositide binding protein Ssh1p (GI:2739044) {Glycine max}; similar to polyphosphoinositide binding protein Ssh2, Glycine max, gb:T05953; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus   chr4:5839680-5842391 FORWARD   Aliases: T8A17.90, T8A17_90	5.2	4.9	0.3	1.1	100.0%	-4.3
6705	AT4G37250.1   leucine-rich repeat family protein / protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr4:17527644-17530500 REVERSE   Aliases: AP22.22, AP22_22	6.6	6.8	-0.2	-1.1	100.0%	-4.6
6706	AT3G62040.1   similar to haloacid dehalogenase-like hydrolase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g59490.1); similar to expressed protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_470321.1); contains InterPro domain HAD-superfamily hydrolase, subfamily IA, variant 3 (InterPro:IPR006402); contains InterPro domain Haloacid dehalogenase-like hydrolase (InterPro:IPR005834)   chr3:22986251-22987558 REVERSE   Aliases: F21F14.210	4.1	3.5	0.6	1.1	100.0%	-3.8
6707	AT2G47840.1   tic20 protein-related, similar to Tic20 (GI:3769673) ( <i>Pisum sativum</i> )   chr2:19601257-19602071 REVERSE   Aliases: F17A22.23	7.9	7.7	0.2	1.1	100.0%	-4.5
6708	AT4G36790.1   transporter-related, low similarity to spinster membrane proteins from ( <i>Drosophila melanogaster</i> ) GI:12003976, GI:12003972, GI:12003974, GI:12003970; contains Pfam profile PF00083: major facilitator superfamily protein   chr4:17336177-17338376 FORWARD   Aliases: AP22.91, AP22_91	5.9	6.1	-0.2	-1.1	100.0%	-4.6
6709	AT1G54770.1   expressed protein   chr1:20438329-20439675 FORWARD   Aliases: T22H22.18, T22H22_18	4.8	5.1	-0.3	-1.1	100.0%	-4.2
6710	AT3G01220.1   homeobox-leucine zipper protein, putative / HD-ZIP transcription factor, putative, similar to homeobox-leucine zipper protein, HAT7 (GB:Q00466) ( <i>Arabidopsis thaliana</i> )   chr3:73488-75545 FORWARD   Aliases: T4P13.9, T4P13_9	3.9	4.1	-0.2	-1.1	100.0%	-4.6
6711	AT3G60360.1   expressed protein   chr3:22323285-22325375 REVERSE   Aliases: T8B10.20	6.1	6.7	-0.5	-1.1	100.0%	-4.2
6712	AT1G54840.2   expressed protein   chr1:20456117-20457916 REVERSE   Aliases: T22H22.23, T22H22_23	3.8	4.0	-0.2	-1.1	100.0%	-4.7
6713	AT2G11000.1   Symbol: ATMAK10   similar to Unknown (protein for MGC:64157) [ <i>Danio rerio</i> ] (GB:AAH53286.1); contains InterPro domain Mak10 subunit, NatC N(alpha)-terminal acetyltransferase (InterPro:IPR007244)   chr2:4348205-4354938 REVERSE   Aliases: F15K19.7, F15K19_7, MAK10	6.3	5.9	0.4	1.1	100.0%	-4.3
6714	AT5G18800.2   NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein, contains Pfam profile: PF05850 NADH-ubiquinone oxidoreductase 19 kDa subunit   chr5:6267067-6268616 FORWARD   Aliases: F17K4.50, F17K4_50	12.3	12.6	-0.2	-1.1	100.0%	-5.0
6715	AT2G34970.1   eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein, similar to SP:Q64350 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) { <i>Rattus norvegicus</i> }; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon   chr2:14753386-14755860 FORWARD   Aliases: F19I3.20, F19I3_20	5.5	5.8	-0.4	-1.1	100.0%	-4.7
6716	AT2G13960.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain   chr2:5866667-5868393 FORWARD   Aliases: F9B22.7, F9B22_7	5.2	4.7	0.5	1.1	100.0%	-3.9
6717	AT5G02320.1   Symbol: MYB3R 5   myb family transcription factor (MYB3R5), contains Pfam profile: PF00249 myb-like DNA binding domain; identical to cDNA putative c-myb-like transcription factor MYB3R-5 (MYB3R5) GI:15375300   chr5:483121-486432 REVERSE   Aliases: T1E22.80, T1E22_80	5.2	4.7	0.5	1.1	100.0%	-3.9
6718	AT1G61560.1   Symbol: MLO6   seven transmembrane MLO family protein / MLO-like protein 6 (MLO6), identical to membrane protein Mlo6 ( <i>Arabidopsis thaliana</i> ) gi:14091582;gb:AAK53799; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 ( <i>Hordeum vulgare</i> )(Barley); contains Pfam profile	2.6	2.7	-0.1	-1.1	100.0%	-4.8
6719	AT5G15330.1   SPX (SYG1/Pho81/XPR1) domain-containing protein, similar to PHO1 protein ( <i>Arabidopsis thaliana</i> ) GI:20069032; contains Pfam profile PF03105: SPX domain   chr5:4980491-4982234 FORWARD   Aliases: F8M21.220, F8M21_220	3.6	3.4	0.2	1.1	100.0%	-4.7
6720	AT2G38250.1   DNA-binding protein-related, contains similarity to DNA-binding protein GI:170271 from ( <i>Nicotiana tabacum</i> )   chr2:16025462-16026578 FORWARD   Aliases: F16M14.18, F16M14_18	5.0	4.4	0.5	1.1	100.0%	-4.3
6721	AT5G53530.1   vacuolar protein sorting-associated protein 26, putative / VPS26, putative, similar to vacuolar sorting protein 26 ( <i>Homo sapiens</i> ) GI:9622852; contains Pfam profile PF03643: Vacuolar protein sorting-associated protein 26   chr5:21763269-21765790 REVERSE   Aliases: MNC6.7, MNC6_7	7.1	6.7	0.4	1.1	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6722	AT4G22510.1   expressed protein   chr4:11855059-11857083 REVERSE   Aliases: F7K2.90, F7K2_90	3.6	3.8	-0.2	-1.1	100.0%	-4.8
6723	AT1G27595.1   expressed protein, similar to Symplekin (SP:Q92797) {Homo sapiens}   chr1:9595480-9603242 FORWARD   Aliases: T22C5.3	3.1	3.3	-0.2	-1.1	100.0%	-4.8
6724	AT2G25625.2   expressed protein   chr2:10913538-10914357 FORWARD   Aliases: None	3.5	3.4	0.2	1.1	100.0%	-4.8
6725	AT1G64350.1   Symbol: SEH1H   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to nuclear pore protein SEH1 (SP:P53011) (Saccharomyces cerevisiae)   chr1:23885175-23886960 FORWARD   Aliases: F15H21.21, seh1 homolog	5.0	5.3	-0.3	-1.1	100.0%	-4.5
6726	NA	4.2	3.7	0.5	1.1	100.0%	-4.6
6727	AT5G61780.1   tudor domain-containing protein / nuclease family protein, contains Pfam domains PF00567: Tudor domain and PF00565: Staphylococcal nuclease homologue   chr5:24838484-24844195 FORWARD   Aliases: MAC9.14, MAC9_14	6.0	5.6	0.5	1.1	100.0%	-4.2
6728	AT5G65550.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase ;similar to flavonol 3-O-glucosyltransferase (anthocyanin rhamnosyl transferase) from Petunia hybrida (SP:Q43716)	4.0	3.7	0.3	1.1	100.0%	-4.5
6729	AT5G41850.1   expressed protein   chr5:16773926-16775019 REVERSE   Aliases: K16L22.14, K16L22_14	3.8	4.1	-0.2	-1.1	100.0%	-4.6
6730	AT4G29600.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase 7 (CDA7) (Arabidopsis thaliana) GI:3818574, cytidine deaminase homolog DesC (Arabidopsis thaliana) GI:4836445; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14515584-14516507 FORWARD   Aliases: T16L4.110, T16L4_110	3.0	3.2	-0.2	-1.1	100.0%	-4.9
6731	AT1G71890.1   sucrose transporter / sucrose-proton symporter (SUC5), nearly identical to sucrose transporter (Arabidopsis thaliana) GI:12057172   chr1:27062101-27064447 FORWARD   Aliases: F17M19.4, F17M19_4	3.2	3.4	-0.2	-1.1	100.0%	-4.5
6732	AT3G09900.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:871510 from (Pisum sativum); contains Pfam profile: PF00071 Ras family   chr3:3034567-3036596 FORWARD   Aliases: F8A24.5	7.8	8.0	-0.2	-1.1	100.0%	-4.4
6733	AT4G37580.1   Symbol: HLS1   N-acetyltransferase, putative / hookless1 (HLS1), contains Pfam profile PF00583: acetyltransferase, GNAT family; identical to cDNA putative N-acetyltransferase hookless1 (HLS1) GI:1277089   chr4:17658606-17660729 FORWARD   Aliases: CONSTITUTIVE PHOTOMORPHOGENIC 3, COP3, F19F18.70, F19F18_70, HOOKLESS 1, UNS2	4.5	4.2	0.2	1.1	100.0%	-4.5
6734	AT1G68990.1   DNA-directed RNA polymerase, mitochondrial (RPOMT), identical to SP:P92969 DNA-directed RNA polymerase, mitochondrial precursor (EC 2.7.7.6) {Arabidopsis thaliana}   chr1:25938307-25944629 REVERSE   Aliases: T6L1.17, T6L1_17	3.9	4.1	-0.2	-1.1	100.0%	-4.6
6735	AT1G03950.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr1:1011235-1013359 REVERSE   Aliases: F21M11.12, F21M11_12	5.6	5.0	0.6	1.1	100.0%	-4.0
6736	AT3G60950.1   C2 domain-containing protein, similar to CLB1 (Lycopersicon esculentum) GI:2789434; contains Pfam profile PF00168: C2 domain   chr3:22535450-22540489 FORWARD   Aliases: T27I15.40	2.9	3.1	-0.3	-1.1	100.0%	-4.6
6737	AT3G61030.1   C2 domain-containing protein, similar to CLB1 (Lycopersicon esculentum) GI:2789434; contains Pfam profile PF00168: C2 domain   chr3:22596630-22601670 FORWARD   Aliases: T27I15.120	2.9	3.1	-0.3	-1.1	100.0%	-4.6
6738	AT3G61050.2   similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g60950.1); similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g61030.1); similar to putative CLB1 protein (calcium-dependent lipid binding) protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477665.1); contains InterPro domain C2 domain (InterPro:IPR000008)   chr3:22608202-22612124 FORWARD   Aliases: T27I15.140	2.9	3.1	-0.3	-1.1	100.0%	-4.6
6739	AT5G41140.1   expressed protein   chr5:16485675-16489774 FORWARD   Aliases: MEE6.21, MEE6_21	3.1	3.7	-0.6	-1.1	100.0%	-4.2
6740	AT2G44690.1   Symbol: ARAC9   Rac-like GTP-binding protein (ARAC9), identical to rac-like protein ARAC9 GI:5381419 from (Arabidopsis thaliana)   chr2:18436339-18437879 FORWARD   Aliases: F16B22.18	5.0	4.8	0.2	1.0	100.0%	-4.4
6741	AT2G33730.1   DEAD box RNA helicase, putative, similar to SP:P23394 Pre-mRNA splicing factor RNA helicase PRP28 {Saccharomyces cerevisiae}; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr2:14272526-14275048 REVERSE   Aliases: T1B8.4, T1B8_4	8.0	8.2	-0.2	-1.0	100.0%	-4.8
6742	AT5G65180.2   expressed protein, contains Pfam domain, PF04818: Protein of unknown function, DUF618   chr5:26062602-26065257 FORWARD   Aliases: MQN23.12, MQN23_12	4.3	4.6	-0.4	-1.0	100.0%	-4.5
6743	AT5G59430.2   telomere repeat-binding protein 1 (TRP1), identical to telomere repeat-binding protein TRP1 (Arabidopsis thaliana) GI:5459298   chr5:23984541-23988171 FORWARD   Aliases: F2O15.20, F2O15_20	2.5	2.7	-0.2	-1.0	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6744	AT1G76620.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr1:28761453-28764191 FORWARD   Aliases: F14G6.22, F14G6_22	2.5	2.3	0.1	1.0	100.0%	-5.0
6745	AT1G15280.2   glycine-rich protein   chr1:5252332-5256746 FORWARD   Aliases: F9L1.22, F9L1_22	3.7	3.5	0.2	1.0	100.0%	-4.5
6746	AT1G11160.1   WD-40 repeat family protein / katanin p80 subunit, putative, similar to contains 6 WD-40 repeats (PF00400); katanin p80 subunit (GI:3005601) (Strongylocentrotus purpuratus)   chr1:3733925-3739703 FORWARD   Aliases: T28P6.17, T28P6_17	2.6	2.8	-0.2	-1.0	100.0%	-4.8
6747	AT1G04100.1   Symbol: IAA10   auxin-responsive protein / indoleacetic acid-induced protein 10 (IAA10), identical to SP:Q38828 Auxin-responsive protein IAA10 (Indoleacetic acid-induced protein 10) {Arabidopsis thaliana}   chr1:1059505-1061190 FORWARD   Aliases: AUXIN INDUCED PROTEIN 10, F20D22.13, F20D22_13	4.6	4.2	0.3	1.0	100.0%	-4.2
6748	AT1G21440.1   mutase family protein, similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from (Arabidopsis thaliana); similar to carboxyphosphoenolpyruvate mutase (GI:47149) (Streptomyces hygrosopicus); contains Prosite PS00161: Isocitrate lyase signature   chr1:7502159-7504140 REVERSE   Aliases: F24J8.7, F24J8_7	9.8	10.4	-0.6	-1.0	100.0%	-4.7
6749	AT5G52230.1   Symbol: MBD13   expressed protein   chr5:21225116-21229035 REVERSE   Aliases: F17P19.13, F17P19_13	2.4	2.6	-0.2	-1.0	100.0%	-4.9
6750	AT1G68110.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, similar to clathrin assembly protein AP180 (GI:6492344) (Xenopus laevis); contains Pfam profile: PF01417 ENTH domain, suggesting involvement in endocytosis or cytoskeletal machinery   chr1:25528381-25529813 FORWARD   Aliases: T23K23.4, T23K23_4	3.0	2.8	0.2	1.0	100.0%	-4.8
6751	ATCG00140.1   Symbol: ATPH   ATPase III subunit   chrC:13262-13507 REVERSE   Aliases: ATPH	9.3	8.7	0.5	1.0	100.0%	-4.3
6752	AT4G19900.1   glycosyl transferase-related, contains Pfam profiles PF01535: PPR repeat, PF04572: Alpha 1,4-glycosyltransferase conserved region, PF04488: Glycosyltransferase sugar-binding region containing DXD motif; several hypothetical proteins - Arabidopsis thaliana   chr4:10786958-10791443 REVERSE   Aliases: F18F4.6, F18F4_6	3.6	3.9	-0.3	-1.0	100.0%	-4.5
6753	AT5G57710.1   heat shock protein-related, contains similarity to 101 kDa heat shock protein; HSP101 (Triticum aestivum) gi:11561808:gb:AAC83689   chr5:23402020-23405579 FORWARD   Aliases: MRI1.7, MRI1_7	6.8	6.4	0.3	1.0	100.0%	-4.4
6754	AT3G17365.1   expressed protein, low similarity to PIR:I46078 endothelin converting enzyme from Bos primigenius taurus	5.9	6.3	-0.3	-1.0	100.0%	-4.7
6755	AT2G19880.1   ceramide glucosyltransferase, putative, similar to ceramide glucosyltransferase (GI:14718995) (Gossypium arboreum); weak similarity to Ceramide glucosyltransferase (Glucosylceramide synthase) (GCS) (UDP-glucose:N-acylsphingosine D-glucosyltransferase) (GLCT-1) (Swiss-Prot:Q16739) (Homo sapiens)	3.8	3.6	0.2	1.0	100.0%	-4.6
6756	AT5G40490.1   RNA recognition motif (RRM)-containing protein, ribonucleoprotein, Xenopus laevis, PIR:S40778; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	9.1	8.6	0.5	1.0	100.0%	-4.3
6757	AT5G65440.1   expressed protein   chr5:26168668-26174324 FORWARD   Aliases: MNA5.17, MNA5_17	5.1	5.4	-0.3	-1.0	100.0%	-4.5
6758	AT2G34470.2   Symbol: UREG   similar to urease accessory protein G [Solanum tuberosum] (GB:CAC33002.1); similar to urease accessory protein G [Solanum tuberosum] (GB:CAC33000.1); contains InterPro domain Urease accessory protein UreG (InterPro:IPR004400); contains InterPro domain HypB/UreG, nucleotide-binding (InterPro:IPR002894)   chr2:14537814-14539584 REVERSE   Aliases: PSKF109, T31E10.19, T31E10_19, UREASE ACCESSORY PROTEIN UREG	10.1	10.4	-0.4	-1.0	100.0%	-4.7
6759	AT3G01320.1   similar to paired amphipathic helix repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g70060.1); similar to paired amphipathic helix repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g59890.1); similar to paired amphipathic helix repeat-containing protein [Arabidopsis thaliana] (TAIR:At5g15020.1); similar to paired amphipathic helix repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g24190.1); similar to transcriptional co-repressor -like [Oryza sativa (japonica cultivar-group)] (GB:XP_549869.1); contains InterPro domain Paired amphipathic helix (InterPro:IPR003822)   chr3:106662-113625 FORWARD   Aliases: T22N4.5, T22N4_5	5.6	6.3	-0.7	-1.0	100.0%	-4.4
6760	AT4G11920.1   WD-40 repeat family protein, contains 6 WD repeats (PF00400); similar to Fzr1 (GI:6463679) {Homo sapiens}; similar to WD repeat protein Srw1 -Schizosaccharomyces pombe,PID:d1023012   chr4:7160270-7163376 REVERSE   Aliases: T26M18.130, T26M18_130	4.7	4.4	0.2	1.0	100.0%	-4.5
6761	AT4G39660.1   Symbol: AGT2   alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative, similar to SP:Q64565 Alanine--glyoxylate aminotransferase 2, mitochondrial precursor (EC 2.6.1.44) (AGT 2) (Beta-alanine-pyruvate aminotransferase) {Rattus norvegicus}; contains Pfam profile PF00202: aminotransferase, class III   chr4:18406767-18409466 FORWARD   Aliases: ALANINE:GLYOXYLATE AMINOTRANSFERASE 2, T19P19.50, T19P19_50	9.6	9.1	0.5	1.0	100.0%	-4.2
6762	AT4G16790.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:9451604-9453273 REVERSE   Aliases: DL4420C, FCAALL.137	4.0	3.8	0.2	1.0	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6763	AT3G55520.1   immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative, POSSIBLE PEPTIDYL-PROLYL CIS-TRANS ISOMERASE (EC 5.2.1.8) (PPIASE) (ROTAMASE) SP:P30416(Mouse);P59 PROTEIN (HSP BINDING IMMUNOPHILIN), rabbit, SWISSPROT:P27124:FKB4_RABBIT   chr3:20604691-20606324 FORWARD   Aliases: T22E16.180	10.7	10.3	0.4	1.0	100.0%	-4.5
6764	AT2G21520.1   similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At4g39170.1); similar to putative hosphatidylinositol/phosphatidylcholine transfer protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464026.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251); contains InterPro domain Cellular retinaldehyde binding/alpha-tocopherol transport (InterPro:IPR001071); contains InterPro domain Cellular retinaldehyde-binding/triple function, N-terminal (InterPro:IPR008273)	6.9	7.4	-0.5	-1.0	100.0%	-4.1
6765	AT4G33080.2   similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At2g19400.1); similar to protein kinase [Raphanus sativus] (GB:BAC76895.1); similar to putative serine/threonine kinase 38 [Oryza sativa (japonica cultivar-group)] (GB:BAD72247.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_914515.1); similar to protein kinase [Spinacia oleracea] (GB:CAA82991.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:15959965-15963980 FORWARD   Aliases: F4I10.10, F4I10_10	5.1	4.8	0.3	1.0	100.0%	-4.4
6766	AT1G23740.1   oxidoreductase, zinc-binding dehydrogenase family protein, contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family   chr1:8398115-8399717 REVERSE   Aliases: F5O8.29, F5O8_29	8.4	8.0	0.4	1.0	100.0%	-4.0
6767	AT1G14750.1   Symbol: SDS   cyclin, putative (SDS), identical to cyclin-like protein (Arabidopsis thaliana) GI:20302467; low similarity to SP:P30278 G2/mitotic-specific cyclin 2 (B-like cyclin) (CycMs2 {Medicago sativa}); contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:5079402-5082515 REVERSE   Aliases: F10B6.15, F10B6_15, SOLO DANCERS	2.9	2.8	0.1	1.0	100.0%	-5.2
6768	AT3G45500.1   expressed protein   chr3:16699403-16700678 REVERSE   Aliases: F9K21.80	2.6	2.9	-0.2	-1.0	100.0%	-4.8
6769	AT2G16340.1   hypothetical protein   chr2:7080216-7080566 FORWARD   Aliases: F16F14.16, F16F14_16	6.6	6.2	0.4	1.0	100.0%	-4.4
6770	AT2G29420.1   Symbol: ATGSTU7   glutathione S-transferase, putative   chr2:12625013-12625976 REVERSE   Aliases: F16P2.20, F16P2_20, GLUTATHIONE S TRANSFERASE 25, GST25	9.2	8.8	0.4	1.0	100.0%	-4.5
6771	AT3G59810.1   small nuclear ribonucleoprotein F, putative / U6 snRNA-associated Sm-like protein, putative / Sm protein F, putative, similar to SWISS-PROT:Q9Y4Y8 U6 snRNA-associated Sm-like protein LSm6 (Mus musculus)   chr3:22107492-22108885 FORWARD   Aliases: F24G16.80	8.2	7.8	0.4	1.0	100.0%	-4.3
6772	AT5G65160.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr5:26048419-26051040 REVERSE   Aliases: MQN23.9, MQN23_9	4.4	4.1	0.3	1.0	100.0%	-4.3
6773	AT4G30810.1   Symbol: SCPL29	8.9	9.3	-0.4	-1.0	100.0%	-4.4
6774	AT1G30160.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g05540.1); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR005174)   chr1:10606235-10607768 FORWARD   Aliases: T2H7.4, T2H7_4	3.1	2.9	0.2	1.0	100.0%	-4.9
6775	AT5G32590.1   myosin heavy chain-related, similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II)(SP:Q99323) {Drosophila melanogaster}   chr5:12238819-12241552 REVERSE   Aliases: F3D18.80, F3D18_80	2.5	2.4	0.1	1.0	100.0%	-5.3
6776	AT2G01510.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:230751-232505 REVERSE   Aliases: F2I9.13, F2I9_13	3.2	3.4	-0.2	-1.0	100.0%	-4.7
6777	AT5G47780.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8; strong similarity to unknown protein (emb:CAB71043.1)   chr5:19365145-19367895 FORWARD   Aliases: MCA23.10, MCA23_10	7.7	8.0	-0.3	-1.0	100.0%	-4.6
6778	AT4G23010.1   UDP-galactose transporter-related, contains weak similarity to UDP-galactose transporter related isozyme 1 (GI:1669562) (Mus musculus)   chr4:12060179-12062827 REVERSE   Aliases: F7H19.200, F7H19_200	6.5	6.0	0.5	1.0	100.0%	-4.3
6779	AT3G20150.1   kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain   chr3:7031418-7036505 FORWARD   Aliases: MAL21.18	2.6	2.9	-0.3	-1.0	100.0%	-4.4
6780	AT1G67890.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:25460842-25466455 FORWARD   Aliases: T23K23.26, T23K23_26	5.6	6.1	-0.5	-1.0	100.0%	-4.2
6781	AT1G66100.1   thionin, putative, similar to thionin (Arabidopsis thaliana) GI:1181533   chr1:24609334-24610200 REVERSE   Aliases: F15E12.20, F15E12_20	2.5	2.6	-0.2	-1.0	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6782	AT1G31380.1   hypothetical protein   chr1:11240432-11241080 REVERSE   Aliases: T8E3.3	2.7	2.8	-0.1	-1.0	100.0%	-5.1
6783	AT5G50410.1   expressed protein   chr5:20545425-20547053 REVERSE   Aliases: MXI22.13, MXI22_13	6.9	6.4	0.4	1.0	100.0%	-3.9
6784	AT4G17170.1   Symbol: AT RAB2   Rab2-like GTP-binding protein (RAB2), identical to Rab2-like protein (At-RAB2) GI:1765896 from (Arabidopsis thaliana)	7.4	7.0	0.4	1.0	100.0%	-4.4
6785	AT4G20020.2   expressed protein   chr4:10844141-10846133 REVERSE   Aliases: F18F4.120, F18F4_120	5.0	5.3	-0.2	-1.0	100.0%	-4.7
6786	AT4G18060.1   SH3 domain-containing protein 3 (SH3P3), nearly identical to SH3 domain-containing protein 3 (Arabidopsis thaliana) GI:16974680; contains Pfam profile PF00018: SH3 domain   chr4:10027492-10029866 REVERSE   Aliases: F15J5.30, F15J5_30	5.5	5.9	-0.4	-1.0	100.0%	-4.1
6787	AT4G00240.1   Symbol: PLDBETA2   phospholipase D beta 2 / PLD beta 2 (PLDBETA2) / PLDdelta1, identical to SP:O23078 Phospholipase D beta 2 (EC 3.1.4.4) (AtPLDbeta2) (PLD beta 2) (PLDdelta1) (Arabidopsis thaliana); contains Pfam profiles: PF00614 phospholipase D.active site motif, PF00168 C2 domain   chr4:106380-110718 REVERSE   Aliases: F5I10.13	5.9	6.3	-0.3	-1.0	100.0%	-4.4
6788	AT1G55190.1   prenylated rab acceptor (PRA1) family protein, contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr1:20592064-20592866 FORWARD   Aliases: F7A10.20, F7A10_20	5.3	5.6	-0.3	-1.0	100.0%	-4.3
6789	AT5G19720.1   tRNA synthetase class I (E and Q) family protein, similar to tRNA-glutamine synthetase (Lupinus luteus) GI:2995455; contains Pfam profile PF03950: tRNA synthetases class I (E and Q), anti-codon binding domain	3.7	3.9	-0.2	-1.0	100.0%	-4.7
6790	AT1G06310.1   Symbol: ACX6   Encodes a putative acyl-CoA oxidase. However, no transcripts have been detected for this gene and no altered phenotypes have been detected in plants mutant for this gene. This suggests that ACX6 does not significantly contribute to seedling beta-oxidation of fatty acids or indole-3-butyric acid in vivo.   chr1:1926790-1930257 FORWARD   Aliases: ACX6, ACYL COA OXIDASE 6, T2D23.2, T2D23_2	2.3	2.5	-0.2	-1.0	100.0%	-5.0
6791	AT5G43860.1   Symbol: ATCLH2	3.5	3.2	0.2	1.0	100.0%	-4.6
6792	AT4G33350.1   chloroplast inner membrane import protein Tic22, putative, similar to Tic22 (Pisum sativum) gi:3769671:gb:AAC64606   chr4:16064552-16066740 REVERSE   Aliases: F17M5.110, F17M5_110	6.0	6.5	-0.4	-1.0	100.0%	-4.2
6793	AT1G08490.1   cysteine desulfurase, putative, similar to nitrogen fixation protein (nifS) GB:D64004 GI:1001701 from (Synechocystis sp); contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V   chr1:2685662-2688592 REVERSE   Aliases: T27G7.17, T27G7_17	5.9	5.6	0.3	1.0	100.0%	-4.2
6794	AT2G47960.1   expressed protein   chr2:19632684-19636180 FORWARD   Aliases: F17A22.35	6.1	6.4	-0.4	-1.0	100.0%	-4.3
6795	AT2G17310.1   Symbol: SON1   F-box family protein, contains F-box domain Pfam:PF00646	3.3	3.1	0.2	1.0	100.0%	-4.6
6796	AT2G48130.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:19692138-19693063 REVERSE   Aliases: F11L15.3	2.7	3.1	-0.5	-1.0	100.0%	-3.8
6797	AT1G71080.1   expressed protein   chr1:26813503-26815427 REVERSE   Aliases: F23N20.7, F23N20_7	8.7	8.1	0.6	1.0	100.0%	-4.2
6798	AT1G04340.1   lesion inducing protein-related, similar to ORF, able to induce HR-like lesions (Nicotiana tabacum)   chr1:1163096-1164850 REVERSE   Aliases: F19P19.23, F19P19_23	7.3	6.9	0.4	1.0	100.0%	-4.4
6799	AT3G17620.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr3:6026452-6027700 REVERSE   Aliases: MKP6.18	3.3	3.4	-0.1	-1.0	100.0%	-4.9
6800	AT4G20910.1   Symbol: HEN1   double-stranded RNA binding protein-related / DsRBD protein-related, contains weak similarity to Pfam profile PF00035: Double-stranded RNA binding motif	3.4	3.7	-0.2	-1.0	100.0%	-4.5
6801	AT5G10930.1   Symbol: CIPK5   CBL-interacting protein kinase 5 (CIPK5), identical to CBL-interacting protein kinase 5 GP:9280632:gb:AAF86504 (Arabidopsis thaliana)   chr5:3445367-3447115 REVERSE   Aliases: CBL INTERACTING PROTEIN KINASE 5, T30N20.200, T30N20_200	5.3	5.6	-0.3	-1.0	100.0%	-4.5
6802	AT1G54510.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	5.0	5.4	-0.3	-1.0	100.0%	-4.5
6803	AT3G06330.2   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At5g18760.1); similar to zinc finger (C3HC4-type RING finger) protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_464222.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr3:1917246-1919931 FORWARD   Aliases: F24P17.21, F24P17_21	4.7	4.2	0.4	1.0	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6804	AT3G05830.1   Encodes alpha-helical IF (intermediate filament)-like protein.   chr3:1736686-1738670 FORWARD   Aliases: F10A16.12, F10A16_12	3.5	3.9	-0.5	-1.0	100.0%	-4.3
6805	AT1G64150.1   expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	4.7	4.5	0.3	1.0	100.0%	-4.3
6806	AT5G55810.1   nicotinamide-nucleotide adenylyltransferase, putative / NAD(+) pyrophosphorylase, putative, similar to nicotinamide mononucleotide adenylyl transferase (Homo sapiens) GI:11245478; contains Pfam profile PF01467: Cytidylyltransferase   chr5:22601294-22603520 REVERSE   Aliases: MDF20.25, MDF20_25	3.6	3.4	0.3	1.0	100.0%	-4.3
6807	AT3G42725.1   expressed protein   chr3:14853888-14854695 REVERSE   Aliases: None	2.5	2.7	-0.1	-1.0	100.0%	-5.3
6808	AT5G14910.1   heavy-metal-associated domain-containing protein, Pfam profile PF00403: Heavy-metal-associated domain   chr5:4823717-4825373 FORWARD   Aliases: F2G14.30, F2G14_30	6.3	6.8	-0.5	-1.0	100.0%	-4.0
6809	AT3G47430.1   peroxisomal biogenesis factor 11 family protein / PEX11 family protein, contains Pfam PF05648: Peroxisomal biogenesis factor 11 (PEX11)   chr3:17491682-17492777 FORWARD   Aliases: T21L8.180	2.5	2.4	0.1	1.0	100.0%	-5.1
6810	AT5G44790.1   Symbol: RAN1   copper-exporting ATPase / responsive-to-antagonist 1 / copper-transporting ATPase (RAN1), identical to SP:Q9S7J8	9.2	8.7	0.5	1.0	100.0%	-4.4
6811	AT2G39080.1   expressed protein   chr2:16316907-16319587 REVERSE   Aliases: T7F6.25, T7F6_25	6.3	6.5	-0.2	-1.0	100.0%	-4.7
6812	AT4G39530.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:18374730-18377234 REVERSE   Aliases: F23K16.160, F23K16_160	2.9	3.1	-0.2	-1.0	100.0%	-4.8
6813	NA	6.2	5.7	0.5	1.0	100.0%	-4.7
6814	AT1G02305.1   cathepsin B-like cysteine protease, putative, similar to cathepsin B-like cysteine proteinase (Nicotiana rustica) GI:609175; contains Pfam profile PF00112: Papain family cysteine protease   chr1:455778-458124 FORWARD   Aliases: None	10.5	9.8	0.6	1.0	100.0%	-4.7
6815	AT4G08430.1   Ulp1 protease family protein, similar to At5g45570, At5g28235; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr4:5347393-5350433 REVERSE   Aliases: C18G5.10, C18G5_10	2.7	2.6	0.1	1.0	100.0%	-5.3
6816	AT5G41330.1   potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain   chr5:16552567-16555131 REVERSE   Aliases: MYC6.4, MYC6_4	4.4	3.9	0.5	1.0	100.0%	-4.2
6817	AT3G03300.1   Symbol: DCL2   DEAD/DEAH box helicase carpel factory-related, similar to RNA helicase GB:AAF03534   chr3:768027-774834 REVERSE   Aliases: T17B22.28	4.8	5.3	-0.5	-1.0	100.0%	-4.6
6818	AT3G18910.1   F-box family protein, contains Pfam:PF00646 F-box domain ; contains TIGRFAM TIGR01640: F-box protein interaction domain ; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:6521766-6523049 FORWARD   Aliases: K13E13.1	5.2	5.0	0.2	1.0	100.0%	-4.5
6819	AT1G04120.1   Symbol: ATMRP5	9.9	9.5	0.4	1.0	100.0%	-4.4
6820	AT1G70630.1   expressed protein   chr1:26634895-26637759 FORWARD   Aliases: F24J13.20, F24J13_20	2.3	2.2	0.1	1.0	100.0%	-5.4
6821	AT1G20010.1   Symbol: TUB5   tubulin beta-5 chain (TUB5), nearly identical to SP:P29513 Tubulin beta-5 chain {Arabidopsis thaliana}   chr1:6937786-6940573 REVERSE   Aliases: T20H2.21, T20H2_21	6.4	6.0	0.4	1.0	100.0%	-4.5
6822	AT2G03690.1   coenzyme Q biosynthesis Coq4 family protein / ubiquinone biosynthesis Coq4 family protein, contains Pfam profile PF05019: Coenzyme Q (ubiquinone) biosynthesis protein Coq4   chr2:1121897-1123168 REVERSE   Aliases: F19B11.14, F19B11_14	6.3	5.9	0.4	1.0	100.0%	-4.2
6823	AT3G09380.1   expressed protein, contains Pfam profile PF01883: Domain of unknown function   chr3:2885271-2886122 REVERSE   Aliases: F3L24.26	3.4	3.2	0.2	1.0	100.0%	-5.0
6824	AT1G29440.1   auxin-responsive family protein, similar to auxin-induced protein 6B (SP:P33083) (Glycine max)   chr1:10304557-10304955 REVERSE   Aliases: F15D2.3, F15D2_3	2.3	2.2	0.1	1.0	100.0%	-5.7
6825	AT1G77510.1   Symbol: ATPDIL1 2   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	8.1	8.8	-0.7	-1.0	100.0%	-4.3
6826	AT1G03060.1   WD-40 repeat family protein / beige-related, similar to BEIGE (GI:3928547) (Rattus norvegicus); Similar to gb:U70015 lysosomal trafficking regulator from Mus musculus and contains 2 Pfam PF00400 WD-40, G-beta repeats. ESTs gb:T43386 and gb:AA395236 come from this gene   chr1:712473-726891 REVERSE   Aliases: F1003.12, F1003_12	4.5	4.9	-0.4	-1.0	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6827	AT3G46920.1   protein kinase family protein, similar to MAP3K delta-1 protein kinase (Arabidopsis thaliana) GI:2253010; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr3:17291415-17295842 REVERSE   Aliases: T6H20.50	4.8	5.1	-0.4	-1.0	100.0%	-4.2
6828	AT3G06570.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr3:2047311-2048559 REVERSE   Aliases: F5E6.10, F5E6_10	6.6	6.3	0.3	1.0	100.0%	-4.3
6829	AT1G12400.1   expressed protein   chr1:4221861-4222835 FORWARD   Aliases: F5O11.12, F5O11_12	7.9	8.3	-0.5	-1.0	100.0%	-4.1
6830	AT5G12470.1   expressed protein   chr5:4044625-4047439 REVERSE   Aliases: None	10.8	10.4	0.4	1.0	100.0%	-4.7
6831	AT1G07140.1   Symbol: SIRANBP   Ran-binding protein 1a (RanBP1a), identical to Ran-binding protein (atranbp1a) GI:2058282 from (Arabidopsis thaliana)	11.3	11.8	-0.4	-1.0	100.0%	-4.8
6832	AT1G55840.1   SEC14 cytosolic factor (SEC14) / phosphoglyceride transfer protein, similar to polyphosphoinositide binding protein SEC14 homolog Ssh1p (GB:AAB94598) (Glycine max); identified in Eur J Biochem 1998 Dec 1;258(2):402-10 as AtSEC14, characterized by functional complementation in S. cerevisiae.   chr1:20877268-20879938 FORWARD   Aliases: F14J16.8, F14J16_8	9.2	9.9	-0.6	-1.0	100.0%	-4.5
6833	AT3G10740.1   Symbol: ASD1   glycosyl hydrolase family protein 51, similar to arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II from GI:13398414 (Hordeum vulgare)   chr3:3360893-3365368 REVERSE   Aliases: T7M13.18	6.8	7.4	-0.6	-1.0	100.0%	-4.1
6834	AT1G20020.1   ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative, strong similarity to Ferredoxin--NADP reductase, chloroplast precursor (EC 1.18.1.2) (FNR) from {Pisum sativum} SP:P10933, {Mesembryanthemum crystallinum} SP:P41343, {Spinacia oleracea} SP:P00455, (Capsicum annuum) GI:6899972   chr1:6942796-6945006 FORWARD   Aliases: T20H2.20, T20H2_20	5.7	6.2	-0.5	-1.0	100.0%	-4.0
6835	AT5G14860.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:4805890-4807762 FORWARD   Aliases: T9L3.160, T9L3_160	3.9	4.3	-0.3	-1.0	100.0%	-4.4
6836	AT3G63010.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr3:23300400-23302459 FORWARD   Aliases: T20O10.110	4.1	3.8	0.2	1.0	100.0%	-4.5
6837	AT5G15580.1   expressed protein, unknown protein F14P3.18 - Arabidopsis thaliana, EMBL:AC009755   chr5:5068304-5072495 REVERSE   Aliases: T20K14.190, T20K14_190	3.5	3.8	-0.3	-1.0	100.0%	-4.4
6838	AT1G48380.1   Symbol: RHL1   root hair initiation protein root hairless 1 (RHL1)   chr1:17881081-17882938 REVERSE   Aliases: F11A17.7, F11A17_7, ROOT HAIRLESS 1	6.4	6.1	0.3	1.0	100.0%	-4.1
6839	AT4G36900.1   Symbol: RAP2.10   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family (RAP2.10). The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.9 and RAP2.1.	6.6	6.2	0.4	1.0	100.0%	-4.3
6840	AT5G18580.1   Symbol: FASS   tonneau 2 (TON2), identical to tonneau 2 protein (TON2) GI:11494362 from (Arabidopsis thaliana); contains Pfam profile: PF00036 EF hand   chr5:6174998-6178569 FORWARD   Aliases: EMB40, EMBRYO DEFECTIVE 40, FASS 1, FS1, GDO, GORDO, T28N17.60, T28N17_60, TON2, TONNEAU 2	8.6	8.2	0.4	1.0	100.0%	-4.4
6841	AT5G11900.1   eukaryotic translation initiation factor SUI1 family protein, similar to SP:O43583 Density-regulated protein (DRP1 protein) (Smooth muscle cell associated protein-3) {Homo sapiens}; contains Pfam profile PF01253: Translation initiation factor SUI1   chr5:3834015-3836247 FORWARD   Aliases: F14F18.70, F14F18_70	6.9	6.5	0.4	1.0	100.0%	-4.0
6842	AT5G25080.1   expressed protein   chr5:8643675-8647061 FORWARD   Aliases: T11H3.90, T11H3_90	4.7	4.2	0.5	1.0	100.0%	-4.5
6843	AT4G10850.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr4:6674994-6676976 FORWARD   Aliases: F25I24.60, F25I24_60	2.5	2.6	-0.1	-1.0	100.0%	-5.1
6844	AT4G14970.1   expressed protein   chr4:8553851-8561661 FORWARD   Aliases: DL3525W, FCAALL.148	2.7	2.9	-0.2	-1.0	100.0%	-4.8
6845	AT2G36490.1   Symbol: ROS1   HhH-GPD base excision DNA repair family protein (ROS1), similar to DEMETER protein (Arabidopsis thaliana) GI:21743571; contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein   chr2:15315100-15321351 REVERSE   Aliases: F1O11.12, F1O11_12	2.5	2.3	0.2	1.0	100.0%	-5.1
6846	AT3G18600.1   DEAD/DEAH box helicase, putative, non-consensus acceptor splice site AT at exon 2; similar to DEAD box helicase protein GB:NP_006764 from (Homo sapiens), contains Pfam profile: PF00270	5.6	6.1	-0.4	-1.0	100.0%	-4.3
6847	AT5G30500.1   galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 GI:5608497 from (Ajuga reptans)   chr5:11632575-11634156 FORWARD   Aliases: None	2.7	2.5	0.1	1.0	100.0%	-5.0
6848	AT5G09760.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:3032376-3034544 FORWARD   Aliases: F17I14.50, F17I14_50	8.7	9.3	-0.5	-1.0	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6849	AT2G18180.1   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminussimilar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus);	3.4	3.2	0.2	1.0	100.0%	-4.6
6850	AT2G28930.3   Symbol: APK1B   similar to protein kinase (APK1a) [Arabidopsis thaliana] (TAIR:At1g07570.2); similar to protein kinase (APK1a) [Arabidopsis thaliana] (TAIR:At1g07570.1); similar to putative protein kinase [Oryza sativa] (GB:XP_493889.1); similar to putative protein kinase [Oryza sativa (japonica cultivar-group)] (GB:NP_910058.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr2:12431381-12434189 FORWARD   Aliases: T9I4.1, T9I4_1	6.3	6.7	-0.4	-1.0	100.0%	-4.2
6851	AT3G04910.2   Symbol: WNK1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g28080.1); similar to mitogen activated protein kinase kinase [Oryza sativa] (GB:AAC32599.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:1354641-1358225 FORWARD   Aliases: T9J14.14, T9J14_14, WITH NO LYSINE (K) 1, ZIK4	5.8	6.1	-0.4	-1.0	100.0%	-4.2
6852	AT4G11200.1   expressed protein, contains weak hit to Pfam profile PF03108: MuDR family transposase   chr4:6827754-6829492 REVERSE   Aliases: T22B4.180, T22B4_180	3.5	3.8	-0.3	-1.0	100.0%	-4.7
6853	AT3G13730.1   Symbol: CYP90D1   Encodes a cytochrome P-450 gene that is involved in brassinosteroid biosynthesis, most likely in the conversion step of teasterone (TE) to 3-dehydroteasterone (3DT), and/or 6-deoxoteasterone (6-deoxoTE) to 6-deoxo-3-dehydroteasterone (6-deoxo3DT); or the conversion of cathasterone (CT) to TE, and/or 6-deoxocathasterone (6-deoxoCT) to 6-deoxoTE. Member of the CYP90C CYP450 family. Similar to Cytochrome P450 90C1 (ROT3).   chr3:4497983-4500927 REVERSE   Aliases: MMM17.20	5.3	5.6	-0.3	-1.0	100.0%	-4.2
6854	AT1G64220.1   preprotein translocase-related, similar to TOM7 protein (Solanum tuberosum) GI:3319774   chr1:23836751-23836984 REVERSE   Aliases: F22C12.30, F22C12_30	2.9	2.8	0.1	1.0	100.0%	-5.0
6855	AT3G49360.1   glucosamine/galactosamine-6-phosphate isomerase family protein, similar to SP:O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) {Homo sapiens}; contains Pfam profile PF01182: Glucosamine-6-phosphate isomerase/6-phosphogluconolactonase   chr3:18314031-18315383 REVERSE   Aliases: F2K15.220	4.9	5.3	-0.4	-1.0	100.0%	-4.2
6856	AT1G75540.1   zinc finger (B-box type) family protein, similar to zinc finger protein GB:BAA33202 GI:3618312 from (Oryza sativa)   chr1:28369720-28371313 FORWARD   Aliases: F10A5.24, F10A5_24	6.1	6.6	-0.6	-1.0	100.0%	-4.1
6857	AT1G72750.1   Symbol: ATTIM23 2   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr1:27387027-27388186 FORWARD   Aliases: F28P22.6, F28P22_6	6.5	5.8	0.7	1.0	100.0%	-3.9
6858	AT2G24270.2   Symbol: ALDH11A3   NADP-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, similar to NADP-dependent glyceraldehyde-3-phosphate dehydrogenase (NON-phosphorylating glyceraldehyde 3-phosphate; glyceraldehyde-3-phosphate dehydrogenase (NADP+)) (Nicotiana plumbaginifolia) SWISS-PROT:P93338   chr2:10334132-10336826 REVERSE   Aliases: F27D4.18, F27D4_18	8.4	8.0	0.5	1.0	100.0%	-4.0
6859	AT1G15000.1   Symbol: SCPL50	6.2	6.0	0.2	1.0	100.0%	-4.5
6860	AT4G09150.1   T-complex protein 11, contains Pfam PF05794: T-complex protein 11   chr4:5828622-5833657 FORWARD   Aliases: F23J3.180, F23J3_180	5.6	5.9	-0.3	-1.0	100.0%	-4.3
6861	AT1G06240.1   expressed protein, contains Pfam domain, PF04305: Protein of unknown function (DUF455)   chr1:1911121-1913179 FORWARD   Aliases: F9P14.10, F9P14_10	4.9	4.6	0.4	1.0	100.0%	-4.1
6862	AT1G24040.2   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr1:8503781-8506792 REVERSE   Aliases: T23E23.19, T23E23_19	5.6	5.3	0.3	1.0	100.0%	-4.3
6863	AT3G02930.1   expressed protein, ; expression supported by MPSS   chr3:655313-658326 FORWARD   Aliases: F13E7.12, F13E7_12	6.1	7.1	-0.9	-1.0	100.0%	-4.0
6864	AT1G59840.2   expressed protein   chr1:22030172-22033044 FORWARD   Aliases: F23H11.16, F23H11_16	6.1	5.5	0.6	1.0	100.0%	-3.7
6865	AT5G57980.1   eukaryotic rpb5 RNA polymerase subunit family protein, similar to SP:P19388 DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) {Homo sapiens}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain	3.0	3.3	-0.3	-1.0	100.0%	-4.6
6866	AT3G51520.1   diacylglycerol acyltransferase family, contains Pfam PF03982: Diacylglycerol acyltransferase   chr3:19121628-19123739 FORWARD   Aliases: F26O13.160	6.5	5.9	0.6	1.0	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6867	AT3G53600.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:19886510-19887037 FORWARD   Aliases: F4P12.300	2.8	2.7	0.1	1.0	100.0%	-5.2
6868	AT3G29400.1   exocyst subunit EXO70 family protein, similar to EXO70 protein (GI:2352998) (Mus musculus); contains Pfam domain PF03081: Exo70 exocyst complex subunit   chr3:11298520-11300857 REVERSE   Aliases: MUO10.14	4.9	4.8	0.1	1.0	100.0%	-5.0
6869	AT3G25840.1   protein kinase family protein, contains Pfam profile: PF00069 eukaryotic protein kinase domain   chr3:9453926-9458791 REVERSE   Aliases: K9I22.6	6.6	6.2	0.3	1.0	100.0%	-4.4
6870	AT2G30220.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	2.6	2.8	-0.2	-1.0	100.0%	-4.9
6871	AT2G30310.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr2:12930132-12931448 FORWARD   Aliases: T9D9.12, T9D9_12	2.6	2.8	-0.2	-1.0	100.0%	-4.9
6872	AT3G20730.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:7247101-7249151 FORWARD   Aliases: MOE17.3	3.5	3.3	0.3	1.0	100.0%	-4.2
6873	AT5G42640.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:17105923-17106825 FORWARD   Aliases: MFO20.6, MFO20_6	2.2	2.3	-0.1	-1.0	100.0%	-5.6
6874	AT2G26530.2   Symbol: AR781   similar to calmodulin-binding protein [Arabidopsis thaliana] (TAIR:At2g15760.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:NP_914731.1)   chr2:11289853-11291289 REVERSE   Aliases: AR781, T9J22.20, T9J22_20	4.7	4.4	0.3	1.0	100.0%	-4.3
6875	AT2G45240.1   Symbol: MAP1A   methionyl aminopeptidase, putative / methionine aminopeptidase, putative / peptidase M, putative, similar to SP:Q01662 Methionine aminopeptidase 1 precursor (EC 3.4.11.18) {Saccharomyces cerevisiae}; contains Pfam profile PF00557: metallopeptidase family M24   chr2:18663040-18666151 FORWARD   Aliases: F4L23.25, METHIONINE AMINOPEPTIDASE 1A	5.5	5.9	-0.4	-1.0	100.0%	-4.3
6876	AT2G20350.1   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr2:8791850-8792477 FORWARD   Aliases: F11A3.10, F11A3_10	2.7	2.5	0.2	1.0	100.0%	-4.9
6877	AT5G62180.1   expressed protein, similar to PrMC3, Pinus radiata, GI:5487873   chr5:24996070-24997075 REVERSE   Aliases: MMI9.26	3.8	3.7	0.2	1.0	100.0%	-4.7
6878	AT1G23820.2   Symbol: SPDS1   spermidine synthase 1 (SPDSYN1) / putrescine aminopropyltransferase 1, identical to SP:Q9ZUB3 Spermidine synthase 1 (EC 2.5.1.16) (Putrescine aminopropyltransferase 1) (SPDSY 1) {Arabidopsis thaliana}   chr1:8420276-8422928 FORWARD   Aliases: F5O8.38, F5O8_38, SPERMIDINE SYNTHASE 1	12.0	12.4	-0.4	-1.0	100.0%	-5.0
6879	AT5G28800.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:10822884-10823642 FORWARD   Aliases: T32B20.90, T32B20_90	3.3	3.2	0.2	1.0	100.0%	-5.0
6880	AT2G18990.1   expressed protein   chr2:8245773-8247077 REVERSE   Aliases: F19F24.19, F19F24_19	4.3	4.6	-0.3	-1.0	100.0%	-4.3
6881	AT4G02690.1   expressed protein, low similarity to N-methyl-D-aspartate receptor-associated protein (Drosophila melanogaster) GI:567104, NMDA receptor glutamate-binding subunit (Rattus sp.) GI:8248741; contains Pfam profile PF01027: Uncharacterized protein family UPF0005   chr4:1186023-1187534 FORWARD   Aliases: T10P11.23, T10P11_23	3.9	3.6	0.2	1.0	100.0%	-4.5
6882	AT5G46190.1   KH domain-containing protein, strong similarity to unknown protein (pir::T04533)	4.4	4.1	0.3	1.0	100.0%	-4.4
6883	AT2G44970.1   lipase-related, contains weak similarity to lipase (Pseudomonas aeruginosa) gi:3550950:gb:AAC34733.   chr2:18555898-18559130 REVERSE   Aliases: T14P1.23, T14P1_23	8.4	8.7	-0.3	-1.0	100.0%	-4.4
6884	AT5G04480.1   expressed protein   chr5:1271516-1277986 REVERSE   Aliases: T32M21.80, T32M21_80	3.9	3.7	0.2	1.0	100.0%	-4.4
6885	AT1G63680.1   Symbol: PDE316	3.8	4.0	-0.3	-1.0	100.0%	-4.5
6886	AT5G59330.1   expressed protein   chr5:23948640-23948903 FORWARD   Aliases: MNC17.24, MNC17_24	3.1	2.9	0.2	1.0	100.0%	-4.8
6887	AT4G25780.1   pathogenesis-related protein, putative, similar to gene PR-1 protein - Medicago truncatula, SP:Q40374; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:13121077-13121964 FORWARD   Aliases: F14M19.60, F14M19_60	5.2	4.9	0.3	1.0	100.0%	-4.1
6888	AT4G37110.1   expressed protein   chr4:17484119-17486265 REVERSE   Aliases: AP22.72, AP22_72	4.4	4.7	-0.3	-1.0	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6889	AT2G01470.1   Symbol: STL2P   St12p protein (ST12p) / SEC12p protein, putative, 99.8% identical to St12p protein (GI:166878) {Arabidopsis thaliana}   chr2:211969-214464 REVERSE   Aliases: ATSEC12, F2I9.9, F2I9_9, SEC12P LIKE PROTEIN	10.2	10.5	-0.4	-1.0	100.0%	-4.4
6890	AT2G21800.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g22140.1); similar to hypothetical protein DDB0205993 [Dictyostelium discoideum] (GB:EAL67624.1); contains domain LYS_RICH (PS50318)   chr2:9305235-9309004 FORWARD   Aliases: F7D8.12, F7D8_12	2.9	3.1	-0.2	-1.0	100.0%	-4.7
6891	AT2G38090.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:15951789-15954163 FORWARD   Aliases: F16M14.2, F16M14_2	6.0	6.3	-0.3	-1.0	100.0%	-4.2
6892	AT3G18780.2   Symbol: ACT2   actin 2 (ACT2), identical to SP:Q96292 Actin 2 {Arabidopsis thaliana}; nearly identical to SP:Q96293 Actin 8 (Arabidopsis thaliana) GI:1669387 and to At1g49240   chr3:6474877-6477210 FORWARD   Aliases: ACTIN 2, ACTIN2, DEFORMED ROOT HAIRS 1, DER1, LIGHT STRESS REGULATED 2, LSR2, MVE11.16	9.3	9.9	-0.6	-1.0	100.0%	-4.4
6893	AT2G02740.1   transcription factor, putative, similar to DNA-binding protein p24 (Solanum tuberosum) GI:9651810, Plant Transcriptional Regulator Pbf-2 (Solanum tuberosum) (GI:21730639, GI:21730638, GI:21730640, GI:21730637)   chr2:769367-772312 FORWARD   Aliases: T20F6.12, T20F6_12	3.3	3.5	-0.2	-1.0	100.0%	-4.5
6894	AT1G01830.1   armadillo/beta-catenin repeat family protein, armadillo/beta-catenin-like repeats, Pfam:PF00514   chr1:298535-300729 REVERSE   Aliases: T1N6.25, T1N6_25	3.8	3.6	0.2	1.0	100.0%	-4.6
6895	AT5G12130.1   Symbol: PDE149	5.5	5.8	-0.3	-1.0	100.0%	-4.5
6896	AT2G34800.1   hypothetical protein   chr2:14689442-14689594 REVERSE   Aliases: F19I3.3, F19I3_3	2.4	2.5	-0.1	-1.0	100.0%	-5.6
6897	AT1G07960.3   Symbol: ATPDIL5 1   thioredoxin family protein, low similarity to protein disulfide isomerase 4 (Giardia intestinalis) GI:13489047; contains Pfam profile PF00085: Thioredoxin   chr1:2467174-2469151 FORWARD   Aliases: ATPDIL5 1, PDI LIKE 5 1, T6D22.5, T6D22_5	7.2	6.9	0.3	1.0	100.0%	-4.7
6898	AT4G39950.1   Symbol: CYP79B2   cytochrome P450 79B2, putative (CYP79B2), identical to cytochrome P450 (79B2) SP:O81346 from (Arabidopsis thaliana)   chr4:18525240-18527573 FORWARD   Aliases: T5J17.120, T5J17_120	3.8	4.3	-0.5	-1.0	100.0%	-3.9
6899	AT5G55030.2   expressed protein   chr5:22344421-22347072 REVERSE   Aliases: K13P22.3, K13P22_3	4.2	4.5	-0.3	-1.0	100.0%	-4.6
6900	AT1G56350.1   peptide chain release factor, putative, similar to SP:P28353 Peptide chain release factor 2 (RF-2). {Salmonella typhi}; contains Pfam profiles PF00472: Peptidyl-tRNA hydrolase domain, PF03462: PCRF domain   chr1:21098443-21101491 FORWARD   Aliases: F13N6.6, F13N6_6	5.9	5.5	0.3	1.0	100.0%	-4.1
6901	AT1G62390.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein, contains Pfam profiles PF00564: PB1 domain, PF00515: TPR Domain   chr1:23087975-23090792 REVERSE   Aliases: F24O1.41, F24O1_41	6.0	6.5	-0.5	-1.0	100.0%	-4.1
6902	AT2G39320.1   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr2:16424670-16425595 REVERSE   Aliases: T16B24.4, T16B24_4	3.0	2.9	0.2	1.0	100.0%	-4.9
6903	AT1G18310.1   glycosyl hydrolase family 81 protein, similar to beta-glucan binding protein GI:6625560 from (Phaseolus vulgaris)   chr1:6301193-6303949 REVERSE   Aliases: F15H18.17, F15H18_17	2.7	2.5	0.2	1.0	100.0%	-5.0
6904	AT4G31770.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.2	3.4	-0.2	-1.0	100.0%	-4.5
6905	AT5G18100.1   Symbol: CSD3   superoxide dismutase (Cu-Zn) / copper/zinc superoxide dismutase (CSD3), identical to copper/zinc superoxide dismutase GI:3273755	7.7	7.4	0.3	1.0	100.0%	-4.5
6906	AT4G16800.1   enoyl-CoA hydratase, putative, similar to AU-binding protein/Enoyl-CoA hydratase (Homo sapiens) GI:780241, (Mus musculus)GI:6840920; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr4:9454835-9456328 REVERSE   Aliases: DL4425C, FCAALL.21	6.9	7.5	-0.6	-1.0	100.0%	-4.3
6907	AT1G06890.1   transporter-related, low similarity to SP:Q9NTN3 UDP-glucuronic acid/UDP-N-acetylgalactosamine transporter {Homo sapiens}, SP:Q95YI5 UDP-sugar transporter UST74c {Drosophila melanogaster}, SP:Q18779 UDP-sugar transporter sqv-7 {Caenorhabditis elegans}; contains 8 predicted transmembrane domains   chr1:2111562-2114533 REVERSE   Aliases: F4H5.5, F4H5_5	8.2	7.9	0.3	1.0	100.0%	-4.5
6908	AT5G49945.1   expressed protein, strong similarity to unknown protein (pir::T09896)   chr5:20334631-20337381 FORWARD   Aliases: None	6.6	7.0	-0.4	-1.0	100.0%	-4.3
6909	AT2G33560.1   spindle checkpoint protein-related, similar to spindle checkpoint protein BubR1 (GI:22128593) (Xenopus laevis); similar to Mitotic checkpoint serine/threonine-protein kinase BUB1 beta (EC 2.7.1.-) (MAD3/BUB1-related protein kinase) (Mitotic checkpoint kinase MAD3L) (Swiss-Prot:Q9Z1S0) (Mus musculus)   chr2:14220680-14223075 REVERSE   Aliases: F4P9.33, F4P9_33	4.8	5.2	-0.5	-1.0	100.0%	-4.3
6910	AT2G10020.1   expressed protein, and genefinder   chr2:3804313-3804513 FORWARD   Aliases: F7B19.16, F7B19_16	6.5	6.1	0.4	1.0	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6911	AT3G15270.1   Symbol: SPL5   squamosa promoter-binding protein-like 5 (SPL5), identical to squamosa promoter binding protein-like 5 (Arabidopsis thaliana) GI:5931629; contains Pfam profile PF03110: SBP domain   chr3:5140396-5141353 REVERSE   Aliases: K7L4.7, SQUAMOSA PROMOTER BINDING PROTEIN LIKE 5	2.8	2.6	0.2	1.0	100.0%	-4.7
6912	AT3G25910.1   expressed protein   chr3:9490486-9492729 FORWARD   Aliases: MPE11.8	8.7	8.2	0.5	1.0	100.0%	-4.2
6913	AT2G36300.1   integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain   chr2:15220139-15221351 REVERSE   Aliases: F2H17.9, F2H17_9	7.4	7.0	0.3	1.0	100.0%	-4.3
6914	AT3G06410.1   similar to zinc finger (CCCH-type) family protein [Arabidopsis thaliana] (TAIR:At5g18550.1); similar to putative floral homeotic protein HUA1 [Oryza sativa (japonica cultivar-group)] (GB:BAD81402.1); contains InterPro domain Zn-finger, C-x8-C-x5-C-x3-H type (InterPro:IPR000571)   chr3:1947310-1949775 REVERSE   Aliases: F24P17.12, F24P17_12	7.1	6.7	0.4	1.0	100.0%	-4.4
6915	AT4G27960.2   Symbol: UBC9   ubiquitin-conjugating enzyme E2-17 kDa 9 (UBC9), E2; identical to gi:297883, SP:P35132; identical to cDNA UBC9 for ubiquitin conjugating enzyme homolog GI:297883   chr4:13915839-13917426 REVERSE   Aliases: T13J8.70, T13J8_70, UBIQUITIN CONJUGATING ENZYME 9, UBIQUITIN PROTEIN LIGASE	13.7	13.3	0.5	1.0	100.0%	-5.6
6916	AT5G53300.2   Symbol: UBC10   ubiquitin-conjugating enzyme 10 (UBC10), E2; identical to gi:297877, SP:P35133   chr5:21649740-21651389 REVERSE   Aliases: None	13.7	13.3	0.5	1.0	100.0%	-5.6
6917	AT1G02850.3   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max)   chr1:630512-633259 FORWARD   Aliases: F22D16.15, F22D16_15	8.2	8.7	-0.6	-1.0	100.0%	-4.0
6918	AT2G01350.2   quinolinate phosphoribosyl transferase family protein, contains Pfam profile: PF01729 quinolinate phosphoribosyl transferase, C-terminal domain   chr2:165145-167246 REVERSE   Aliases: F10A8.23, F10A8_23	9.7	10.0	-0.3	-1.0	100.0%	-4.6
6919	AT2G40790.1   thioredoxin family protein, contains Pfam profile: PF00085 thioredoxin   chr2:17030041-17031346 REVERSE   Aliases: T7D17.3, T7D17_3	4.0	3.7	0.3	1.0	100.0%	-4.5
6920	AT3G25690.1   Symbol: CHUP1   hydroxyproline-rich glycoprotein family protein, Common family members: At4g18570, At4g04980, At5g61090 (Arabidopsis thaliana);	5.4	5.9	-0.5	-1.0	100.0%	-4.0
6921	AT5G05680.1   nuclear pore complex protein-related, contains weak similarity to Nuclear pore complex protein Nup88 (Nucleoporin Nup88) (88 kDa nuclear pore complex protein) (Swiss-Prot:Q99567) (Homo sapiens)   chr5:1698271-1702616 FORWARD   Aliases: MJJ3.8, MJJ3_8	5.5	5.8	-0.3	-1.0	100.0%	-4.5
6922	AT2G37650.1   scarecrow-like transcription factor 9 (SCL9), identical to cDNA scarecrow-like 9 (SCL9) mRNA, partial cds GI:4580524   chr2:15799701-15802313 FORWARD   Aliases: F13M22.15, F13M22_15	3.7	3.4	0.3	1.0	100.0%	-4.5
6923	AT5G14590.1   isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative, strong similarity to isocitrate dehydrogenase (NADP+) (Nicotiana tabacum) GI:3021512; contains Pfam domain PF00180: dehydrogenase, isocitrate/isopropylmalate family   chr5:4703301-4706738 REVERSE   Aliases: T15N1.80, T15N1_80	10.1	10.5	-0.4	-1.0	100.0%	-4.4
6924	AT1G56520.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:21179279-21182585 REVERSE   Aliases: F25P12.102, F25P12_102	3.4	3.1	0.2	1.0	100.0%	-4.6
6925	AT1G74040.1   Symbol: IMS1   2-isopropylmalate synthase 1 (IMS1), identical to 2-isopropylmalate synthase (IMS1) (Arabidopsis thaliana) GI:12330687; identical to cDNA 2-isopropylmalate synthase (IMS1) GI:12330686	7.8	8.2	-0.4	-1.0	100.0%	-4.2
6926	AT5G40950.1   50S ribosomal protein L27, chloroplast, putative (RPL27), identical to SP:Q9FLN4 ribosomal protein L27, chloroplast precursor {Arabidopsis thaliana}; similar to SP:P30155 50S ribosomal protein L27, chloroplast precursor (CL27) {Nicotiana tabacum}   chr5:16428037-16429284 FORWARD   Aliases: MMG1.7	6.8	7.4	-0.6	-1.0	100.0%	-4.0
6927	AT4G36060.2   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.5	2.4	0.1	1.0	100.0%	-4.8
6928	AT5G29050.1   hypothetical protein, predicted protein, Arabidopsis thaliana   chr5:11111696-11112287 FORWARD   Aliases: F23C8.20, F23C8_20	2.3	2.2	0.1	1.0	100.0%	-5.3
6929	AT1G29660.1   GDSL-motif lipase/hydrolase family protein, low similarity to family II lipase EXL1 (Arabidopsis thaliana) GI:15054382; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr1:10371825-10373743 FORWARD   Aliases: F15D2.21, F15D2_21	2.0	1.9	0.1	1.0	100.0%	-5.5
6930	AT5G17210.2   expressed protein   chr5:5656435-5658149 FORWARD   Aliases: MKP11.6, MKP11_6	7.5	6.9	0.6	1.0	100.0%	-4.1
6931	AT5G17720.1   hydrolase, alpha/beta fold family protein, low similarity to SP:P27747 Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Ralstonia eutropha) {Alcaligenes eutrophus}, SP:P24640 Lipase 3 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Moraxella sp}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:5845936-5847655 FORWARD   Aliases: MVA3.7, MVA3_7	3.5	3.8	-0.2	-1.0	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6932	AT3G19450.1   Symbol: CAD4   cinnamyl-alcohol dehydrogenase (CAD), identical to SP:P48523 Cinnamyl-alcohol dehydrogenase (EC 1.1.1.195) (CAD) (Arabidopsis thaliana)   chr3:6744769-6747220 FORWARD   Aliases: ATCAD4, CAD, CAD C, CINNAMYL ALCOHOL DEHYDROGENASE 4, MLD14.30	7.9	8.5	-0.7	-1.0	100.0%	-4.0
6933	AT4G27430.1   Symbol: CIP7   COP1-interacting protein 7 (CIP7), identical to COP1-Interacting Protein 7 (CIP7) GI:3327868 from (Arabidopsis thaliana)	4.3	4.6	-0.3	-1.0	100.0%	-4.3
6934	AT3G07300.2   similar to eukaryotic translation initiation factor 2B family protein / eIF-2B family protein [Arabidopsis thaliana] (TAIR:At2g44070.1); similar to putative translation initiation factor 2B beta subunit [Oryza sativa (japonica cultivar-group)] (GB:AAP53571.1); contains InterPro domain Initiation factor 2B (InterPro:IPR000649)   chr3:2324623-2327630 REVERSE   Aliases: T1B9.3	5.4	5.7	-0.3	-1.0	100.0%	-4.4
6935	AT5G48460.1   fimbrin-like protein, putative, strong similarity to fimbrin-like protein AtFim2 (Arabidopsis thaliana) GI:2737926; contains Pfam profile PF00307: Calponin homology (CH) domain	6.0	6.2	-0.2	-1.0	100.0%	-4.7
6936	AT1G67820.1   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase 2C emb:CAA72341.1   chr1:25433516-25435725 FORWARD   Aliases: F12A21.5, F12A21_5	9.1	8.7	0.4	1.0	100.0%	-4.1
6937	AT3G25800.2   Symbol: PDF1   similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit A (RCN1) [Arabidopsis thaliana] (TAIR:At1g25490.1); similar to serine/threonine protein phosphatase 2A (PP2A) 65 kDa regulatory subunit, putative [Arabidopsis thaliana] (TAIR:At1g13320.1); similar to protein phosphatase [Cicer arietinum] (GB:CAA10285.1); similar to serine/threonine protein phosphatase type 2A regulatory subunit A (GB:AAB60713.1); similar to Ser/Thr specific protein phosphatase 2A A regulatory subunit beta isoform [Medicago sativa subsp. x varia] (GB:AAG29594.1); similar to protein phosphatase 2A [Nicotiana tabacum] (GB:CAA66487.1); similar to phosphatase 2A regulatory A subunit [Oryza sativa (japonica cultivar-group)] (GB:XP_450276.1); contains InterPro domain HEAT repeat (InterPro:IPR000357)   chr3:9423825-9427281 REVERSE   Aliases: K13N2.2, PR 65, PR65	8.1	8.5	-0.4	-1.0	100.0%	-4.2
6938	AT5G18340.1   U-box domain-containing protein, weak similarity to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain   chr5:6070642-6072200 REVERSE   Aliases: F20L16.60, F20L16_60	4.2	3.9	0.2	1.0	100.0%	-4.5
6939	AT3G13130.1   expressed protein   chr3:4223015-4223620 FORWARD   Aliases: MJG19.8	3.2	3.4	-0.2	-1.0	100.0%	-4.9
6940	AT3G56720.1   expressed protein   chr3:21022032-21024398 FORWARD   Aliases: T8M16.50	8.3	7.9	0.4	1.0	100.0%	-4.5
6941	AT3G09480.1   histone H2B, putative, similar to histone from Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP:O22582, H2B-3 GB:CAA12231 from (Lycopersicon esculentum); contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr3:2914896-2915276 REVERSE   Aliases: F11F8.5	7.5	7.9	-0.5	-1.0	100.0%	-4.1
6942	AT4G12490.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:7409618-7410403 REVERSE   Aliases: T1P17.80, T1P17_80	2.6	2.5	0.1	1.0	100.0%	-4.9
6943	AT4G31750.1   protein phosphatase 2C, putative / PP2C, putative, protein phosphatase 2C, Medicago sativa, PID:g2582800	8.3	8.0	0.3	1.0	100.0%	-4.6
6944	AT2G27750.1   nucleolar matrix protein-related, contains Pfam domain, PF04935: Surfeit locus protein 6	2.9	3.0	-0.2	-1.0	100.0%	-5.0
6945	AT5G19750.1   peroxisomal membrane 22 kDa family protein, similar to SP:P42925 22 kDa peroxisomal membrane protein {Mus musculus}; contains Pfam profile PF04117: Mpv17 / PMP22 family	4.2	4.5	-0.3	-1.0	100.0%	-4.6
6946	AT5G52100.1   dihydrodipicolinate reductase family protein, weak similarity to dihydrodipicolinate reductase (Corynebacterium glutamicum) GI:311768; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus   chr5:21187371-21189571 FORWARD   Aliases: MSG15.20, MSG15_20	3.1	3.3	-0.2	-1.0	100.0%	-4.7
6947	AT4G02750.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:1221116-1223461 REVERSE   Aliases: T5J8.5, T5J8_5	4.7	5.2	-0.5	-1.0	100.0%	-4.0
6948	AT1G64320.1   myosin heavy chain-related, similar to myosin heavy chain (GI:4249703) (Rana catesbeiana); similar to smooth muscle myosin heavy chain SM2 (GI:2352945) (Homo sapiens)   chr1:23872699-23874211 FORWARD   Aliases: F15H21.20, F15H21_20	2.4	2.5	-0.1	-1.0	100.0%	-5.5
6949	AT4G11860.1   expressed protein, contains Pfam domain PF04424: Protein of unknown function (DUF544)   chr4:7134078-7138497 REVERSE   Aliases: T26M18.70, T26M18_70	6.8	7.3	-0.5	-1.0	100.0%	-4.2
6950	AT1G20960.1   Symbol: EMB1507   U5 small nuclear ribonucleoprotein helicase, putative, similar to SP:O75643 U5 small nuclear ribonucleoprotein 200 kDa helicase {Homo sapiens}; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF02889: Sec63 domain   chr1:7302580-7309903 REVERSE   Aliases: EMB1507, EMBRYO DEFECTIVE 1507, F9H16.5, F9H16_5	7.2	7.6	-0.4	-1.0	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6951	AT2G44560.1   glycosyl hydrolase family 9 protein   chr2:18398990-18400730 REVERSE   Aliases: F16B22.5	3.1	3.3	-0.2	-1.0	100.0%	-4.9
6952	AT3G04690.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:1273392-1275944 REVERSE   Aliases: F7O18.16, F7O18_16	2.6	2.4	0.1	1.0	100.0%	-5.0
6953	AT1G05410.2   similar to tropomyosin-related [Arabidopsis thaliana] (TAIR:At5g48160.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_469730.1); contains domain CYS_RICH (PS50311)   chr1:1585370-1587773 REVERSE   Aliases: T25N20.6, T25N20_6	6.3	6.6	-0.3	-1.0	100.0%	-4.3
6954	AT5G15600.1   expressed protein   chr5:5078203-5079094 FORWARD   Aliases: T20K14.210, T20K14_210	7.3	6.9	0.4	1.0	100.0%	-4.0
6955	AT1G01080.2   similar to 33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative [Arabidopsis thaliana] (TAIR:At3g52380.1); similar to unnamed protein product [Nicotiana tabacum] (GB:CAA37879.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr1:45296-47019 REVERSE   Aliases: T25K16.19, T25K16_19	4.2	4.5	-0.3	-1.0	100.0%	-4.3
6956	AT3G43930.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g26270.1); similar to unknown [Oryza sativa (japonica cultivar-group)] (GB:AAO72659.1); contains InterPro domain BRCT (InterPro:IPR001357)   chr3:15771885-15774317 REVERSE   Aliases: T15B3.70	2.7	2.6	0.2	1.0	100.0%	-4.9
6957	AT2G26830.1   Symbol: EMB1187   choline/ethanolamine kinase family protein, similar to SP:Q9HBU6 Ethanolamine kinase (EC 2.7.1.82) (EKI){Homo sapiens}, GmCK3p (Glycine max) GI:1438883; contains Pfam profile PF01633: Choline/ethanolamine kinase   chr2:11450639-11454184 FORWARD   Aliases: EMB1187, EMBRYO DEFECTIVE 1187, F12C20.13, F12C20_13	5.4	5.8	-0.5	-1.0	100.0%	-4.1
6958	AT2G10465.1   replication protein-related, weak similarity to Replication Protein A 70	2.6	2.7	-0.1	-1.0	100.0%	-5.3
6959	AT5G67060.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	2.9	0.1	1.0	100.0%	-5.0
6960	AT5G45240.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18330933-18336316 FORWARD   Aliases: K18C1.12, K18C1_12	2.6	2.7	-0.1	-1.0	100.0%	-5.1
6961	AT3G44330.1   expressed protein   chr3:16017685-16021952 FORWARD   Aliases: T22K7.10	5.7	6.3	-0.5	-1.0	100.0%	-4.3
6962	AT2G34930.1   disease resistance family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.1 (Lycopersicon pimpinellifolium) gi:1184075:gb:AAC15779   chr2:14744145-14746983 REVERSE   Aliases: F19I3.16, F19I3_16	3.0	2.8	0.2	1.0	100.0%	-4.8
6963	AT1G20620.5   Symbol: CAT3   similar to catalase 1 [Arabidopsis thaliana] (TAIR:At1g20630.1); similar to catalase 2 [Arabidopsis thaliana] (TAIR:At4g35090.1); similar to catalase 1 [Nicotiana tabacum] (GB:AAB71764.1); similar to catalase [Brassica juncea] (GB:AAD17935.1); similar to catalase [Prunus persica] (GB:CAD42908.1); similar to catalase [Brassica napus] (GB:AAB53101.2); similar to catalase 2 [Raphanus sativus] (GB:AAD30291.2); contains InterPro domain Catalase (InterPro:IPR002226)	7.9	7.1	0.8	1.0	100.0%	-4.1
6964	AT1G63210.1   expressed protein, contains Pfam profile: PF04283 protein of unknown function (DUF439)   chr1:23447353-23451019 FORWARD   Aliases: F16M19.22, F16M19_22	3.6	3.4	0.2	1.0	100.0%	-4.6
6965	AT5G65570.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:26221194-26223410 FORWARD   Aliases: K21L13.8, K21L13_8	3.2	3.1	0.2	1.0	100.0%	-5.1
6966	AT1G73880.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:27788642-27790465 FORWARD   Aliases: F2P9.25, F2P9_25	10.8	10.0	0.8	1.0	100.0%	-4.0
6967	AT5G66540.1   expressed protein, ; supported by full-length cDNA gi:12057175 from (Arabidopsis thaliana)   chr5:26573576-26576653 REVERSE   Aliases: K1F13.21, K1F13_21	3.9	4.1	-0.2	-1.0	100.0%	-4.6
6968	AT5G48710.1   ubiquitin-related, similar to SP:O13351 Ubiquitin-like protein smt3/pmt3 {Schizosaccharomyces pombe}   chr5:19772291-19772798 REVERSE   Aliases: K24G6.4, K24G6_4	4.2	3.9	0.3	1.0	100.0%	-4.6
6969	AT1G65370.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, contains Pfam profile PF00917: MATH domain   chr1:24288136-24289806 REVERSE   Aliases: T8F5.15, T8F5_15	6.9	7.4	-0.5	-1.0	100.0%	-3.9
6970	AT4G15570.1   tRNA-splicing endonuclease positive effector-related, contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease (Saccharomyces cerevisiae) gi:172574:gb:AAB63976   chr4:8892637-8898994 FORWARD   Aliases: DL3825W, FCAALL.334	3.9	4.2	-0.3	-1.0	100.0%	-4.4
6971	AT4G22640.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr4:11911611-11912019 FORWARD   Aliases: T12H17.30	3.6	4.2	-0.6	-1.0	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6972	AT5G27150.1   Symbol: NHX1   sodium proton exchanger / Na <sup>+</sup> /H <sup>+</sup> antiporter (NHX1), identical to Na <sup>+</sup> /H <sup>+</sup> exchanger (Arabidopsis thaliana) gi:6650177:gb:AAF21755 and sodium proton exchanger Nhx1 (Arabidopsis thaliana) gi:4324597:gb:AAD16946; Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563   chr5:9553441-9557516 FORWARD   Aliases: AT NHX1, ATNHX, ATNHX1, NA(+)/H(+) ANTIPORTER, NA <sup>+</sup> /H <sup>+</sup> EXCHANGER, T21B4.60, T21B4_60	7.2	6.8	0.5	1.0	100.0%	-4.1
6973	AT1G02740.1   MRG family protein, member of Pfam PF05712: MRG; similar to Transcription factor-like protein MRG15 (MORF-related gene 15 protein) (MSL3-1 protein) (Protein HSPC008/HSPC061) (SP:Q9UBU8) {Homo sapiens}	5.6	5.2	0.4	1.0	100.0%	-4.1
6974	AT3G19120.1   expressed protein   chr3:6609418-6611065 REVERSE   Aliases: MVI11.2	4.0	4.3	-0.3	-1.0	100.0%	-4.3
6975	AT4G01990.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr4:871145-872913 REVERSE   Aliases: T7B11.26, T7B11_26	4.5	4.9	-0.4	-1.0	100.0%	-4.4
6976	AT2G23240.2   plant EC metallothionein-like family 15 protein, identical to EC protein homolog 2 (SP:Q42377) {Arabidopsis thaliana}; identical to an EST: GB:X92116:ATECPRHOM; contains a vertebrate metallothionein signature (PS00203); contains Pfam profile PF02068: Plant PEC family metallothionein   chr2:9902935-9903405 REVERSE   Aliases: T20D16.13, T20D16_13	3.5	3.2	0.3	1.0	100.0%	-4.6
6977	AT3G16010.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:5434020-5436270 FORWARD   Aliases: MSL1.5	4.6	5.0	-0.5	-1.0	100.0%	-4.4
6978	AT4G12690.1   expressed protein   chr4:7480804-7481867 FORWARD   Aliases: T20K18.40, T20K18_40	3.6	3.4	0.2	1.0	100.0%	-4.5
6979	AT1G33600.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to gi:9294355:dbj:BAB02252 (Arabidopsis thaliana)   chr1:12180756-12182305 FORWARD   Aliases: T1E4.2, T1E4_2	2.4	2.6	-0.1	-1.0	100.0%	-5.1
6980	AT1G60010.1   expressed protein   chr1:22099025-22100242 REVERSE   Aliases: T2K10.6, T2K10_6	5.0	4.5	0.5	1.0	100.0%	-4.1
6981	AT5G62610.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	9.4	9.1	0.3	1.0	100.0%	-4.3
6982	AT1G22590.2   MADS-box family protein, similar to putative DNA-binding protein GI:6714399 from (Arabidopsis thaliana); MADS-box protein AGL87   chr1:7983500-7984224 FORWARD   Aliases: F12K8.7, F12K8_7	3.4	3.3	0.2	1.0	100.0%	-4.9
6983	AT1G14850.1   Symbol: NUP155	4.4	4.8	-0.4	-1.0	100.0%	-4.2
6984	AT1G10830.1   sodium symporter-related, contains five transmembrane domains; Interpro IPR001991 Sodium:dicarboxylate symporter; EST gb:F13926 comes from this gene   chr1:3605590-3607494 REVERSE   Aliases: T16B5.3, T16B5_3	6.1	5.8	0.4	1.0	100.0%	-4.4
6985	AT5G53410.1   hypothetical protein, similar to unknown protein (gb AAC73044.1)	3.9	3.5	0.4	1.0	100.0%	-4.6
6986	AT4G27080.1   Symbol: ATPDIL5 4   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	6.6	7.2	-0.6	-1.0	100.0%	-4.3
6987	AT3G13610.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to desacetoxyvindoline 4-hydroxylase (Catharanthus roseus)(GI:1916643), flavonol synthase 1 (SP:Q96330); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr3:4449455-4451184 FORWARD   Aliases: K20M4.9	2.8	3.2	-0.4	-1.0	100.0%	-4.0
6988	AT2G26250.1   Symbol: FDH   beta-ketoacyl-CoA synthase family (FIDDLEHEAD) (FDH), identical to GB:AJ010713 (fiddlehead protein)   chr2:11177496-11180220 REVERSE   Aliases: FIDDLEHEAD, T1D16.11, T1D16_11	2.5	2.9	-0.4	-1.0	100.0%	-3.9
6989	AT1G67860.1   expressed protein   chr1:25448468-25448926 REVERSE   Aliases: T23K23.29, T23K23_29	3.0	2.8	0.2	1.0	100.0%	-4.9
6990	AT1G49660.1   expressed protein   chr1:18382365-18383467 REVERSE   Aliases: F14J22.11, F14J22_11	6.8	7.4	-0.6	-1.0	100.0%	-4.0
6991	AT5G47200.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303750 from (Pisum sativum)	9.5	10.1	-0.6	-1.0	100.0%	-4.4
6992	AT3G57940.1   expressed protein, contains Pfam profile PF05127: Putative ATPase (DUF699)   chr3:21460275-21466938 FORWARD   Aliases: T10K17.150	4.2	4.6	-0.4	-1.0	100.0%	-4.1
6993	AT2G32660.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4 (Lycopersicon hirsutum) gi:2808683:emb:CAA05268   chr2:13860836-13863189 REVERSE   Aliases: F24L7.20, F24L7_20	3.3	3.5	-0.2	-1.0	100.0%	-5.1
6994	AT1G75450.1   Symbol: CKX6   FAD-binding domain-containing protein / cytokinin oxidase family protein, similar to GB:CAA77151 from (Zea mays) (SP:Q9T0N8) (Plant J. 17 (6), 615-626 (1999))   chr1:28318582-28321793 REVERSE   Aliases: CYTOKININ OXIDASE 6, F1B16.2, F1B16_2	4.7	4.3	0.4	1.0	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
6995	AT4G37370.1   Symbol: CYP81D8   cytochrome P450, putative, similar to Cytochrome P450 91A1 (SP:Q9FG65 )(Arabidopsis thaliana); cytochrome P450, Glycyrrhiza echinata, AB001379   chr4:17569822-17571698 REVERSE   Aliases: F6G17.20, F6G17_20	4.9	5.5	-0.6	-1.0	100.0%	-3.8
6996	AT1G50110.1   branched-chain amino acid aminotransferase 6 / branched-chain amino acid transaminase 6 (BCAT6), contains Pfam profile: PF01063 aminotransferase class IV; identical to SP:Q9LPM9 Branched-chain amino acid aminotransferase 6 (EC 2.6.1.42) (Atbcat-6) {Arabidopsis thaliana}   chr1:18561685-18563940 REVERSE   Aliases: F2J10.4, F2J10_4	6.4	6.7	-0.4	-1.0	100.0%	-4.0
6997	AT4G33370.1   DEAD-box protein abstrakt, putative, RNA helicase DBP2 - Saccharomyces cerevisiae, PID:g5272   chr4:16069672-16071408 REVERSE   Aliases: F17M5.130, F17M5_130	3.8	3.5	0.2	1.0	100.0%	-4.6
6998	AT1G70770.1   expressed protein   chr1:26691892-26694939 REVERSE   Aliases: F5A18.5, F5A18_5	8.2	8.7	-0.5	-1.0	100.0%	-4.3
6999	AT4G25434.2   similar to MutT/nudix family protein [Arabidopsis thaliana] (TAIR:At5g47650.1); similar to OSJNBa0079A21.19 [Oryza sativa (japonica cultivar-group)] (GB:XP_473408.1); contains InterPro domain Anti-sense to fibroblast growth factor protein GFG (InterPro:IPR003293); contains InterPro domain NUDIX hydrolase (InterPro:IPR000086)   chr4:13003986-13005873 REVERSE   Aliases: None	4.0	4.1	-0.2	-1.0	100.0%	-4.8
7000	AT2G25930.1   Symbol: ELF3   hydroxyproline-rich glycoprotein family protein, identical to cDNA nematode responsive protein GI:2213418   chr2:11066113-11070402 FORWARD   Aliases: EARLY FLOWERING 3, F17H15.25, PYK20	6.3	6.7	-0.4	-1.0	100.0%	-4.3
7001	AT5G24670.1   similar to novel protein [Danio rerio] (GB:CAD43470.1); contains InterPro domain Cytidine/deoxycytidylate deaminase, zinc-binding region (InterPro:IPR002125)   chr5:8448100-8451221 FORWARD   Aliases: MXC17.5, MXC17_5	5.8	6.3	-0.5	-1.0	100.0%	-4.2
7002	AT3G57210.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr3:21184341-21184670 REVERSE   Aliases: F28O9.60	2.7	2.5	0.1	1.0	100.0%	-4.9
7003	AT2G19330.1   leucine-rich repeat family protein, contains leucine rich repeats, Pfam:PF00560   chr2:8380029-8381535 FORWARD   Aliases: F27F23.13, F27F23_13	2.1	2.2	-0.1	-1.0	100.0%	-5.4
7004	AT1G58150.1   expressed protein   chr1:21533768-21534123 FORWARD   Aliases: T15M6.2	6.1	5.6	0.5	1.0	100.0%	-4.2
7005	AT5G18920.1   expressed protein   chr5:6310066-6310848 FORWARD   Aliases: F17K4.170, F17K4_170	3.9	4.2	-0.3	-1.0	100.0%	-4.2
7006	AT5G13610.1   expressed protein   chr5:4383016-4385032 FORWARD   Aliases: T6I14.13	7.1	7.4	-0.4	-1.0	100.0%	-4.4
7007	AT1G68340.1   expressed protein   chr1:25617860-25619066 REVERSE   Aliases: T22E19.3, T22E19_3	4.3	4.1	0.2	1.0	100.0%	-4.6
7008	AT1G24240.1   ribosomal protein L19 family protein, similar to plastid ribosomal protein L19 precursor (Spinacia oleracea) gi:7582403:gb:AAF64312   chr1:8586342-8588070 FORWARD   Aliases: F3I6.17, F3I6_17	4.9	4.7	0.2	1.0	100.0%	-4.5
7009	AT2G25430.1   epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain;	6.0	5.6	0.4	1.0	100.0%	-4.3
7010	AT3G06700.3   similar to 60S ribosomal protein L29 (RPL29B) [Arabidopsis thaliana] (TAIR:At3g06680.1); similar to P0475H04.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_914175.1); contains InterPro domain Ribosomal L29e protein (InterPro:IPR002673)   chr3:2117361-2117960 REVERSE   Aliases: T8E24.8	10.9	11.4	-0.5	-1.0	100.0%	-4.6
7011	AT4G21990.1   Symbol: APR3   5'-adenylylsulfate reductase (APR3) / PAPS reductase homolog (PRH26), identical to 5'-adenylylsulfate reductase (Arabidopsis thaliana) GI:2738760; identical to cDNA PAPS reductase homolog (PRH26) GI:1710113   chr4:11657020-11659069 REVERSE   Aliases: 5' ADENYLYLPHOSPHOSULFATE REDUCTASE, APS REDUCTASE 3, ATAPR3, F1N20.90, F1N20_90, PAPS REDUCTASE HOMOLOG 26, PRH 26, PRH26	6.5	7.1	-0.6	-1.0	100.0%	-4.3
7012	AT1G24520.1   Symbol: BCP1   anther-specific protein agp1, identical to agp1 GI:780177 from (Arabidopsis thaliana)   chr1:8688617-8689251 FORWARD   Aliases: F21J9.18, F21J9_18	4.9	4.6	0.3	1.0	100.0%	-4.4
7013	AT1G12790.1   expressed protein   chr1:4359149-4361267 REVERSE   Aliases: F13K23.4, F13K23_4	2.9	2.7	0.2	1.0	100.0%	-4.9
7014	AT1G69160.1   expressed protein   chr1:26003877-26005251 FORWARD   Aliases: F4N2.12, F4N2_12	2.7	2.8	-0.1	-1.0	100.0%	-5.1
7015	AT1G24450.1   ribonuclease III family protein, contains similarity to Swiss-Prot:P51837 ribonuclease III (EC 3.1.26.3) (RNase III) (Coxiella burnetii)	5.9	5.4	0.5	1.0	100.0%	-4.3
7016	AT2G15660.1   similar to MADS-box family protein [Arabidopsis thaliana] (TAIR:At2g40210.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_908461.1); similar to putative MADS-box protein AGL35 [Oryza sativa (japonica cultivar-group)] (GB:BAD86857.1)   chr2:6831328-6832658 REVERSE   Aliases: F9O13.21	2.8	2.9	-0.1	-1.0	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7017	AT2G25730.1   expressed protein   chr2:10963380-10979807 REVERSE   Aliases: F3N11.1, F3N11_1	7.1	7.3	-0.3	-1.0	100.0%	-4.6
7018	AT2G36990.1   Symbol: SIGF   RNA polymerase sigma subunit SigF (sigF) / sigma-like factor (SIG6), identical to RNA polymerase sigma subunit SigF (Arabidopsis thaliana) GI:7209640; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2; identical to cDNA partial mRNA for putative sigma-like transcription factor (sig6 gene) GI:6273429   chr2:15544337-15547218 REVERSE   Aliases: RNA POLYMERASE SIGMA 70 FACTOR, SIG6, T1J8.17, T1I8_17	5.8	6.2	-0.3	-1.0	100.0%	-4.2
7019	AT5G50170.1   C2 domain-containing protein / GRAM domain-containing protein, low similarity to SP:P40748 Synaptotagmin III (SytlIII) {Rattus norvegicus}; contains Pfam profiles PF00168: C2 domain, PF02893: GRAM domain   chr5:20438299-20442812 FORWARD   Aliases: K6A12.3, K6A12_3	5.3	5.7	-0.4	-1.0	100.0%	-4.1
7020	AT5G19830.1   similar to peptidyl-tRNA hydrolase family protein [Arabidopsis thaliana] (TAIR:At5g16140.1); similar to CRS2 [Zea mays] (GB:AAF27939.1); similar to A Chain A, Crystal Structure Of The Chloroplast Group Ii Intron Splicing Factor Crs2 (GB:1RYB); contains InterPro domain Peptidyl-tRNA hydrolase (InterPro:IPR001328)   chr5:6703152-6705248 FORWARD   Aliases: T29J13.250, T29J13_250	6.8	6.4	0.4	1.0	100.0%	-3.9
7021	AT2G20490.2   Symbol: NOP10   expressed protein, similar to hypothetical protein LOC548917 [Xenopus tropicalis] (GB:NP_001016163.1); contains InterPro domain Nucleolar RNA-binding protein Nop10p (InterPro:IPR007264)   chr2:8838797-8839997 FORWARD   Aliases: NOP10, T13C7.8, T13C7_8	7.0	7.6	-0.6	-1.0	100.0%	-4.0
7022	AT2G18280.2   similar to F-box family protein / tubby family protein [Arabidopsis thaliana] (TAIR:At1g47270.1); similar to F-box family protein / tubby family protein [Arabidopsis thaliana] (TAIR:At2g47900.1); similar to putative tubby-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_467371.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Tubby (InterPro:IPR000007)   chr2:7953080-7955550 FORWARD   Aliases: T30D6.21, T30D6_21	8.8	8.3	0.5	1.0	100.0%	-4.2
7023	AT2G28330.1   expressed protein   chr2:12106967-12107834 REVERSE   Aliases: T1B3.15, T1B3_15	3.8	3.6	0.2	1.0	100.0%	-4.7
7024	AT3G62080.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr3:22997151-22999743 FORWARD   Aliases: T17J13.40	2.7	2.9	-0.3	-1.0	100.0%	-4.9
7025	ATCG00740.1   Symbol: RPOA   RNA polymerase alpha subunit   chrC:77901-78890 REVERSE   Aliases: RPOA	9.5	10.2	-0.7	-1.0	100.0%	-4.2
7026	AT5G40180.1   hypothetical protein, predicted protein, Arabidopsis thaliana   chr5:16085151-16085434 FORWARD   Aliases: MSN9.8, MSN9_8	2.9	2.8	0.1	1.0	100.0%	-5.2
7027	AT1G56230.1   expressed protein   chr1:21049699-21052690 REVERSE   Aliases: F14G9.16, F14G9_16	6.6	7.1	-0.4	-1.0	100.0%	-4.3
7028	AT2G34310.3   expressed protein   chr2:14484820-14487041 REVERSE   Aliases: F13P17.27	6.5	6.8	-0.3	-1.0	100.0%	-4.4
7029	AT4G05050.2   Symbol: UBQ11   similar to polyubiquitin (UBQ14) [Arabidopsis thaliana] (TAIR:At4g02890.1); similar to polyubiquitin (UBQ3) [Arabidopsis thaliana] (TAIR:At5g03240.2); similar to polyubiquitin (UBQ4) [Arabidopsis thaliana] (TAIR:At5g20620.1); similar to polyubiquitin (UBQ14) [Arabidopsis thaliana] (TAIR:At4g02890.2); similar to polyubiquitin (UBQ14) [Arabidopsis thaliana] (TAIR:At4g02890.3); similar to ubiquitin-like protein [Phaseolus vulgaris] (GB:AAB36545.1); similar to polyubiquitin [Fragaria x ananassa] (GB:AAB68045.1); similar to pentameric polyubiquitin (GB:AAA34124.1); contains InterPro domain Ubiquitin domain (InterPro:IPR000626)   chr4:2588002-2589137 REVERSE   Aliases: C17L7.6, UBIQUITIN_11	13.6	13.3	0.3	1.0	100.0%	-5.3
7030	AT5G40420.1   Symbol: OLEO2   glycine-rich protein / oleosin   chr5:16190621-16192011 REVERSE   Aliases: OLEOSIN TYPE 2, PA23	3.0	2.8	0.3	1.0	100.0%	-4.6
7031	AT3G52590.1   Symbol: UBQ1   ubiquitin extension protein 1 (UBQ1) / 60S ribosomal protein L40 (RPL40B), identical to GI:166929, GI:166930   chr3:19516614-19517910 FORWARD   Aliases: EMB2167, EMBRYO DEFECTIVE 2167, F3C22.8, UBIQUITIN EXTENSION PROTEIN 1	12.2	12.4	-0.2	-1.0	100.0%	-4.6
7032	AT1G73530.1   RNA recognition motif (RRM)-containing protein, low similarity to SP:Q03251 Glycine-rich RNA-binding protein 8 (CCR1 protein) {Arabidopsis thaliana}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:27647294-27649047 REVERSE   Aliases: T9L24.48, T9L24_48	4.7	5.1	-0.3	-1.0	100.0%	-4.1
7033	AT3G49910.1   60S ribosomal protein L26 (RPL26A), 60S RIBOSOMAL PROTEIN L26, Brassica rapa, EMBL:BRD495   chr3:18515241-18515952 FORWARD   Aliases: F3A4.4	9.0	9.4	-0.4	-1.0	100.0%	-4.3
7034	AT2G12940.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g13150.1); similar to transcription factor VSF-1 [Lycopersicon esculentum] (GB:CAA05898.1); similar to vsf-1 [Lycopersicon esculentum] (GB:CAA52015.1); similar to vsf-1 protein - tomato (GB:S52203); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr2:5324557-5325483 FORWARD   Aliases: T19K21.9, T19K21_9	2.3	2.2	0.1	1.0	100.0%	-5.2
7035	AT3G42550.1   aspartyl protease family protein, weak similarity to CND41, chloroplast nucleoid DNA binding protein (Nicotiana tabacum) GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease	2.2	2.4	-0.2	-1.0	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7036	AT5G65940.2   Symbol: CHY1   similar to 3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative [Arabidopsis thaliana] (TAIR:At2g30660.1); similar to putative enoyl-CoA-hydratase [Oryza sativa (japonica cultivar-group)] (GB:AAP54951.1); similar to enoyl-CoA hydratase [Prunus armeniaca] (GB:AAB88874.1); contains InterPro domain Enoyl-CoA hydratase/isomerase (InterPro:IPR001753)   chr5:26393917-26396460 REVERSE   Aliases: BETA HYDROXYISOBUTYRYL COA HYDROLASE 1, COA THIOESTER HYDROLASE, K14B20.11, K14B20_11	6.3	5.9	0.4	1.0	100.0%	-4.5
7037	AT1G10560.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:3484581-3486966 FORWARD   Aliases: T10O24.19, T10O24_19	4.9	4.5	0.4	1.0	100.0%	-4.4
7038	AT4G15040.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo)   chr4:8581368-8584117 REVERSE   Aliases: DL3561C, FCAALL.176	2.4	2.3	0.1	1.0	100.0%	-5.3
7039	AT5G37380.2   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9QYI4 DnaJ homolog subfamily B member 12 {Mus musculus}; contains Pfam profile PF00226: DnaJ domain	5.4	6.2	-0.8	-1.0	100.0%	-4.3
7040	AT2G42620.1   Symbol: MAX2   F-box family protein (ORE9), E3 ubiquitin ligase SCF complex F-box subunit; identical to F-box containing protein ORE9 GI:15420162 from (Arabidopsis thaliana)   chr2:17763217-17765545 FORWARD   Aliases: F14N22.11, F14N22_11, MORE AXILLARY BRANCHES 2, ORE9, ORESARA 9	6.5	6.9	-0.5	-1.0	100.0%	-4.3
7041	AT4G17650.1   aromatic-rich family protein, contains Pfam PF03654: Aromatic-Rich Protein Family   chr4:9827532-9829668 FORWARD   Aliases: DL4860W, FCAALL.381	4.6	5.0	-0.5	-1.0	100.0%	-4.3
7042	AT3G51300.1   Symbol: ROP1   Rac-like GTP-binding protein (ARAC11) / Rho-like GTP-binding protein (ROP1), identical to GTP binding protein Rop1At (Arabidopsis thaliana) GI:2558666, rac-like GTP binding protein Arac11 (Arabidopsis thaliana) GI:3603426   chr3:19053866-19055330 FORWARD   Aliases: F24M12.340, ROP1AT	2.7	3.0	-0.3	-1.0	100.0%	-4.3
7043	AT2G18980.1   peroxidase, putative, identical to peroxidase ATP22a (Arabidopsis thaliana) gi:1620369:emb:CAA70034   chr2:8240417-8242394 REVERSE   Aliases: F19F24.18, F19F24_18	2.6	2.8	-0.1	-1.0	100.0%	-4.9
7044	AT4G18580.2   expressed protein   chr4:10234421-10236028 REVERSE   Aliases: F28J12.240, F28J12_240	7.8	7.1	0.6	1.0	100.0%	-4.2
7045	AT1G80690.1   expressed protein   chr1:30333961-30335695 REVERSE   Aliases: F23A5.4, F23A5_4	5.2	5.5	-0.3	-1.0	100.0%	-4.4
7046	AT4G35480.1   Symbol: RHA3B   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:16852079-16852952 REVERSE   Aliases: F15J1.50, F15J1_50, RING H2 FINGER PROTEIN RHA3B	5.3	4.7	0.6	1.0	100.0%	-3.9
7047	AT4G39050.1   kinesin-related protein (MKRP2), kinesin motor protein - Ustilago maydis, PID:g2062750; identical to cDNA MKRP2 mRNA for kinesin-related protein GI:16902293, kinesin-related protein (Arabidopsis thaliana) GI:16902294   chr4:18193129-18200691 FORWARD   Aliases: F19H22.150, F19H22_150	3.4	4.2	-0.8	-1.0	100.0%	-4.3
7048	AT3G58760.1   ankyrin protein kinase, putative, similar to ankyrin-kinase (Medicago truncatula) gi:18700701:gb:AAL78674   chr3:21739691-21742904 FORWARD   Aliases: T20N10.110	4.5	4.2	0.3	1.0	100.0%	-4.6
7049	AT5G61865.1   expressed protein   chr5:24864553-24867018 FORWARD   Aliases: None	3.5	3.7	-0.2	-1.0	100.0%	-4.7
7050	AT3G46070.1   zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	3.3	3.1	0.2	1.0	100.0%	-4.8
7051	AT4G31240.2   expressed protein   chr4:15176461-15178514 REVERSE   Aliases: F8F16.60, F8F16_60	4.3	3.9	0.3	1.0	100.0%	-4.2
7052	AT5G38660.1   Symbol: APE1   expressed protein, similar to unknown protein (pir::S75762)   chr5:15490363-15492765 REVERSE   Aliases: ACCLIMATION OF PHOTOSYNTHESIS TO ENVIRONMENT, MBB18.21, MBB18_21	10.0	9.3	0.6	1.0	100.0%	-4.3
7053	AT2G26210.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:11164230-11166369 FORWARD   Aliases: T1D16.15, T1D16_15	4.9	4.6	0.3	1.0	100.0%	-4.2
7054	AT1G63940.4   monodehydroascorbate reductase, putative, similar to monodehydroascorbate reductase GB:AAD28178 (Brassica juncea)   chr1:23733769-23737555 FORWARD   Aliases: T12P18.4, T12P18_4	9.4	10.2	-0.7	-1.0	100.0%	-4.4
7055	AT5G48120.1   expressed protein, low similarity to MMS19 (Mus musculus) GI:14029390   chr5:19525177-19532000 REVERSE   Aliases: MDN11.21, MDN11_21	4.4	4.7	-0.2	-1.0	100.0%	-4.5
7056	AT3G52490.1   heat shock protein-related, contains similarity to 101 kDa heat shock protein; HSP101 (Triticum aestivum) gi:11561808:gb:AAC83689   chr3:19466677-19469897 REVERSE   Aliases: F22O6.130	5.3	5.8	-0.5	-1.0	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7057	AT3G27300.2   Symbol: G6PD5   similar to glucose-6-phosphate 1-dehydrogenase / G6PD (ACG12) [Arabidopsis thaliana] (TAIR:At5g40760.1); similar to G6PD_MEDSA Glucose-6-phosphate 1-dehydrogenase, cytoplasmic isoform (G6PD) (GB:Q42919); similar to glucose-6-phosphate dehydrogenase [Nicotiana tabacum] (GB:CAA04992.1); similar to glucose-6-phosphate 1-dehydrogenase [Solanum tuberosum] (GB:CAA52442.1); similar to cytosolic glucose-6-phosphate dehydrogenase 2 [Petroselinum crispum] (GB:AAB69319.1); similar to glucose-6-phosphate dehydrogenase [Nicotiana tabacum] (GB:CAA04993.1); contains InterPro domain Glucose-6-phosphate dehydrogenase (InterPro:IPR001282)   chr3:10084305-10087889 REVERSE   Aliases: G6PD5, GLUCOSE 6 PHOSPHATE DEHYDROGENASE 5, K17E12.12	6.0	6.8	-0.9	-1.0	100.0%	-4.2
7058	AT1G28300.1   Symbol: LEC2   transcriptional factor B3 family protein / leafy cotyledon 2 (LEC2), nearly identical to LEAFY COTYLEDON 2 (Arabidopsis thaliana) GI:15987516; contains Pfam profile PF02362: B3 DNA binding domain   chr1:9896854-9899863 REVERSE   Aliases: F3H9.5, F3H9_5, LEAFY COTYLEDON 2	2.4	2.6	-0.2	-1.0	100.0%	-5.1
7059	AT5G41800.1   amino acid transporter family protein, similar to amino acid permease 1 (Nicotiana glauca) GI:976402; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II   chr5:16751059-16753219 FORWARD   Aliases: K16L22.8, K16L22_8	6.2	5.9	0.3	1.0	100.0%	-4.3
7060	AT1G05400.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr1:1584341-1585243 FORWARD   Aliases: T25N20.5, T25N20_5	4.0	3.7	0.4	1.0	100.0%	-4.5
7061	AT2G15790.1   Symbol: SQN   peptidyl-prolyl cis-trans isomerase / cyclophilin-40 (CYP40) / rotamase, identical to cyclophilin-40 (Arabidopsis thaliana) GI:13442983; supporting cDNA gi:13442982:gb:AY026065.1:   chr2:6884857-6887980 REVERSE   Aliases: CYCLOPHILIN 40, CYP40, F19G14.21, F19G14_21, SQUINT	3.5	4.1	-0.6	-1.0	100.0%	-4.2
7062	AT5G58680.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeats (4 copies)   chr5:23725338-23726577 REVERSE   Aliases: MZN1.14, MZN1_14	4.6	4.4	0.3	1.0	100.0%	-4.6
7063	AT1G07000.1   exocyst subunit EXO70 family protein, similar to leucine zipper protein GI:10177020 from (Arabidopsis thaliana) contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr1:2150193-2152324 REVERSE   Aliases: F10K1.28, F10K1_28	4.8	4.4	0.4	1.0	100.0%	-4.2
7064	AT2G22960.1   serine carboxypeptidase S10 family protein, contains Pfam profile: PF00450 serine carboxypeptidase ;similar to sinapoylglucose:malate sinapoyltransferase GI:8699619 from (Arabidopsis thaliana)	2.6	2.4	0.1	1.0	100.0%	-5.4
7065	AT1G04000.1   expressed protein, Location of ESTs 203I24T7, gb:H76794 and 203I24XP, gb:AA605510   chr1:1028105-1029118 REVERSE   Aliases: F21M11.6, F21M11_6	3.7	3.4	0.2	1.0	100.0%	-4.6
7066	AT3G14630.1   Symbol: CYP72A9   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4917505-4919416 FORWARD   Aliases: MIE1.13	3.0	2.8	0.2	1.0	100.0%	-4.7
7067	AT4G39510.1   Symbol: CYP96A12   cytochrome P450 family protein, contains Pfam PF00067: Cytochrome P450; similar to Cytochrome P450 86A2 (SP:O23066) (Arabidopsis thaliana)   chr4:18368797-18370646 REVERSE   Aliases: F23K16.140, F23K16_140	4.7	4.3	0.4	1.0	100.0%	-4.4
7068	AT4G20740.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:11126162-11128345 FORWARD   Aliases: F21C20.90, F21C20_90	3.8	3.9	-0.2	-1.0	100.0%	-4.6
7069	AT1G19320.1   pathogenesis-related thaumatin family protein, similar to SP:P28493 Pathogenesis-related protein 5 precursor (PR-5) from (Arabidopsis thaliana), thaumatin-like protein (Arabidopsis thaliana) GI:2435406; contains Pfam profile PF00314: Thaumatin family   chr1:6679272-6680242 FORWARD   Aliases: F18O14.4, F18O14_4	2.7	3.0	-0.3	-1.0	100.0%	-4.3
7070	AT5G14180.1   lipase family protein, similar to SP:Q64194 Lysosomal acid lipase/cholesteryl ester hydrolase precursor (EC 3.1.1.13) {Rattus norvegicus}; contains Pfam profile PF04083: ab-hydrolase associated lipase region   chr5:4571341-4574464 REVERSE   Aliases: MUA22.18, MUA22_18	3.1	3.0	0.1	1.0	100.0%	-5.1
7071	AT4G10950.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr4:6711498-6713508 REVERSE   Aliases: F25I24.160, F25I24_160	2.4	2.6	-0.1	-1.0	100.0%	-5.2
7072	AT5G43320.1   casein kinase, putative, similar to casein kinase I (CKI2) (Arabidopsis thaliana) gi:1103322:emb:CAA55397; contains protein kinase domain, Pfam:PF00069   chr5:17403095-17406629 REVERSE   Aliases: MWF20.1, MWF20_1	6.3	6.6	-0.4	-1.0	100.0%	-4.5
7073	AT3G31300.1   hypothetical protein   chr3:12676906-12677097 FORWARD   Aliases: T22B15.1	2.2	2.3	-0.1	-1.0	100.0%	-5.7
7074	AT1G51700.1   Symbol: ADOF1   Dof-type zinc finger domain-containing protein (ADOF1), identical to cDNA adof1 mRNA for dof zinc finger protein, GI:3608260; contains Pfam profile PF02701: Dof domain, zinc finger   chr1:19177738-19178857 FORWARD   Aliases: ADOF1, F19C24.9, F19C24_9	6.3	6.0	0.3	1.0	100.0%	-4.3
7075	AT3G58840.1   expressed protein   chr3:21768289-21769749 REVERSE   Aliases: T20N10.190	8.0	8.6	-0.6	-1.0	100.0%	-4.2
7076	AT3G57290.1   Symbol: EIF3E   eukaryotic translation initiation factor 3E / eIF3e (TIF3E1), identical to eukaryotic initiation factor 3E subunit (Arabidopsis thaliana) gi:12407658:gb:AAG53613   chr3:21207533-21210127 REVERSE   Aliases: ATEIF3E 1, EIF3E, F28O9.140, INT 6, TIF3E1	8.2	9.0	-0.7	-1.0	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7077	AT1G16790.1   ribosomal protein-related, similar to Chloroplast 30S ribosomal protein S8 (SP:P21508) (Euglena gracilis)   chr1:5744558-5745202 FORWARD   Aliases: F17F16.10, F17F16_10	5.3	5.7	-0.4	-1.0	100.0%	-4.2
7078	AT1G21170.1   expressed protein   chr1:7413039-7419400 FORWARD   Aliases: T22I11.1	3.0	3.3	-0.2	-1.0	100.0%	-4.9
7079	AT1G05510.1   expressed protein   chr1:1629452-1630862 FORWARD   Aliases: T25N20.16	2.8	2.7	0.2	1.0	100.0%	-4.9
7080	AT4G12750.1   expressed protein   chr4:7497811-7503640 REVERSE   Aliases: T20K18.100, T20K18_100	4.5	4.7	-0.3	-1.0	100.0%	-4.5
7081	AT1G32570.1   hypothetical protein   chr1:11777281-11777537 FORWARD   Aliases: T9G5.6, T9G5_6	4.6	4.2	0.4	1.0	100.0%	-4.3
7082	AT3G29260.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to 3-beta-hydroxysteroiddehydrogenase Gl:15983819 from (Digitalis lanata)   chr3:11217189-11218103 REVERSE   Aliases: MXO21.13	4.1	3.8	0.3	1.0	100.0%	-4.4
7083	AT4G16900.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:9512026-9516560 REVERSE   Aliases: DL4480C, FCAALL.310	2.5	2.3	0.2	1.0	100.0%	-4.8
7084	AT3G20290.2   similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At4g05520.2); similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At4g05520.1); similar to OSJNBa0043A12.19 [Oryza sativa (japonica cultivar-group)] (GB:XP_474282.1); similar to putative receptor Mediated Endocytosis RME-1 [Oryza sativa (japonica cultivar-group)] (GB:BAD28174.1); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048); contains InterPro domain EPS15 homology (EH) (InterPro:IPR000261)   chr3:7074823-7078789 REVERSE   Aliases: MQC12.3	8.4	8.0	0.4	1.0	100.0%	-4.7
7085	AT1G21900.1   emp24/gp25L/p24 family protein, similar to SP:O35587 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Mesocricetus auratus}; contains Pfam profile PF01105: emp24/gp25L/p24 family   chr1:7690859-7692370 REVERSE   Aliases: T26F17.12, T26F17_12	8.2	7.8	0.4	1.0	100.0%	-4.9
7086	AT4G25870.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr4:13149700-13152286 REVERSE   Aliases: F14M19.150, F14M19_150	7.2	7.4	-0.2	-1.0	100.0%	-4.8
7087	AT5G56790.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:22985165-22988756 FORWARD   Aliases: MIK19.26, MIK19_26	7.3	7.0	0.3	1.0	100.0%	-4.4
7088	AT1G42470.1   patched family protein, similar to SP:O15118 Niemann-Pick C1 protein precursor from Homo sapiens (GB:AAB63982) (Gl:2276463); contains Pfam profile PF02460 Patched family   chr1:15929427-15937648 FORWARD   Aliases: F7F22.1, F7F22_1	7.1	7.5	-0.4	-1.0	100.0%	-4.6
7089	AT5G15610.2   proteasome family protein, contains Pfam domain, PF01399: PCI domain   chr5:5079516-5082208 FORWARD   Aliases: T20K14.220, T20K14_220	6.1	6.4	-0.3	-1.0	100.0%	-4.3
7090	AT2G35800.1   mitochondrial substrate carrier family protein, contains INTERPRO:IPR001993 Mitochondrial substrate carrier family, INTERPRO:IPR002048 calcium-binding EF-hand domain   chr2:15051124-15055682 FORWARD   Aliases: F11F19.29, F11F19_29	4.9	5.2	-0.2	-1.0	100.0%	-4.5
7091	AT5G54070.1   Symbol: AT HSFA9   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr5:21961209-21962545 FORWARD   Aliases: HSFA9, MJP23.4, MJP23_4	2.7	2.6	0.1	1.0	100.0%	-5.3
7092	AT2G28370.1   expressed protein, contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (Gl:22135858) (Arabidopsis thaliana)   chr2:12138651-12140776 FORWARD   Aliases: T1B3.11, T1B3_11	5.6	4.8	0.8	1.0	100.0%	-4.2
7093	AT3G02810.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:608467-610992 REVERSE   Aliases: F13E7.25, F13E7_25	2.5	2.4	0.1	1.0	100.0%	-5.1
7094	AT1G47730.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain; identical to hypothetical protein GB:AAD46016 Gl:5668790 from (Arabidopsis thaliana)   chr1:17566371-17567546 REVERSE   Aliases: T2E6.20	2.5	2.7	-0.1	-1.0	100.0%	-5.4
7095	AT3G55420.1   expressed protein   chr3:20558694-20559744 FORWARD   Aliases: T22E16.80	5.6	5.3	0.4	1.0	100.0%	-4.5
7096	AT3G11270.1   26S proteasome non-ATPase regulatory subunit 7, putative / 26S proteasome regulatory subunit S12, putative / MOV34 protein, putative, contains similarity to 26S proteasome regulatory subunit S12 (MOV34) SP:P26516 from (Mus musculus)	6.9	7.7	-0.8	-1.0	100.0%	-4.2
7097	AT4G32840.1   phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) Gl:17432243; contains Pfam profile PF00365: Phosphofructokinase   chr4:15844784-15848445 REVERSE   Aliases: T16I18.50, T16I18_50	4.9	5.2	-0.3	-1.0	100.0%	-4.7
7098	AT4G36020.1   cold-shock DNA-binding family protein, contains Pfam domains, PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle	9.5	9.1	0.3	1.0	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7099	AT2G24120.2   Symbol: PDE319	3.9	4.1	-0.2	-1.0	100.0%	-4.6
7100	AT2G14050.1   minichromosome maintenance family protein / MCM family protein, low similarity to SP:P49736 DNA replication licensing factor MCM2 {Homo sapiens}; contains Pfam profile PF00493: MCM2/3/5 family	3.1	3.3	-0.2	-1.0	100.0%	-4.8
7101	AT5G02420.1   expressed protein   chr5:523387-524074 FORWARD   Aliases: T22P11.10, T22P11_10	3.2	2.7	0.5	1.0	100.0%	-4.2
7102	AT3G06440.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr3:1972628-1975760 REVERSE   Aliases: F24P17.7, F24P17_7	4.2	4.5	-0.2	-1.0	100.0%	-4.5
7103	AT3G52260.2   pseudouridine synthase family protein, similar to SP:P39219 Ribosomal large subunit pseudouridine synthase A (EC 4.2.1.70) (Pseudouridylate synthase) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF00849: RNA pseudouridylate synthase   chr3:19394254-19397453 REVERSE   Aliases: T25B15.30	4.2	3.9	0.3	1.0	100.0%	-4.3
7104	AT3G56090.1   Symbol: ATFER3	7.2	7.9	-0.7	-1.0	100.0%	-3.8
7105	AT3G52220.1   expressed protein   chr3:19380340-19382033 REVERSE   Aliases: T25B15.5	10.8	10.4	0.3	1.0	100.0%	-4.5
7106	AT1G48490.2   similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g17850.1); similar to incomplete root hair elongation (IRE) / protein kinase, putative [Arabidopsis thaliana] (TAIR:At5g62310.1); similar to putative AGC family protein kinase [Dictyostelium discoideum] (GB:EAL71293.1); similar to similar to cell wall biosynthesis kinase; Cbk1p [Saccharomyces cerevisiae] [Dictyostelium discoideum] (GB:AAS45329.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)	7.8	6.9	0.9	1.0	100.0%	-4.3
7107	AT3G17850.1   protein kinase, putative, similar to IRE (incomplete root hair elongation) (Arabidopsis thaliana) gi:6729346:dbj:BAA89783; contains protein kinase domain Pfam:PF00069   chr3:6109711-6116464 REVERSE   Aliases: MEB5.7	7.8	6.9	0.9	1.0	100.0%	-4.3
7108	AT3G05890.1   Symbol: RCI2B   hydrophobic protein (RCI2B) / low temperature and salt responsive protein (LTI6B), identical to SP:Q9ZNS6 Hydrophobic protein RCI2B (Low temperature and salt responsive protein LTI6B) {Arabidopsis thaliana}   chr3:1757637-1758498 REVERSE   Aliases: F2O10.15, F2O10_15, RARE COLD INDUCIBLE 2B	5.7	4.9	0.8	1.0	100.0%	-4.1
7109	AT5G64890.1   expressed protein   chr5:25951798-25952735 FORWARD   Aliases: MXK3.12, MXK3_12	3.9	4.5	-0.6	-1.0	100.0%	-4.2
7110	AT1G79390.1   expressed protein   chr1:29867946-29869214 REVERSE   Aliases: T8K14.19, T8K14_19	7.8	7.5	0.3	1.0	100.0%	-4.6
7111	AT5G64730.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to Will die slowly protein (SP:Q9V3J8) (Fruit fly) {Drosophila m.}   chr5:25890361-25892409 FORWARD   Aliases: MVP7.5, MVP7_5	6.0	5.6	0.4	1.0	100.0%	-4.4
7112	AT3G56580.3   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At2g40830.1); similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At2g40830.3); similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At2g40830.2); similar to putative ring finger protein 126 isoform 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD68141.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr3:20972568-20974728 FORWARD   Aliases: T5P19.5	3.0	3.3	-0.3	-1.0	100.0%	-4.7
7113	AT1G43260.1   hypothetical protein, contains Pfam domain, PF04937: Protein of unknown function (DUF 659)   chr1:16320693-16321674 FORWARD   Aliases: F1I21.5, F1I21_5	2.5	2.4	0.1	1.0	100.0%	-5.2
7114	AT1G64370.1   expressed protein   chr1:23892583-23893324 FORWARD   Aliases: F15H21.1, F15H21_1	3.9	3.6	0.3	1.0	100.0%	-4.3
7115	AT3G54270.1   sucrose-phosphatase 3 (SPP3), nearly identical to sucrose-phosphatase (SPP3) (Arabidopsis thaliana) GI:16904077   chr3:20098060-20100713 REVERSE   Aliases: F24B22.230	3.2	3.5	-0.2	-1.0	100.0%	-4.7
7116	AT3G13680.1   F-box family protein, contains F-box domain Pfam:PF00646	4.1	3.7	0.4	1.0	100.0%	-4.5
7117	AT5G19260.1   expressed protein, various predicted proteins   chr5:6479402-6480448 REVERSE   Aliases: F7K24.10, F7K24_10	4.9	4.6	0.3	1.0	100.0%	-4.4
7118	AT5G51850.1   expressed protein, similar to unknown protein (emb:CAB81354.1)   chr5:21096478-21098704 FORWARD   Aliases: MIO24.1, MIO24_1	2.1	2.2	-0.1	-1.0	100.0%	-5.4
7119	AT4G17960.1   expressed protein   chr4:9970859-9972468 FORWARD   Aliases: T6K21.140, T6K21_140	5.7	6.2	-0.5	-1.0	100.0%	-4.3
7120	AT5G11590.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr5:3727790-3728500 REVERSE   Aliases: T22P22.1	2.5	2.4	0.1	1.0	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7121	AT1G14480.1   similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At1g14500.1); similar to ankyrin-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD30891.1); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr1:4956252-4957966 FORWARD   Aliases: F14L17.26, F14L17_26	3.8	3.5	0.3	1.0	100.0%	-4.5
7122	AT2G22340.1   expressed protein   chr2:9499959-9501035 REVERSE   Aliases: F14M13.26, F14M13_26	2.7	3.0	-0.2	-1.0	100.0%	-4.9
7123	AT5G59730.2   similar to exocyst subunit EXO70 family protein [Arabidopsis thaliana] (TAIR:At2g28650.1); similar to putative leucine zipper protein [Oryza sativa (japonica cultivar-group)] (GB:BAB86177.1); contains InterPro domain Exo70 exocyst complex subunit (InterPro:IPR004140)   chr5:24081173-24083396 REVERSE   Aliases: MTH12.6, MTH12_6	5.1	4.9	0.2	1.0	100.0%	-4.6
7124	AT5G45530.1   expressed protein, contains Pfam domain, PF04578: Protein of unknown function, DUF594   chr5:18471543-18474504 REVERSE   Aliases: MFC19.20, MFC19_20	3.4	3.2	0.3	1.0	100.0%	-4.7
7125	AT1G32990.1   Symbol: PRPL11	6.5	7.0	-0.6	-1.0	100.0%	-3.7
7126	AT5G58140.4   Symbol: PHOT2   protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1), contains Pfam domains, PF00069: Protein kinase domain and PF00785: PAC motif; similar to SP:O48963 Nonphototropic hypocotyl protein 1	4.0	3.8	0.2	1.0	100.0%	-4.8
7127	AT5G04720.1   Symbol: ADR1 L2   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:1360713-1363885 FORWARD   Aliases: ADR1 L2, ADR1 LIKE 2, MUK11.4	7.3	6.9	0.5	1.0	100.0%	-4.2
7128	AT5G40850.1   Symbol: UPM1   uroporphyrin III methylase (UPM1), identical to uroporphyrin III methylase (GI:1146165) (Arabidopsis thaliana); similar to s-adenosyl-L-methionine-dependent uroporphyrinogen III methyltransferase (GI:1490606) (Arabidopsis thaliana); similar to Diphthine synthase (Diphtamide biosynthesis methyltransferase) (DPH5) (SP:P32469) (Saccharomyces cerevisiae); contains Pfam PF00590 : Tetrapyrrole (Corrin/Porphyrin) Methylases domain; contains TIGRFAM PF00590: Tetrapyrrole (Corrin/Porphyrin) Methylases   chr5:16383742-16386327 FORWARD   Aliases: MHK7.8, MHK7_8, UROPHORPHYRIN METHYLASE 1	7.8	7.5	0.4	1.0	100.0%	-4.5
7129	NA	2.2	2.2	-0.1	-1.0	100.0%	-5.4
7130	AT1G66740.1   ASF1-like anti-silencing protein, putative, similar to SP:P32447 Anti-silencing protein 1 {Saccharomyces cerevisiae}; contains Pfam profile PF04729: Anti-silencing protein, ASF1-like; supporting cDNA gi:27530935:dbj:AB078339.1:   chr1:24896003-24897429 FORWARD   Aliases: F4N21.13, F4N21_13	4.3	4.7	-0.4	-1.0	100.0%	-4.4
7131	AT3G28760.2   similar to conserved protein [Methanothermobacter thermautotrophicus str. Delta H] (GB:AAB85086.1); contains InterPro domain Protein of unknown function DUF109 (InterPro:IPR002812)   chr3:10794192-10796541 REVERSE   Aliases: T19N8.5	4.6	4.9	-0.4	-1.0	100.0%	-4.1
7132	AT1G43620.2   UDP-glucose:sterol glucosyltransferase, putative, similar to UDP-glucose:sterol glucosyltransferase (Arabidopsis thaliana) GI:2462931; contains Pfam profile: PF03033 glycosyltransferase family 28 N-terminal domain   chr1:16427872-16432606 REVERSE   Aliases: T10P12.7, T10P12_7	4.5	5.0	-0.5	-1.0	100.0%	-4.3
7133	AT4G00360.1   Symbol: CYP86A2   cytochrome P450, putative   chr4:160768-163002 FORWARD   Aliases: A_IG005I10.21, A_IG005I10_21, F5I10.21, F5I10_21	4.2	3.8	0.5	1.0	100.0%	-4.0
7134	AT3G51680.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to short-chain alcohol dehydrogenase GI:1877480 from (Tripsacum dactyloides)   chr3:19184601-19185646 REVERSE   Aliases: T18N14.60	3.0	3.2	-0.1	-1.0	100.0%	-5.1
7135	AT1G76400.1   ribophorin I family protein, similar to ribophorin I (Sus scrofa) GI:9857227; contains Pfam profile PF04597: Ribophorin I   chr1:28663126-28666604 REVERSE   Aliases: F15M4.10, F15M4_10	7.3	8.1	-0.8	-1.0	100.0%	-4.4
7136	AT1G31780.1   similar to Component of oligomeric golgi complex 6 [Xenopus tropicalis] (GB:AAH75361.1)   chr1:11391210-11394729 FORWARD   Aliases: F5M6.21, F5M6_21	6.5	7.1	-0.5	-1.0	100.0%	-4.1
7137	AT3G09440.1   heat shock cognate 70 kDa protein 3 (HSC70-3) (HSP70-3), identical to SP:O65719 Heat shock cognate 70 kDa protein 3 (Hsc70.3) {Arabidopsis thaliana}   chr3:2903205-2905728 REVERSE   Aliases: F3L24.33	7.3	7.8	-0.5	-1.0	100.0%	-4.2
7138	AT3G42630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:14733254-14734843 FORWARD   Aliases: T12K4.80	5.1	5.4	-0.3	-1.0	100.0%	-4.4
7139	AT1G79560.1   Symbol: EMB1047/FTSH12	4.8	5.2	-0.4	-1.0	100.0%	-4.4
7140	AT5G64560.2   magnesium transporter CorA-like family protein (MRS2-2), weak similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg2+ transporter protein   chr5:25824347-25826821 REVERSE   Aliases: MUB3.8, MUB3_8	4.3	4.7	-0.3	-1.0	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7141	AT4G10610.2   Symbol: RBP37   similar to RNA-binding protein, putative [Arabidopsis thaliana] (TAIR:At1g32790.1); similar to putative RNA-binding protein RBP37 [Oryza sativa (japonica cultivar-group)] (GB:XP_479783.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr4:6557173-6559591 FORWARD   Aliases: ATRBP37, CID12, RNA BINDING PROTEIN 37, T4F9.70, T4F9_70	9.5	9.0	0.5	1.0	100.0%	-4.5
7142	AT5G13260.1   expressed protein   chr5:4243031-4246880 FORWARD   Aliases: T31B5.80, T31B5_80	5.5	6.0	-0.5	-1.0	100.0%	-4.2
7143	AT5G02820.1   Symbol: RHL2   DNA topoisomerase VIA (SPO11), identical to topoisomerase 6 subunit A (spo11) (Arabidopsis thaliana) GI:12331186	7.2	7.6	-0.4	-1.0	100.0%	-4.1
7144	AT5G47060.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);   chr5:19134034-19135273 FORWARD   Aliases: MQD22.20, MQD22_20	6.6	6.1	0.4	1.0	100.0%	-4.4
7145	AT1G24050.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g70220.1); similar to hypothetical protein DDB0191031 [Dictyostelium discoideum] (GB:EAL72551.1)   chr1:8507009-8508853 FORWARD   Aliases: T23E23.20, T23E23_20	9.9	9.4	0.5	1.0	100.0%	-4.6
7146	AT2G21440.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:9180640-9186246 REVERSE   Aliases: F3K23.20, F3K23_20	7.8	8.3	-0.5	-1.0	100.0%	-4.2
7147	AT3G13320.1   Symbol: CAX2   calcium exchanger (CAX2), almost identical to low affinity calcium antiporter CAX2 (GI:1488267) (Arabidopsis thaliana); Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563   chr3:4314536-4318358 FORWARD   Aliases: ATCAX2, CATION EXCHANGER 2, CAX2, MDC11.19	5.9	5.6	0.3	1.0	100.0%	-4.5
7148	AT3G44990.1   Symbol: XTR8   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative   chr3:16457960-16459749 REVERSE   Aliases: ATXTR8, F14D17.60	6.6	6.2	0.4	1.0	100.0%	-4.3
7149	AT3G12380.1   Symbol: ATARP5	6.8	7.0	-0.2	-1.0	100.0%	-4.6
7150	AT3G26060.1   peroxiredoxin Q, putative, similar to peroxiredoxin Q (Sedum lineare) GI:6899842; contains Pfam profile: PF00578 AhpC/TSA (alkyl hydroperoxide reductase and thiol-specific antioxidant) family   chr3:9526013-9527611 FORWARD   Aliases: MPE11.21	7.2	7.9	-0.7	-1.0	100.0%	-3.7
7151	AT1G18150.2   Symbol: ATMPK8	5.6	5.9	-0.4	-1.0	100.0%	-4.3
7152	AT5G14500.1   aldose 1-epimerase family protein, similar to apospory-associated protein C, Chlamydomonas reinhardtii, EMBL:AF195243 Pfam profile PF01263: Aldose 1-epimerase   chr5:4674236-4676768 REVERSE   Aliases: T15N1.5	4.8	4.5	0.3	1.0	100.0%	-4.3
7153	AT3G19280.1   Symbol: FUT11   glycoprotein 3-alpha-L-fucosyltransferase A / FucTA / core alpha-(1,3)-fucosyltransferase (FUT11), identical to Glycoprotein 3-alpha-L-fucosyltransferase A (Core alpha-(1,3)-fucosyltransferase)(Fuc-T C3) (FucTA) (FucT1) (AtFUT11)(SP:Q9LJK1) from (Arabidopsis thaliana); contains Pfam profile PF00852: Fucosyl transferase; identical to cDNA alpha1,3-fucosyltransferase (FucTA) GI:13992482   chr3:6681303-6683898 REVERSE   Aliases: ATFUT11, FUCT1, FUCTA, MVI11.20	4.4	4.6	-0.2	-1.0	100.0%	-4.7
7154	AT1G23000.1   heavy-metal-associated domain-containing protein, similar to farnesylated protein ATPF3 (GI:4097547); contains PF00403 Heavy-metal-associated domain   chr1:8143393-8145059 FORWARD   Aliases: F19G10.6, F19G10_6	2.6	2.7	-0.1	-1.0	100.0%	-5.1
7155	AT3G55400.1   methionyl-tRNA synthetase / methionine--tRNA ligase / MetRS (cpMetRS), identical to methionyl-tRNA synthetase MEtRS (Arabidopsis thaliana) GI:2266985   chr3:20546608-20550044 REVERSE   Aliases: T22E16.60	8.0	8.4	-0.4	-1.0	100.0%	-3.9
7156	AT5G42890.1   sterol carrier protein 2 (SCP-2) family protein, similar to sterol carrier protein-2 (Homo sapiens) GI:432973; contains Pfam profile PF02036: SCP-2 sterol transfer family   chr5:17211500-17213260 REVERSE   Aliases: MBD2.8, MBD2_8	9.7	10.0	-0.4	-1.0	100.0%	-4.4
7157	AT4G23630.1   reticulon family protein (RTNLB1), weak similarity to Nogo-C protein (Rattus norvegicus) GI:6822251; contains Pfam profile PF02453: Reticulon   chr4:12317834-12319947 FORWARD   Aliases: F9D16.100, F9D16_100	9.2	8.5	0.8	1.0	100.0%	-4.3
7158	AT1G27680.1   Symbol: APL2   glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase, identical to SP:P55230   chr1:9631272-9634584 FORWARD   Aliases: APL2, T22C5.13, T22C5_13	5.1	5.4	-0.3	-1.0	100.0%	-4.1
7159	AT5G49120.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);   chr5:19926026-19926558 REVERSE   Aliases: K20J1.9, K20J1_9	2.6	2.5	0.1	1.0	100.0%	-5.2
7160	AT4G18930.1   cyclic phosphodiesterase, identical to cyclic phosphodiesterase (Arabidopsis thaliana) gi:2065013:emb:CAA72363   chr4:10370715-10372056 FORWARD   Aliases: F13C5.100, F13C5_100	9.2	9.5	-0.3	-1.0	100.0%	-4.4
7161	AT2G43020.1   amine oxidase family protein, similar to polyamine oxidase SP:O64411 (Zea mays); contains Pfam profile PF01593 amine oxidase, flavin-containing   chr2:17898580-17901712 FORWARD   Aliases: MFL8.12, MFL8_12	7.3	7.0	0.3	1.0	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7162	AT2G46540.1   expressed protein   chr2:19117544-19118841 REVERSE   Aliases: F13A10.7, F13A10_7	12.3	12.4	-0.1	-1.0	100.0%	-5.4
7163	AT3G01960.1   expressed protein   chr3:324588-325094 REVERSE   Aliases: F28J7.29, F28J7_29	2.3	2.2	0.1	1.0	100.0%	-5.3
7164	AT3G53430.1   60S ribosomal protein L12 (RPL12B), 60S RIBOSOMAL PROTEIN L12, Prunus armeniaca, SWISSPROT:RL12_PRUAR   chr3:19820665-19821447 REVERSE   Aliases: F4P12.130	10.0	10.5	-0.6	-1.0	100.0%	-4.2
7165	AT3G57680.1   peptidase S41 family protein, similar to PSII D1 protein processing enzyme (GI::7268527) (Arabidopsis thaliana); similar to SP:Q55669 Carboxyl-terminal processing protease precursor (Photosystem II D1 protein processing peptidase) (EC 3.4.21.102) (strain PCC 6803) {Synechocystis sp.}; contains Pfam profile PF03572: Peptidase family S41B   chr3:21392031-21394606 FORWARD   Aliases: F15B8.130	5.8	5.1	0.6	1.0	100.0%	-4.1
7166	AT1G22360.2   Symbol: AT2   similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22380.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22340.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22400.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At1g22370.2); similar to glycosyltransferase NTGT5a [Nicotiana tabacum] (GB:BAD93689.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyl transferase (InterPro:IPR002213)   chr1:7894847-7897580 REVERSE   Aliases: None	5.2	5.9	-0.7	-1.0	100.0%	-3.9
7167	AT5G59250.1   sugar transporter family protein, similar to D-xylose-H+ symporter from Lactobacillus brevis GI:2895856, sugar-porter family protein 2 (Arabidopsis thaliana) GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:23921119-23924202 FORWARD   Aliases: MNC17.15, MNC17_15	6.9	6.6	0.3	1.0	100.0%	-4.4
7168	AT1G09820.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3190290-3192416 REVERSE   Aliases: F21M12.21, F21M12_21	4.1	4.3	-0.3	-1.0	100.0%	-4.4
7169	AT1G27400.1   60S ribosomal protein L17 (RPL17A), similar to GB:P51413 from (Arabidopsis thaliana); similar to ESTs gb:L33542 and gb:AA660016   chr1:9515122-9516912 FORWARD   Aliases: F17L21.19, F17L21_19	9.9	10.5	-0.6	-1.0	100.0%	-4.1
7170	AT1G71060.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to CRP1 (Zea mays) GI:3289002; contains Pfam profile PF01535: PPR repeat   chr1:26809313-26810845 REVERSE   Aliases: F23N20.5, F23N20_5	3.6	3.4	0.3	1.0	100.0%	-4.3
7171	AT3G50270.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr3:18646902-18648323 FORWARD   Aliases: F11C1.110	3.4	3.6	-0.1	-1.0	100.0%	-5.0
7172	AT3G23880.1   F-box family protein, contains F-box domain Pfam:PF00646	3.7	3.2	0.5	1.0	100.0%	-3.9
7173	AT1G13330.1   expressed protein, similar to nuclear receptor coactivator GT198 (GI:16506273) {Rattus norvegicus}; similar to TBP-1 interacting protein (GI:7328534) (Homo sapiens)   chr1:4567932-4570565 FORWARD   Aliases: T6J4.9, T6J4_9	4.1	4.4	-0.3	-1.0	100.0%	-4.3
7174	AT2G45380.2   similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:At4g22740.1); similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:At4g22740.2); similar to putative glycine-rich protein [Oryza sativa (japonica cultivar-group)] (GB:XP_479799.1)	2.8	2.6	0.3	1.0	100.0%	-4.2
7175	AT4G34460.3   Symbol: AGB1   guanine nucleotide-binding protein beta subunit (GB1) / GTP-binding protein beta subunit (AGB1) / transducin, contains 7 WD-40 repeats (PF00400); identical to Guanine nucleotide-binding protein beta subunit.SP:P49177 (Arabidopsis thaliana); Weiss, CA et al, PNAS 91:9954 (1994)   chr4:16477194-16479510 REVERSE   Aliases: ARABIDOPSIS G PROTEIN BETA SUBUNIT, ELK4, ERECTA LIKE 4, GTP BINDING PROTEIN BETA 1, T4L20.40, T4L20_40	3.7	3.1	0.6	1.0	100.0%	-4.2
7176	AT2G21640.1   expressed protein   chr2:9261539-9262705 FORWARD   Aliases: F2G1.9, F2G1_9	4.2	4.0	0.3	1.0	100.0%	-4.3
7177	AT1G20290.1   expressed protein   chr1:7025538-7029688 REVERSE   Aliases: F14O10.11, F14O10_11	2.5	2.4	0.1	1.0	100.0%	-5.4
7178	AT5G64420.1   DNA polymerase V family, contains Pfam domain PF04931: DNA polymerase V   chr5:25773558-25778567 FORWARD   Aliases: MSJ1.26, MSJ1_26	5.7	6.0	-0.3	-1.0	100.0%	-4.5
7179	AT5G47600.1   heat shock protein-related, contains weak similarity to Heat shock 22 kDa protein, mitochondrial precursor (Swiss-Prot:P46254) (Pisum sativum)   chr5:19317008-19317703 REVERSE   Aliases: MNJ7.19, MNJ7_19	4.2	3.7	0.5	1.0	100.0%	-4.4
7180	AT3G52570.1   expressed protein, contains Interpro entry IPR000379   chr3:19512108-19513977 FORWARD   Aliases: F3C22.3	7.3	7.0	0.3	1.0	100.0%	-4.5
7181	AT3G50120.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function; expression supported by MPSS   chr3:18596140-18598229 REVERSE   Aliases: F3A4.200	2.6	2.5	0.2	1.0	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7182	AT1G62020.1   coatomer protein complex, subunit alpha, putative, contains Pfam PF00400: WD domain, G-beta repeat; similar to Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) (SP:P53621) (Homo sapiens)   chr1:22923479-22927689 FORWARD   Aliases: F8K4.21, F8K4_21	8.1	8.6	-0.5	-1.0	100.0%	-4.3
7183	AT5G22290.1   Symbol: ANAC089   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain   chr5:7375926-7377626 REVERSE   Aliases: ANAC089, T6G21.9	9.1	8.6	0.5	1.0	100.0%	-4.3
7184	AT2G38400.1   Symbol: AGT3   alanine--glyoxylate aminotransferase, putative / beta-alanine-pyruvate aminotransferase, putative / AGT, putative, similar to SP:Q64565 Alanine--glyoxylate aminotransferase 2, mitochondrial precursor (EC 2.6.1.44) (AGT 2) (Beta-alanine-pyruvate aminotransferase) {Rattus norvegicus}; contains Pfam profile PF00202: aminotransferase, class III   chr2:16090769-16093427 FORWARD   Aliases: ALANINE:GLYOXYLATE AMINOTRANSFERASE 2 HOMOLOG, ALANINE:GLYOXYLATE AMINOTRANSFERASE 3, T19C21.11, T19C21_11	7.2	7.6	-0.4	-1.0	100.0%	-4.4
7185	AT5G56910.1   expressed protein   chr5:23040148-23041428 FORWARD   Aliases: MHM17.2, MHM17_2	8.8	8.2	0.5	1.0	100.0%	-4.1
7186	AT4G39590.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:18387325-18388726 REVERSE   Aliases: F23K16.220, F23K16_220	3.1	3.4	-0.3	-1.0	100.0%	-4.6
7187	AT4G22030.1   F-box family protein, PF0064: F-box domain; similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)	3.0	3.3	-0.2	-1.0	100.0%	-4.9
7188	AT3G03100.2   similar to NADH:ubiquinone oxidoreductase B17.2-like subunit [Chlamydomonas reinhardtii] (GB:AAQ64638.1); contains InterPro domain NADH:ubiquinone oxidoreductase 17.2 kD subunit (InterPro:IPR007763)   chr3:705388-707657 REVERSE   Aliases: T17B22.21, T17B22_21	11.7	12.0	-0.3	-1.0	100.0%	-4.9
7189	AT5G26960.1   kelch repeat-containing F-box family protein, predicted proteins, Arabidopsis thaliana and Oryza sativa; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr5:9484777-9486152 REVERSE   Aliases: F2P16.220, F2P16_220	6.3	5.9	0.4	1.0	100.0%	-4.4
7190	AT5G02410.1   DIE2/ALG10 family, contains Pfam PF04922: DIE2/ALG10 family   chr5:517210-519754 REVERSE   Aliases: T1E22.170, T1E22_170	3.6	3.9	-0.3	-1.0	100.0%	-4.4
7191	AT3G10830.1   hypothetical protein   chr3:3390255-3390698 FORWARD   Aliases: T7M13.9	2.2	2.1	0.1	1.0	100.0%	-5.4
7192	AT2G41330.1   glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	3.6	3.3	0.3	1.0	100.0%	-4.4
7193	AT1G54370.1   sodium proton exchanger, putative (NHX5), contains similarity to Na <sup>+</sup> /H <sup>+</sup> antiporter GI:1655701 from (Xenopus laevis); Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563; contains non-consensus AT-AC splice sites at introns 3 and 10   chr1:20296818-20300796 REVERSE   Aliases: F20D21.19, F20D21_19	2.9	3.3	-0.4	-1.0	100.0%	-4.0
7194	AT3G51530.1   F-box family protein, various predicted proteins, Arabidopsis thaliana; contains Pfam profile PF00646: F-box domain   chr3:19123399-19125622 REVERSE   Aliases: F26O13.170	7.0	7.4	-0.4	-1.0	100.0%	-4.2
7195	AT2G18410.2   expressed protein   chr2:7997847-7999856 FORWARD   Aliases: T30D6.8, T30D6_8	4.3	4.5	-0.2	-1.0	100.0%	-4.8
7196	AT3G59090.3   similar to transmembrane protein-related (TOM1) [Arabidopsis thaliana] (TAIR:At4g21790.1); similar to P0046E05.19 [Oryza sativa (japonica cultivar-group)] (GB:NP_916134.1)   chr3:21850175-21853732 FORWARD   Aliases: F17J16.140	4.0	3.7	0.3	1.0	100.0%	-4.2
7197	AT5G20920.2   Symbol: EIF2 BETA   eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative, similar to SP:P41035 Eukaryotic translation initiation factor 2 subunit (eIF-2-beta) {Oryctolagus cuniculus}; contains Pfam profile PF01873: Domain found in IF2B/IF5   chr5:7094721-7097077 REVERSE   Aliases: EMB1401, EMBRYO DEFECTIVE 1401, F22D1.90, F22D1_90	8.7	8.4	0.3	1.0	100.0%	-4.5
7198	AT2G47970.2   NPL4 family protein, contains Pfam domain, PF05021: NPL4 family   chr2:19636544-19638208 FORWARD   Aliases: T9J23.1	7.5	7.2	0.3	1.0	100.0%	-4.6
7199	AT3G58670.1   expressed protein   chr3:21714367-21717027 REVERSE   Aliases: T20N10.20	4.6	4.9	-0.3	-1.0	100.0%	-4.3
7200	AT2G46505.1   Symbol: SDH4   expressed protein   chr2:19096801-19097621 REVERSE   Aliases: None	8.5	9.2	-0.6	-1.0	100.0%	-4.2
7201	AT5G05080.1   ubiquitin-conjugating enzyme, putative, similar to SP:Q16763 Ubiquitin-conjugating enzyme E2-24 kDa (EC 6.3.2.19) (Ubiquitin- protein ligase) (Ubiquitin carrier protein) {Homo sapiens}; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr5:1498556-1500780 REVERSE   Aliases: MUG13.6, MUG13_6	7.8	8.4	-0.7	-1.0	100.0%	-4.2
7202	AT1G50620.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr1:18752205-18755006 FORWARD   Aliases: F17J6.14, F17J6_14	3.0	3.1	-0.1	-1.0	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7203	AT3G62120.2   tRNA synthetase class II (G, H, P and S) family protein, similar to SP:P07814 Bifunctional aminoacyl-tRNA synthetase (Includes: Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase)) {Homo sapiens}; contains Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF03129: Anticodon binding domain	8.7	9.4	-0.7	-1.0	100.0%	-4.2
7204	AT3G45130.1   cycloartenol synthase, putative / 2,3-epoxysqualene--cycloartenol cyclase, putative / (S)-2,3-epoxysqualene mutase, putative, 77% similar to cycloartenol synthase (SP:P38605:gi:452446) (PMID: 7505443); oxidosqualene cyclase LcOSC2 - Luffa cylindrica, EMBL:AB033335   chr3:16523256-16528507 REVERSE   Aliases: T14D3.70	3.4	3.1	0.3	1.0	100.0%	-4.3
7205	AT5G67630.1   DNA helicase, putative, similar to RuvB-like DNA helicase reptin (Danio rerio) GI:27733814, reptin (Drosophila melanogaster) GI:7243682   chr5:26984607-26986620 REVERSE   Aliases: K9I9.20, K9I9_20	3.2	3.6	-0.4	-1.0	100.0%	-4.6
7206	AT1G75640.1   leucine-rich repeat family protein / protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr1:28407261-28410683 REVERSE   Aliases: F10A5.16, F10A5_16	3.0	3.2	-0.2	-1.0	100.0%	-4.6
7207	AT5G17200.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Lycopersicon esculentum) GI:4325090; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:5653526-5655338 REVERSE   Aliases: MKP11.14, MKP11_14	3.0	2.8	0.2	1.0	100.0%	-4.8
7208	AT2G36090.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr2:15165710-15166663 FORWARD   Aliases: F9C22.2, F9C22_2	6.4	5.8	0.6	1.0	100.0%	-4.0
7209	AT5G64500.1   membrane protein-related, contains weak similarity to spinster type IV (GI:12003976) (Drosophila melanogaster)   chr5:25797608-25800880 FORWARD   Aliases: T12B11.9, T12B11_9	8.7	8.4	0.3	1.0	100.0%	-4.5
7210	AT5G18930.1   adenosylmethionine decarboxylase family protein, contains Pfam profile: PF01536 adenosylmethionine decarboxylase	2.8	3.0	-0.1	-1.0	100.0%	-5.3
7211	AT5G15090.1   porin, putative / voltage-dependent anion-selective channel protein, putative, similar to SP:P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin; identical to cDNA voltage-dependent anion-selective channel protein GI:4006940   chr5:4889298-4891475 REVERSE   Aliases: F2G14.210, F2G14_210	8.3	8.9	-0.5	-1.0	100.0%	-4.7
7212	AT1G06145.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At5g66520.1); similar to putative pentatricopeptide (PPR) repeat-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_450548.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr1:1867014-1868871 REVERSE   Aliases: None	4.3	4.5	-0.2	-1.0	100.0%	-4.6
7213	AT1G07770.2   Symbol: RPS15A	11.2	11.5	-0.2	-1.0	100.0%	-4.7
7214	AT2G20980.1   expressed protein   chr2:9018735-9020937 REVERSE   Aliases: F26H11.26, F26H11_26	4.2	4.6	-0.3	-1.0	100.0%	-4.4
7215	AT4G22830.1   expressed protein   chr4:11990149-11991379 REVERSE   Aliases: F7H19.1	3.1	2.9	0.2	1.0	100.0%	-4.5
7216	AT5G20410.1   Symbol: MGD2   1,2-diacylglycerol 3-beta-galactosyltransferase, putative / monogalactosyldiacylglycerol synthase, putative / MGDG synthase, putative, identical to monogalactosyldiacylglycerol synthase (gi:3367638) from Arabidopsis thaliana, similar to MGDG synthase type A (gi:9884651) from Glycine max   chr5:6896679-6898785 FORWARD   Aliases: ATMGD2, F5O24.300, F5O24_300	5.4	5.0	0.4	1.0	100.0%	-4.1
7217	AT5G14530.1   transducin family protein / WD-40 repeat family protein, similar to Will die slowly protein (SP:Q9V3J8) (Drosophila melanogaster) ; contains Pfam PF00400: WD domain, G-beta repeat (4 copies, 1 weak)   chr5:4684623-4686912 REVERSE   Aliases: T15N1.20, T15N1_20	6.0	5.6	0.4	1.0	100.0%	-4.1
7218	AT3G14350.3   leucine-rich repeat transmembrane protein kinase, putative, similar to leucine-rich repeat transmembrane protein kinase 1 GB:AAC27894 from (Zea mays)   chr3:4782764-4787174 REVERSE   Aliases: MLN21.15	5.3	5.7	-0.4	-1.0	100.0%	-4.2
7219	AT1G03260.1   expressed protein   chr1:795532-798463 REVERSE   Aliases: F15K9.14, F15K9_14	5.2	5.0	0.3	1.0	100.0%	-4.5
7220	AT5G09790.1   PHD finger family protein / SET domain-containing protein, contains Pfam domain, PF00628: PHD-finger and PF00856: SET domain   chr5:3038979-3041045 REVERSE   Aliases: F17I14.20, F17I14_20	3.7	4.0	-0.3	-1.0	100.0%	-4.2
7221	AT4G00390.1   expressed protein, contains Pfam profile: PF04504 protein of unknown function, DUF573   chr4:171497-172843 REVERSE   Aliases: A_IG005I10.6, A_IG005I10_6, F5I10.6, F5I10_6	3.9	3.6	0.3	1.0	100.0%	-4.5
7222	AT4G16970.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:9551478-9555839 REVERSE   Aliases: DL4515C, FCAALL.319	3.6	3.9	-0.3	-1.0	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7223	AT1G76090.1   Symbol: SMT3   S-adenosyl-methionine-sterol-C-methyltransferase, identical to S-adenosyl-methionine-sterol-C-methyltransferase GI:2246456 from ( <i>Arabidopsis thaliana</i> )   chr1:28555303-28556675 REVERSE   Aliases: SMT3, T23E18.40, T23E18_40	5.6	5.0	0.6	1.0	100.0%	-4.5
7224	AT1G34440.1   expressed protein   chr1:12591326-12592715 REVERSE   Aliases: F12K21.23, F12K21_23	3.2	3.4	-0.2	-1.0	100.0%	-4.9
7225	AT1G09240.1   nicotianamine synthase, putative, similar to nicotianamine synthase ( <i>Lycopersicon esculentum</i> )(GI:4753801), nicotianamine synthase 2 ( <i>Hordeum vulgare</i> )(GI:4894912)   chr1:2984883-2986132 FORWARD   Aliases: T12M4.5, T12M4_5	3.3	3.1	0.2	1.0	100.0%	-4.8
7226	AT4G29210.2   gamma-glutamyltranspeptidase family protein, similar to SP:P07314 Gamma-glutamyltranspeptidase precursor (EC 2.3.2.2) (Gamma-glutamyltransferase) (GGT) { <i>Rattus norvegicus</i> }; contains Pfam profilePF01019: Gamma-glutamyltranspeptidase	5.6	5.9	-0.3	-1.0	100.0%	-4.3
7227	AT5G20400.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to naringenin,2-oxoglutarate 3-dioxygenase (flavonone-3-hydroxylase) (SP:Q06942)( <i>Malus domestica</i> ); contains PF031712OG-Fe(II) oxygenase superfamily domain   chr5:6894856-6896351 FORWARD   Aliases: F5O24.290, F5O24_290	7.6	7.9	-0.3	-1.0	100.0%	-4.6
7228	AT3G13650.1   disease resistance response protein-related/ dirigent protein-related, similar to dirigent protein ( <i>Thuja plicata</i> ) gi:6694699:gb:AAF25360; similar to pathogenesis-related protein ( <i>Pisum sativum</i> ) gi:4585273:gb:AAD25355   chr3:4462899-4463879 FORWARD   Aliases: MMM17.15	5.5	6.0	-0.5	-1.0	100.0%	-4.1
7229	AT4G34200.1   D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative, similar to phosphoglycerate dehydrogenase, <i>Arabidopsis thaliana</i> , SP:O04130   chr4:16373850-16376626 REVERSE   Aliases: F10M10.7	8.3	9.2	-0.9	-1.0	100.0%	-4.0
7230	AT5G14105.1   expressed protein   chr5:4551991-4553053 REVERSE   Aliases: None	8.9	9.2	-0.3	-1.0	100.0%	-4.3
7231	AT1G20540.1   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to Rbap46 polypeptide (GI:9454362) ( <i>Gallus gallus</i> )   chr1:7112611-7115810 FORWARD   Aliases: F5M15.14, F5M15_14	8.6	9.0	-0.4	-1.0	100.0%	-4.4
7232	AT2G39170.1   expressed protein   chr2:16341708-16343288 REVERSE   Aliases: T16B24.19, T16B24_19	6.4	6.1	0.3	1.0	100.0%	-4.3
7233	AT5G38150.1   expressed protein   chr5:15240346-15242165 REVERSE   Aliases: MXA21.20, MXA21_20	4.3	4.7	-0.4	-1.0	100.0%	-4.2
7234	AT5G11850.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain; identical to cDNA MAP3K delta-1 protein kinase GI:2253009   chr5:3816347-3821073 REVERSE   Aliases: F14F18.20, F14F18_20	4.9	5.1	-0.2	-1.0	100.0%	-4.6
7235	AT5G47070.1   protein kinase, putative, similar to protein kinase ( <i>Lophopyrum elongatum</i> ) gi:13022177:gb:AAK11674   chr5:19135770-19138136 REVERSE   Aliases: K14A3.2, K14A3_2	6.3	5.8	0.5	1.0	100.0%	-4.2
7236	AT1G55560.1   Symbol: SKS14   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)( <i>Brassica napus</i> ); contains Pfam profile: PF00394 Multicopper oxidase   chr1:20757989-20760320 REVERSE   Aliases: SKS14, T5A14.2, T5A14_2	2.2	2.3	-0.1	-1.0	100.0%	-5.6
7237	AT3G08930.2   LMBR1 integral membrane family protein, contains 5 transmembrane domains; contains Pfam PF04791: LMBR1-like conserved region; similar to unknown protein GB:BAA83351 ( <i>Oryza sativa</i> )   chr3:2713410-2717318 FORWARD   Aliases: T16O11.13	7.5	7.0	0.5	1.0	100.0%	-4.4
7238	AT3G17150.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) { <i>Actinidia chinensis</i> }; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr3:5847297-5849550 FORWARD   Aliases: K14A17.27	2.9	2.7	0.2	1.0	100.0%	-4.8
7239	AT5G63730.1   IBR domain-containing protein, contains similarity to Swiss-Prot:Q94981 ariadne-1 protein (Ari-1) ( <i>Drosophila melanogaster</i> ) and Pfam:PF01485 IBR domain   chr5:25525326-25526932 REVERSE   Aliases: MBK5.21, MBK5_21	3.2	3.0	0.2	1.0	100.0%	-4.9
7240	AT3G60480.1   expressed protein   chr3:22358426-22359213 REVERSE   Aliases: T8B10.140	9.1	8.8	0.2	1.0	100.0%	-4.5
7241	AT2G04700.1   ferredoxin thioredoxin reductase catalytic beta chain family protein, contains Pfam profile: PF02943 ferredoxin thioredoxin reductase catalytic beta   chr2:1646805-1648554 FORWARD   Aliases: F28I8.26, F28I8_26	7.3	7.0	0.3	1.0	100.0%	-4.7
7242	AT3G24140.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain	2.8	2.7	0.2	1.0	100.0%	-4.9
7243	AT2G29250.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 ( <i>Arabidopsis thaliana</i> ) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr2:12585986-12587857 REVERSE   Aliases: F16P2.37, F16P2_37	2.6	2.5	0.1	1.0	100.0%	-5.2
7244	AT2G31820.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr2:13537427-13539639 FORWARD   Aliases: F20M17.14, F20M17_14	8.0	7.8	0.2	1.0	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7245	AT2G28590.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:12256912-12258745 FORWARD   Aliases: T8O18.12, T8O18_12	5.1	5.4	-0.3	-1.0	100.0%	-4.4
7246	AT1G07010.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.4	6.0	0.4	1.0	100.0%	-4.1
7247	AT2G18710.1   preprotein translocase secY subunit, chloroplast (CpSecY), identical to SP:Q38885 Preprotein translocase secY subunit, chloroplast precursor (CpSecY) {Arabidopsis thaliana}   chr2:8119166-8121559 REVERSE   Aliases: MSF3.9, MSF3_9	7.6	6.8	0.7	1.0	100.0%	-4.2
7248	AT5G56380.1   F-box family protein, similar to unknown protein (emb:CAB62440.1); contains Pfam profile PF00646: F-box domain   chr5:22855898-22858241 REVERSE   Aliases: MCD7.14, MCD7_14	4.0	4.3	-0.3	-1.0	100.0%	-4.5
7249	AT1G06820.1   Symbol: CRTISO	5.4	5.6	-0.3	-1.0	100.0%	-4.6
7250	AT3G15540.1   Symbol: IAA19   auxin-responsive protein / indoleacetic acid-induced protein 19 (IAA19), identical to SP:O24409 Auxin-responsive protein IAA19 (Indoleacetic acid-induced protein 19) {Arabidopsis thaliana}   chr3:5264031-5265683 FORWARD   Aliases: MJK13.22, MSG2	5.2	5.5	-0.3	-1.0	100.0%	-4.4
7251	AT3G46290.1   protein kinase, putative, similar to receptor-like protein kinase (Catharanthus roseus) gi:1644291:emb:CAA97692   chr3:17023994-17026772 FORWARD   Aliases: F12M12.260	2.8	2.7	0.1	1.0	100.0%	-4.9
7252	AT3G29185.2   expressed protein   chr3:11156166-11158444 REVERSE   Aliases: MXO21.1	6.5	6.8	-0.3	-1.0	100.0%	-4.3
7253	AT5G04190.1   phytochrome kinase substrate-related, contains similarity to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 (Arabidopsis thaliana)   chr5:1150893-1152482 FORWARD   Aliases: F21E1.110, F21E1_110	2.3	2.4	-0.1	-1.0	100.0%	-5.3
7254	AT1G63870.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:23710794-23715564 REVERSE   Aliases: T12P18.11, T12P18_11	2.7	2.8	-0.1	-1.0	100.0%	-5.2
7255	AT1G59940.1   Symbol: ARR3   two-component responsive regulator / response regulator 3 (ARR3), identical to response regulator 3 GI:3953595 from (Arabidopsis thaliana)   chr1:22069282-22070638 REVERSE   Aliases: F23H11.25, F23H11_25, RESPONSE REGULATOR 3	3.9	4.1	-0.3	-1.0	100.0%	-4.3
7256	AT5G11500.1   expressed protein, contains Pfam profile PF05670: Domain of unknown function (DUF814)   chr5:3676641-3679347 FORWARD   Aliases: F15N18.90, F15N18_90	11.1	10.8	0.3	1.0	100.0%	-5.0
7257	AT1G73320.2   similar to Expressed protein [Arabidopsis thaliana] (TAIR:At1g08125.1); similar to P0684C02.12 [Oryza sativa (japonica cultivar-group)] (GB:NP_915768.1)	4.6	4.2	0.4	1.0	100.0%	-4.2
7258	AT5G49170.1   expressed protein, similar to unknown protein (gb:AAF63814.1)   chr5:19955802-19956797 REVERSE   Aliases: K21P3.4, K21P3_4	2.5	2.7	-0.1	-1.0	100.0%	-5.1
7259	AT2G42130.5   expressed protein, contains weak hit to Pfam PF04755: PAP_fibrillin   chr2:17573301-17575182 FORWARD   Aliases: T24P15.4, T24P15_4	5.1	5.5	-0.4	-1.0	100.0%	-4.3
7260	AT3G57570.1   expressed protein   chr3:21323475-21331276 FORWARD   Aliases: T8H10.170	3.4	3.6	-0.2	-1.0	100.0%	-4.6
7261	AT1G67800.3   copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens}   chr1:25424443-25427386 REVERSE   Aliases: F12A21.7, F12A21_7	5.6	5.3	0.2	1.0	100.0%	-4.5
7262	AT4G38940.1   kelch repeat-containing F-box family protein, low similarity to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr4:18152691-18154106 FORWARD   Aliases: F19H22.40, F19H22_40	5.5	5.3	0.3	1.0	100.0%	-4.7
7263	AT5G57030.1   Symbol: LUT2   lycopene epsilon cyclase, identical to lycopene epsilon cyclase (GI:1399181)   chr5:23094491-23097262 FORWARD   Aliases: LUTEIN DEFICIENT 2, LYCOPENE EPSILON CYCLASE, MHM17.16, MHM17_16	4.8	5.1	-0.3	-1.0	100.0%	-4.4
7264	AT4G35320.1   expressed protein, predicted protein, Arabidopsis thaliana   chr4:16805874-16806660 REVERSE   Aliases: F23E12.120, F23E12_120	3.7	3.5	0.2	1.0	100.0%	-4.8
7265	AT4G21810.1   Der1-like family protein / degradation in the ER-like family protein, contains Pfam profile: PF04511 Der1-like family   chr4:11575271-11577165 REVERSE   Aliases: T8O5.20, T8O5_20	6.2	5.8	0.4	1.0	100.0%	-4.5
7266	AT1G76460.1   RNA recognition motif (RRM)-containing protein, low similarity to RRM-containing protein SEB-4 (Xenopus laevis) GI:8895698; contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr1:28691023-28694015 REVERSE   Aliases: F15M4.25	3.3	2.9	0.4	1.0	100.0%	-4.3
7267	AT5G40140.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr5:16074575-16076227 FORWARD   Aliases: MSN9.4, MSN9_4	4.8	4.4	0.4	1.0	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7268	AT5G23780.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr5:8017195-8019029 REVERSE   Aliases: MRO11.18, MRO11_18	2.9	3.1	-0.2	-1.0	100.0%	-5.1
7269	AT2G44450.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) (Prunus serotina)   chr2:18348042-18350820 FORWARD   Aliases: F4I1.26	5.7	6.0	-0.3	-1.0	100.0%	-4.2
7270	AT5G54880.1   DTW domain-containing protein, contains Pfam domain, PF03942: DTW domain	3.4	3.6	-0.2	-1.0	100.0%	-4.7
7271	AT4G31780.2   Symbol: MGD1   1,2-diacylglycerol 3-beta-galactosyltransferase, putative / monogalactosyldiacylglycerol synthase, putative / MGDG synthase, putative, similar to MGD synthase type A from Arabidopsis thaliana (gi:9927297), similar to monogalactosyldiacylglycerol synthase, Cucumis sativus, PID:g1805254   chr4:15374005-15377140 FORWARD   Aliases: F11C18.2, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE 1, MONOGALACTOSYLDIACYLGLYCEROL SYNTHASE A	8.3	8.1	0.2	1.0	100.0%	-4.7
7272	AT1G69170.2   squamosa promoter-binding protein-like 6 (SPL6), identical to squamosa promoter binding protein-like 6 (Arabidopsis thaliana) GI:5931683; contains Pfam profile PF03110: SBP domain   chr1:26008761-26013907 FORWARD   Aliases: F4N2.13, F4N2_13	4.1	3.9	0.3	1.0	100.0%	-4.6
7273	AT1G14810.1   semialdehyde dehydrogenase family protein, similar to SP:O31219 Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11) (ASA dehydrogenase) (ASADH) {Legionella pneumophila}; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain   chr1:5102419-5104684 REVERSE   Aliases: F10B6.22, F10B6_22	11.4	10.8	0.5	1.0	100.0%	-4.1
7274	AT2G35510.1   Symbol: SRO1   Encodes a WWE domain-containing protein with 76% similarity to RCD1. The protein also contains a PARP signature upstream of the C-terminal protein interaction domain. The PARP signature may bind NAD+ and attach the ADP-ribose-moiety from NAD+ to the target molecule. Its presence suggests a role for the protein in ADP ribosylation.   chr2:14923803-14927456 REVERSE   Aliases: SIMILAR TO RCD ONE 1, SIMILAR TO RCD ONE 1, SRO1, T32F12.11, T32F12_11	6.2	5.9	0.3	1.0	100.0%	-4.3
7275	AT1G03360.1   exonuclease family protein, similar to Exosome complex exonuclease RRP4 (Ribosomal RNA processing protein 4)(SP:P38792) {Saccharomyces cerevisiae}   chr1:824561-826179 FORWARD   Aliases: F15K9.4, F15K9_4	7.4	7.9	-0.5	-1.0	100.0%	-3.9
7276	AT1G08550.2   Symbol: NPQ1   similar to violaxanthin de-epoxidase-related [Arabidopsis thaliana] (TAIR:At2g21860.1); similar to violaxanthin de-epoxidase [Camellia sinensis] (GB:AAL67858.2)	6.0	5.6	0.4	1.0	100.0%	-4.1
7277	AT2G38440.1   Symbol: ITB1   Encodes a subunit of the WAVE complex. The WAVE complex is required for activation of ARP2/3 complex which functions in actin microfilament nucleation and branching. Mutants have distorted trichomes (branches have shorter length) and abnormal epidermal cell adhesion. Contains an N terminal SCAR domain and C terminal WA domain.	5.9	6.2	-0.3	-1.0	100.0%	-4.6
7278	AT4G31890.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr4:15426298-15429113 REVERSE   Aliases: F11C18.90, F11C18_90	3.6	4.1	-0.5	-1.0	100.0%	-4.3
7279	AT1G80550.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:30289838-30291596 REVERSE   Aliases: T21F11.12, T21F11_12	3.8	3.5	0.2	1.0	100.0%	-4.5
7280	AT5G34870.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr5:13202751-13205176 FORWARD   Aliases: T2L5.20, T2L5_20	2.2	2.1	0.1	1.0	100.0%	-5.1
7281	AT5G06250.1   DNA-binding protein, putative, similar to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857 and RAV2 GI:3868859, AP2 domain containing protein RAP2.8 (Arabidopsis thaliana) GI:2281641; contains Pfam profile PF02362: B3 DNA binding domain   chr5:1892715-1894059 REVERSE   Aliases: MHF15.23, MHF15_23	2.7	2.6	0.1	1.0	100.0%	-5.0
7282	AT5G43840.1   Symbol: AT HSFA6A   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr5:17642664-17643591 REVERSE   Aliases: HSFA6A, MQD19.20, MQD19_20	3.2	3.0	0.1	1.0	100.0%	-5.1
7283	AT3G54420.1   Symbol: ATEP3   class IV chitinase (CHIV), almost identical to class IV chitinase from GI:2597826 (Arabidopsis thaliana)   chr3:20156888-20158041 FORWARD   Aliases: ATCHITIV, CHIV, T14E10.4	4.2	4.7	-0.5	-1.0	100.0%	-4.2
7284	AT1G71140.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:26828424-26830410 FORWARD   Aliases: F23N20.13, F23N20_13	4.3	4.6	-0.3	-1.0	100.0%	-4.4
7285	AT5G64660.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain   chr5:25859139-25860663 REVERSE   Aliases: MUB3.18, MUB3_18	6.0	5.7	0.3	1.0	100.0%	-4.5
7286	AT5G66930.2   expressed protein, similar to unknown protein (pir::T38383)   chr5:26743168-26744977 FORWARD   Aliases: MUD21.19, MUD21_19	4.9	4.4	0.5	1.0	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7287	AT5G23590.2   similar to DNAJ heat shock protein, mitochondrially targeted (GFA2) [Arabidopsis thaliana] (TAIR:At5g48030.1); similar to PREDICTED: similar to hypothetical protein FLJ10634 [Canis familiaris] (GB:XP_535435.1); contains InterPro domain Heat shock protein DnaJ (InterPro:IPR003095); contains InterPro domain Heat shock protein DnaJ, N-terminal (InterPro:IPR001623)   chr5:7953532-7955625 REVERSE   Aliases: MQM1.14, MQM1_14	9.6	9.2	0.4	1.0	100.0%	-4.1
7288	AT5G40250.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHX1a (Arabidopsis thaliana) GI:3790591; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:16103284-16104414 FORWARD   Aliases: MSN9.150, MSN9_150	8.7	8.9	-0.2	-1.0	100.0%	-4.8
7289	AT1G31970.1   DEAD/DEAH box helicase, putative, similar to p68 RNA helicase (Schizosaccharomyces pombe) GI:173419   chr1:11479846-11482870 FORWARD   Aliases: F5M6.3	9.3	9.7	-0.3	-1.0	100.0%	-4.7
7290	AT4G36360.2   Symbol: BGAL3   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase precursor SP:P48980 from (Lycopersicon esculentum)   chr4:17176345-17181245 REVERSE   Aliases: F23E13.200, F23E13_200	5.9	6.4	-0.5	-1.0	100.0%	-4.2
7291	AT5G47420.1   expressed protein, contains Pfam domain, PF01987: Protein of unknown function   chr5:19250063-19252286 FORWARD   Aliases: MQL5.28, MQL5_28	5.3	5.8	-0.5	-1.0	100.0%	-4.1
7292	AT3G42320.1   expressed protein, various predicted Helicases, Arabidopsis thaliana   chr3:14489392-14493635 REVERSE   Aliases: T14K23.30	2.5	2.3	0.1	1.0	100.0%	-5.3
7293	AT4G27530.1   expressed protein   chr4:13752646-13753236 FORWARD   Aliases: T29A15.20, T29A15_20	3.1	3.0	0.2	1.0	100.0%	-4.9
7294	AT4G18770.1   Symbol: MYB98   myb family transcription factor (MYB98), identical to transcription factor (MYB98) GI:15375282 from (Arabidopsis thaliana)   chr4:10311041-10313250 FORWARD   Aliases: F28A21.180, F28A21_180	3.5	3.3	0.2	1.0	100.0%	-4.7
7295	AT2G34320.1   hypothetical protein   chr2:14492038-14492916 FORWARD   Aliases: F13P17.16, F13P17_16	3.0	2.8	0.2	1.0	100.0%	-4.9
7296	AT5G50110.1   methyltransferase-related, contains weak similarity to Methyltransferase gidB (EC 2.1.-.-) (Glucose inhibited division protein B). (Swiss-Prot:Q93D95) (Streptococcus mutans)   chr5:20390794-20393433 FORWARD   Aliases: MPF21.12, MPF21_12	7.5	7.1	0.4	1.0	100.0%	-4.1
7297	AT3G58870.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:21776856-21778275 REVERSE   Aliases: T20N10.220	2.6	2.7	-0.1	-1.0	100.0%	-5.1
7298	AT1G49310.1   expressed protein   chr1:18241531-18242030 REVERSE   Aliases: F13F21.30, F13F21_30	4.8	4.0	0.7	1.0	100.0%	-4.1
7299	AT2G02380.1   Symbol: ATGSTZ2   glutathione S-transferase, putative, similar to gi:167970 gb:AAA72320 gb:AY052332   chr2:626841-628675 FORWARD   Aliases: T16F16.17, T16F16_17	2.9	2.7	0.2	1.0	100.0%	-4.8
7300	AT1G26850.3   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr1:9300860-9304120 REVERSE   Aliases: T2P11.4, T2P11_4	10.0	10.3	-0.3	-1.0	100.0%	-4.5
7301	AT1G13880.1   ELM2 domain-containing protein, contains Pfam profile: PF01448 ELM2 domain   chr1:4748926-4751208 FORWARD   Aliases: F16A14.9, F16A14_9	4.8	4.3	0.6	1.0	100.0%	-4.3
7302	AT5G40840.2   Symbol: SYN2   cohesion family protein SYN2 (SYN2), identical to cohesion family protein SYN2 (Arabidopsis thaliana) GI:12006360; supporting cDNA gi:12006359:gb:AF281154.1:AF281154   chr5:16376658-16381020 REVERSE   Aliases: MHK7.7, MHK7_7	3.3	3.6	-0.2	-1.0	100.0%	-4.7
7303	AT1G42480.1   expressed protein   chr1:15938670-15941301 FORWARD   Aliases: T8D8.4, T8D8_4	5.9	6.2	-0.2	-1.0	100.0%	-4.6
7304	AT2G33260.1   tryptophan/tyrosine permease family protein, contains Pfam profile PF03222: Tryptophan/tyrosine permease family   chr2:14107917-14109329 REVERSE   Aliases: F4P9.3, F4P9_3	2.9	3.1	-0.2	-1.0	100.0%	-4.6
7305	AT2G47420.1   dimethyladenosine transferase, putative, similar to SP:P41819 Dimethyladenosine transferase (EC 2.1.1.-) (S-adenosylmethionine-6-N', N'-adenosyl (rRNA) dimethyltransferase) {Saccharomyces cerevisiae}; contains Pfam profile PF00398: ribosomal RNA adenine dimethylase family protein   chr2:19464555-19465951 FORWARD   Aliases: T30B22.28	6.9	6.4	0.4	1.0	100.0%	-4.3
7306	AT1G63840.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHA1a (GI:3790554) (Arabidopsis thaliana)' similar to BRH1 RING finger protein (Arabidopsis thaliana) GI:4689366; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:23693360-23694470 REVERSE   Aliases: T12P18.14, T12P18_14	7.4	7.0	0.3	1.0	100.0%	-4.5
7307	AT3G46680.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:17206303-17207728 REVERSE   Aliases: F12A12.200	3.2	3.4	-0.2	-1.0	100.0%	-4.8
7308	AT1G62840.1   expressed protein   chr1:23275146-23276072 FORWARD   Aliases: F23N19.19, F23N19_19	5.6	5.1	0.5	1.0	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7309	AT1G73100.1   Symbol: SUVH3   SET domain-containing protein (SUVH3), identical to SUVH3 (Arabidopsis thaliana) GI:13517747; contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH3 (SUVH3) GI:14625477   chr1:27494885-27497843 FORWARD   Aliases: F3N23.30, F3N23_30, SU(VAR)3 9 HOMOLOG 3	4.9	4.6	0.3	1.0	100.0%	-4.3
7310	AT1G05370.1   expressed protein   chr1:1569191-1572279 REVERSE   Aliases: YUP8H12.1	2.6	2.8	-0.2	-1.0	100.0%	-4.8
7311	AT1G64070.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:23783612-23787112 FORWARD   Aliases: F22C12.17, F22C12_17	2.3	2.2	0.1	1.0	100.0%	-5.1
7312	AT2G40360.1   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); similar to block of proliferation protein Bop1 (GI:1679772) (Mus musculus)   chr2:16859958-16863768 REVERSE   Aliases: T3G21.13, T3G21_13	9.1	9.3	-0.3	-1.0	100.0%	-4.6
7313	AT1G63030.1   Symbol: DDF2   encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (DDF2). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. Overexpression of this gene results in the reduction of gibberellic acid biosynthesis. This gene is expressed in all tissues examined, but most abundantly expressed in rosette leaves and stems. Overexpression of DDF1, a putative paralog of this gene, also reduces gibberellic acid biosynthesis and makes the plants more tolerant to high-salinity levels.   chr1:23371177-23371813 REVERSE   Aliases: DDF2, DWARF AND DELAYED FLOWERING 2, F16P17.20, F16P17_20	2.0	1.9	0.1	1.0	100.0%	-5.4
7314	AT1G71690.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr1:26951439-26952726 FORWARD   Aliases: F14O23.3, F14O23_3	3.8	3.5	0.3	1.0	100.0%	-4.4
7315	AT1G79260.1   expressed protein   chr1:29818154-29819202 FORWARD   Aliases: YUP8H12R.14, YUP8H12R_14	7.6	8.1	-0.5	-1.0	100.0%	-4.1
7316	AT4G13840.1   transferase family protein, low similarity to acetyl-CoA:benzylalcohol acetyltransferase (Clarkia concinna) GI:6166328; contains Pfam profile PF02458: Transferase family	4.4	4.1	0.2	1.0	100.0%	-4.8
7317	AT5G40710.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:16312264-16314232 FORWARD   Aliases: MNF13.27, MNF13_27	4.3	4.6	-0.3	-1.0	100.0%	-4.6
7318	AT3G42800.1   expressed protein, hypothetical proteins - Arabidopsis thaliana; expression supported by MPSS   chr3:14916825-14917850 FORWARD   Aliases: T21C14.20	3.2	3.1	0.1	1.0	100.0%	-5.0
7319	AT2G44000.1   expressed protein   chr2:18221400-18222647 FORWARD   Aliases: F6E13.13	2.3	2.2	0.1	1.0	100.0%	-5.5
7320	AT1G09310.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:3009057-3009882 FORWARD   Aliases: T31J12.3, T31J12_3	3.0	3.1	-0.1	-1.0	100.0%	-4.9
7321	AT4G02280.1   sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative, strong similarity to sucrose synthase GI:6682841 from (Citrus unshiu)   chr4:994927-998963 FORWARD   Aliases: T2H3.8, T2H3_8	5.6	5.2	0.3	1.0	100.0%	-4.1
7322	AT5G05570.1   transducin family protein / WD-40 repeat family protein, similar to unknown protein (pir::T04661); contains Pfam PF00400: WD domain, G-beta repeat (4 copies, 2 weak):8683726:gb:AV524198.1:AV524198   chr5:1656567-1663930 FORWARD   Aliases: MOP10.11, MOP10_11	5.7	6.2	-0.5	-1.0	100.0%	-4.4
7323	AT1G77540.1   expressed protein, similar to GB:AAD41433   chr1:29142570-29143103 REVERSE   Aliases: T5M16.13, T5M16_13	9.1	8.7	0.5	1.0	100.0%	-4.1
7324	AT1G48360.1   similar to Similar to Caenorhabditis elegans cosmid C01G5; Pfam family PF00096 (U50068) [Oryza sativa (japonica cultivar-group)] (GB:XP_493957.1)   chr1:17872318-17876699 FORWARD   Aliases: F11A17.9, F11A17_9	5.9	5.4	0.5	1.0	100.0%	-4.4
7325	AT3G49400.1   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); low similarity (47%) to Agamous-like MADS box protein AGL5 (SP:P29385) {Arabidopsis thaliana}   chr3:18330234-18335467 REVERSE   Aliases: F2K15.260	3.2	3.0	0.2	1.0	100.0%	-4.5
7326	AT5G63890.2   Symbol: ATHDH   histidinol dehydrogenase, putative / HDH, putative, strong similarity to SP:P24226 Histidinol dehydrogenase, chloroplast precursor (EC 1.1.1.23) (HDH) {Brassica oleracea var.capitata}; contains Pfam profile PF00815: histidinol dehydrogenase   chr5:25582657-25585421 REVERSE   Aliases: HISTIDINOL DEHYDROGENASE, MGI19.9, MGI19_9	9.1	9.6	-0.5	-1.0	100.0%	-4.2
7327	AT3G05290.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr3:1505897-1507706 REVERSE   Aliases: T12H1.26, T12H1_26	8.1	8.4	-0.3	-1.0	100.0%	-4.6
7328	AT3G55190.1   esterase/lipase/thioesterase family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379   chr3:20468984-20470867 FORWARD   Aliases: T26I12.70	2.2	2.2	0.1	1.0	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7329	AT2G21990.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr2:9366436-9367744 REVERSE   Aliases: F7D8.31, F7D8_31	3.1	3.3	-0.2	-1.0	100.0%	-4.7
7330	AT2G17360.1   40S ribosomal protein S4 (RPS4A), contains ribosomal protein S4 signature from residues 8 to 22   chr2:7553567-7555395 FORWARD   Aliases: F5J6.12, F5J6_12	9.0	9.6	-0.6	-1.0	100.0%	-4.3
7331	AT2G03270.1   DNA-binding protein, putative, similar to Swiss-Prot:Q60560 DNA-binding protein SMUBP-2 (Immunoglobulin MU binding protein 2) (SMUBP-2) (Insulin II gene enhancer-binding protein)(RIPE3B-binding complex 3B2 P110 subunit) (RIP-1)(Mesocricetus auratus); identical to putative helicase (atpc-2 gene) cDNA NCBI_gi:11191230   chr2:993780-996125 FORWARD   Aliases: T4M8.30, T4M8_30	6.5	6.9	-0.4	-1.0	100.0%	-4.3
7332	AT5G40190.1   Identified in a screen for calmodulin-binding proteins obtained from an auxin treated cDNA library.   chr5:16086430-16087163 REVERSE   Aliases: MSN9.9, MSN9_9	7.2	7.0	0.3	1.0	100.0%	-4.6
7333	AT5G57580.1   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum)   chr5:23331942-23335351 REVERSE   Aliases: MUA2.16, MUA2_16	3.4	3.2	0.2	1.0	100.0%	-4.6
7334	AT2G01700.1   hypothetical protein   chr2:314843-315157 REVERSE   Aliases: T8O11.13, T8O11_13	2.0	2.1	-0.1	-1.0	100.0%	-5.5
7335	AT3G59040.2   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:21832326-21835289 REVERSE   Aliases: F17J16.90	5.4	5.8	-0.3	-1.0	100.0%	-4.4
7336	AT1G22790.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g34010.1); similar to light stress-responsive one-helix protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD52885.1)   chr1:8069502-8071429 FORWARD   Aliases: T22J18.4, T22J18_4	5.1	4.8	0.3	1.0	100.0%	-4.5
7337	AT1G07080.1   gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein, similar to SP:P13284 Gamma-interferon inducible lysosomal thiol reductase precursor {Homo sapiens}; contains Pfam profile PF03227: Gamma interferon inducible lysosomal thiol reductase (GILT)   chr1:2170009-2172193 FORWARD   Aliases: F10K1.21, F10K1_21	7.4	7.0	0.5	1.0	100.0%	-4.3
7338	AT5G45230.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18319374-18325530 REVERSE   Aliases: K18C1.11, K18C1_11	4.5	4.4	0.1	1.0	100.0%	-5.0
7339	AT5G20350.1   Symbol: TIP1   similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At2g14250.1); similar to putative ankyrin repeat-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464354.1); contains InterPro domain Zn-finger, DHHC type (InterPro:IPR001594); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr5:6876591-6881272 FORWARD   Aliases: F5O24.240, F5O24_240, TIP GROWTH DEFECTIVE 1	8.1	8.3	-0.2	-1.0	100.0%	-4.6
7340	AT3G29265.1   hypothetical protein   chr3:11232949-11233659 FORWARD   Aliases: MMF24.1	2.1	2.2	-0.1	-1.0	100.0%	-5.4
7341	AT1G06130.2   hydroxyacylglutathione hydrolase, putative / glyoxalase II, putative, similar to glyoxalase II isozyme GB:AAC49865 GI:2570338 from (Arabidopsis thaliana)   chr1:1857766-1860697 REVERSE   Aliases: T21E18.18, T21E18_18	5.4	4.9	0.5	1.0	100.0%	-4.0
7342	AT2G46840.1   expressed protein, ; expression supported by MPSS   chr2:19256260-19256978 REVERSE   Aliases: F19D11.12	2.5	2.4	0.2	1.0	100.0%	-5.0
7343	AT5G16990.1   NADP-dependent oxidoreductase, putative, strong similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana   chr5:5581661-5584032 REVERSE   Aliases: F2K13.140, F2K13_140	9.9	9.5	0.4	1.0	100.0%	-4.4
7344	AT1G44000.1   expressed protein   chr1:16710509-16712153 REVERSE   Aliases: F9C16.20, F9C16_20	7.2	7.5	-0.3	-1.0	100.0%	-4.3
7345	AT1G34310.1   Symbol: ARF12   transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related, contains Pfam profile: PF02309 AUX/IAA family   chr1:12508526-12511498 REVERSE   Aliases: ARF12, AUXIN RESPONSE FACTOR 12, F23M19.4, F23M19_4	4.3	4.7	-0.4	-1.0	100.0%	-4.4
7346	AT5G53820.1   expressed protein, similar to ABA-inducible protein (Fagus sylvatica) GI:3901016, cold-induced protein kin1 (Brassica napus) GI:167146   chr5:21870623-21871343 FORWARD   Aliases: MGN6.21, MGN6_21	2.8	2.9	-0.1	-1.0	100.0%	-5.3
7347	AT3G55080.2   similar to SET domain-containing protein [Arabidopsis thaliana] (TAIR:At3g07670.1); similar to putative ribulose-1,5 bisphosphate carboxylase/oxygenase large subunit N-methyltransferase, chloroplast precursor [Oryza sativa (japonica cultivar-group)] (GB:BAD28364.1)   chr3:20422380-20426896 REVERSE   Aliases: T15C9.90	5.5	5.2	0.3	1.0	100.0%	-4.2
7348	AT1G49720.1   Symbol: ABF1   ABA-responsive element-binding protein / abscisic acid responsive elements-binding factor (ABRE), identical to abscisic acid responsive elements-binding factor GB:AAF27179 GI:6739274 from (Arabidopsis thaliana); identical to cDNA abscisic acid responsive elements-binding factor (ABRE) mRNA, complete cds GI:6739273   chr1:18403760-18406735 FORWARD   Aliases: ABSCISIC ACID RESPONSIVE ELEMENT BINDING FACTOR 1, F14J22.7, F14J22_7	5.1	4.8	0.3	1.0	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7349	AT1G74055.1   expressed protein   chr1:27852891-27853473 FORWARD   Aliases: None	4.3	4.1	0.2	1.0	100.0%	-4.6
7350	AT5G15020.1   paired amphipathic helix repeat-containing protein, similar to transcription co-repressor Sin3 (Xenopus laevis) GI:4960210; contains Pfam profile PF02671: Paired amphipathic helix repeat   chr5:4859141-4865572 REVERSE   Aliases: F2G14.140, F2G14_140	3.2	3.4	-0.2	-1.0	100.0%	-4.7
7351	AT3G11670.2   Symbol: DGD1   digalactosyldiacylglycerol synthase 1 (DGD1) / MGDG:MGDG galactosyltransferase / galactolipid galactosyltransferase, identical to digalactosyldiacylglycerol synthase (DGD1) GI:5354158 (Arabidopsis thaliana)   chr3:3681612-3684552 REVERSE   Aliases: DIGALACTOSYL DIACYLGLYCEROL DEFICIENT 1, DIGALACTOSYLDIACYLGLYCEROL SYNTHASE 1, T19F11.7	6.2	5.7	0.4	1.0	100.0%	-4.3
7352	AT3G57610.1   adenylosuccinate synthetase (ADSS), identical to adenylosuccinate synthetase, chloroplast precursor (EC 6.3.4.4) (IMP-- aspartate ligase) (AdSS) (AMPSase) (Swiss-Prot:Q96529) (Arabidopsis thaliana)   chr3:21345261-21347635 REVERSE   Aliases: F15B8.200, F15B8_200	11.2	11.6	-0.4	-1.0	100.0%	-4.5
7353	AT1G79040.1   photosystem II 10 kDa polypeptide, identical to photosystem II 10 kDa polypeptide, chloroplast (precursor) SP:P27202 from (Arabidopsis thaliana); contains Pfam profile: PF04725 photosystem II 10 kDa polypeptide PsbR   chr1:29740911-29741831 FORWARD   Aliases: YUP8H12R.34, YUP8H12R_34	11.5	11.2	0.3	1.0	100.0%	-4.5
7354	AT1G65740.1   F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.3	-0.1	-1.0	100.0%	-5.2
7355	AT2G19930.1   RNA-dependent RNA polymerase family protein, contains Pfam domain, PF05183: RNA dependent RNA polymerase	5.2	5.6	-0.4	-1.0	100.0%	-4.2
7356	AT2G45720.2   similar to armadillo/beta-catenin repeat family protein [Arabidopsis thaliana] (TAIR:At1g01830.1); similar to arm repeat containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_478704.1); contains InterPro domain Armadillo repeat (InterPro:IPR000225)   chr2:18841223-18843448 FORWARD   Aliases: F4I18.30	7.1	6.8	0.3	1.0	100.0%	-4.5
7357	AT5G47360.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:19231672-19233105 REVERSE   Aliases: MQL5.22, MQL5_22	6.3	5.9	0.4	1.0	100.0%	-4.3
7358	AT3G63080.1   Symbol: ATGPX5	7.4	6.6	0.8	1.0	100.0%	-4.2
7359	AT5G32440.1   expressed protein   chr5:12094126-12095787 FORWARD   Aliases: F18O9.50, F18O9_50	8.0	7.6	0.4	1.0	100.0%	-4.4
7360	AT1G41880.1   60S ribosomal protein L35a (RPL35aB), identical to GB:CAB81600 from (Arabidopsis thaliana)   chr1:15653564-15654932 REVERSE   Aliases: F5A13.4, F5A13_4	11.3	11.7	-0.4	-1.0	100.0%	-4.0
7361	AT3G55750.1   60S ribosomal protein L35a (RPL35aD), ribosomal protein L35a.e.c15, Saccharomyces cerevisiae, PIR:S44069	11.3	11.7	-0.4	-1.0	100.0%	-4.0
7362	AT4G02730.1   transducin family protein / WD-40 repeat family protein, similar to C. elegans putative WD-repeat protein C14B1.4 (SP:Q17963)   chr4:1207725-1209287 FORWARD   Aliases: T5J8.2, T5J8_2	5.9	6.6	-0.7	-1.0	100.0%	-4.3
7363	AT2G47180.1   galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 GI:5608497 from (Ajuga reptans)   chr2:19375868-19377511 REVERSE   Aliases: T8I13.2	4.5	4.8	-0.3	-1.0	100.0%	-4.2
7364	AT4G08500.2   Symbol: MEKK1   similar to mitogen-activated protein kinase, putative [Arabidopsis thaliana] (TAIR:At4g08480.1); similar to MAP3K beta 1 protein kinase [Brassica napus] (GB:CAA08997.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:5403754-5407298 REVERSE   Aliases: ARAKIN, ATMEKK1, MAPKKK8, MYTOGEN ACTIVATED PROTEIN KINASE KINASE, T15F16.5, T15F16_5	3.8	3.4	0.4	1.0	100.0%	-4.2
7365	AT1G40390.1   expressed protein   chr1:15435017-15437115 REVERSE   Aliases: F9D18.22, F9D18_22	2.8	2.7	0.1	1.0	100.0%	-5.1
7366	AT5G09470.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:2949242-2950514 REVERSE   Aliases: T5E8.270, T5E8_270	3.4	3.1	0.3	1.0	100.0%	-4.2
7367	AT4G31200.3   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein, related to DAN26 (Homo sapiens) gi:1770394:emb:CAA69591   chr4:15161642-15164914 REVERSE   Aliases: F8F16.10, F8F16_10	5.7	5.9	-0.2	-1.0	100.0%	-4.6
7368	AT1G12650.2   similar to similar to CG8461-PA [Apis mellifera] (GB:XP_394556.1); contains domain LYS_RICH (PS50318)   chr1:4305958-4307957 FORWARD   Aliases: T12C24.18, T12C24_18	8.0	8.4	-0.4	-1.0	100.0%	-4.1
7369	AT2G01820.1   Symbol: CYCJ18	5.4	5.9	-0.5	-1.0	100.0%	-4.3
7370	AT1G03870.1   Symbol: FLA9   fasciclin-like arabinogalactan-protein (FLA9), identical to gi_13377784_gb_AAK20861   chr1:982508-983539 REVERSE   Aliases: F21M11.20, F21M11_20, fasciclin like arabinogalactan protein 9	4.8	4.5	0.3	1.0	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7371	AT2G45580.1   Symbol: CYP76C3   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome p450   chr2:18789400-18791417 REVERSE   Aliases: F17K2.11	4.6	4.4	0.2	1.0	100.0%	-4.5
7372	AT1G62360.1   Symbol: STM   homeobox protein SHOOT MERISTEMLESS (STM), identical to homeobox protein SHOOT MERISTEMLESS (STM) SP:Q38874 from (Arabidopsis thaliana)   chr1:23062248-23065387 REVERSE   Aliases: BUM, BUM1, BUMBERSHOOT, F24O1.38, F24O1_38, HOMEBOX PROTEIN SHOOTMERISTEMLESS, SHL, SHOOT MERISTEMLESS, SHOOTLESS, SHOOTMERISTEMLESS, STM, WALDMEISTER, WAM, WAM1	2.7	2.5	0.1	1.0	100.0%	-5.1
7373	AT3G53160.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:19713434-19714954 REVERSE   Aliases: T4D2.90	3.3	3.5	-0.3	-1.0	100.0%	-4.6
7374	AT3G11580.2   DNA-binding protein, putative, similar to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857 and RAV2 GI:3868859, AP2 domain containing protein RAP2.8 (Arabidopsis thaliana) GI:2281641; contains Pfam profile PF02362: B3 DNA binding domain   chr3:3650546-3651323 REVERSE   Aliases: F24K9.25	5.6	5.1	0.5	1.0	100.0%	-4.2
7375	AT3G18560.1   expressed protein   chr3:6393916-6394783 FORWARD   Aliases: K24M9.5	4.4	4.0	0.4	1.0	100.0%	-4.0
7376	AT1G49975.1   expressed protein   chr1:18508484-18509265 FORWARD   Aliases: None	2.3	2.2	0.1	1.0	100.0%	-5.4
7377	AT2G35020.1   UTP--glucose-1-phosphate uridylyltransferase family protein, similar to SP:Q16222 UDP-N-acetylhexosamine pyrophosphorylase (Antigen X) {Homo sapiens}; contains Pfam profile PF01704: UTP--glucose-1-phosphate uridylyltransferase   chr2:14763790-14767768 FORWARD   Aliases: F19I3.25, F19I3_25	5.6	5.9	-0.3	-1.0	100.0%	-4.7
7378	AT1G32440.1   pyruvate kinase, putative, similar to pyruvate kinase isozyme G, chloroplast precursor (Nicotiana tabacum) SWISS-PROT:Q40546   chr1:11712142-11715092 FORWARD   Aliases: F5D14.22, F5D14_22, F5F19.10, F5F19_10	5.5	6.1	-0.5	-1.0	100.0%	-4.5
7379	AT5G12270.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similarity to ripening protein E8, tomato, PIR:S01642; contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr5:3970132-3971302 REVERSE   Aliases: None	3.3	3.5	-0.2	-1.0	100.0%	-4.9
7380	AT1G67280.1   lactoylglutathione lyase, putative / glyoxalase I, putative, similar to putative lactoylglutathione lyase SP:Q39366, GI:2494843 from (Brassica oleracea)	9.3	8.7	0.5	1.0	100.0%	-4.4
7381	AT5G58870.1   Symbol: FTSH9   encodes an FtsH protease that is localized to the chloroplast   chr5:23787038-23791006 REVERSE   Aliases: FTSH9, K19M22.17, K19M22_17	6.8	7.1	-0.3	-1.0	100.0%	-4.7
7382	AT3G12950.1   expressed protein   chr3:4132535-4135140 REVERSE   Aliases: MGH6.6	6.2	5.9	0.3	1.0	100.0%	-4.4
7383	AT5G58560.1   phosphatidate cytidylyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidylyltransferase   chr5:23687641-23690513 FORWARD   Aliases: MZN1.8, MZN1_8	6.4	6.1	0.3	1.0	100.0%	-4.4
7384	AT3G07720.1   kelch repeat-containing protein, similar to epithiospecifier (GI:16118838) (Arabidopsis thaliana); contains Pfam PF01344: Kelch motif (5 repeats)   chr3:2465371-2467239 FORWARD   Aliases: MLP3.17, MLP3_17	7.7	7.3	0.4	1.0	100.0%	-4.1
7385	AT2G47990.1   Symbol: SWA1   transducin family protein / WD-40 repeat family protein, similar to Vegetatible incompatibility protein HET-E-1 (SP:Q00808) {Podospora anserina}; contains 5 WD-40 repeats (PF00400); similar to	6.4	6.9	-0.5	-1.0	100.0%	-4.3
7386	AT3G01750.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr3:270236-272873 FORWARD   Aliases: F28J7.8	3.8	3.6	0.2	1.0	100.0%	-4.5
7387	AT4G17730.1   Symbol: SYP23   syntaxin 23 (SYP23) / PEP12-like protein, identical to SP:O04378 Syntaxin 23 (AtSYP23) (AtPLP) (AtPEP12-like protein) {Arabidopsis thaliana}   chr4:9865158-9866983 FORWARD   Aliases: ATSYP23, DL4901W, FCAALL.117	6.9	6.5	0.4	1.0	100.0%	-4.4
7388	AT3G45320.1   hypothetical protein   chr3:16642631-16643131 FORWARD   Aliases: F18N11.80	2.3	2.2	0.1	1.0	100.0%	-5.2
7389	AT1G56670.1   GDSL-motif lipase/hydrolase family protein, similarity to early early nodulin ENOD8 (Medicago sativa) GI:304037, lanatoside 15'-O-acetylesterase (Digitalis lanata) GI:3688284, elicitor-induced glycoprotein iEP4 (Daucus carota) GI:1911765; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr1:21245350-21247712 FORWARD   Aliases: F25P12.90, F25P12_90	4.8	5.0	-0.2	-1.0	100.0%	-4.7
7390	AT4G02610.1   tryptophan synthase, alpha subunit, putative, similar to A. thaliana tryptophan synthase alpha chain (EC 4.2.1.20), GenBank accession number U18993 (gi:619753)   chr4:1147634-1149577 FORWARD   Aliases: T10P11.11, T10P11_11	8.5	8.9	-0.5	-1.0	100.0%	-4.1
7391	AT5G24610.1   expressed protein, similar to unknown protein (emb:CAB62459.1)   chr5:8428081-8429255 FORWARD   Aliases: K18P6.15, K18P6_15	6.7	7.3	-0.6	-1.0	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7392	AT1G04820.1   Symbol: TUA4   tubulin alpha-2/alpha-4 chain (TUA4), nearly identical to SP:P29510 Tubulin alpha-2/alpha-4 chain from (Arabidopsis thaliana)   chr1:1356190-1358374 REVERSE   Aliases: F13M7.19	8.1	7.1	1.0	1.0	100.0%	-4.2
7393	AT2G05000.1   hypothetical protein, and genefinder   chr2:1761801-1762375 REVERSE   Aliases: F1O13.13, F1O13_13	2.4	2.5	-0.1	-1.0	100.0%	-5.3
7394	AT4G24890.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.4	2.3	0.1	1.0	100.0%	-5.3
7395	AT5G62230.1   Symbol: ERL1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:25013659-25019356 FORWARD   Aliases: ERECTA LIKE 1, MMI9.14, MMI9_14	3.2	3.1	0.1	1.0	100.0%	-5.0
7396	AT4G34520.1   Symbol: FAE1   fatty acid elongase 1 (FAE1), identical to fatty acid elongase 1 (GI:881615)   chr4:16494210-16495847 FORWARD   Aliases: FATTY ACID ELONGATION1, T4L20.100, T4L20_100	2.9	2.7	0.2	1.0	100.0%	-4.9
7397	AT1G71100.1   ribose 5-phosphate isomerase-related, similar to ribose-5-phosphate isomerase GI:18654317 from (Spinacia oleracea)   chr1:26818294-26819333 FORWARD   Aliases: F23N20.9, F23N20_9	3.2	3.0	0.2	1.0	100.0%	-4.5
7398	AT3G06360.1   Symbol: AGP27   arabinogalactan-protein (AGP27)	2.7	2.8	-0.2	-1.0	100.0%	-4.8
7399	AT3G07570.1   membrane protein, putative, similar to membrane protein SDR2 (GI:1747306) (Mus musculus)	6.6	7.0	-0.3	-1.0	100.0%	-4.2
7400	AT2G38270.1   Symbol: CXIP2   CAX-interacting protein, putative, identical to cDNA CAXIP1-like protein GI:27752306; contains Pfam profile PF00462: Glutaredoxin; contains TIGRfam profile TIGR00365: glutaredoxin-related protein   chr2:16038340-16040154 REVERSE   Aliases: CAX INTERACTING PROTEIN 2, F16M14.20, F16M14_20	7.0	6.7	0.3	1.0	100.0%	-4.5
7401	AT1G16700.1   NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial, putative, very strong similarity to SP:Q42599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD) (Complex I- 28.5KD) (CI-28.5KD) {Arabidopsis thaliana}; contains Pfam profile PF00037: iron-sulfur cluster-binding protein   chr1:5709718-5711889 FORWARD   Aliases: F19K19.1, F19K19_1	10.4	9.5	1.0	1.0	100.0%	-3.7
7402	AT1G79010.1   NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial (TYKY), identical to SP:Q42599 NADH-ubiquinone oxidoreductase 23 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-23KD) (CI-23KD) (Complex I- 28.5KD) (CI-28.5KD) {Arabidopsis thaliana}   chr1:29729814-29731910 REVERSE   Aliases: YUP8H12R.37, YUP8H12R_37	10.4	9.5	1.0	1.0	100.0%	-3.7
7403	AT3G22800.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965   chr3:8062895-8064563 REVERSE   Aliases: MWI23.17	3.4	3.7	-0.3	-1.0	100.0%	-4.2
7404	NA	5.7	5.3	0.4	1.0	100.0%	-4.8
7405	AT1G47830.1   clathrin coat assembly protein, putative, similar to clathrin coat assembly protein AP17 GB:CAA65533 GI:2959358 from (Zea mays); contains Pfam profile: PF01217 clathrin adaptor complex small chain   chr1:17615538-17617355 REVERSE   Aliases: T2E6.6, T2E6_6	7.6	7.9	-0.3	-1.0	100.0%	-4.3
7406	AT4G18390.1   TCP family transcription factor, putative, similar to TFPD (GI:6681577) (Arabidopsis thaliana); teosinte branched1 protein - Zea mays, PIR2:T04347   chr4:10162964-10165573 REVERSE   Aliases: F28J12.50, F28J12_50	5.4	5.1	0.3	1.0	100.0%	-4.6
7407	AT5G14250.2   Symbol: COP13   expressed protein, similar to hypothetical protein LOC549992 [Xenopus tropicalis] (GB:NP_001017238.1)   chr5:4597889-4600762 FORWARD   Aliases: CONSTITUTIVE PHOTOMORPHOGENIC 13, CSN3, F18O22.40, F18O22_40, FUS11, FUSCA 11	7.9	8.2	-0.2	-1.0	100.0%	-4.4
7408	AT4G16845.2   Symbol: VRN2   vernalization 2 protein (VRN2), identical to vernalization 2 protein (Arabidopsis thaliana) gi:16945788:gb:AAL32135   chr4:9476174-9479895 FORWARD   Aliases: REDUCED VERNALIZATION RESPONSE 2	5.8	6.1	-0.3	-1.0	100.0%	-4.7
7409	AT1G22340.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase; similar to UDP-glucose glucosyltransferase GI:3928543 from (Arabidopsis thaliana)   chr1:7890453-7892079 REVERSE   Aliases: T16E15.5, T16E15_5	5.5	5.2	0.3	1.0	100.0%	-4.5
7410	AT1G71200.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.2	3.0	0.2	1.0	100.0%	-4.7
7411	AT2G37240.1   expressed protein, weak similarity to fmHP (GI:22902096) (Takifugu rubripes)   chr2:15647018-15648842 REVERSE   Aliases: F3G5.3, F3G5_3	8.0	7.6	0.4	1.0	100.0%	-4.0
7412	AT5G51400.1   expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614   chr5:20895839-20897360 REVERSE   Aliases: MFG13.11, MFG13_11	7.8	7.4	0.4	1.0	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7413	AT2G38940.1   Symbol: ATPT2   phosphate transporter (PT2), identical to phosphate transporter (AtPT2) (Arabidopsis thaliana) GI:1502430   chr2:16264318-16267300 FORWARD   Aliases: PHOSPHATE TRANSPORTER 2, PHT4, T7F6.11, T7F6_11	1.9	2.0	-0.1	-1.0	100.0%	-5.3
7414	AT1G66680.1   Symbol: AR401   S locus-linked protein, putative, similar to S locus-linked protein SLL2 (Brassica napus) GI:1518113   chr1:24869758-24872638 REVERSE   Aliases: AR401, F4N21.18, F4N21_18	7.7	8.1	-0.4	-1.0	100.0%	-4.5
7415	AT4G20130.1   ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N-methyltransferase-related, contains weak similarity to Swiss-Prot:P94026 ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N- methyltransferase, chloroplast precursor (Ribulose- biphosphate-carboxylase)-lysine N-methyltransferase, RuBisCO methyltransferase, RuBisco LSMT, rbcMT) (Nicotiana tabacum)   chr4:10878916-10881939 FORWARD   Aliases: F1C12.4	3.2	3.3	-0.1	-1.0	100.0%	-5.3
7416	AT1G69040.2   Symbol: ACR4   ACT domain containing protein (ACR4), low similarity to uridylyltransferase (Gluconacetobacter diazotrophicus) GI:17226253; contains Pfam profile PF01842: ACT domain   chr1:25961482-25963970 FORWARD   Aliases: ACT REPEAT 4, F4N2.2, F4N2_2	4.7	4.5	0.2	1.0	100.0%	-4.6
7417	AT4G15090.1   Symbol: FAR1   far-red impaired response protein (FAR1) / far-red impaired responsive protein (FAR1), identical to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr4:8614063-8618142 FORWARD   Aliases: DL3590W, FAR RED IMPAIRED RESPONSE 1, FCAALL.134	5.2	5.5	-0.3	-1.0	100.0%	-4.4
7418	AT3G06120.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.6	2.8	-0.2	-1.0	100.0%	-4.7
7419	AT4G28020.1   expressed protein, contains Pfam PF01980: Uncharacterised protein family	5.1	4.9	0.2	1.0	100.0%	-4.5
7420	AT5G50230.1   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g49660.1); similar to TipD [Dictyostelium discoideum] (GB:AAB70659.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr5:20465596-20468107 REVERSE   Aliases: K6A12.9, K6A12_9	6.6	6.3	0.3	1.0	100.0%	-4.6
7421	AT5G08180.1   ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein, Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.   chr5:2631658-2633449 REVERSE   Aliases: T22D6.120, T22D6_120	7.1	7.4	-0.3	-1.0	100.0%	-4.3
7422	AT2G35870.1   expressed protein   chr2:15068888-15069190 REVERSE   Aliases: F11F19.22, F11F19_22	3.0	2.8	0.2	1.0	100.0%	-4.9
7423	AT3G44050.1   kinesin motor protein-related, KLP2 protein, Xenopus laevis, PIR:T30335   chr3:15829725-15835848 FORWARD   Aliases: F26G5.1	4.9	5.2	-0.3	-1.0	100.0%	-4.6
7424	AT1G31850.3   dehydration-responsive protein, putative, strong similarity to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase	7.6	8.1	-0.5	-1.0	100.0%	-4.4
7425	AT2G47710.1   universal stress protein (USP) family protein, similar to ER6 protein (Lycopersicon esculentum) GI:5669654; contains Pfam profile PF00582: universal stress protein family   chr2:19561904-19563135 REVERSE   Aliases: F17A22.10	11.3	10.8	0.5	1.0	100.0%	-4.2
7426	AT5G65700.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:26298986-26302473 FORWARD   Aliases: MPA24.5, MPA24_5	5.3	5.8	-0.6	-1.0	100.0%	-4.1
7427	AT1G55490.2   Symbol: CPN60B	10.9	11.4	-0.4	-1.0	100.0%	-4.1
7428	AT5G63910.1   expressed protein   chr5:25589116-25591313 REVERSE   Aliases: MGI19.4, MGI19_4	6.1	5.9	0.3	1.0	100.0%	-4.5
7429	AT1G14780.1   expressed protein   chr1:5090985-5094147 FORWARD   Aliases: F10B6.18, F10B6_18	3.3	3.8	-0.5	-1.0	100.0%	-4.1
7430	AT3G50410.1   Symbol: OBP1   Dof-type zinc finger domain-containing protein   chr3:18720729-18721724 FORWARD   Aliases: F11C1.250, OBF BINDING PROTEIN	6.1	6.6	-0.6	-1.0	100.0%	-3.8
7431	AT1G07980.1   histone-like transcription factor (CBF/NF-Y) family protein, contains Pfam profile PF00808: Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to Chromatin accessibility complex protein 1 (CHRAC-1) (CHRAC-15) (HuCHRAC15) (DNA polymerase epsilon subunit p15) (SP:Q9NRG0) {Homo sapiens}   chr1:2473162-2474924 REVERSE   Aliases: T6D22.7, T6D22_7	6.6	6.3	0.3	1.0	100.0%	-4.4
7432	AT5G27830.2   expressed protein   chr5:9861293-9862900 FORWARD   Aliases: T1G16.160, T1G16_160	8.2	7.6	0.6	1.0	100.0%	-4.4
7433	AT5G64380.1   fructose-1,6-bisphosphatase family protein, similar to SP:P22418 Fructose-1,6-bisphosphatase, chloroplast precursor (EC 3.1.3.11) (D-fructose-1,6-bisphosphate 1-phosphohydrolase) (FBPase) {Spinacia oleracea}; contains Pfam profile PF00316: fructose-1,6-bisphosphatase   chr5:25758475-25760424 FORWARD   Aliases: MSJ1.22, MSJ1_22	5.0	4.6	0.3	1.0	100.0%	-4.2
7434	AT1G71730.1   expressed protein   chr1:26989750-26990571 REVERSE   Aliases: F14O23.11, F14O23_11	5.5	5.0	0.5	1.0	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7435	AT1G01910.3   similar to anion-transporting ATPase family protein [Arabidopsis thaliana] (TAIR:At5g60730.1); similar to ENSANGP00000018739 [Anopheles gambiae str. PEST] (GB:XP_315798.2); contains InterPro domain Anion-transporting ATPase (InterPro:IPR003348)   chr1:313210-315902 REVERSE   Aliases: F22M8.4, F22M8_4	6.5	7.1	-0.6	-1.0	100.0%	-4.1
7436	AT5G62880.1   Symbol: ARAC10	4.7	5.0	-0.3	-1.0	100.0%	-4.4
7437	AT3G12890.1   Symbol: ASML2   expressed protein   chr3:4099206-4100476 FORWARD   Aliases: ACTIVATOR OF SPOMIN::LUC2, MJM20.3	2.8	2.7	0.1	1.0	100.0%	-5.2
7438	AT4G30950.1   Symbol: FAD6   omega-6 fatty acid desaturase, chloroplast (FAD6) (FADC), identical to GI:493068	10.4	10.0	0.4	1.0	100.0%	-4.3
7439	AT4G18360.1   (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative, similar to (S)-2-hydroxy-acid oxidase, peroxisomal (Glycolate oxidase, GOX) (Short chain alpha-hydroxy acid oxidase) (Spinacia oleracea) SWISS-PROT:P05414   chr4:10145930-10148693 REVERSE   Aliases: F28J12.20, F28J12_20	7.3	7.7	-0.4	-1.0	100.0%	-4.4
7440	AT1G49590.1   formin-binding protein-related, similar to formin binding protein 21 (GI:3550080) (Homo sapiens); similar to formin binding protein 21 (GI:3550077) (Mus musculus); similar to Dinap1-interacting protein 1 (GI:8745458) (Cryptocodium cohnii)   chr1:18358488-18360310 FORWARD   Aliases: F14J22.17, F14J22_17	5.5	5.1	0.3	1.0	100.0%	-4.3
7441	AT1G72530.1   plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (required for chloroplast differentiation) GB:Q38732 (Antirrhinum majus)   chr1:27316661-27317599 FORWARD   Aliases: F28P22.28, F28P22_28	4.2	4.0	0.2	1.0	100.0%	-4.4
7442	AT3G12203.1   Symbol: SCPL17	3.2	3.1	0.2	1.0	100.0%	-4.8
7443	AT1G79150.1   expressed protein, ; expression supported by MPSS   chr1:29779996-29782767 REVERSE   Aliases: YUP8H12R.24, YUP8H12R_24	7.0	7.5	-0.5	-1.0	100.0%	-4.5
7444	AT1G77370.1   glutaredoxin, putative, similar to glutaredoxin (Ricinus communis) gi:1732424:emb:CAA89699   chr1:29078741-29079683 FORWARD   Aliases: F2P24.8, F2P24_8	9.7	9.4	0.3	1.0	100.0%	-4.8
7445	AT3G11730.1   Symbol: AFTP8   Ras-related GTP-binding protein, putative, similar to Rab1-like small GTP-binding protein GI:4096662 from (Petunia x hybrida)   chr3:3709332-3711489 REVERSE   Aliases: AFTP8, F26K24.2	8.5	8.7	-0.3	-1.0	100.0%	-4.4
7446	AT2G16510.1   Symbol: AVA P1	9.5	8.9	0.6	1.0	100.0%	-4.4
7447	AT4G22890.3   expressed protein   chr4:12006997-12009529 FORWARD   Aliases: F7H19.70, F7H19_70	9.7	9.3	0.4	1.0	100.0%	-4.4
7448	AT1G01800.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)   chr1:293342-295040 FORWARD   Aliases: T1N6.22, T1N6_22	11.3	11.8	-0.5	-1.0	100.0%	-4.6
7449	AT1G64810.2   Symbol: APO1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g57930.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g57930.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_467639.1); contains InterPro domain Arabidopsis thaliana protein of unknown function DUF794 (InterPro:IPR008512)   chr1:24090402-24092201 FORWARD   Aliases: ACCUMULATION OF PHOTOSYSTEM ONE 1, F13O11.11, F13O11_11	5.6	5.3	0.3	1.0	100.0%	-4.2
7450	AT1G69325.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr1:26066868-26067399 FORWARD   Aliases: None	3.4	2.6	0.8	1.0	100.0%	-3.8
7451	AT4G36700.1   cupin family protein, low similarity to preproMP27-MP32 from Cucurbita cv. Kurokawa Amakuri (GI:691752); contains Pfam profile PF00190: Cupin   chr4:17298204-17300371 REVERSE   Aliases: AP22.80, AP22_80	3.4	3.2	0.3	1.0	100.0%	-4.5
7452	AT5G03160.1   DNAJ heat shock N-terminal domain-containing protein, similar to P58 protein, Bos primigenius taurus, PIR:A56534; similar to p58 (GI:1353270) {Homo sapiens}; contains Pfam PF00226: Dnaj domain; contains Pfam PF00515: TPR Domain   chr5:750121-753656 FORWARD   Aliases: F15A17.190, F15A17_190	6.2	6.5	-0.3	-1.0	100.0%	-4.3
7453	AT5G37450.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:14870031-14874328 REVERSE   Aliases: T25O11.15, T25O11_15	2.6	2.8	-0.2	-1.0	100.0%	-4.6
7454	AT1G20690.1   expressed protein   chr1:7174428-7176367 FORWARD   Aliases: F2D10.18, F2D10_18	2.1	2.3	-0.2	-1.0	100.0%	-5.2
7455	AT1G67880.1   glycosyl transferase family 17 protein, low similarity to beta-1,4-mannosyl-glycoprotein beta-1,4-N-acetylglucosaminyltransferase (EC 2.4.1.144) from Mus musculus (SP:Q10470), Rattus norvegicus (SP:Q02527), Homo sapiens (SP:Q09327) ; contains Pfam profile PF04724 :Glycosyltransferase family 17   chr1:25457584-25459398 REVERSE   Aliases: T23K23.27, T23K23_27	5.0	4.6	0.4	1.0	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7456	AT4G02630.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	6.3	5.9	0.4	1.0	100.0%	-4.3
7457	AT5G38520.1   hydrolase, alpha/beta fold family protein, low similarity to hydrolase (Terrabacter sp. DBF63) GI:14196240; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:15438804-15440661 FORWARD   Aliases: MBB18.5, MBB18_5	5.2	4.8	0.4	1.0	100.0%	-4.0
7458	AT4G36390.1   radical SAM domain-containing protein / TRAM domain-containing protein, similar to CDK5 activator-binding protein (Rattus norvegicus) GI:7330738; contains Pfam profiles PF00919: UPF0004 family protein, PF01938: TRAM domain, PF04055: radical SAM domain protein   chr4:17194591-17197134 REVERSE   Aliases: AP22.85, AP22_85	6.3	6.6	-0.3	-1.0	100.0%	-4.6
7459	AT2G47260.1   Symbol: WRKY23	6.2	6.5	-0.3	-1.0	100.0%	-4.3
7460	AT1G10500.1   Symbol: ATCPISCA   Involved in chloroplast Fe-S cluster	7.9	7.6	0.3	1.0	100.0%	-4.3
7461	AT4G30200.3   expressed protein, contains weak similarities to Pfam profiles: PF00041 Fibronectin type III domain, PF00628 PHD-finger; supporting cDNA gi:11177136:dbj:AB050977.1:   chr4:14786639-14790479 REVERSE   Aliases: F9N11.50, F9N11_50	5.1	5.5	-0.4	-1.0	100.0%	-4.5
7462	AT3G10330.1   transcription initiation factor IIB-2 / general transcription factor TFIIB-2 (TFIIB2), identical to SP:Q9SS44 Transcription initiation factor IIB-2 (General transcription factor TFIIB-2) (AtTFIIB2) {Arabidopsis thaliana}   chr3:3199775-3201860 FORWARD   Aliases: F14P13.7	7.2	6.7	0.5	1.0	100.0%	-4.5
7463	AT1G43590.1   expressed protein, contains Pfam domain, PF04827: Protein of unknown function (DUF635)   chr1:16416561-16417067 FORWARD   Aliases: T10P12.13, T10P12_13	2.3	2.4	-0.1	-1.0	100.0%	-5.3
7464	AT2G38960.2   Symbol: AERO2   endoplasmic reticulum oxidoreductin 1 (ERO1) family protein, contains Pfam domain, PF04137: Endoplasmic Reticulum Oxidoreductin 1 (ERO1)   chr2:16272533-16274870 FORWARD   Aliases: T7F6.13, T7F6_13	4.3	4.1	0.2	1.0	100.0%	-4.4
7465	AT5G46700.1   senescence-associated protein, putative, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr5:18968188-18969995 FORWARD   Aliases: MZA15.11, MZA15_11	6.7	7.2	-0.5	-1.0	100.0%	-4.2
7466	AT1G36756.1   expressed protein   chr1:13918543-13919028 FORWARD   Aliases: T32O22.6, T32O22_6	2.2	2.1	0.1	1.0	100.0%	-5.3
7467	AT5G58440.1   phox (PX) domain-containing protein, similar to SP:O60749 Sorting nexin 2 {Homo sapiens}; contains Pfam profile PF00787: PX domain   chr5:23641133-23644013 REVERSE   Aliases: MQJ2.4, MQJ2_4	6.2	6.6	-0.4	-1.0	100.0%	-4.4
7468	AT3G44980.1   expressed protein   chr3:16452008-16453083 FORWARD   Aliases: F14D17.50	3.3	3.2	0.1	1.0	100.0%	-5.1
7469	AT1G55160.1   expressed protein   chr1:20582084-20583677 FORWARD   Aliases: T7N22.11	6.1	6.4	-0.3	-1.0	100.0%	-4.3
7470	AT2G35260.1   expressed protein   chr2:14856615-14859048 FORWARD   Aliases: T4C15.7, T4C15_7	3.3	3.4	-0.2	-1.0	100.0%	-4.9
7471	AT1G24470.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to b-keto acyl reductase GI:2586127 from (Hordeum vulgare)   chr1:8674044-8676265 FORWARD   Aliases: F21J9.13	3.0	3.2	-0.2	-1.0	100.0%	-4.8
7472	AT1G22040.1   kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	5.0	4.7	0.3	1.0	100.0%	-4.4
7473	AT3G49020.1   F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.9	-0.2	-1.0	100.0%	-5.1
7474	AT1G61670.1   expressed protein, similar to membrane protein PTM1 precursor isolog GI:1931644 from (Arabidopsis thaliana)   chr1:22773694-22776091 FORWARD   Aliases: T13M11.2, T13M11_2	6.1	6.5	-0.4	-1.0	100.0%	-4.0
7475	AT1G47885.1   leucine-rich repeat family protein, contains 2 leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr1:17646066-17646474 REVERSE   Aliases: T6B12.8	2.7	2.9	-0.1	-1.0	100.0%	-5.0
7476	AT3G21140.1   expressed protein   chr3:7409463-7412231 REVERSE   Aliases: MSA6.18	6.1	6.4	-0.4	-1.0	100.0%	-4.2
7477	AT5G33280.1   chloride channel-like (CLC) protein, putative, similar to CLC-c, At5g49890 (Arabidopsis thaliana) and chloride channel protein CIC-1 - Nicotiana tabacum, PIR:T02939   chr5:12566510-12569737 FORWARD   Aliases: F19N2.1	4.4	4.7	-0.3	-1.0	100.0%	-4.3
7478	AT3G05680.1   Symbol: EMB2016   expressed protein   chr3:1660558-1671052 REVERSE   Aliases: EMB2016, EMBRYO DEFECTIVE 2016, F18C1.5, F18C1_5	3.4	3.6	-0.2	-1.0	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7479	AT1G78800.1   glycosyl transferase family 1 protein, contains similarity to glycosyltransferase GI:871530 from ( <i>Saccharomyces cerevisiae</i> ), Alg2 mannosyltransferase (gi:3868942) from <i>Rhizomucor pusillus</i> ; contains Pfam profile: PF00534 Glycosyl transferases group 1   chr1:29630552-29632862 REVERSE   Aliases: F9K20.16, F9K20_16	4.4	4.2	0.2	1.0	100.0%	-4.7
7480	AT3G14910.1   expressed protein   chr3:5015437-5017573 FORWARD   Aliases: K15M2.5	4.3	4.1	0.2	1.0	100.0%	-4.7
7481	AT2G44310.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr2:18316288-18316902 FORWARD   Aliases: F4I1.12	10.1	9.7	0.4	1.0	100.0%	-4.2
7482	AT5G40155.1   Encodes a defensin-like (DEFL) family protein.   chr5:16079119-16079965 FORWARD   Aliases: None	3.0	2.8	0.2	1.0	100.0%	-5.0
7483	AT1G66160.2   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 ( <i>Petroselinum crispum</i> ) GI:14582200; contains Pfam profile PF04564: U-box domain   chr1:24640859-24642271 FORWARD   Aliases: F15E12.6, F15E12_6	4.9	4.6	0.4	1.0	100.0%	-4.4
7484	AT5G02830.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:643609-648451 REVERSE   Aliases: F9G14.140, F9G14_140	7.2	7.5	-0.4	-1.0	100.0%	-4.0
7485	AT3G32270.1   expressed protein, similar to putative replication protein A1 GB:AAC95163 GI:4006821 from ( <i>Arabidopsis thaliana</i> )	4.6	4.2	0.3	1.0	100.0%	-4.4
7486	AT2G35930.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 ( <i>Petroselinum crispum</i> ) GI:14582200; contains Pfam profile PF04564: U-box domain   chr2:15089934-15091552 REVERSE   Aliases: F11F19.16, F11F19_16	5.2	5.7	-0.5	-1.0	100.0%	-4.2
7487	AT2G41650.1   expressed protein   chr2:17370985-17371512 FORWARD   Aliases: T32G6.17, T32G6_17	10.0	10.3	-0.3	-1.0	100.0%	-4.5
7488	AT1G12210.1   Symbol: RFL1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.9	3.1	-0.2	-1.0	100.0%	-4.8
7489	AT1G16730.1   expressed protein   chr1:5726610-5727305 REVERSE   Aliases: F19K19.18	3.3	3.1	0.2	1.0	100.0%	-4.8
7490	AT5G66310.1   kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain   chr5:26502911-26508608 REVERSE   Aliases: K1L20.9, K1L20_9	3.8	4.0	-0.2	-1.0	100.0%	-4.9
7491	AT5G49000.1   similar to kelch repeat-containing F-box family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g39550.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Kelch repeat (InterPro:IPR006652)   chr5:19881739-19882981 FORWARD   Aliases: K19E20.13, K19E20_13	7.0	7.2	-0.2	-1.0	100.0%	-4.9
7492	AT2G21630.1   transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A ( <i>Homo sapiens</i> )   chr2:9257403-9260995 FORWARD   Aliases: F2G1.10, F2G1_10	3.5	3.7	-0.2	-1.0	100.0%	-4.8
7493	AT3G24830.1   60S ribosomal protein L13A (RPL13aB), similar to 60S RIBOSOMAL PROTEIN L13A GB:P35427 from ( <i>Rattus norvegicus</i> )   chr3:9064570-9066089 FORWARD   Aliases: K7P8.13	10.7	10.3	0.4	1.0	100.0%	-4.6
7494	AT2G28810.1   Dof-type zinc finger domain-containing protein, similar to zinc finger protein OBP2 GI:5059394 from ( <i>Arabidopsis thaliana</i> )   chr2:12370707-12372454 FORWARD   Aliases: F8N16.10, F8N16_10	4.5	4.4	0.2	1.0	100.0%	-4.6
7495	AT5G22390.1   expressed protein   chr5:7418119-7419252 REVERSE   Aliases: MWD9.19, MWD9_19	2.9	2.7	0.2	1.0	100.0%	-4.9
7496	AT5G01090.1   legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain   chr5:32831-34325 FORWARD   Aliases: F7J8.70, F7J8_70	7.1	6.8	0.3	1.0	100.0%	-4.4
7497	AT3G62710.1   glycosyl hydrolase family 3 protein, exhydrolase II - <i>Zea mays</i> , EMBL:AF064707   chr3:23208634-23211611 REVERSE   Aliases: F26K9.140	2.5	2.6	-0.1	-1.0	100.0%	-5.0
7498	AT5G18475.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:6129257-6131017 REVERSE   Aliases: None	5.2	4.9	0.4	1.0	100.0%	-4.5
7499	AT4G18630.1   expressed protein, contains Pfam profile: PF05097 protein of unknown function (DUF688)   chr4:10257089-10258954 FORWARD   Aliases: F28A21.40, F28A21_40	3.3	3.5	-0.2	-1.0	100.0%	-4.5
7500	AT3G46690.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:17208614-17210322 REVERSE   Aliases: T6H20.280	3.7	4.2	-0.5	-1.0	100.0%	-3.9
7501	AT1G67980.2   Symbol: CCoAMT	3.5	3.7	-0.2	-1.0	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7502	AT1G32660.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr1:11811020-11812360 FORWARD   Aliases: F6N18.5, F6N18_5	3.0	2.8	0.2	1.0	100.0%	-4.8
7503	AT5G47700.1   60S acidic ribosomal protein P1 (RPP1C)   chr5:19345029-19346209 REVERSE   Aliases: MCA23.2, MCA23_2	10.1	10.4	-0.3	-1.0	100.0%	-4.2
7504	AT5G18420.3   expressed protein, non-consensus GC donor splice site at exon 1, unknown (C40) protein, Homo sapiens, EMBL:AF103798   chr5:6105524-6109380 REVERSE   Aliases: F20L16.140, F20L16_140	8.6	9.0	-0.4	-1.0	100.0%	-4.3
7505	AT3G10730.1   sad1/unc-84-like 2 family protein, contains 1 transmembrane domain; similar to Sad1 unc-84 domain protein 2 (GI:6538749) (Homo sapiens); similar to Sad1/unc-84-like protein 2 (Fragment) (Swiss-Prot:Q9UH99) (Homo sapiens)   chr3:3358333-3360687 REVERSE   Aliases: T7M13.19	4.4	4.7	-0.3	-1.0	100.0%	-4.6
7506	AT5G66730.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:26658878-26661628 REVERSE   Aliases: MSN2.12, MSN2_12	4.7	4.5	0.2	1.0	100.0%	-4.4
7507	AT1G13060.1   Symbol: PBE1   20S proteasome beta subunit E1 (PBE1) (PRCE), identical to GB:O23717; identical to cDNA proteasome subunit prce GI:2511595   chr1:4452269-4454872 FORWARD   Aliases: 20S PROTEASOME BETA SUBUNIT PBE1, F3F19.8, F3F19_8	12.0	12.4	-0.4	-1.0	100.0%	-4.7
7508	AT3G26340.1   20S proteasome beta subunit E, putative, very strong similarity to SP:O23717 Proteasome subunit beta type 5 precursor (EC 3.4.25.1) (20S proteasome subunit E) (Proteasome epsilon chain) {Arabidopsis thaliana}	12.0	12.4	-0.4	-1.0	100.0%	-4.7
7509	AT3G57140.2   patatin-related, contains Patatin domain PF01734	2.7	2.6	0.1	1.0	100.0%	-5.1
7510	AT5G55320.1   membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related, similar to wax synthase (Simmondsia chinensis) GI:5020219 (EC 2.3.1.75)   chr5:22452906-22453925 REVERSE   Aliases: MTE17.3, MTE17_3	3.1	3.3	-0.2	-1.0	100.0%	-4.8
7511	AT4G35520.1   DNA mismatch repair family protein, similar to SP:Q9UHC1 DNA mismatch repair protein Mlh3 (MutL protein homolog 3) {Homo sapiens}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF01119: DNA mismatch repair protein, C-terminal domain   chr4:16865493-16871769 FORWARD   Aliases: F8D20.30, F8D20_30	3.4	3.2	0.2	1.0	100.0%	-4.7
7512	AT4G11190.1   disease resistance-responsive family protein / dirigent family protein, similar to dirigent protein (Forsythia x intermedia) gi:6694693:gb:AAF25357; similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669   chr4:6826673-6827379 FORWARD   Aliases: T22B4.170, T22B4_170	2.7	3.0	-0.2	-1.0	100.0%	-4.3
7513	AT1G18610.1   kelch repeat-containing protein, contains Pfam profile PF01344: Kelch motif   chr1:6405771-6408823 FORWARD   Aliases: F25I16.5, F25I16_5	3.0	3.2	-0.2	-1.0	100.0%	-5.3
7514	AT5G38840.1   forkhead-associated domain-containing protein / FHA domain-containing protein, related to adaptor protein kanadaplin (Homo sapiens) gi:13562130:gb:AAK29177   chr5:15568526-15572300 FORWARD   Aliases: K15E6.5, K15E6_5	7.9	8.6	-0.7	-1.0	100.0%	-4.2
7515	AT3G14067.1   subtilase family protein, contains similarity to cucumisin-like serine protease GI:3176874 from (Arabidopsis thaliana)   chr3:4658428-4660761 REVERSE   Aliases: MAG2.15	4.2	3.3	0.9	0.9	100.0%	-4.2
7516	AT1G77270.1   expressed protein   chr1:29032672-29036122 FORWARD   Aliases: T14N5.12, T14N5_12	2.8	2.7	0.1	0.9	100.0%	-5.4
7517	AT2G36820.1   expressed protein   chr2:15445489-15447772 REVERSE   Aliases: F13K3.22, F13K3_22	3.5	3.1	0.4	0.9	100.0%	-4.2
7518	AT4G31360.1   expressed protein   chr4:15221892-15223633 FORWARD   Aliases: F8F16.180, F8F16_180	6.6	6.2	0.4	0.9	100.0%	-4.0
7519	AT3G11760.1   expressed protein   chr3:3718535-3721129 FORWARD   Aliases: F26K24.5	5.3	5.6	-0.3	-0.9	100.0%	-4.4
7520	AT1G03590.1   protein phosphatase 2C family protein / PP2C family protein, similar to protein phosphatase-2C; PP2C (GI:3643088) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain;   chr1:894254-896439 REVERSE   Aliases: F21B7.20	6.1	5.9	0.2	0.9	100.0%	-4.6
7521	AT1G36970.1   expressed protein   chr1:14018826-14020797 REVERSE   Aliases: T32E20.31, T32E20_31	3.0	3.3	-0.2	-0.9	100.0%	-4.7
7522	AT4G21320.1   (2R)-phospho-3-sulfolactate synthase-related, contains weak similarity to Swiss-Prot:Q57703 (2R)-phospho-3-sulfolactate synthase (PSL synthase) (Methanococcus jannaschii)   chr4:11340435-11341887 FORWARD   Aliases: T6K22.50, T6K22_50	5.5	5.2	0.3	0.9	100.0%	-4.2
7523	AT3G07750.2   3' exoribonuclease family domain 1-containing protein, similar to SP:Q15024 Exosome complex exonuclease RRP42 (EC 3.1.13.-) (Ribosomal RNA processing protein 42) {Homo sapiens}; contains Pfam profile PF01138: 3' exoribonuclease family, domain 1   chr3:2473247-2475398 FORWARD   Aliases: F17A17.9, F17A17_9, MLP3.20	7.1	7.6	-0.4	-0.9	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7524	AT2G01150.1   Symbol: RHA2B   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:100648-101494 FORWARD   Aliases: F10A8.3, F10A8_3, RING H2 FINGER PROTEIN 2B, RING H2 FINGER PROTEIN RHA2B	5.5	5.1	0.3	0.9	100.0%	-4.3
7525	AT3G58580.1   endonuclease/exonuclease/phosphatase family protein, similar to SP:P31384 Glucose-repressible alcohol dehydrogenase transcriptional effector (Carbon catabolite repressor protein 4) {Saccharomyces cerevisiae}; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr3:21671843-21674674 REVERSE   Aliases: F14P22.170	5.0	5.4	-0.4	-0.9	100.0%	-4.4
7526	AT2G42490.1   copper amine oxidase, putative, similar to copper methylamine oxidase precursor (MAOXII) (Arthrobacter sp.) SWISS-PROT:Q07123   chr2:17698497-17702926 REVERSE   Aliases: MHK10.21, MHK10_21	8.5	8.8	-0.3	-0.9	100.0%	-4.8
7527	AT5G59500.1   expressed protein   chr5:24003155-24004607 FORWARD   Aliases: F2O15.18, F2O15_18	4.8	5.1	-0.3	-0.9	100.0%	-4.3
7528	AT3G29800.1   AAA-type ATPase family, contains Pfam profile: ATPase family PF00004   chr3:11722575-11724582 FORWARD   Aliases: K17E7.10	2.6	2.8	-0.2	-0.9	100.0%	-4.8
7529	AT5G47040.1   Lon protease homolog 1, mitochondrial (LON), identical to Lon protease homolog 1	5.7	5.3	0.4	0.9	100.0%	-4.3
7530	AT3G18440.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	4.6	4.9	-0.3	-0.9	100.0%	-4.5
7531	AT1G26795.1   self-incompatibility protein-related, similar to S3 self-incompatibility protein (Papaver rhoeas) GI:1107841   chr1:9276368-9276941 FORWARD   Aliases: None	3.3	3.2	0.1	0.9	100.0%	-5.2
7532	AT5G46270.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18782099-18786068 REVERSE   Aliases: MPL12.5, MPL12_5	2.8	2.6	0.1	0.9	100.0%	-5.1
7533	AT2G06010.1   Symbol: ORG4   expressed protein   chr2:2336815-2338899 FORWARD   Aliases: F5K7.23, F5K7_23, OBP3 RESPONSIVE GENE 4	5.1	4.9	0.2	0.9	100.0%	-4.4
7534	AT1G15690.1   Symbol: AVP1   pyrophosphate-energized vacuolar membrane proton pump / pyrophosphate-energized inorganic pyrophosphatase (AVP-3), identical to pyrophosphate-energized vacuolar membrane proton pump (pyrophosphate-energized inorganic pyrophosphatase) SP:P31414 from (Arabidopsis thaliana)   chr1:5398985-5402949 FORWARD   Aliases: ATAVP3, AVP 3, F7H2.3, F7H2_3, VACUOLAR H+ PYROPHOSPHATASE AVP 3	9.9	10.4	-0.4	-0.9	100.0%	-4.7
7535	ATCG00280.1   Symbol: PSBC   chloroplast gene encoding a CP43 subunit of the photosystem II reaction center. promoter contains a blue-light responsive element.   chrC:33720-35141 FORWARD   Aliases: CP43, PSBC	7.7	8.6	-0.9	-0.9	100.0%	-4.2
7536	AT4G25800.1   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum)   chr4:13124996-13127913 FORWARD   Aliases: F14M19.80, F14M19_80	3.8	3.6	0.2	0.9	100.0%	-4.9
7537	AT5G63310.1   Symbol: NDPK2   nucleotide diphosphate kinase II, chloroplast (NDPK2), identical to SP:O64903 Nucleoside diphosphate kinase II, chloroplast precursor (NDK II) (NDP kinase II) (NDPK II) (NDPK Ia) (Arabidopsis thaliana); contains Pfam PF00334 : Nucleoside diphosphate kinase domain; contains Pfam profile PF00334: Nucleoside diphosphate kinase   chr5:25389130-25391081 REVERSE   Aliases: MDC12.28, MDC12_28, NDPK IA, NDPK IA IA, NDPK1A, NUCLEOSIDE DIPHOSPHATE KINASE 2, NUCLEOSIDE DIPHOSPHATE KINASE IA	9.4	9.9	-0.4	-0.9	100.0%	-4.0
7538	AT1G53600.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:20004931-20009463 FORWARD   Aliases: F22G10.27	5.5	5.2	0.3	0.9	100.0%	-4.5
7539	AT4G36930.1   Symbol: SPT   basic helix-loop-helix (bHLH) protein SPATULA (SPT), identical to SPATULA (SPT) GI:11245493 from (Arabidopsis thaliana)   chr4:17414124-17416291 FORWARD   Aliases: AP22.25, AP22_25, SPATULA	4.0	3.6	0.4	0.9	100.0%	-4.2
7540	AT3G63190.1   ribosome recycling factor, chloroplast, putative / ribosome releasing factor, chloroplast, putative, similar to SP:P82231 Ribosome recycling factor, chloroplast precursor (Ribosome releasing factor, chloroplast) (RRF) (CpFrr) (RRFHCP) {Spinacia oleracea}; contains Pfam profile PF01765: ribosome recycling factor	5.4	5.8	-0.4	-0.9	100.0%	-4.2
7541	AT1G35900.1   expressed protein   chr1:13348716-13349645 REVERSE   Aliases: F10O5.7, F10O5_7	3.5	3.2	0.2	0.9	100.0%	-4.5
7542	AT4G34700.1   complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)   chr4:16556850-16558851 FORWARD   Aliases: T4L20.280, T4L20_280	11.9	11.5	0.4	0.9	100.0%	-5.0
7543	AT5G49100.1   expressed protein   chr5:19914596-19916340 REVERSE   Aliases: K20J1.7, K20J1_7	6.4	7.1	-0.6	-0.9	100.0%	-3.9
7544	AT5G44470.1   expressed protein   chr5:17935966-17936391 FORWARD   Aliases: MFC16.13, MFC16_13	2.6	2.5	0.1	0.9	100.0%	-5.2
7545	AT3G54970.2   expressed protein   chr3:20379199-20381066 REVERSE   Aliases: T15C9.1	4.6	4.3	0.3	0.9	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7546	AT5G55900.1   sucrase-related, similar to sucrase (Solanum tuberosum) GI:1200257   chr5:22654757-22656987 FORWARD   Aliases: MYN21.1, MYN21_1	5.5	5.2	0.3	0.9	100.0%	-4.4
7547	AT4G34850.1   chalcone and stilbene synthase family protein, similar to chalcone synthase homolog PrChS1, Pinus radiata, gb:U90341; similar to anther-specific protein (Nicotiana glauca)(GI:2326774), YY2 protein (Oryza sativa)(GI:2645170)   chr4:16608318-16610253 FORWARD   Aliases: F11I11.90, F11I11_90	3.9	3.6	0.3	0.9	100.0%	-4.6
7548	AT1G53035.1   expressed protein   chr1:19765368-19766219 REVERSE   Aliases: None	5.3	5.5	-0.2	-0.9	100.0%	-4.6
7549	AT4G36990.1   Symbol: HSF4   heat shock factor protein 4 (HSF4) / heat shock transcription factor 4 (HSTF4), identical to heat shock transcription factor 4 (HSF4) SP:Q96320 from (Arabidopsis thaliana)   chr4:17440287-17442145 FORWARD   Aliases: AP22.9, AP22_9, AT HSF4, ATHSF4, HEAT SHOCK FACTOR 4, HEAT SHOCK TRANSCRIPTION FACTOR 4, HSF4	8.2	8.9	-0.6	-0.9	100.0%	-4.5
7550	AT1G09680.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3134109-3135932 REVERSE   Aliases: F21M12.7, F21M12_7	5.2	5.5	-0.3	-0.9	100.0%	-4.3
7551	AT1G59510.1   Symbol: CF9   expressed protein	3.7	3.5	0.2	0.9	100.0%	-4.5
7552	AT4G01510.1   Symbol: ARV2   similar to transmembrane ARV1-like family protein [Arabidopsis thaliana] (TAIR:At1g01020.1); similar to hypothetical protein DDB0188786 [Dictyostelium discoideum] (GB:EAL62332.1); contains InterPro domain Arv1-like protein (InterPro:IPR007290)   chr4:642733-644336 FORWARD   Aliases: ARV2, F11O4.16, F11O4_16	5.4	5.1	0.3	0.9	100.0%	-4.4
7553	AT4G27000.1   RNA-binding protein 45 (RBP45), putative, DNA binding protein ACBF - Nicotiana glauca, PID:g1899188   chr4:13554632-13557860 REVERSE   Aliases: ATRBP45C, F10M23.340, F10M23_340	7.7	7.1	0.6	0.9	100.0%	-4.2
7554	AT1G37020.1   Ulp1 protease family protein   chr1:14049176-14052183 FORWARD   Aliases: T32E20.20, T32E20_20	2.7	2.8	-0.1	-0.9	100.0%	-5.4
7555	AT3G49320.1   expressed protein, contains Pfam profile PF03690: Uncharacterised protein family (UPF0160)   chr3:18299232-18301643 REVERSE   Aliases: F2K15.180	6.4	6.8	-0.3	-0.9	100.0%	-4.2
7556	AT3G18830.1   Symbol: ATPLT5	6.5	6.3	0.2	0.9	100.0%	-4.7
7557	AT5G11870.1   expressed protein   chr5:3825533-3827242 FORWARD   Aliases: F14F18.40, F14F18_40	3.5	3.2	0.2	0.9	100.0%	-4.5
7558	AT2G27530.2   60S ribosomal protein L10A (RPL10aB)   chr2:11770332-11771821 REVERSE   Aliases: F10A12.22	10.5	10.9	-0.4	-0.9	100.0%	-4.3
7559	AT5G26010.1   similar to protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana] (TAIR:At4g32950.1); similar to putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] (GB:XP_465582.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr5:9085396-9087375 REVERSE   Aliases: T1N24.8, T1N24_8	4.7	4.2	0.6	0.9	100.0%	-4.0
7560	AT2G33380.2   Symbol: RD20   similar to Ca+2-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At5g29560.1); similar to Ca+2-binding EF hand protein [Glycine max] (GB:AAB71227.1); contains InterPro domain Caleosin related (InterPro:IPR007736)   chr2:14151907-14153547 REVERSE   Aliases: F4P9.15, F4P9_15, RESPONSIVE TO DESSICATION 20	2.4	2.3	0.1	0.9	100.0%	-5.4
7561	AT5G24850.1   cryptochrome dash (CRYD), nearly identical to cryptochrome dash (Arabidopsis thaliana) GI:28971609; similar to Deoxyribodipyrimidine photolyase (DNA photolyase) (Photoreactivating enzyme)(SP:Q55081){Synechocystis sp.}   chr5:8535285-8538110 REVERSE   Aliases: F6A4.60, F6A4_60	5.7	5.4	0.3	0.9	100.0%	-4.3
7562	AT5G54430.1   universal stress protein (USP) family protein, low similarity to early nodulin ENOD18 (Vicia faba) GI:11602747, ER6 protein (Lycopersicon esculentum) GI:5669654; contains Pfam profile PF00582: universal stress protein family	6.7	6.5	0.2	0.9	100.0%	-4.5
7563	AT3G02890.1   PHD finger protein-related, contains low similarity to PHD-finger domain proteins   chr3:641050-645310 FORWARD   Aliases: F13E7.16, F13E7_16	3.7	4.0	-0.3	-0.9	100.0%	-4.3
7564	AT4G21480.1   glucose transporter, putative, similar to glucose transporter (Sugar carrier) STP1, Arabidopsis thaliana, SP:P23586; contains Pfam profile PF00083: major facilitator superfamily protein   chr4:11433314-11435296 REVERSE   Aliases: F18E5.100, F18E5_100	7.8	7.3	0.5	0.9	100.0%	-4.0
7565	AT1G12600.1   expressed protein   chr1:4286412-4288860 REVERSE   Aliases: F5O11.33, F5O11_33	3.2	3.0	0.2	0.9	100.0%	-4.8
7566	AT4G12590.1   expressed protein, contains Pfam PF05863: Eukaryotic protein of unknown function (DUF850)   chr4:7451001-7453085 REVERSE   Aliases: T1P17.180, T1P17_180	9.5	8.3	1.3	0.9	100.0%	-4.2
7567	AT1G10730.1   clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	4.2	4.0	0.2	0.9	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7568	AT3G15950.2   similar to caldesmon-related [Arabidopsis thaliana] (TAIR:At1g52410.2); similar to caldesmon-related [Arabidopsis thaliana] (TAIR:At1g52410.1); similar to hypothetical protein FG09227.1 [Gibberella zeae PH-1] (GB:EAA76462.1)	3.3	3.6	-0.3	-0.9	100.0%	-4.6
7569	AT4G27830.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max)   chr4:13861743-13864506 REVERSE   Aliases: T27E11.70, T27E11_70	4.7	4.5	0.2	0.9	100.0%	-4.6
7570	AT3G23790.1   AMP-binding protein, putative, similar to AMP-binding protein GB:CAA96521 from (Brassica napus) (Plant Mol. Biol. (1997) 33 (5), 911-922); contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA acyl-CoA synthetase-like protein GI:20799732   chr3:8575174-8581119 FORWARD   Aliases: MYM9.14	4.3	4.0	0.3	0.9	100.0%	-4.3
7571	AT4G38500.1   expressed protein, contains Pfam profile: PF04765 protein of unknown function (DUF616)   chr4:18007750-18011343 FORWARD   Aliases: F20M13.60, F20M13_60	6.1	6.6	-0.4	-0.9	100.0%	-4.3
7572	AT3G20210.1   Symbol: DELTA VPE   vacuolar processing enzyme, putative / asparaginyl endopeptidase, putative, similar to asparaginyl endopeptidase (VmPE-1) (Vigna mungo) GI:4589396; contains Pfam profile PF01650: Peptidase C13 family; identical to cDNA vacuolar processing enzyme delta preproprotein (At3g20210) GI:24850432   chr3:7052426-7054749 FORWARD   Aliases: DELTAVPE, MAL21.27	2.2	2.1	0.1	0.9	100.0%	-5.3
7573	AT1G67250.1   proteasome maturation factor UMP1 family protein, contains Pfam profile PF05348: Proteasome maturation factor UMP1   chr1:25167305-25168715 REVERSE   Aliases: F1N21.7	11.1	10.7	0.4	0.9	100.0%	-4.6
7574	AT2G45940.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At4g16080.1); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR005174)   chr2:18910086-18911387 FORWARD   Aliases: F4I18.8	2.6	2.5	0.2	0.9	100.0%	-5.0
7575	AT4G39230.1   isoflavone reductase, putative, similar to allergenic isoflavone reductase-like protein Bet v 6.0102 (Betula pendula)(GI:10764491); contains Pfam profile PF02716: Isoflavone reductase   chr4:18265879-18267718 REVERSE   Aliases: T22F8.130, T22F8_130	6.9	7.7	-0.7	-0.9	100.0%	-4.0
7576	AT5G49030.2   similar to isoleucyl-tRNA synthetase, putative / isoleucine--tRNA ligase, putative [Arabidopsis thaliana] (TAIR:At4g10320.1); similar to COG0060: Isoleucyl-tRNA synthetase [Anabaena variabilis ATCC 29413] (GB:ZP_00158029.2); similar to COG0060: Isoleucyl-tRNA synthetase [Crocospaera watsonii WH 8501] (GB:ZP_00178195.1); similar to COG0060: Isoleucyl-tRNA synthetase [Trichodesmium erythraeum IMS101] (GB:ZP_00327549.1); similar to COG0060: Isoleucyl-tRNA synthetase [Nostoc punctiforme PCC 73102] (GB:ZP_00106717.1); similar to isoleucyl-tRNA synthetase [Nostoc sp. PCC 7120] (GB:BAB73030.1); contains InterPro domain Aminoacyl-tRNA synthetase, class I (InterPro:IPR001412); contains InterPro domain Isoleucyl-tRNA synthetase, class Ia (InterPro:IPR002301); contains InterPro domain Aminoacyl-tRNA synthetase, class Ia (InterPro:IPR002300)   chr5:19893392-19899688 REVERSE   Aliases: K19E20.18, K19E20_18	7.2	7.6	-0.3	-0.9	100.0%	-4.3
7577	AT1G28710.1   expressed protein, similar to GI:2827651, GI:7527728, GI:4406788, GI:6063544, GI:10764853 from (Arabidopsis thaliana)   chr1:10086623-10088044 REVERSE   Aliases: F1K23.9, F1K23_9	2.9	3.3	-0.4	-0.9	100.0%	-4.5
7578	AT4G22150.1   Symbol: pux3   UBX domain-containing protein, similar to XY40 protein (Rattus norvegicus) GI:2547025; contains Pfam profile PF00789: UBX domain	8.6	8.9	-0.3	-0.9	100.0%	-4.4
7579	AT5G44980.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.7	-0.1	-0.9	100.0%	-5.4
7580	AT4G10560.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.6	0.2	0.9	100.0%	-5.1
7581	AT4G05210.1   bacterial transferase hexapeptide repeat-containing protein, similar to SP:P32203 UDP-3-O-(3-hydroxymyristoyl) glucosamine N-acyltransferase (EC 2.3.1.-) {Yersinia enterocolitica}; contains Pfam profile PF00132: Bacterial transferase hexapeptide (three repeats)   chr4:2682865-2684897 FORWARD   Aliases: C17L7.130, C17L7_130	3.9	4.2	-0.3	-0.9	100.0%	-4.5
7582	AT5G62550.1   expressed protein   chr5:25122864-25125177 REVERSE   Aliases: K19B1.16, K19B1_16	3.9	4.5	-0.6	-0.9	100.0%	-4.2
7583	AT3G11290.1   expressed protein   chr3:3535616-3537849 REVERSE   Aliases: F11B9.20	4.1	4.0	0.1	0.9	100.0%	-5.1
7584	AT3G05990.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to leaf senescence-associated receptor-like protein kinase (Phaseolus vulgaris) gi:9837280:gb:AAG00510   chr3:1796871-1799876 REVERSE   Aliases: F2O10.5, F2O10_5	6.9	7.2	-0.3	-0.9	100.0%	-4.6
7585	AT4G22680.1   Symbol: MYB85   myb family transcription factor (MYB85), similar to myb DNA-binding protein GI:1020155 from (Arabidopsis thaliana)   chr4:11922351-11924227 REVERSE   Aliases: T12H17.70, T12H17_70	2.7	2.8	-0.1	-0.9	100.0%	-5.1
7586	AT3G49220.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:18260769-18264824 FORWARD   Aliases: F2K15.80, F2K15_80	7.5	7.1	0.4	0.9	100.0%	-4.2
7587	AT3G45750.1   expressed protein   chr3:16804596-16808918 REVERSE   Aliases: T6D9.80	3.5	3.7	-0.2	-0.9	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7588	AT1G33780.1   expressed protein, similar to At3g29240 (Arabidopsis thaliana); contains Pfam profile PF02622: Uncharacterized ACR, COG1678   chr1:12244565-12246168 REVERSE   Aliases: F14M2.10, F14M2_10	7.0	7.3	-0.3	-0.9	100.0%	-4.5
7589	AT3G45830.1   expressed protein   chr3:16852262-16856526 FORWARD   Aliases: F16L2.40	6.3	6.6	-0.3	-0.9	100.0%	-4.8
7590	AT3G23490.1   Symbol: CYN   cyanate lyase family, contains Pfam profile: PF02560 cyanate lyase C-terminal domain   chr3:8423042-8424659 REVERSE   Aliases: CYANASE, MEE5.3	7.4	6.8	0.6	0.9	100.0%	-4.1
7591	AT1G77000.1   F-box family protein, similar to GP:21554029: F-box protein AtFBL5 from (Arabidopsis thaliana); similar to F-box protein FBL2 GI:6063090 from (Homo sapiens)   chr1:28945726-28947490 FORWARD   Aliases: F22K20.10, F22K20_10	6.3	5.9	0.4	0.9	100.0%	-4.5
7592	AT1G58220.1   myb family transcription factor, contains Pfam profile: PF00249: Myb-like DNA-binding domain   chr1:21561908-21566630 REVERSE   Aliases: F16M22.4, F16M22_4	5.1	5.4	-0.3	-0.9	100.0%	-4.3
7593	AT1G33760.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr1:12237858-12238478 FORWARD   Aliases: F14M2.12, F14M2_12	2.2	2.1	0.1	0.9	100.0%	-5.3
7594	AT5G66890.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr5:26730170-26731609 REVERSE   Aliases: MUD21.15, MUD21_15	2.8	2.6	0.2	0.9	100.0%	-5.0
7595	AT5G53550.1   transporter, putative, similar to iron-phytosiderophore transporter protein yellow stripe 1 (Zea mays) GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein   chr5:21773307-21776002 FORWARD   Aliases: MNC6.9, MNC6_9	4.9	4.4	0.5	0.9	100.0%	-4.1
7596	AT3G23270.1   regulator of chromosome condensation (RCC1) family protein, contains Pfam domain PF00415: Regulator of chromosome condensation (RCC1); similar to zinc finger protein (GI:15811367) (Arabidopsis thaliana); similar to chromosome condensation regulator protein (GI:22770461) (Cicer arietinum)	2.3	2.2	0.1	0.9	100.0%	-5.5
7597	AT1G26800.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:9285086-9286311 REVERSE   Aliases: T24P13.19, T24P13_19	4.5	4.1	0.4	0.9	100.0%	-4.3
7598	AT3G09760.1   zinc finger (C3HC4-type RING finger) family protein, ; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:2992659-2995639 REVERSE   Aliases: F11F8.35	3.4	3.2	0.2	0.9	100.0%	-4.9
7599	AT1G18180.1   expressed protein   chr1:6255896-6257590 FORWARD   Aliases: T10F20.18	5.9	6.3	-0.4	-0.9	100.0%	-4.4
7600	AT5G15840.2   Symbol: CO   similar to zinc finger protein CONSTANS-LIKE 1 (COL1) [Arabidopsis thaliana] (TAIR:At5g15850.1); similar to constans [Brassica napus] (GB:AAC27694.1); contains InterPro domain Zn-finger, CONSTANS type (InterPro:IPR002926); contains InterPro domain Zn-finger, B-box (InterPro:IPR000315)   chr5:5171186-5172738 REVERSE   Aliases: CONSTANS, F14F8.220, F14F8_220, FG	3.4	3.2	0.1	0.9	100.0%	-5.0
7601	AT1G31730.1   epsilon-adaptin, putative, similar to SP:Q9UPM8 Adapter-related protein complex 4 epsilon 1 subunit (Epsilon subunit of AP-4) (AP-4 adapter complex epsilon subunit) {Homo sapiens}; contains Pfam profile: PF01602 Adaptin N terminal region   chr1:11359623-11364269 FORWARD   Aliases: F27M3.7, F27M3_7	5.1	5.3	-0.3	-0.9	100.0%	-4.6
7602	AT3G09580.1   amine oxidase family protein, low similarity to SP:P28553 Phytoene dehydrogenase, chloroplast precursor (Phytoene desaturase) from Glycine max; contains Pfam profile PF01593 amine oxidase, flavin-containing   chr3:2942509-2944083 REVERSE   Aliases: F11F8.15	4.1	4.2	-0.2	-0.9	100.0%	-4.8
7603	AT1G43850.1   Symbol: SEU   SEUSS transcriptional co-regulator, identical to SEUSS transcriptional co-regulator (Arabidopsis thaliana) gi:18033922:gb:AAL57277   chr1:16619592-16624489 FORWARD   Aliases: F28H19.10, F28H19_10, SEUSS	4.5	4.8	-0.2	-0.9	100.0%	-4.6
7604	AT1G50320.1   Symbol: ATHX   thioredoxin x, nearly identical to thioredoxin x GB:AAF15952 GI:6539616 from (Arabidopsis thaliana)   chr1:18642098-18643196 REVERSE   Aliases: F14I3.8, F14I3_8	7.6	7.3	0.3	0.9	100.0%	-4.5
7605	AT1G52760.1   esterase/lipase/thioesterase family protein, low similarity to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379   chr1:19655013-19656411 FORWARD   Aliases: F14G24.3, F14G24_3	9.0	9.4	-0.4	-0.9	100.0%	-4.7
7606	AT1G77050.1   DEAD/DEAH box helicase, putative, similar to RNA helicase GI:3776027 from (Arabidopsis thaliana)	2.8	3.0	-0.2	-0.9	100.0%	-5.0
7607	AT1G14770.2   expressed protein   chr1:5086625-5088621 REVERSE   Aliases: F10B6.17, F10B6_17	3.9	4.1	-0.2	-0.9	100.0%	-4.7
7608	AT4G10925.2   F-box family protein, contains Pfam PF00646: F-box domain   chr4:6702766-6704618 REVERSE   Aliases: None	5.9	5.7	0.3	0.9	100.0%	-4.5
7609	AT4G30520.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr4:14908006-14911313 REVERSE   Aliases: F17I23.140, F17I23_140	6.2	5.9	0.3	0.9	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7610	AT3G13360.1   expressed protein   chr3:4338366-4340403 REVERSE   Aliases: MDC11.20	7.8	8.3	-0.4	-0.9	100.0%	-4.1
7611	AT3G47660.1   regulator of chromosome condensation (RCC1) family protein, contains Pfam domain PF00415: Regulator of chromosome condensation (RCC1)   chr3:17582289-17585790 FORWARD   Aliases: F1P2.210	2.1	2.2	-0.1	-0.9	100.0%	-5.3
7612	AT4G39200.1   40S ribosomal protein S25 (RPS25E), ribosomal protein S25, Lycopersicon esculentum, PIR2:S40089   chr4:18257330-18258670 FORWARD   Aliases: T22F8.100, T22F8_100	11.2	11.5	-0.3	-0.9	100.0%	-4.4
7613	AT1G70540.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.9	2.8	0.1	0.9	100.0%	-5.3
7614	AT5G05540.1   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr5:1636307-1638940 FORWARD   Aliases: MOP10.8, MOP10_8	4.3	4.6	-0.3	-0.9	100.0%	-4.4
7615	AT5G24070.1   peroxidase family protein, similar to cationic peroxidase, Peanut (Arachis hypogaea) GP:166475:gb:AAA32676; contains Pfam profile PF00141: Peroxidase   chr5:8134304-8135994 REVERSE   Aliases: MZF18.4, MZF18_4	2.5	2.3	0.2	0.9	100.0%	-5.0
7616	AT2G25280.1   expressed protein   chr2:10769101-10771819 REVERSE   Aliases: T22F11.13, T22F11_13	7.7	8.3	-0.5	-0.9	100.0%	-4.4
7617	AT3G01790.2   ribosomal protein L13 family protein, similar to putative ribosomal protein L13 GB:AAC07691 (Aquifex aeolicus)   chr3:283697-285744 REVERSE   Aliases: F28J7.12, F28J7_12	7.7	8.2	-0.5	-0.9	100.0%	-4.1
7618	AT4G18530.1   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr4:10217123-10220511 FORWARD   Aliases: F28J12.190, F28J12_190	3.9	3.7	0.2	0.9	100.0%	-4.7
7619	AT1G49480.1   Symbol: RTV1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr1:18317846-18320313 REVERSE   Aliases: F13F21.8, F13F21_8, RELATED TO VERNALIZATION1 1, RTV1	6.4	6.0	0.3	0.9	100.0%	-4.6
7620	AT3G60030.1   squamosa promoter-binding protein-like 12 (SPL12), identical to squamosa promoter binding protein-like 12 (Arabidopsis thaliana) GI:6006395; contains Pfam profiles PF03110: SBP domain, PF00023: Ankyrin repeat	6.7	6.2	0.5	0.9	100.0%	-4.4
7621	AT3G61910.1   Symbol: ANAC066   no apical meristem (NAM) family protein, no apical meristem (NAM) - Petunia hybrida, EMBL:PHDNANAM   chr3:22939981-22941417 REVERSE   Aliases: ANAC066, F21F14.80	2.4	2.3	0.1	0.9	100.0%	-5.0
7622	AT5G23320.1   Symbol: ATSTE14   isoprenylcysteine carboxyl methyltransferase family protein / ICMT family protein, similar to SP:O12947 Protein-S isoprenylcysteine O-methyltransferase (EC 2.1.1.100) (Isoprenylcysteine carboxylmethyltransferase) (Farnesyl cysteine carboxyl methyltransferase) (FCMT) {Xenopus laevis}; contains Pfam profile PF04140: Isoprenylcysteine carboxyl methyltransferase (ICMT) family   chr5:7853371-7853964 FORWARD   Aliases: MKD15.18, MKD15_18, PRENYLCYSTEINE ALPHA CARBOXYL METHYLTRANSFERASE, STE14	4.2	3.9	0.3	0.9	100.0%	-4.4
7623	AT5G66610.1   LIM domain-containing protein, contains Pfam profile PF00412: LIM domain	3.0	2.9	0.2	0.9	100.0%	-4.8
7624	AT1G53850.1   Symbol: PAE1   20S proteasome alpha subunit E1 (PAE1), identical to 20S proteasome subunit PAE1 GI:3421087 from (Arabidopsis thaliana)   chr1:20107622-20109663 REVERSE   Aliases: 20S PROTEASOME SUBUNIT PAE1, T18A20.8, T18A20_8	8.8	9.2	-0.4	-0.9	100.0%	-4.5
7625	AT4G22212.1   Encodes a defensin-like (DEFL) family protein.   chr4:11753998-11754700 FORWARD   Aliases: None	10.2	9.9	0.3	0.9	100.0%	-4.9
7626	AT5G01800.1   saposin B domain-containing protein, contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1   chr5:306967-308905 FORWARD   Aliases: T20L15.70, T20L15_70	6.7	6.1	0.6	0.9	100.0%	-4.3
7627	AT2G01740.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:326135-327814 REVERSE   Aliases: T8O11.9, T8O11_9	4.3	4.6	-0.3	-0.9	100.0%	-4.5
7628	AT3G28600.1   similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At5g40000.1); similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At3g28610.1); similar to Cell Division Protein AAA ATPase family [Triticum aestivum] (GB:CAH10209.1); similar to Cell Division Protein AAA ATPase family [Triticum aestivum] (GB:CAH10201.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr3:10723674-10725232 FORWARD   Aliases: MZN14.12	2.8	2.9	-0.1	-0.9	100.0%	-5.3
7629	AT5G10510.1   similar to ovule development protein, putative [Arabidopsis thaliana] (TAIR:At5g65510.1); similar to AP2/EREBP transcription factor BABY BOOM2 [Brassica napus] (GB:AAM33801.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr5:3316037-3320009 FORWARD   Aliases: F12B17.140, F12B17_140	2.2	2.3	-0.1	-0.9	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7630	AT5G08550.1   expressed protein   chr5:2765982-2770283 REVERSE   Aliases: MAH20.11, MAH20_11	3.5	3.7	-0.3	-0.9	100.0%	-4.7
7631	AT1G01520.1   myb family transcription factor, similar to myb-related protein GI:2505876 from (Arabidopsis thaliana)   chr1:190596-192139 FORWARD   Aliases: F22L4.18, F22L4_18	2.5	2.4	0.1	0.9	100.0%	-5.4
7632	AT5G49620.1   myb family transcription factor (MYB78), contains Pfam profile: myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB78) mRNA, partial cds GI:3941509   chr5:20154620-20156610 REVERSE   Aliases: K6M13.18, K6M13_18	4.5	4.3	0.2	0.9	100.0%	-4.7
7633	AT5G54540.1   expressed protein   chr5:22173738-22175280 FORWARD   Aliases: MRB17.4, MRB17_4	9.5	8.9	0.6	0.9	100.0%	-4.3
7634	AT2G21880.1   Ras-related GTP-binding protein, putative, similar to Ras family GTP-binding protein SP:Q43463 from (Glycine max)   chr2:9331713-9333401 REVERSE   Aliases: F7D8.20, F7D8_20	3.0	3.3	-0.3	-0.9	100.0%	-4.3
7635	AT1G05890.1   zinc finger protein-related, contains low similarity to zinc finger proteins and Pfam PF01485: IBR domain   chr1:1779356-1784521 FORWARD   Aliases: T20M3.16, T20M3_16	5.7	5.3	0.4	0.9	100.0%	-4.3
7636	AT1G23930.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr1:8459071-8461449 REVERSE   Aliases: T23E23.10, T23E23_10	2.6	2.7	-0.1	-0.9	100.0%	-5.5
7637	AT4G09370.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr4:5943637-5946067 FORWARD   Aliases: T15G18.210, T15G18_210	2.6	2.7	-0.1	-0.9	100.0%	-5.5
7638	AT4G28960.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr4:14280534-14282870 FORWARD   Aliases: F25O24.80, F25O24_80	2.6	2.7	-0.1	-0.9	100.0%	-5.5
7639	AT5G33230.1   hypothetical protein   chr5:12493907-12494364 FORWARD   Aliases: T29A4.40, T29A4_40	2.6	2.7	-0.1	-0.9	100.0%	-5.5
7640	AT5G37390.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr5:14848662-14851085 REVERSE   Aliases: T25O11.4, T25O11_4	2.6	2.7	-0.1	-0.9	100.0%	-5.5
7641	AT5G44415.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr5:17911173-17913602 FORWARD   Aliases: None	2.6	2.7	-0.1	-0.9	100.0%	-5.5
7642	AT2G26970.2   similar to OSJNBa0079M09.9 [Oryza sativa (japonica cultivar-group)] (GB:XP_471716.1); contains InterPro domain Exonuclease (InterPro:IPR006055)   chr2:11516799-11518992 REVERSE   Aliases: T20P8.2, T20P8_2	5.6	5.4	0.3	0.9	100.0%	-4.6
7643	AT3G20710.1   F-box protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; contains weak hit to Pfam PF00646: F-box domain   chr3:7237917-7239005 REVERSE   Aliases: F3H11.11	4.0	4.3	-0.3	-0.9	100.0%	-4.4
7644	AT1G28060.1   small nuclear ribonucleoprotein family protein / snRNP family protein, contains similarity to U4/U6 small nuclear ribonucleoprotein hPrp3 (Homo sapiens) gi:2708307:gb:AAC51926   chr1:9779125-9782687 FORWARD   Aliases: F13K9.16, F13K9_16	7.2	7.0	0.2	0.9	100.0%	-5.0
7645	AT4G39680.1   SAP domain-containing protein, contains Pfam domain PF02037: SAP domain   chr4:18414300-18417524 REVERSE   Aliases: T19P19.70, T19P19_70	3.8	4.3	-0.6	-0.9	100.0%	-4.3
7646	AT2G36145.1   expressed protein   chr2:15175620-15176585 FORWARD   Aliases: None	5.5	5.1	0.4	0.9	100.0%	-3.9
7647	AT5G54800.1   glucose-6-phosphate/phosphate translocator, putative, identical to glucose 6 phosphate/phosphate translocator (Arabidopsis thaliana) gi:7229675:gb:AAF42936   chr5:22278497-22281111 FORWARD   Aliases: MBG8.6, MBG8_6	7.6	6.7	0.9	0.9	100.0%	-4.1
7648	AT4G22110.2   alcohol dehydrogenase, putative, similar to alcohol dehydrogenase ADH GI:7705214 from (Lycopersicon esculentum); contains Pfam zinc-binding dehydrogenase domain PF00107	3.3	3.7	-0.4	-0.9	100.0%	-4.1
7649	AT3G22020.1   receptor-like protein kinase-related, contains Pfam profile: PF01657 Domain of unknown function; weak similarity to receptor-like protein kinase 5 (GI:13506747) (Arabidopsis thaliana); weak similarity to receptor-like protein kinase homolog RK20-1 (GI:4530126) (Phaseolus vulgaris)   chr3:7756584-7757453 FORWARD   Aliases: MZN24.20	3.0	2.8	0.2	0.9	100.0%	-4.8
7650	AT1G12360.1   Symbol: KEU   cytokinesis-related Sec1 protein (KEULE), similar to cytokinesis-related Sec1 protein KEULE (Arabidopsis thaliana) gi:12659318:gb:AAK01291; contains Pfam domain, PF00995: Sec1 family   chr1:4200874-4206385 FORWARD   Aliases: F5O11.8, F5O11_8, KEULE	7.4	7.8	-0.4	-0.9	100.0%	-4.4
7651	AT3G09650.1   Symbol: HCF152	7.0	7.4	-0.4	-0.9	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7652	AT1G05790.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr1:1733038-1737484 FORWARD   Aliases: T20M3.5, T20M3_5	6.5	6.2	0.4	0.9	100.0%	-4.3
7653	AT3G49210.1   expressed protein   chr3:18249033-18252208 REVERSE   Aliases: F2K15.70	4.2	3.8	0.4	0.9	100.0%	-4.1
7654	AT4G33400.1   dem protein-related / defective embryo and meristems protein-related, identical to dem Gl:2190419 from (Lycopersicon esculentum)	7.0	7.6	-0.6	-0.9	100.0%	-4.1
7655	AT1G31812.1   acyl-CoA binding protein / ACBP, identical to acyl-CoA-binding protein (ACBP) (Arabidopsis thaliana) SWISS-PROT:P57752   chr1:11410857-11412170 REVERSE   Aliases: F5M6.27, F5M6_27	12.7	12.9	-0.2	-0.9	100.0%	-4.9
7656	AT5G17690.1   Symbol: TFL2   like heterochromatin protein (LHP1), identical to like heterochromatin protein LHP1 (Arabidopsis thaliana) Gl:15625407; contains Pfam profile PF00385: 'chromo' (CHRromatin Organization MODifier)   chr5:5827173-5829684 REVERSE   Aliases: LHP1, LIKE HETEROCHROMATIN PROTEIN 1, MVA3.4, MVA3_4, TERMINAL FLOWER 2	4.1	3.9	0.2	0.9	100.0%	-4.9
7657	AT5G51170.1   expressed protein   chr5:20811024-20812625 REVERSE   Aliases: MWD22.11, MWD22_11	6.5	6.1	0.5	0.9	100.0%	-4.3
7658	AT3G08630.1   expressed protein   chr3:2620838-2622226 FORWARD   Aliases: F17O14.10	7.4	6.6	0.8	0.9	100.0%	-4.0
7659	AT4G26690.1   glycerophosphoryl diester phosphodiesterase family protein, weak similarity to glycerophosphodiester phosphodiesterase (Borrelia hermsii) Gl:1399038; contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family   chr4:13456034-13460025 REVERSE   Aliases: F10M23.30, F10M23_30	3.7	3.4	0.3	0.9	100.0%	-4.7
7660	AT1G59820.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Mus musculus (SP:P70704), {Bos taurus} SP:Q29449; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:22014993-22023959 FORWARD   Aliases: F23H11.14, F23H11_14	5.2	4.9	0.2	0.9	100.0%	-4.5
7661	AT2G25180.1   Symbol: ARR12   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain   chr2:10731380-10734040 REVERSE   Aliases: ARABIDOPSIS RESPONSE REGULATOR 12, F13D4.140, F13D4_140	5.3	4.9	0.4	0.9	100.0%	-4.1
7662	AT4G35500.2   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr4:16857358-16859608 FORWARD   Aliases: F8D20.10, F8D20_10	4.7	4.3	0.3	0.9	100.0%	-4.5
7663	AT1G21750.2   Symbol: ATPDIL1 1   protein disulfide isomerase, putative, similar to SP:P29828 Protein disulfide isomerase precursor (PDI) (EC 5.3.4.1) {Medicago sativa}; isoform contains non-consensus GA donor splice site at intron 9   chr1:7645690-7648688 FORWARD   Aliases: ATPDIL1_1, F8K7.19, F8K7_19, PDI LIKE 1 1	6.9	7.5	-0.6	-0.9	100.0%	-4.5
7664	AT5G59740.1   UDP-galactose/UDP-glucose transporter-related, weak similarity to UDP-galactose/UDP-glucose transporter (Arabidopsis thaliana) Gl:22651763   chr5:24087277-24090243 REVERSE   Aliases: MTH12.11, MTH12_11	6.0	6.3	-0.3	-0.9	100.0%	-4.4
7665	AT4G08210.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:5183810-5185870 REVERSE   Aliases: T12G13.50, T12G13_50	2.8	3.0	-0.1	-0.9	100.0%	-5.0
7666	AT4G21090.3   similar to adrenodoxin-like ferredoxin 2 [Arabidopsis thaliana] (TAIR:At4g05450.1); similar to putative ferredoxin [Oryza sativa (japonica cultivar-group)] (GB:XP_476404.1); contains InterPro domain Adrenodoxin (InterPro:IPR001055); contains InterPro domain Ferredoxin (InterPro:IPR001041)   chr4:11256470-11258598 REVERSE   Aliases: F7J7.30, F7J7_30	7.1	7.4	-0.3	-0.9	100.0%	-4.4
7667	AT2G26680.1   expressed protein, similar to NLPE1 (Gl:13022100) (Rhizobium etli);   chr2:11350879-11352480 REVERSE   Aliases: F18A8.5, F18A8_5	5.0	5.3	-0.2	-0.9	100.0%	-4.5
7668	AT1G32090.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) Gl:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr1:11540151-11544059 REVERSE   Aliases: F3C3.11, F3C3_11	3.2	3.4	-0.2	-0.9	100.0%	-4.8
7669	AT3G06380.1   F-box family protein / tubby family protein, similar to phosphodiesterase (Gl:467578) (Mus musculus); similar to C-terminal half of tubby protein (A mutation in the tub gene causes maturity-onset obesity, insulin resistance, and sensory deficits) (GB:P50586) (Gl:6730158)(Mus musculus); contains Pfam PF00646: F-box domain and Pfam PF01167: Tub family; similar to Tubby protein homolog (Swiss-Prot:O88808) (Rattus norvegicus)   chr3:1936130-1938227 FORWARD   Aliases: F24P17.15, F24P17_15	4.7	4.5	0.3	0.9	100.0%	-4.5
7670	AT5G55390.1   Symbol: EDM2   hydroxyproline-rich glycoprotein family protein   chr5:22465192-22471640 REVERSE   Aliases: MTE17.10, MTE17_10	4.5	5.1	-0.5	-0.9	100.0%	-4.4
7671	AT1G67040.1   expressed protein, ; expression supported by MPSS   chr1:25022768-25025585 REVERSE   Aliases: F1O19.10, F1O19_10	3.9	4.2	-0.2	-0.9	100.0%	-4.4
7672	AT3G24490.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) Gl:18149189   chr3:8911029-8912182 FORWARD   Aliases: MOB24.1	7.2	6.9	0.3	0.9	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7673	AT2G17550.1   expressed protein   chr2:7641365-7644693 REVERSE   Aliases: MJB20.11, MJB20_11	4.5	4.4	0.2	0.9	100.0%	-4.9
7674	AT5G63130.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, contains Pfam profile PF00564: PB1 domain   chr5:25340335-25341498 FORWARD   Aliases: MDC12.9, MDC12_9	3.5	3.2	0.3	0.9	100.0%	-4.5
7675	AT1G05150.1   calcium-binding EF hand family protein, low similarity to O-linked GlcNAc transferase (Homo sapiens) GI:2266994; contains Pfam profiles PF00036: EF hand, PF00515: TPR Domain   chr1:1484066-1486959 REVERSE   Aliases: YUP8H12.24, YUP8H12_24	5.0	5.6	-0.6	-0.9	100.0%	-4.6
7676	AT3G22370.1   Symbol: AOX1A   alternative oxidase 1a, mitochondrial (AOX1A), identical to GB:Q39219 (SP:Q39219) from (Arabidopsis thaliana)   chr3:7906800-7908747 FORWARD   Aliases: MCB17.10	8.4	7.8	0.6	0.9	100.0%	-4.2
7677	AT1G33090.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:11993278-11996692 FORWARD   Aliases: T9L6.17, T9L6_17	3.0	2.9	0.2	0.9	100.0%	-4.8
7678	AT1G33100.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:11997663-12001288 FORWARD   Aliases: T9L6.18, T9L6_18	3.0	2.9	0.2	0.9	100.0%	-4.8
7679	AT1G51570.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr1:19125844-19128356 REVERSE   Aliases: F19C24.20, F19C24_20	5.3	5.6	-0.3	-0.9	100.0%	-4.4
7680	AT3G20500.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	10.3	9.9	0.4	0.9	100.0%	-4.5
7681	AT1G04920.1   sucrose-phosphate synthase, putative, similar to GB:Y11795 from (Craterostigma plantagineum)   chr1:1391501-1395863 REVERSE   Aliases: F13M7.9, F13M7_9	3.1	3.4	-0.3	-0.9	100.0%	-4.6
7682	AT5G37490.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain   chr5:14904708-14906281 FORWARD   Aliases: MPA22.3, MPA22_3	3.7	3.9	-0.2	-0.9	100.0%	-4.7
7683	AT1G51210.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:18991477-18992778 FORWARD   Aliases: F11M15.8, F11M15_8	5.7	5.3	0.4	0.9	100.0%	-4.5
7684	AT2G45830.2   expressed protein   chr2:18873135-18875616 FORWARD   Aliases: F4I18.19	4.8	4.4	0.4	0.9	100.0%	-4.3
7685	AT1G56320.1   expressed protein   chr1:21089213-21090124 REVERSE   Aliases: F14G9.7, F14G9_7	3.9	4.4	-0.5	-0.9	100.0%	-4.0
7686	AT3G20050.1   Symbol: ATTCP 1   T-complex protein 1 alpha subunit / TCP-1-alpha / chaperonin (CCT1), identical to SWISS-PROT:P28769- T-complex protein 1, alpha subunit (TCP-1-alpha) (Arabidopsis thaliana)   chr3:6998260-7002407 REVERSE   Aliases: MAL21.5, MAL21_5	9.0	9.6	-0.6	-0.9	100.0%	-4.3
7687	AT2G04880.2   Symbol: ZAP1   WRKY family transcription factor (ZAP1), identical to ZAP1 GI:1064883 from (Arabidopsis thaliana); contains Pfam profile: PF03106 WRKY DNA -binding domain   chr2:1717890-1720971 FORWARD   Aliases: ATWRKY1, F1O13.1, F1O13_1, WRKY1, ZAP1	6.5	6.8	-0.3	-0.9	100.0%	-4.5
7688	AT4G38680.1   Symbol: GRP2   cold-shock DNA-binding family protein, contains Pfam domains PF00313: 'Cold-shock' DNA-binding domain and PF00098: Zinc knuckle   chr4:18071878-18073176 REVERSE   Aliases: GRP 2, T9A14.9	6.4	6.0	0.3	0.9	100.0%	-4.4
7689	AT5G05150.1   transport protein-related, contains 2 WD-40 repeats (PF00400); similar to transport protein Gsa12p (GI:18307769) (Pichia pastoris)   chr5:1524842-1526200 REVERSE   Aliases: K2A11.2, K2A11_2	3.3	3.1	0.2	0.9	100.0%	-4.7
7690	AT4G02010.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:881185-885399 FORWARD   Aliases: T10M13.2, T10M13_2	5.5	5.9	-0.4	-0.9	100.0%	-4.3
7691	AT1G56540.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:21185329-21188971 FORWARD   Aliases: F25P12.101, F25P12_101	2.3	2.4	-0.1	-0.9	100.0%	-5.3
7692	AT3G10520.1   Symbol: AHB2   non-symbiotic hemoglobin 2 (HB2) (GLB2), identical to SP:O24521 Non-symbiotic hemoglobin 2 (Hb2) (ARATH GLB2) {Arabidopsis thaliana}   chr3:3276235-3277865 REVERSE   Aliases: ARATH GLB2, F13M14.20, GLB2, HEMOGLOBIN, NSHB2	3.7	3.8	-0.2	-0.9	100.0%	-4.9
7693	AT2G13100.1   glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative, similar to glycerol-3-phosphate transporter (glycerol 3-phosphate permease) (Homo sapiens) GI:7543982; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:5397288-5399011 FORWARD   Aliases: T17A11.9, T17A11_9	6.8	6.6	0.2	0.9	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7694	AT1G75410.1   Symbol: BLH3   BEL1-like homeodomain 3 protein (BLH3), identical to BEL1-like homeodomain 3 (GI:13877515) (Arabidopsis thaliana)   chr1:28303453-28306232 REVERSE   Aliases: BEL1 like homeodomain 3, F1B16.6, F1B16_6	5.1	4.6	0.5	0.9	100.0%	-4.3
7695	AT5G60270.1   lectin protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain, PF00139: Legume lectins beta domain, and PF00138: Legume lectins alpha domain   chr5:24274987-24276993 FORWARD   Aliases: F15L12.9, F15L12_9	2.8	2.7	0.1	0.9	100.0%	-5.1
7696	AT1G05020.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, Similar to clathrin assembly protein gb:X68878 (AP180) from Rattus norvegicus; contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; EST gb:W43552 comes from this gene	3.8	3.5	0.3	0.9	100.0%	-4.7
7697	AT1G48920.1   nucleolin, putative, similar to nuM1 protein GI:1279562 from (Medicago sativa)   chr1:18101776-18105291 FORWARD   Aliases: F27K7.6, F27K7_6	9.6	9.2	0.4	0.9	100.0%	-4.3
7698	AT3G07740.2   Symbol: ADA2A   transcriptional adaptor (ADA2a), identical to transcriptional adaptor ADA2a (Arabidopsis thaliana) gi:13591698:gb:AAK31319   chr3:2469789-2473085 REVERSE   Aliases: ATADA2A, HAC10, HXA02, HXA2, MLP3.19	5.3	5.7	-0.4	-0.9	100.0%	-4.5
7699	AT5G53830.1   VQ motif-containing protein, contains PF05678: VQ motif   chr5:21874276-21875210 FORWARD   Aliases: MGN6.22, MGN6_22	2.5	2.6	-0.1	-0.9	100.0%	-5.2
7700	AT1G32470.1   glycine cleavage system H protein, mitochondrial, putative, similar to SP:P25855 Glycine cleavage system H protein 1, mitochondrial precursor {Arabidopsis thaliana}; contains Pfam profile PF01597: Glycine cleavage H-protein   chr1:11739284-11740308 REVERSE   Aliases: F5D14.25, F5D14_25	6.8	7.4	-0.6	-0.9	100.0%	-3.9
7701	AT3G19710.1   branched-chain amino acid aminotransferase, putative / branched-chain amino acid transaminase, putative (BCAT4), similar to branched-chain amino acid transaminase 6 (Arabidopsis thaliana) GI:13810195; contains Pfam profile: PF01063 aminotransferase class IV   chr3:6846996-6849503 REVERSE   Aliases: MMB12.20	3.1	3.6	-0.5	-0.9	100.0%	-3.9
7702	AT4G19510.2   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:10633715-10638174 FORWARD   Aliases: F24J7.70, F24J7_70	3.7	3.4	0.2	0.9	100.0%	-4.7
7703	AT3G63090.1   expressed protein   chr3:23324403-23325964 FORWARD   Aliases: T20O10.190	4.6	4.9	-0.3	-0.9	100.0%	-4.4
7704	AT3G09220.1   laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)(GI:13661201), laccase GB:CAA74105 (Populus balsamifera subsp. trichocarpa); contains Pfam profile: Multicopper oxidases   chr3:2827245-2830548 REVERSE   Aliases: F3L24.9	3.9	4.3	-0.3	-0.9	100.0%	-4.3
7705	AT3G19570.2   expressed protein, contains Pfam domain, PF04484: Family of unknown function (DUF566)   chr3:6797491-6801738 FORWARD   Aliases: MMB12.3	2.8	3.0	-0.2	-0.9	100.0%	-4.9
7706	AT3G21750.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:7664352-7666202 FORWARD   Aliases: MSD21.8	5.2	5.7	-0.5	-0.9	100.0%	-3.8
7707	AT2G41740.1   Symbol: VLN2   villin 2 (VLN2), nearly identical to villin 2 (VLN2) (Arabidopsis thaliana) GI:3415115   chr2:17417793-17424667 REVERSE   Aliases: T11A7.16, T11A7_16, VILLIN 2	4.3	4.5	-0.2	-0.9	100.0%	-4.6
7708	AT3G16050.1   Symbol: A37   stress-responsive protein, putative, similar to ethylene-inducible protein HEVER (Hevea brasiliensis) SWISS-PROT:Q39963; contains Pfam domain, PF01680: SOR/SNZ family   chr3:5443957-5445335 REVERSE   Aliases: MSL1.3	8.6	8.1	0.5	0.9	100.0%	-4.2
7709	AT5G67490.1   expressed protein   chr5:26951379-26952178 REVERSE   Aliases: K9I9.5, K9I9_5	10.4	10.1	0.3	0.9	100.0%	-4.3
7710	AT5G60870.2   regulator of chromosome condensation (RCC1) family protein, weak similarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	6.8	6.4	0.4	0.9	100.0%	-4.1
7711	AT5G47370.1   Symbol: HAT2   homeobox-leucine zipper protein 2 (HAT2) / HD-ZIP protein 2, identical to homeobox-leucine zipper protein HAT2 (HD-ZIP protein 2) (Arabidopsis thaliana) SP:P46601; contains Pfam profiles PF04618: HD-ZIP protein N terminus, PF02183: Homeobox associated leucine zipper, PF00046: Homeobox domain   chr5:19233539-19235136 REVERSE   Aliases: MQL5.23, MQL5_23	6.9	7.4	-0.4	-0.9	100.0%	-4.3
7712	AT4G35050.1   Symbol: MSI3   WD-40 repeat protein (MSI3), contains 5 WD-40 repeats (PF0400); identical to WD-40 repeat protein MSI3 (SP:O22469) (Arabidopsis thaliana)   chr4:16682585-16684853 REVERSE   Aliases: M4E13.110, M4E13_110	4.7	5.2	-0.5	-0.9	100.0%	-4.6
7713	AT5G07860.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:2511443-2513096 FORWARD   Aliases: F13G24.60, F13G24_60	5.0	5.2	-0.2	-0.9	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7714	AT5G02140.1   thaumatin-like protein, putative, similar to SP:P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}; contains Pfam profile PF00314: Thaumatin family   chr5:423381-424434 FORWARD   Aliases: T7H20.190, T7H20_190	2.8	3.0	-0.2	-0.9	100.0%	-4.8
7715	AT3G24670.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa)   chr3:9006212-9008808 REVERSE   Aliases: MSD24.10	5.6	5.1	0.6	0.9	100.0%	-4.2
7716	AT1G26940.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr1:9343113-9345132 FORWARD   Aliases: T2P11.13, T2P11_13	5.2	5.5	-0.3	-0.9	100.0%	-4.4
7717	AT4G33750.1   expressed protein   chr4:16188358-16188927 FORWARD   Aliases: T16L1.240, T16L1_240	4.9	5.7	-0.8	-0.9	100.0%	-4.4
7718	AT1G17190.1   Symbol: ATGSTU26   glutathione S-transferase, putative, One of three repeated glutathione transferases. 65% identical to glutathione transferase (Arabidopsis thaliana) (gi:4006934). Location of est 141C5T7 (gb:T46669); supported by fl cDNA gi:14326476gb:AF385691.	2.7	3.1	-0.4	-0.9	100.0%	-3.9
7719	AT5G10470.1   kinesin motor protein-related, TH65 protein, Arabidopsis thaliana, EMBL:AJ001729; contains Pfam profile PF00225: Kinesin motor domain   chr5:3290122-3297249 REVERSE   Aliases: F12B17.180, F12B17_180	3.5	3.9	-0.4	-0.9	100.0%	-4.4
7720	AT3G52200.1   Symbol: LTA3   dihydrolipoamide S-acetyltransferase, putative, similar to dihydrolipoamide acetyltransferase (E2) subunit of PDC (Arabidopsis thaliana) GI:559395; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain; supporting cDNA gi:5881964:gb:AF066080.1:AF066080   chr3:19371184-19377365 FORWARD   Aliases: DIHYDROLIPOAMIDE S ACETYLTRANSFERASE, T25B15.141	7.2	7.8	-0.6	-0.9	100.0%	-4.3
7721	AT3G18310.1   expressed protein   chr3:6284362-6287150 REVERSE   Aliases: MYF24.3	5.0	5.2	-0.2	-0.9	100.0%	-4.8
7722	AT1G21830.1   expressed protein, EST gb:T21171 comes from this gene   chr1:7661149-7662595 REVERSE   Aliases: AT1G21820, T26F17.4	3.4	3.5	-0.2	-0.9	100.0%	-4.9
7723	AT3G48530.1   CBS domain-containing protein, low similarity to SP:Q9UGI9 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) {Homo sapiens}; contains Pfam profile PF00571: CBS domain	6.2	6.6	-0.4	-0.9	100.0%	-4.3
7724	AT3G24210.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr3:8753481-8756072 REVERSE   Aliases: MUJ8.11	3.2	3.4	-0.2	-0.9	100.0%	-4.7
7725	AT5G24080.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:8139256-8141125 REVERSE   Aliases: MZF18.3, MZF18_3	2.7	3.2	-0.4	-0.9	100.0%	-4.0
7726	AT1G54870.1   similar to short-chain dehydrogenase/reductase (SDR) family protein [Arabidopsis thaliana] (TAIR:At3g05260.1); similar to putative TAG-associated factor [Lupinus angustifolius] (GB:AAN75426.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)   chr1:20462673-20464314 FORWARD   Aliases: F14C21.43, F14C21_43	2.6	2.7	-0.1	-0.9	100.0%	-5.2
7727	AT3G53230.1   cell division cycle protein 48, putative / CDC48, putative, very strong similarity to SP:P54609 Cell division cycle protein 48 homolog {Arabidopsis thaliana}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain   chr3:19734353-19737650 FORWARD   Aliases: T4D2.160	6.8	6.4	0.3	0.9	100.0%	-4.4
7728	AT4G23440.1   expressed protein   chr4:12237775-12240818 FORWARD   Aliases: F16G20.140, F16G20_140	3.6	3.8	-0.2	-0.9	100.0%	-4.7
7729	AT2G22940.1   expressed protein, ; expression supported by MPSS   chr2:9768735-9770542 REVERSE   Aliases: T20K9.15, T20K9_15	2.4	2.3	0.1	0.9	100.0%	-5.5
7730	AT1G01320.1   tetratricopeptide repeat (TPR)-containing protein, low similarity to SP:P46825 Kinesin light chain (KLC) {Loligo pealeii}; contains Pfam profile PF00515: TPR Domain   chr1:121134-130099 REVERSE   Aliases: F6F3.12, F6F3_12	3.7	3.9	-0.3	-0.9	100.0%	-4.4
7731	AT1G06690.1   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:2049601-2052059 REVERSE   Aliases: F12K11.2, F12K11_2	6.6	6.9	-0.4	-0.9	100.0%	-4.2
7732	AT1G76180.1   Symbol: ERD14   dehydrin (ERD14), identical to SP:P42763 Dehydrin ERD14 {Arabidopsis thaliana}   chr1:28591667-28592771 REVERSE   Aliases: EARLY RESPONSE TO DEHYDRATION 14, ERD14, T23E18.12, T23E18_12	10.6	11.0	-0.5	-0.9	100.0%	-4.8
7733	AT5G65900.1   DEAD/DEAH box helicase, putative, contains Pfam profiles	4.4	4.7	-0.3	-0.9	100.0%	-4.4
7734	AT4G02920.2   expressed protein   chr4:1292640-1294861 FORWARD   Aliases: T4I9.20	5.9	5.7	0.3	0.9	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7735	AT1G30810.1   transcription factor jumonji (jnj) family protein / zinc finger (C5HC2 type) family protein, contains similarity to Swiss-Prot:P29375 retinoblastoma-binding protein 2 (RBBP-2) (Homo sapiens); contains Pfam domains PF02375: jnjN domain and PF02373: jnjC domain; intron between exons 6 and 7 was required to circumvent a frameshift. There could be an underlying sequence error.	4.2	4.0	0.3	0.9	100.0%	-4.5
7736	AT4G08790.1   nitrilase, putative, similar to nitrilase 1 (Mus musculus) GI:3228668; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family   chr4:5608237-5611212 REVERSE   Aliases: T32A17.100, T32A17_100	5.4	5.6	-0.3	-0.9	100.0%	-4.3
7737	AT3G30300.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr3:11923677-11926884 REVERSE   Aliases: T6J22.5	6.1	6.4	-0.3	-0.9	100.0%	-4.4
7738	AT2G43980.1   inositol 1,3,4-trisphosphate 5/6-kinase family protein, contains Pfam profile PF05770: Inositol 1, 3, 4-trisphosphate 5/6-kinase; contains Prosite PS00591: Glycosyl hydrolases family 10 active site; similar to inositol 1,3,4-trisphosphate 5/6-kinase (GI:1322038) (Homo sapiens)   chr2:18215349-18218712 REVERSE   Aliases: F6E13.11	4.0	4.3	-0.3	-0.9	100.0%	-4.7
7739	AT1G03410.1   Symbol: 2A6   2-oxoglutarate-dependent dioxygenase, putative, identical to 2A6 (GI:599622), a homolog of the tomato ethylene synthesis regulatory protein E8; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr1:844435-846484 REVERSE   Aliases: 2A6, F21B7.3	3.0	3.0	0.1	0.9	100.0%	-5.4
7740	AT1G08450.2   Symbol: CRT3   calreticulin 3 (CRT3), identical to similar to SP:O04153 Calreticulin 3 precursor {Arabidopsis thaliana}	8.6	8.8	-0.3	-0.9	100.0%	-4.7
7741	AT4G16050.1   expressed protein   chr4:9092238-9094369 FORWARD   Aliases: DL4065W, FCAALL.267	2.7	2.8	-0.1	-0.9	100.0%	-5.4
7742	AT2G43370.1   U1 small nuclear ribonucleoprotein 70 kDa, putative   chr2:18020454-18022531 FORWARD   Aliases: T1O24.11	4.9	4.7	0.3	0.9	100.0%	-4.3
7743	AT5G02430.1   WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); rab11 binding protein, Bos taurus, EMBL:AF117897   chr5:526590-529837 FORWARD   Aliases: T22P11.20, T22P11_20	5.1	5.5	-0.4	-0.9	100.0%	-4.4
7744	AT2G31810.3   acetolactate synthase small subunit, putative, similar to gi:5931761 from Nicotiana plumbaginifolia   chr2:13531299-13535578 FORWARD   Aliases: F20M17.15, F20M17_15	9.2	8.7	0.5	0.9	100.0%	-4.3
7745	AT1G47610.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to En/Spm-like transposon protein (GI:2739374) (Arabidopsis thaliana)   chr1:17507223-17508404 FORWARD   Aliases: F16N3.9, F16N3_9	3.9	3.5	0.3	0.9	100.0%	-4.4
7746	AT3G48010.1   Symbol: ATCNGC16   cyclic nucleotide-regulated ion channel, putative (CNGC16), similar to cyclic nucleotide and calmodulin-regulated ion channel (cngc6) GI:4581207 from (Arabidopsis thaliana)	2.4	2.3	0.1	0.9	100.0%	-5.4
7747	AT3G63290.2   expressed protein   chr3:23392659-23394513 FORWARD   Aliases: MAA21.8	3.5	3.7	-0.2	-0.9	100.0%	-4.6
7748	AT3G52890.2   Symbol: KIPK   protein kinase (KIPK), identical to protein kinase KIPK (KCBP-interacting protein kinase) (Arabidopsis thaliana) gi:7716430:gb:AAF68383   chr3:19618935-19623164 FORWARD   Aliases: F8J2.60, KCBP INTERACTING PROTEIN KINASE, PROTEIN KINASE KIPK	5.2	5.4	-0.2	-0.9	100.0%	-4.7
7749	AT2G45190.1   Symbol: AFO   axial regulator YABBY1 (YABBY1) / abnormal floral organs protein (AFO) / filamentous flower protein (FIL), identical to YABBY1 (Arabidopsis thaliana) GI:4928749, abnormal floral organs protein (AFO) (Arabidopsis thaliana) GI:4322477; supporting cDNA gi:4322476:gb:AF087015.1:AF087015   chr2:18635339-18637786 REVERSE   Aliases: ABNORMAL FLORAL ORGANS, ABNORMAL FLORAL ORGANS PROTEIN, F4L23.30, FIL, FILAMENTOUS FLOWER, YAB1, YABBY1	2.7	2.9	-0.2	-0.9	100.0%	-4.9
7750	AT3G55010.2   phosphoribosylformylglycinamide cyclo-ligase, chloroplast / phosphoribosyl-aminoimidazole synthetase / AIR synthase (PUR5), identical to phosphoribosylformylglycinamide cyclo-ligase, chloroplast precursor SP:Q05728 from (Arabidopsis thaliana); contains Pfam profiles: PF02769 AIR synthase related protein, C-terminal domain, PF00586 AIR synthase related protein, N-terminal domain	8.0	8.4	-0.5	-0.9	100.0%	-4.3
7751	AT5G58700.2   similar to phosphoinositide-specific phospholipase C family protein [Arabidopsis thaliana] (TAIR:At2g40116.1); similar to phosphoinositide-specific phospholipase C (PLC2) [Arabidopsis thaliana] (TAIR:At3g08510.1); similar to 1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase [Nicotiana rustica] (GB:CAA72681.1); similar to phospholipase C [Pisum sativum] (GB:CAA75546.2); contains InterPro domain Phosphoinositide-specific phospholipase C (PLC) (InterPro:IPR001192); contains InterPro domain C2 domain (InterPro:IPR000008); contains InterPro domain Phosphatidylinositol-specific phospholipase C, X domain (InterPro:IPR000909); contains InterPro domain Phosphatidylinositol-specific phospholipase C, Y domain (InterPro:IPR001711)	7.6	7.8	-0.2	-0.9	100.0%	-4.4
7752	AT3G22530.1   expressed protein, contains Pfam profile:PF00011 HSP20:Hsp20/alpha crystallin family   chr3:7977611-7978642 REVERSE   Aliases: F16J14.9	6.2	6.1	0.2	0.9	100.0%	-5.0
7753	AT1G72500.1   inter-alpha-trypsin inhibitor heavy chain-related, low similarity to Inter-alpha-inhibitor H4 heavy chain (Rattus norvegicus) GI:2292988; contains Pfam profile PF00092: von Willebrand factor type A domain   chr1:27298998-27302218 REVERSE   Aliases: T10D10.3, T10D10_3	9.0	9.3	-0.3	-0.9	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7754	AT1G11950.1   transcription factor jumonji (jnjC) domain-containing protein, contains Pfam domain, PF02373: jnjC domain; non-consensus TG acceptor splice site at exon boundary 79262   chr1:4034585-4038308 REVERSE   Aliases: F12F1.18, F12F1_18	4.2	4.4	-0.2	-0.9	100.0%	-4.7
7755	AT1G29390.2   Symbol: COR314 TM2   stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi:18449100:gb:AAL69988; similar to stress-regulated protein SAP1 (Xerophyta viscosa) gi:21360378:gb:AAM47505   chr1:10286279-10288089 REVERSE   Aliases: F15D2.42	8.6	8.1	0.4	0.9	100.0%	-4.2
7756	AT4G00560.3   methionine adenosyltransferase regulatory beta subunit-related, contains weak similarity to methionine adenosyltransferase regulatory beta subunit (GI:6815285) (Homo sapiens)   chr4:240676-242379 REVERSE   Aliases: F6N23.17, F6N23_17	4.2	3.9	0.2	0.9	100.0%	-4.9
7757	AT2G31270.1   hydroxyproline-rich glycoprotein family protein   chr2:13336092-13338907 FORWARD   Aliases: F16D14.11, F16D14_11	3.2	3.4	-0.2	-0.9	100.0%	-4.6
7758	AT2G17650.1   AMP-dependent synthetase and ligase family protein, similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501; identical to cDNA adenosine monophosphate binding protein 2 AMPBP2 (AMPBP2) GI:20799712   chr2:7678099-7680113 FORWARD   Aliases: T17A5.12, T17A5_12	4.6	4.3	0.3	0.9	100.0%	-4.5
7759	AT2G22400.1   NOL1/NOP2/sun family protein, contains Pfam profile PF01189: NOL1/NOP2/sun family   chr2:9511739-9515955 REVERSE   Aliases: F14M13.20, F14M13_20	6.4	6.9	-0.5	-0.9	100.0%	-4.4
7760	AT3G18770.1   expressed protein   chr3:6459890-6463058 REVERSE   Aliases: MVE11.13	3.2	3.0	0.2	0.9	100.0%	-4.8
7761	AT3G08780.2   similar to P0458H05.113 [Oryza sativa (japonica cultivar-group)] (GB:XP_478579.1)   chr3:2666447-2667539 REVERSE   Aliases: F17O14.25	5.6	5.3	0.2	0.9	100.0%	-4.5
7762	ATCG00760.1   Symbol: RPL36   encodes a chloroplast ribosomal protein L36, a constituent of the large subunit of the ribosomal complex   chrC:79489-79602 REVERSE   Aliases: RPL36	8.4	9.4	-1.0	-0.9	100.0%	-4.8
7763	AT4G14370.1   disease resistance protein (TIR-NBS-LRR class), putative, similar to zinc finger protein (GI:15811367) (Arabidopsis thaliana); similar to TIR-NBS-LRR (GI:27466164) (Arabidopsis thaliana); similar to disease resistance protein RPP1-WsB (GI:3860165) (Arabidopsis thaliana)   chr4:8274309-8283259 REVERSE   Aliases: DL3225C, FCAALL.185	2.3	2.2	0.1	0.9	100.0%	-5.6
7764	AT1G12370.2   Symbol: PHR1   type II CPD photolyase PHR1 (PHR1), nearly identical to type II CPD photolyase PHR1 (Arabidopsis thaliana) GI:2984707; similar to class II DNA photolyase (GI:5081541) (Chlamydomonas reinhardtii); supporting cDNA gi:2984706:gb:AF053365.1:AF053365   chr1:4206372-4208949 REVERSE   Aliases: F5O11.9, F5O11_9, PHOTOLYASE 1, PHR1, TYPE II CPD PHOTOLYASE, UV RESISTANCE2, UVR2	5.7	5.9	-0.2	-0.9	100.0%	-4.7
7765	AT4G17150.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g23540.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g14290.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464484.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr4:9638454-9641790 FORWARD   Aliases: DL4610W, FCAALL.363	5.3	5.6	-0.3	-0.9	100.0%	-4.6
7766	AT5G01260.2   glycoside hydrolase starch-binding domain-containing protein, low similarity to SP:P31797 Cyclomaltodextrin glucanotransferase precursor (EC 2.4.1.19) (Cyclodextrin-glycosyltransferase) (CGTase) {Bacillus stearothermophilus}; contains Pfam profile PF00686: Starch binding domain   chr5:105324-107404 FORWARD   Aliases: F7J8.240, F7J8_240	6.0	5.5	0.5	0.9	100.0%	-4.2
7767	AT2G16910.1   Symbol: AMS   basic helix-loop-helix (bHLH) family protein   chr2:7338803-7341815 FORWARD   Aliases: ABORTED MICROSPORES, F12A24.9, F12A24_9	3.3	3.1	0.2	0.9	100.0%	-4.9
7768	AT5G03850.1   40S ribosomal protein S28 (RPS28B), ribosomal protein S28, Arabidopsis thaliana, EMBL:ATRP28A   chr5:1028339-1029120 REVERSE   Aliases: MED24.14	12.0	12.2	-0.2	-0.9	100.0%	-5.3
7769	AT5G65540.1   expressed protein   chr5:26212915-26215913 FORWARD   Aliases: K21L13.5, K21L13_5	4.6	4.8	-0.3	-0.9	100.0%	-4.5
7770	AT4G18670.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	2.3	2.5	-0.2	-0.9	100.0%	-4.8
7771	AT5G64740.1   Symbol: CESA6   cellulose synthase, catalytic subunit, putative, similar to gi:2827141 cellulose synthase catalytic subunit (Ath-A), Arabidopsis thaliana   chr5:25898292-25903920 FORWARD   Aliases: CELLULASE SYNTHASE 6, E112, ISOXABEN RESISTANT 2, IXR2, MVP7.7, MVP7_7, PRC1, PROCUSTE 1	7.5	7.1	0.4	0.9	100.0%	-4.4
7772	AT1G44960.1   expressed protein   chr1:17001989-17004169 FORWARD   Aliases: T12C22.23, T12C22_23	5.2	4.8	0.4	0.9	100.0%	-4.3
7773	AT5G58740.1   nuclear movement family protein, contains Pfam profile: PF03593 nuclear movement protein	10.8	10.5	0.3	0.9	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7774	AT5G06160.1   splicing factor-related, contains some similarity to splicing factor SP:Q12874 from (Homo sapiens)   chr5:1862370-1866383 REVERSE   Aliases: MBL20.3, MBL20_3	5.1	5.4	-0.3	-0.9	100.0%	-4.6
7775	AT4G00335.3   Symbol: RHB1A   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At5g41350.1); similar to putative RING-H2 finger protein RHB1a [Oryza sativa (japonica cultivar-group)] (GB:AAP52079.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr4:145928-148258 FORWARD   Aliases: RING H2 FINGER PROTEIN RHB1A	4.2	3.9	0.3	0.9	100.0%	-4.5
7776	AT3G27350.1   expressed protein   chr3:10127272-10129192 FORWARD   Aliases: K1G2.6	5.8	6.1	-0.3	-0.9	100.0%	-4.4
7777	AT1G76310.1   Symbol: CYCB2;4   cyclin, putative, similar to B-like cyclin Gl:780267 from (Medicago sativa); contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:28632940-28635093 REVERSE   Aliases: CYCLIN B2;4, F15M4.19	3.1	3.0	0.1	0.9	100.0%	-5.3
7778	AT1G73620.1   thaumatin-like protein, putative / pathogenesis-related protein, putative, strong similarity to SP:P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}, pathogenesis-related group 5 protein (Brassica rapa) Gl:2749943; contains Pfam profile: PF00314 thaumatin family   chr1:27685069-27686790 FORWARD   Aliases: F25P22.3, F25P22_3	2.7	2.9	-0.2	-0.9	100.0%	-4.8
7779	AT2G26670.1   Symbol: HY1   heme oxygenase 1 (HO1) (HY1), identical to plastid heme oxygenase (HY1) (Arabidopsis thaliana) Gl:4877362, heme oxygenase 1 (Arabidopsis thaliana) Gl:4530591 GB:AF132475; annotation updated per Seth J. Davis at University of Wisconsin-Madison   chr2:11348762-11350650 FORWARD   Aliases: ATHO1, ELONGATED HYPOCOTYL 1, F18A8.4, F18A8_4, GENOMES UNCOUPLED 2, GUN2, HEME OXYGENASE, HEME OXYGENASE 1, HO1, PLASTID HEME OXYGENASE, TED 4	8.2	7.8	0.5	0.9	100.0%	-4.3
7780	AT3G45460.1   expressed protein   chr3:16689750-16691028 REVERSE   Aliases: F9K21.40	2.7	2.8	-0.2	-0.9	100.0%	-5.1
7781	AT4G24560.1   Symbol: UBP16   ubiquitin-specific protease 16, putative (UBP16), similar to ubiquitin-specific protease 16 Gl:11993477 (Arabidopsis thaliana)   chr4:12679220-12684949 REVERSE   Aliases: F22K18.240, F22K18_240, UBIQUITIN SPECIFIC PROTEASE 16	4.6	5.0	-0.4	-0.9	100.0%	-4.4
7782	AT2G46620.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr2:19145871-19147817 REVERSE   Aliases: F13A10.15	3.8	3.6	0.3	0.9	100.0%	-4.4
7783	AT2G17370.1   Symbol: HMG2   3-hydroxy-3-methylglutaryl-CoA reductase 2 / HMG-CoA reductase 2 (HMGR2), identical to SP:P43256 3-hydroxy-3-methylglutaryl-coenzyme A reductase 2 (EC 1.1.1.34) (HMG- CoA reductase 2) (HMGR2) {Arabidopsis thaliana}   chr2:7556857-7559283 FORWARD   Aliases: F5J6.1, F5J6_1	6.6	6.4	0.2	0.9	100.0%	-4.6
7784	AT1G31840.1   pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR domains: Pfam profile: PF01535: PPR repeat   chr1:11423987-11426059 FORWARD   Aliases: F5M6.15, F5M6_15	2.6	2.8	-0.1	-0.9	100.0%	-5.1
7785	AT3G16480.1   Symbol: MPPALPHA   mitochondrial processing peptidase alpha subunit, putative, similar to mitochondrial processing peptidase alpha subunit, mitochondrial precursor, Alpha-MPP (Ubiquinol-cytochrome C reductase subunit II) (Potato) SWISS-PROT:P29677	7.2	7.8	-0.6	-0.9	100.0%	-4.2
7786	AT3G27620.1   Symbol: AOX1C   alternative oxidase 1c, mitochondrial (AOX1C), identical to alternative oxidase 1c precursor GB:O22048 (SP:O22048) from (Arabidopsis thaliana)   chr3:10230282-10231939 REVERSE   Aliases: MGF10.1	3.9	3.7	0.2	0.9	100.0%	-4.7
7787	AT5G42820.2   U2 snRNP auxiliary factor small subunit, putative, strong similarity to U2 snRNP auxiliary factor, small subunit (Oryza sativa) Gl:3850816   chr5:17186511-17188897 REVERSE   Aliases: MJB21.20, MJB21_20	7.1	6.8	0.3	0.9	100.0%	-4.5
7788	AT1G51430.1   expressed protein   chr1:19071909-19073444 FORWARD   Aliases: F5D21.20, F5D21_20	4.7	4.4	0.3	0.9	100.0%	-4.5
7789	AT1G32770.1   Symbol: ANAC012   no apical meristem (NAM) family protein, similar to OsNAC7 protein GB:BAA89801 Gl:6730944 from (Oryza sativa)	2.3	2.4	-0.2	-0.9	100.0%	-5.2
7790	AT5G62650.1   expressed protein   chr5:25169851-25173154 REVERSE   Aliases: MRG21.7, MRG21_7	7.1	6.9	0.3	0.9	100.0%	-4.4
7791	AT2G30980.1   shaggy-related protein kinase delta / ASK-delta / ASK-dzeta (ASK4), identical to shaggy-related protein kinase delta (ASK-delta) (ASK- dzeta) (Arabidopsis thaliana) SWISS-PROT:Q39010   chr2:13189148-13193026 REVERSE   Aliases: F7F1.19, F7F1_19	6.1	6.8	-0.7	-0.9	100.0%	-4.2
7792	AT1G60890.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) Gl:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr1:22415911-22420898 REVERSE   Aliases: T7P1.4, T7P1_4	4.0	4.4	-0.4	-0.9	100.0%	-4.2
7793	AT1G72200.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:27173457-27174983 REVERSE   Aliases: T9N14.11, T9N14_11	3.2	2.8	0.3	0.9	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7794	AT5G05350.1   expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614; expression supported by MPSS   chr5:1585758-1587338 FORWARD   Aliases: K18I23.15, K18I23_15	4.2	4.4	-0.2	-0.9	100.0%	-4.6
7795	AT5G16680.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr5:5467537-5473504 REVERSE   Aliases: MTG13.4, MTG13_4	6.6	7.1	-0.5	-0.9	100.0%	-4.6
7796	AT1G66730.1   ATP dependent DNA ligase family protein, contains Pfam profile: PF01068 ATP dependent DNA ligase domain   chr1:24888571-24895486 FORWARD   Aliases: F4N21.14, F4N21_14	3.2	3.3	-0.1	-0.9	100.0%	-5.0
7797	AT3G50540.1   hypothetical protein   chr3:18768730-18769121 FORWARD   Aliases: T20E23.140	5.9	5.5	0.4	0.9	100.0%	-4.5
7798	AT3G54640.1   Symbol: TSA1   tryptophan synthase, alpha subunit (TSA1), identical to gi:619753   chr3:20234137-20236501 REVERSE   Aliases: TRP3, TRYPTOPHAN SYNTHASE ALPHA CHAIN	8.9	9.6	-0.6	-0.9	100.0%	-4.4
7799	AT3G54080.1   expressed protein   chr3:20036245-20038000 FORWARD   Aliases: F24B22.40	6.1	6.4	-0.3	-0.9	100.0%	-4.5
7800	AT5G58450.1   expressed protein, predicted proteins from D.melanogaster, C.elegans and S.pombe	6.9	7.6	-0.6	-0.9	100.0%	-4.1
7801	AT5G54870.1   expressed protein, strong similarity to unknown protein (pir::T04825)   chr5:22306361-22309025 FORWARD   Aliases: MBG8.14, MBG8_14	9.4	9.0	0.4	0.9	100.0%	-4.7
7802	AT5G19370.1   rhodanese-like domain-containing protein / PPIC-type PPIASE domain-containing protein, low similarity to MPT-synthase sulfurylase (Synechococcus sp. PCC 7942) GI:2950364; contains Pfam profiles PF00581: Rhodanese-like domain, PF00639: PPIC-type PPIASE domain; identical to cDNA peptidyl-prolyl cis-trans isomerase GI:2246379   chr5:6524148-6526668 REVERSE   Aliases: F7K24.120, F7K24_120	10.4	10.7	-0.2	-0.9	100.0%	-4.6
7803	AT3G10850.1   Symbol: GLX2 2	9.0	8.4	0.7	0.9	100.0%	-4.4
7804	AT5G06000.1   Symbol: EIF3G2	6.5	6.2	0.4	0.9	100.0%	-4.0
7805	AT3G15000.1   expressed protein, similar to DAG protein (required for chloroplast differentiation and palisade development) GB:Q38732 (Antirrhinum majus)   chr3:5050271-5052439 FORWARD   Aliases: K15M2.14	7.3	7.6	-0.4	-0.9	100.0%	-4.1
7806	AT4G09850.1   expressed protein, ; expression supported by MPSS   chr4:6192509-6193127 FORWARD   Aliases: F17A8.200, F17A8_200	2.6	2.4	0.2	0.9	100.0%	-5.2
7807	AT3G28790.1   expressed protein   chr3:10814571-10816936 REVERSE   Aliases: T19N8.9	3.1	3.0	0.1	0.9	100.0%	-5.0
7808	AT4G29360.2   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr4:14451419-14453733 REVERSE   Aliases: F17A13.180, F17A13_180	3.1	3.2	-0.1	-0.9	100.0%	-4.9
7809	AT1G14980.1   Symbol: CPN10   10 kDa chaperonin (CPN10), identical to SP:P34893 from (Arabidopsis thaliana)   chr1:5165623-5166740 REVERSE   Aliases: CHAPERONIN 10, MITOCHONDRIAL CHAPERONIN 10, T15D22.2, T15D22_2	9.9	10.3	-0.4	-0.9	100.0%	-4.3
7810	AT5G18900.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Rattus norvegicus (GI:474940), Mus musculus (SP:Q60715), Homo sapiens (GI:18073925); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr5:6304217-6306287 REVERSE   Aliases: F17K4.150, F17K4_150	6.9	6.2	0.6	0.9	100.0%	-4.3
7811	AT1G50000.2   similar to COG1385: Uncharacterized protein conserved in bacteria [Rhodospirillum rubrum] (GB:ZP_00267954.1); contains InterPro domain Conserved hypothetical protein 46 (InterPro:IPR004382)   chr1:18518737-18520913 REVERSE   Aliases: F2J10.21, F2J10_21	5.2	4.9	0.3	0.9	100.0%	-4.5
7812	AT5G42110.1   expressed protein   chr5:16849284-16849454 REVERSE   Aliases: MJC20.22, MJC20_22	4.7	4.8	-0.2	-0.9	100.0%	-4.9
7813	AT3G50960.1   expressed protein   chr3:18948325-18951365 REVERSE   Aliases: F18B3.240	7.1	6.8	0.4	0.9	100.0%	-4.5
7814	AT2G35920.1   helicase domain-containing protein, similar to DEIH-box RNA/DNA helicase (Arabidopsis thaliana) GI:5881579; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr2:15082676-15087891 FORWARD   Aliases: F11F19.17, F11F19_17	4.4	4.1	0.3	0.9	100.0%	-4.5
7815	AT4G36280.1   ATP-binding region, ATPase-like domain-containing protein, low similarity to microrchidia (Mus musculus) GI:5410255; contains Pfam profile PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein   chr4:17165334-17169378 REVERSE   Aliases: F23E13.170, F23E13_170	3.0	3.2	-0.2	-0.9	100.0%	-4.9
7816	AT1G78430.1   tropomyosin-related, similar to Tropomyosin 1 (Baker's yeast)(SP:P17536) {Saccharomyces cerevisiae}; similar to enterophilin-2L (GI:12718845) (Cavia porcellus); similar to latent nuclear antigen (GI:5669894) (Human herpesvirus 8); similar to multiple ligand-binding protein 1 (GI:1403575) (Streptococcus sp.)   chr1:29514498-29515788 FORWARD   Aliases: F3F9.6, F3F9_6	6.0	6.4	-0.4	-0.9	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7817	AT1G32870.1   Symbol: ANAC013   no apical meristem (NAM) family protein, similar to NAC2 (GI:645671) (Arabidopsis thaliana); contains Pfam PF02365: No apical meristem (NAM) protein   chr1:11911701-11913927 FORWARD   Aliases: ANAC013, F9L11.7, F9L11_7	4.6	4.4	0.2	0.9	100.0%	-4.8
7818	AT1G23730.1   carbonic anhydrase, putative / carbonate dehydratase, putative, similar to SP:P27140 Carbonic anhydrase, chloroplast precursor (EC 4.2.1.1) (Carbonate dehydratase) {Arabidopsis thaliana}; contains Pfam profile PF00484: Carbonic anhydrase   chr1:8395546-8398497 FORWARD   Aliases: F5O8.28, F5O8_28	3.5	3.9	-0.3	-0.9	100.0%	-4.4
7819	NA	7.0	6.5	0.5	0.9	100.0%	-4.4
7820	AT2G39280.1   RabGAP/TBC domain-containing protein, contains Pfam profile PF00566: TBC domain   chr2:16408837-16413728 REVERSE   Aliases: T16B24.8, T16B24_8	2.7	2.5	0.1	0.9	100.0%	-5.1
7821	AT1G15940.1   expressed protein, similar To androgen-induced prostate proliferative shutoff associated protein (GI:4559410) (Homo sapiens)   chr1:5473584-5478246 FORWARD   Aliases: T24D18.4, T24D18_4	5.8	6.1	-0.3	-0.9	100.0%	-4.5
7822	AT2G37900.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr2:15871474-15873486 REVERSE   Aliases: T8P21.19, T8P21_19	3.5	3.6	-0.2	-0.9	100.0%	-4.8
7823	AT4G35600.1   Symbol: CONNEXIN 32   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:16896242-16898881 FORWARD   Aliases: F8D20.110, F8D20_110	4.6	5.0	-0.3	-0.9	100.0%	-4.4
7824	AT3G59770.2   Symbol: SAC9   similar to phosphoinositide phosphatase family protein [Arabidopsis thaliana] (TAIR:At1g17340.1); similar to P0458A05.20 [Oryza sativa (japonica cultivar-group)] (GB:NP_918862.1); contains InterPro domain Synaptojanin, N-terminal (InterPro:IPR002013); contains InterPro domain WW/Rsp5/WWP domain (InterPro:IPR001202)   chr3:22090010-22097126 REVERSE   Aliases: F24G16.40	3.9	4.3	-0.4	-0.9	100.0%	-4.4
7825	AT3G06340.2   similar to DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] (TAIR:At5g18750.1); similar to B1045D11.23 [Oryza sativa (japonica cultivar-group)] (GB:NP_918758.1); similar to DNAJ heat shock N-terminal domain-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD61387.1); contains InterPro domain Heat shock protein DnaJ (InterPro:IPR003095); contains InterPro domain Heat shock protein DnaJ, N-terminal (InterPro:IPR001623)   chr3:1920213-1923317 REVERSE   Aliases: F24P17.19, F24P17_19	3.8	4.1	-0.3	-0.9	100.0%	-4.3
7826	AT1G54270.1   Symbol: EIF4A 2   eukaryotic translation initiation factor 4A-2 / eIF-4A-2, similar to eukaryotic translation initiation factor 4A GI:19696 from (Nicotiana glauca)   chr1:20263359-20265933 FORWARD   Aliases: F20D21.9, F20D21_9	9.9	9.5	0.4	0.9	100.0%	-4.5
7827	AT3G42950.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to polygalacturonase precursor (Cucumis melo) GI:3320460; contains PF00295: Glycosyl hydrolases family 28   chr3:15026128-15029059 FORWARD   Aliases: F18P9.110	3.4	3.6	-0.2	-0.9	100.0%	-4.6
7828	AT2G18190.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr2:7921387-7922954 REVERSE   Aliases: F8D23.3, F8D23_3	3.7	3.4	0.2	0.9	100.0%	-4.6
7829	AT1G25330.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.3	-0.1	-0.9	100.0%	-5.6
7830	AT1G66630.1   seven in absentia (SINA) family protein, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr1:24858949-24860377 REVERSE   Aliases: T12I7.8, T12I7_8	1.9	2.0	-0.1	-0.9	100.0%	-5.6
7831	AT3G50050.1   aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease   chr3:18564967-18568191 REVERSE   Aliases: F3A4.130	3.6	3.8	-0.2	-0.9	100.0%	-4.7
7832	AT1G51410.1   similar to Eucalyptus gunnii alcohol dehydrogenase of unknown physiological function (GI:1143445), apple tree, PIR:T16995; NOT a cinnamyl-alcohol dehydrogenase   chr1:19063553-19065092 FORWARD   Aliases: F5D21.12, F5D21_12	3.5	3.6	-0.1	-0.9	100.0%	-5.0
7833	AT2G22950.1   calcium-transporting ATPase, plasma membrane-type, putative / Ca <sup>2+</sup> -ATPase, putative (ACA7), identical to SP:O64806 Potential calcium-transporting ATPase 7, plasma membrane-type (EC 3.6.3.8) (Ca <sup>2+</sup> )-ATPase isoform 7) {Arabidopsis thaliana}; strong similarity to SP:O81108 Calcium-transporting ATPase 2, plasma membrane-type (EC 3.6.3.8) (Ca <sup>2+</sup> )-ATPase isoform 2) {Arabidopsis thaliana} Belongs to plant 2B ATPase??s with an N-terminal autoinhibitor.   chr2:9773207-9776846 FORWARD   Aliases: T20K9.16, T20K9_16	3.3	3.1	0.2	0.9	100.0%	-4.9
7834	AT1G48480.1   Symbol: RKL1   leucine-rich repeat transmembrane protein kinase, putative, contains similarity to many predicted protein kinases   chr1:17922059-17924653 FORWARD   Aliases: T1N15.9, T1N15_9	2.8	2.9	-0.1	-0.9	100.0%	-4.9
7835	AT1G62450.1   Rho GDP-dissociation inhibitor family protein, similar to SP:P52565 Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) {Homo sapiens}; contains Pfam profile PF02115: RHO protein GDP dissociation inhibitor   chr1:23119623-23121035 REVERSE   Aliases: F24O1.20	2.7	2.6	0.1	0.9	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7836	AT4G36510.1   hypothetical protein   chr4:17228780-17229454 FORWARD   Aliases: AP22.52, AP22_52	4.3	4.1	0.2	0.9	100.0%	-4.8
7837	AT1G51310.1   tRNA methyl transferase family protein, contains Pfam PF03054: tRNA methyl transferase profile; similar to tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61). (Swiss-Prot:Q8ZPZ4) (Salmonella typhimurium)   chr1:19022647-19025175 REVERSE   Aliases: F11M15.16, F11M15_16	4.8	5.0	-0.3	-0.9	100.0%	-4.3
7838	AT3G20550.1   Symbol: DDL   forkhead-associated domain-containing protein / FHA domain-containing protein, weak similarity to SP:Q28147 Nuclear inhibitor of protein phosphatase-1 (NIPP-1) (Protein phosphatase 1, regulatory inhibitor subunit 8) {Bos taurus}; contains Pfam profile PF00498: FHA domain   chr3:7174470-7177943 REVERSE   Aliases: DAWDLE, K10D20.9	5.4	5.1	0.3	0.9	100.0%	-4.6
7839	AT5G03570.1   iron-responsive transporter-related, similar to iron-regulated transporter IREG1 (Mus musculus) GI:7264727   chr5:904488-906663 FORWARD   Aliases: F12E4.370, F12E4_370	3.8	3.3	0.5	0.9	100.0%	-3.9
7840	AT3G54620.1   Symbol: BZO2H4	5.3	4.7	0.5	0.9	100.0%	-4.1
7841	AT3G44800.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein   chr3:16354320-16357014 FORWARD   Aliases: T32N15.3	2.2	2.3	-0.1	-0.9	100.0%	-5.5
7842	AT4G01910.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.9	5.2	-0.3	-0.9	100.0%	-4.2
7843	AT4G08130.1   hypothetical protein   chr4:5093870-5095313 FORWARD   Aliases: F9M13.12, F9M13_12	2.1	2.2	-0.1	-0.9	100.0%	-5.5
7844	AT5G25150.1   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At4g02730.1); similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g49660.1); similar to putative TATA box binding protein-associated factor [Oryza sativa (japonica cultivar-group)] (GB:XP_477065.1); contains InterPro domain WD40 associated region in TFIID subunit (InterPro:IPR007582); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr5:8677094-8682208 FORWARD   Aliases: F21J6.5	5.4	5.6	-0.3	-0.9	100.0%	-4.4
7845	AT4G26630.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g55660.1); similar to putative BRI1-KD interacting protein 112 [Oryza sativa (japonica cultivar-group)] (GB:BAD88036.1); contains domain GLU_RICH (PS50313)	7.6	7.2	0.3	0.9	100.0%	-4.3
7846	AT4G28720.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenases YUCCA (gi:16555352), YUCCA2 (gi:16555354), and YUCCA3 (gi:16555356) from Arabidopsis thaliana   chr4:14192589-14194262 FORWARD   Aliases: F16A16.170, F16A16_170	5.0	4.7	0.3	0.9	100.0%	-4.6
7847	AT1G76470.1   cinnamoyl-CoA reductase family, similar to cinnamoyl-CoA reductase GB:CAA56103 (Eucalyptus gunnii), Pinus taeda (GI:17978649); contains non-consensus GG acceptor splice site at exon 4   chr1:28694849-28696328 REVERSE   Aliases: F14G6.7, F14G6_7	3.2	3.4	-0.2	-0.9	100.0%	-4.7
7848	AT3G05590.1   Symbol: RPL18   60S ribosomal protein L18 (RPL18B), similar to GB:P42791   chr3:1621486-1623020 FORWARD   Aliases: CYTOPLASMIC RIBOSOMAL PROTEIN L18, F18C1.14, F18C1_14, RIBOSOMAL PROTEIN L18	11.1	11.3	-0.2	-0.9	100.0%	-4.6
7849	AT1G73650.3   expressed protein   chr1:27691784-27693968 REVERSE   Aliases: F25P22.7, F25P22_7	7.4	6.7	0.7	0.9	100.0%	-4.3
7850	AT1G64010.1   serpin, putative / serine protease inhibitor, putative, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr1:23754547-23755104 REVERSE   Aliases: F22C12.29, F22C12_29	2.9	3.0	-0.2	-0.9	100.0%	-5.0
7851	AT1G67530.1   armadillo/beta-catenin repeat family protein / U-box domain-containing family protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:25311321-25314971 FORWARD   Aliases: F12B7.8, F12B7_8	6.1	6.4	-0.2	-0.9	100.0%	-4.4
7852	AT3G47980.1   integral membrane HPP family protein, contains Pfam domain, PF04982: HPP family   chr3:17721462-17723786 FORWARD   Aliases: T17F15.150	4.0	3.8	0.2	0.9	100.0%	-4.8
7853	AT5G55170.1   Symbol: SUM3   small ubiquitin-like modifier 3 (SUMO), similar to SP:O13351 Ubiquitin-like protein smt3/pmt3 {Schizosaccharomyces pombe}; identical to cDNA small ubiquitin-like modifier 3 (SUMO) GI:22652845   chr5:22402694-22403297 REVERSE   Aliases: MCO15.12, MCO15_12, SMALL UBIQUITIN LIKE MODIFIER 3, SUMO 3, SUMO3	4.6	4.2	0.4	0.9	100.0%	-4.1
7854	AT5G20160.2   ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein, Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.   chr5:6803838-6805197 REVERSE   Aliases: F5O24.50, F5O24_50	9.0	9.5	-0.5	-0.9	100.0%	-4.3
7855	AT4G30080.1   Symbol: ARF16   transcriptional factor B3 family protein, contains Pfam profile: PF02362 B3 DNA binding domain   chr4:14703233-14706342 REVERSE   Aliases: ARF16, AUXIN RESPONSE FACTOR 16, F6G3.110, F6G3_110	4.6	4.3	0.3	0.9	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7856	AT3G52710.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:19545563-19546996 FORWARD   Aliases: F3C22.110	2.7	2.5	0.2	0.9	100.0%	-4.8
7857	AT4G07430.1   expressed protein, similar to At2g10840, At5g35280, At2g10500, At2g05860, At4g07310, At1g39270   chr4:4222504-4223524 REVERSE   Aliases: F28D6.17, F28D6_17	2.0	2.1	-0.1	-0.9	100.0%	-5.4
7858	AT4G00840.1   similar to zinc finger (DHHC type) family protein [Arabidopsis thaliana] (TAIR:At3g60800.1); similar to Zdhhc2-prov protein [Xenopus laevis] (GB:AAH78093.1); contains InterPro domain Zn-finger, DHHC type (InterPro:IPR001594)	4.0	3.7	0.3	0.9	100.0%	-4.2
7859	AT4G31985.1   60S ribosomal protein L39 (RPL39C)   chr4:15469901-15470565 FORWARD   Aliases: None	10.6	11.0	-0.4	-0.9	100.0%	-5.0
7860	AT5G02160.1   expressed protein   chr5:426352-427252 FORWARD   Aliases: T7H20.210, T7H20_210	3.5	3.3	0.2	0.9	100.0%	-4.6
7861	AT4G31020.2   expressed protein   chr4:15108107-15110153 REVERSE   Aliases: F6I18.70, F6I18_70	2.8	2.7	0.1	0.9	100.0%	-5.1
7862	AT5G53890.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:21894087-21897687 FORWARD   Aliases: K19P17.5, K19P17_5	5.2	5.5	-0.3	-0.9	100.0%	-4.4
7863	AT3G06830.1   pectinesterase family protein, contains Pfam profiles: PF01095 pectinesterase, PF04043 plant invertase/pectin methylesterase inhibitor   chr3:2153870-2156154 FORWARD   Aliases: F3E22.3	2.9	3.1	-0.2	-0.9	100.0%	-5.0
7864	AT5G23810.2   Symbol: AAP7   similar to amino acid carrier, putative / amino acid permease, putative [Arabidopsis thaliana] (TAIR:At1g77380.1); similar to putative amino acid transport protein AAP2 [Oryza sativa (japonica cultivar-group)] (GB:AAL87189.1); contains InterPro domain Amino acid/polyamine transporter, family II (InterPro:IPR002422)   chr5:8028381-8030166 FORWARD   Aliases: MRO11.15, MRO11_15	4.3	4.0	0.3	0.9	100.0%	-4.3
7865	AT2G39220.1   patatin family protein, similar to patatin-like latex allergen (Hevea brasiliensis)(PMID:10589016); contains patatin domain PF01734   chr2:16381974-16384098 REVERSE   Aliases: T16B24.14, T16B24_14	7.3	7.7	-0.4	-0.9	100.0%	-4.0
7866	AT1G55930.1   CBS domain-containing protein / transporter associated domain-containing protein, contains Pfam profiles PF00571: CBS domain, PF03471: Transporter associated domain, PF01595: Domain of unknown function   chr1:20922385-20925891 FORWARD   Aliases: F14J16.20, F14J16_20	6.4	7.0	-0.6	-0.9	100.0%	-4.4
7867	AT3G06110.2   dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain   chr3:1843487-1844782 FORWARD   Aliases: F28L1.5, F28L1_5	6.8	6.6	0.2	0.9	100.0%	-4.7
7868	AT3G29575.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g13740.1); similar to ABRC5 [Helianthus annuus] (GB:AAR06258.1)   chr3:11384710-11386443 REVERSE   Aliases: MWE13.5	6.7	7.0	-0.3	-0.9	100.0%	-4.5
7869	AT3G15400.1   Symbol: ATA20   anther development protein, putative, similar to anther development protein ATA20 GB:AAC50042 GI:2708813 from (Arabidopsis thaliana)   chr3:5201651-5203204 FORWARD   Aliases: ATA20, MJK13.6	3.3	3.1	0.2	0.9	100.0%	-5.1
7870	AT1G15060.1   expressed protein   chr1:5183623-5186936 REVERSE   Aliases: F9L1.1	3.7	3.5	0.2	0.9	100.0%	-4.8
7871	AT1G66200.2   Symbol: ATGSR2	9.3	8.7	0.6	0.9	100.0%	-4.1
7872	AT2G18876.2   expressed protein   chr2:8176630-8179605 FORWARD   Aliases: None	4.2	4.7	-0.6	-0.9	100.0%	-3.8
7873	AT1G23910.1   hypothetical protein   chr1:8451057-8451278 REVERSE   Aliases: T23E23.8, T23E23_8	2.8	2.9	-0.1	-0.9	100.0%	-5.3
7874	AT2G27590.1   expressed protein   chr2:11784714-11786928 REVERSE   Aliases: F10A12.26, F10A12_26	4.8	5.0	-0.2	-0.9	100.0%	-4.6
7875	AT1G47485.1   expressed protein   chr1:17424888-17425506 FORWARD   Aliases: None	2.6	2.5	0.1	0.9	100.0%	-5.5
7876	AT2G17590.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.2	2.4	-0.2	-0.9	100.0%	-4.8
7877	AT2G33680.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:14256684-14258867 FORWARD   Aliases: T1B8.1, T1B8_1	3.6	3.8	-0.2	-0.9	100.0%	-4.7
7878	AT1G64800.1   expressed protein, ; expression supported by MPSS   chr1:24088749-24089096 FORWARD   Aliases: F13O11.33, F13O11_33	3.1	3.3	-0.2	-0.9	100.0%	-4.7
7879	AT1G50510.1   indigoidine synthase A family protein, similar to IndA protein (GI:7576263) (Erwinia chrysanthemi); contains Pfam profile PF04227: Indigoidine synthase A like protein   chr1:18719796-18722996 FORWARD   Aliases: F11F12.14	8.2	7.6	0.5	0.9	100.0%	-4.2
7880	AT1G47655.1   Dof-type zinc finger domain-containing protein   chr1:17527805-17528746 FORWARD   Aliases: None	3.8	4.0	-0.3	-0.9	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7881	AT1G64550.1   Symbol: ATGCN3	5.8	6.5	-0.8	-0.9	100.0%	-4.2
7882	AT4G32890.1   zinc finger (GATA type) family protein, GATA transcription factor 3, Arabidopsis thaliana, gb:Y13650   chr4:15875474-15876766 FORWARD   Aliases: F26P21.10, F26P21_10	2.8	2.6	0.1	0.9	100.0%	-5.2
7883	AT1G48310.1   SNF2 domain-containing protein / helicase domain-containing protein, contains similarity to DNA-dependent ATPase A Gl:6651385 from (Bos taurus)); contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2   chr1:17851314-17857475 REVERSE   Aliases: F11A17.14, F11A17_14	4.5	4.7	-0.2	-0.9	100.0%	-4.5
7884	AT1G33980.1   Smg-4/UPF3 family protein, contains Pfam PF03467: Smg-4/UPF3 family; similar to hUPF3B (Gl:12232324) (Homo sapiens)   chr1:12351573-12355003 FORWARD   Aliases: F12G12.20, F12G12_20	4.7	4.3	0.4	0.9	100.0%	-4.1
7885	AT5G09240.3   transcriptional coactivator p15 (PC4) family protein, similar to SP:P11031 Activated RNA polymerase II transcriptional coactivator p15 precursor (PC4) (p14) (Single-stranded DNA binding protein p9) {Mus musculus}; contains Pfam profile PF02229: Transcriptional Coactivator p15 (PC4)   chr5:2873589-2874785 REVERSE   Aliases: T2K12.3	5.3	5.0	0.3	0.9	100.0%	-4.2
7886	AT1G33520.1   KOW domain-containing protein / D111/G-patch domain-containing protein, contains Pfam profiles PF01585: G-patch domain, PF00467: KOW motif   chr1:12157136-12158933 REVERSE   Aliases: F10C21.16, F10C21_16	7.3	7.0	0.4	0.9	100.0%	-4.5
7887	AT5G51640.1   Symbol: YLS7   leaf senescence protein-related (YLS7 ), annotation temporarily based on supporting cDNA gi:13122291:dbj:AB047810.1.; identical to cDNA YLS7 leaf-senescence-related protein Gl:13122291	6.8	6.5	0.3	0.9	100.0%	-4.3
7888	AT3G13840.1   scarecrow transcription factor family protein   chr3:4555312-4556844 REVERSE   Aliases: MCP4.6	2.9	2.7	0.2	0.9	100.0%	-4.7
7889	AT2G44500.2   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'axi 1 protein from Nicotiana tabacum -related' based on similarity to axi 1 protein (GB:X80301) (Gl:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	3.5	2.8	0.7	0.9	100.0%	-4.1
7890	AT5G03200.1   zinc finger (C3HC4-type RING finger) family protein, contains weak similarity to zinc finger proteins   chr5:760320-761802 REVERSE   Aliases: F15A17.230, F15A17_230	6.3	6.1	0.2	0.9	100.0%	-5.0
7891	AT4G32610.1   mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SP:P40513 Mitochondrial acidic protein MAM33, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF02330: Mitochondrial glycoprotein   chr4:15726279-15730362 REVERSE   Aliases: F4D11.190, F4D11_190	6.6	7.1	-0.5	-0.9	100.0%	-4.1
7892	AT1G10150.1   Symbol: ATPP2 A10   expressed protein, similar to ESTs gb:T20511, gb:T45308, gb:H36493, and gb:AA651176	7.6	7.4	0.2	0.9	100.0%	-4.7
7893	AT1G74660.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, contains Pfam PF04770: ZF-HD protein dimerisation region; contains TIGRFAM TIGR01566: ZF-HD homeobox protein Cys/His-rich dimerization domain; similar to ZF-HD homeobox protein (Gl:13374061) (Flaveria bidentis)   chr1:28051237-28051788 REVERSE   Aliases: F1M20.34, F1M20_34	5.3	4.9	0.5	0.9	100.0%	-4.4
7894	AT3G27190.1   uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative, similar to SP:O65583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Arabidopsis thaliana}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family   chr3:10040535-10044254 REVERSE   Aliases: K17E12.1	5.9	5.6	0.3	0.9	100.0%	-4.3
7895	AT3G45640.1   Symbol: ATMPK3	5.8	5.3	0.5	0.9	100.0%	-4.5
7896	AT1G08050.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to SP:P79263 Inter-alpha-trypsin inhibitor heavy chain H4 precursor {Sus scrofa}; contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF00092: von Willebrand factor type A domain   chr1:2498833-2501388 REVERSE   Aliases: T6D22.13, T6D22_13	5.5	5.1	0.4	0.9	100.0%	-4.6
7897	AT5G19570.1   expressed protein   chr5:6606702-6607205 FORWARD   Aliases: T20D1.90, T20D1_90	7.8	7.5	0.3	0.9	100.0%	-4.4
7898	AT2G14540.1   serpin family protein / serine protease inhibitor family protein, similar to phloem serpin-1 (Cucurbita maxima) Gl:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr2:6204745-6206488 REVERSE   Aliases: T13P21.8, T13P21_8	2.3	2.4	-0.1	-0.9	100.0%	-5.1
7899	AT5G49360.1   Symbol: BXL1   glycosyl hydrolase family 3 protein   chr5:20029105-20033968 REVERSE   Aliases: ATBXL1, BETA XYLOSIDASE 1, K7J8.3, K7J8_3	3.6	3.5	0.2	0.9	100.0%	-4.7
7900	AT3G09970.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 Calcineurin-like phosphoesterase	10.7	10.5	0.2	0.9	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7901	AT2G17990.1   expressed protein   chr2:7834004-7835836 FORWARD   Aliases: T27K22.14, T27K22_14	8.7	8.5	0.3	0.9	100.0%	-4.6
7902	AT1G32230.2   Symbol: RCD1   WWE domain-containing protein / ceo protein, putative (CEO), contains Pfam domain, PF02825: WWE domain; identical to cDNA for ceo protein (ceo gene) GI:11044956	7.2	6.8	0.4	0.9	100.0%	-4.3
7903	AT4G38840.1   auxin-responsive protein, putative, auxin-inducible SAUR gene, Raphanus sativus,AB000708	2.9	2.8	0.2	0.9	100.0%	-4.8
7904	AT5G45390.1   Symbol: CLPP4   ATP-dependent Clp protease proteolytic subunit (ClpP4), identical to nClpP4 GI:5360593 from (Arabidopsis thaliana)   chr5:18413530-18415343 FORWARD   Aliases: MFC19.6, MFC19_6, NCLPP3, NCLPP4	6.2	6.7	-0.5	-0.9	100.0%	-4.2
7905	AT1G54860.1   expressed protein   chr1:20461088-20462232 REVERSE   Aliases: F14C21.37, F14C21_37	3.4	3.2	0.1	0.9	100.0%	-5.2
7906	AT5G51940.1   DNA-directed RNA polymerase II, putative, similar to SP:O88828 DNA-directed RNA polymerase II 14.4 kDa polypeptide (EC 2.7.7.6) (RPB6) (RPB14.4) {Rattus norvegicus}; contains Pfam profile PF01192: RNA polymerases K / 14 to 18 kDa subunit   chr5:21121813-21123157 FORWARD   Aliases: MSG15.2, MSG15_2	10.8	10.9	-0.1	-0.9	100.0%	-5.2
7907	AT2G03170.1   Symbol: ASK14   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At14), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1b GI:3068809, UIP2 GI:3719211 from (Arabidopsis thaliana)   chr2:961319-961768 FORWARD   Aliases: ARABIDOPSIS SKP1 LIKE 14, ASK14, T18E12.16, T18E12_16	2.6	2.9	-0.2	-0.9	100.0%	-4.9
7908	AT5G05820.1   phosphate translocator-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, glucose-6-phosphate/phosphate-translocator precursor (Zea mays) GI:2997589; contains Pfam profile PF00892: Integral membrane protein   chr5:1751689-1754179 REVERSE   Aliases: MJJ3.24, MJJ3_24	5.4	5.7	-0.3	-0.9	100.0%	-4.4
7909	AT3G57280.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)   chr3:21204820-21206695 FORWARD   Aliases: F28O9.130	10.1	9.8	0.2	0.9	100.0%	-4.6
7910	AT5G65730.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endo-xyloglucan transferase GI:2244732 from (Gossypium hirsutum)   chr5:26316263-26317704 FORWARD   Aliases: MPA24.8, MPA24_8	2.4	2.5	-0.1	-0.9	100.0%	-5.4
7911	AT5G67380.2   Symbol: CKA1   similar to casein kinase II alpha chain 2 [Arabidopsis thaliana] (TAIR:At3g50000.1); similar to casein kinase 2 catalytic subunit [Nicotiana tabacum] (GB:BAC02726.1); similar to casein kinase 2 catalytic subunit [Nicotiana tabacum] (GB:BAC02727.1); similar to protein kinase CK2 alpha chain [Nicotiana tabacum] (GB:CAD27342.1); similar to protein kinase CK2 alpha chain [Nicotiana tabacum] (GB:CAD27341.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:26898192-26900634 REVERSE   Aliases: ATCKA1, ATPK12D, K8K14.10, K8K14_10	9.5	9.8	-0.3	-0.9	100.0%	-4.6
7912	AT5G15350.1   plastocyanin-like domain-containing protein, contains plastocyanin-like domain Pfam:PF02298   chr5:4984962-4986221 REVERSE   Aliases: F8M21.240, F8M21_240	8.8	8.2	0.6	0.9	100.0%	-4.3
7913	AT3G49080.1   ribosomal protein S9 family protein, contains Pfam profile PF00380: ribosomal protein S9	6.7	6.9	-0.3	-0.9	100.0%	-4.5
7914	AT2G17050.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr2:7417917-7422692 REVERSE   Aliases: F6P23.20, F6P23_20	2.4	2.6	-0.2	-0.9	100.0%	-4.7
7915	AT5G59670.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:24058720-24062878 FORWARD   Aliases: MTH12.12, MTH12_12	2.8	3.0	-0.1	-0.9	100.0%	-5.2
7916	AT3G43210.1   Symbol: TES   kinesin motor family protein (NACK2), contains Pfam profile: PF00225 kinesin motor domain	5.1	5.3	-0.2	-0.9	100.0%	-4.7
7917	AT3G26730.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:9824924-9828675 FORWARD   Aliases: MLJ15.12	5.6	5.4	0.2	0.9	100.0%	-4.9
7918	AT3G17450.1   hAT dimerisation domain-containing protein, contains Pfam profile PF04937: Protein of unknown function (DUF 659)	6.1	6.4	-0.3	-0.9	100.0%	-4.5
7919	AT3G50480.1   Symbol: HR4   broad-spectrum mildew resistance RPW8 family protein, contains Pfam PF05659: Arabidopsis broad-spectrum mildew resistance protein RPW8   chr3:18744143-18745369 FORWARD   Aliases: HOMOLOG OF RPW8 4, T20E23.80	4.3	4.6	-0.3	-0.9	100.0%	-4.6
7920	AT1G71310.3   expressed protein   chr1:26882239-26883673 REVERSE   Aliases: F3I17.4, F3I17_4	4.9	4.5	0.4	0.9	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7921	AT4G16480.1   sugar transporter family protein, similar to SP:Q96QE2 Proton myo-inositol co-transporter (Hmit) (Homo sapiens); contains Pfam profile PF00083: major facilitator superfamily protein   chr4:9291141-9293225 FORWARD   Aliases: DL4265W, FCAALL.375	6.2	6.5	-0.3	-0.9	100.0%	-4.6
7922	AT5G01920.1   Symbol: STN8   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:359127-362901 FORWARD   Aliases: T20L15.190, T20L15_190	7.9	7.7	0.2	0.9	100.0%	-4.5
7923	AT4G34720.1   vacuolar ATP synthase 16 kDa proteolipid subunit 1 / V-ATPase 16 kDa proteolipid subunit 1 (AVAP1) (AVA-P1), identical to SP:P59227 Vacuolar ATP synthase 16 kDa proteolipid subunit 1/3/5 (EC 3.6.3.14) (V-ATPase 16 kDa proteolipid subunit 1/3/5) {Arabidopsis thaliana}; contains Pfam profile PF00137: ATP synthase subunit C   chr4:16567829-16569300 REVERSE   Aliases: T4L20.300	9.8	9.5	0.4	0.9	100.0%	-4.8
7924	AT1G19090.1   Symbol: RKF2   serine/threonine protein kinase (RKF2), nearly identical to receptor-like serine/threonine kinase GI:2465925 from (Arabidopsis thaliana); intron 3 was added to circumvent a frameshift. Either a sequencing error exists or this may be a pseudogene.	2.4	2.3	0.1	0.9	100.0%	-5.3
7925	AT2G02980.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:868358-870384 FORWARD   Aliases: T17M13.15, T17M13_15	2.8	2.9	-0.1	-0.9	100.0%	-5.2
7926	AT2G20210.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr2:8728518-8732208 REVERSE   Aliases: F11A3.24, F11A3_24	2.8	2.9	-0.1	-0.9	100.0%	-5.4
7927	AT1G21700.1   Symbol: CHB4   SWIRM domain-containing protein / DNA-binding family protein, contains similarity to SWI/SNF complex 170 KDa subunit (Homo sapiens) gi:1549241:gb:AAC50694; contains Pfam domain PF04433: SWIRM domain, PF00249: Myb-like DNA-binding domain   chr1:7619990-7624125 REVERSE   Aliases: ATSWI3D, F8K7.13, F8K7_13	6.9	7.5	-0.6	-0.9	100.0%	-4.3
7928	AT1G72630.1   expressed protein   chr1:27347932-27349238 FORWARD   Aliases: F28P22.18, F28P22_18	5.9	6.1	-0.2	-0.9	100.0%	-4.7
7929	AT4G15060.1   F-box protein-related, contains weak similarity to F-box domain Pfam:PF00646   chr4:8599031-8601757 FORWARD   Aliases: DL3575W, FCAALL.180	2.7	2.6	0.1	0.9	100.0%	-5.2
7930	AT2G04305.1   magnesium transporter CorA-like protein-related   chr2:1501405-1503782 REVERSE   Aliases: T23O15.7, T23O15_7	3.6	3.5	0.2	0.9	100.0%	-4.8
7931	AT3G16490.1   calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612   chr3:5603968-5605637 REVERSE   Aliases: MDC8.12	3.5	3.7	-0.2	-0.9	100.0%	-4.7
7932	AT1G76070.1   expressed protein   chr1:28551276-28552505 FORWARD   Aliases: T23E18.1, T23E18_1	3.2	2.9	0.2	0.9	100.0%	-4.4
7933	AT3G10840.1   hydrolase, alpha/beta fold family protein, low similarity to hydrolase (Terrabacter sp. DBF63) GI:14196240; contains Pfam profile: PF00561 alpha/beta hydrolase fold   chr3:3391070-3393295 REVERSE   Aliases: T7M13.8	5.6	6.0	-0.4	-0.9	100.0%	-4.0
7934	AT2G16620.1   protein kinase-related, contains similarity to protein kinases   chr2:7212473-7213000 REVERSE   Aliases: T24I21.3, T24I21_3	2.7	2.8	-0.1	-0.9	100.0%	-5.6
7935	AT1G31650.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr1:11326282-11330644 REVERSE   Aliases: F27M3.15, F27M3_15, KINASE PARTNER PROTEIN LIKE, KPP LIKE	2.5	2.6	-0.1	-0.9	100.0%	-5.0
7936	AT5G20650.1   Symbol: COPT5   copper transporter family protein, similar to SP:Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}; contains Pfam profile PF04145: Ctr copper transporter family   chr5:6985300-6986039 REVERSE   Aliases: T1M15.50, T1M15_50	7.4	7.9	-0.5	-0.9	100.0%	-4.2
7937	AT4G15500.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr4:8857093-8858520 REVERSE   Aliases: DL3790C, FCAALL.307	4.1	4.7	-0.6	-0.9	100.0%	-4.0
7938	AT1G45050.1   Symbol: ATUBC2 1   ubiquitin-conjugating enzyme 15 (UBC15), E2; identical to ubiquitin-conjugating enzyme 15 GI:2801442 from (Arabidopsis thaliana)   chr1:17033721-17035638 FORWARD   Aliases: F27F5.13, F27F5_13	6.2	6.7	-0.4	-0.9	100.0%	-4.3
7939	AT4G04980.1   hydroxyproline-rich glycoprotein family protein, Common family members: At4g18570, At3g25690, At5g61090 (Arabidopsis thaliana)   chr4:2544208-2546831 REVERSE   Aliases: C17L7.1	2.6	2.8	-0.2	-0.9	100.0%	-4.9
7940	AT2G16380.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; similar to phosphatidylinositol transfer-like protein III (GI:14486705) (Lotus japonicus)   chr2:7092880-7096239 FORWARD   Aliases: F16F14.12, F16F14_12	3.1	3.0	0.2	0.9	100.0%	-5.0
7941	AT1G78110.1   expressed protein   chr1:29396730-29398079 FORWARD   Aliases: T11I11.5, T11I11_5	7.4	6.8	0.7	0.9	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7942	AT1G54230.1   expressed protein   chr1:20254621-20255894 FORWARD   Aliases: F20D21.5, F20D21_5	2.5	2.4	0.1	0.9	100.0%	-5.2
7943	AT4G28570.1   alcohol oxidase-related, low similarity to long chain fatty alcohol oxidase from <i>Candida cloacae</i> (GI:6983581), <i>Candida tropicalis</i> (GI:6983594)   chr4:14119460-14122093 FORWARD   Aliases: T5F17.20, T5F17_20	7.4	7.8	-0.4	-0.9	100.0%	-4.6
7944	AT5G66180.3   similar to NOL1/NOP2/sun family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g06560.1); similar to phosphate/phosphoenolpyruvate translocator-like [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:BAD28956.1); contains InterPro domain Bacterial Sun/eukaryotic nucleolar Nop1/Nop2 (InterPro:IPR001678)   chr5:26466196-26468434 FORWARD   Aliases: K2A18.26, K2A18_26	7.1	6.7	0.4	0.9	100.0%	-4.2
7945	AT5G01010.1   expressed protein   chr5:1279-4993 REVERSE   Aliases: TOPELOMERE.1, TOPELOMERE_1	3.4	3.7	-0.3	-0.9	100.0%	-4.7
7946	AT1G17200.1   integral membrane family protein, Location of est 136A23T7 (gb:T45563); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr1:5878422-5879984 FORWARD   Aliases: F20D23.10, F20D23_10	2.4	2.6	-0.1	-0.9	100.0%	-5.0
7947	AT3G22220.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g15020.1); similar to transposase-like protein [ <i>Musa acuminata</i> ] (GB:AAR96007.1); contains InterPro domain BED finger (InterPro:IPR003656); contains InterPro domain HAT dimerisation (InterPro:IPR008906); contains InterPro domain Protein of unknown function DUF659 (InterPro:IPR007021)	4.9	5.4	-0.5	-0.9	100.0%	-4.6
7948	AT1G76870.1   expressed protein   chr1:28862144-28863301 FORWARD   Aliases: F7O12.4, F7O12_4	3.1	3.2	-0.1	-0.9	100.0%	-5.2
7949	AT1G05840.1   aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease   chr1:1762767-1766280 REVERSE   Aliases: T20M3.11, T20M3_11	7.7	7.4	0.2	0.9	100.0%	-4.5
7950	AT3G32900.1   Ulp1 protease family protein, similar to At1g32840, At4g04010, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210   chr3:13462616-13466130 FORWARD   Aliases: T7B9.14	2.4	2.2	0.2	0.9	100.0%	-5.1
7951	AT5G47630.1   acyl carrier family protein / ACP family protein, similar to acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) from { <i>Arabidopsis thaliana</i> } SP:P53665, { <i>Neurospora crassa</i> } SP:P11943; contains Pfam profile PF00550: Phosphopantetheine attachment site   chr5:19323373-19324629 FORWARD   Aliases: MNJ7.22, MNJ7_22	6.9	6.4	0.5	0.9	100.0%	-3.8
7952	AT1G52400.2   Symbol: BGL1   similar to glycosyl hydrolase family 1 protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g21370.1); similar to glycosyl hydrolase family 1 protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g09260.1); similar to glycosyl hydrolase family 1 protein / anther-specific protein ATA27 [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g75940.1); similar to beta-glucosidase [ <i>Brassica nigra</i> ] (GB:AAB38784.1); contains InterPro domain Glycoside hydrolase, family 1 (InterPro:IPR001360)   chr1:19518838-19521880 FORWARD   Aliases: BETA GLUCOSIDASE HOMOLOG 1, F19K6.15, F19K6_15	3.5	3.3	0.2	0.9	100.0%	-4.8
7953	AT5G39260.1   Symbol: ATEXPA21   expansin, putative (EXP21), similar to alpha-expansin GI:6573157 from ( <i>Regnellidium diphyllum</i> ); alpha-expansin gene family, PMID:11641069   chr5:15743606-15744686 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A21, ATEXP21, ATHEXP ALPHA 1.20, EXP21, K3K3.110, K3K3_110	3.0	3.1	-0.2	-0.9	100.0%	-4.7
7954	AT5G35600.1   histone deacetylase, putative (HDA7), similar to SP:O22446 Histone deacetylase (HD) { <i>Arabidopsis thaliana</i> }; contains Pfam profile PF00850: Histone deacetylase family   chr5:13787351-13788942 REVERSE   Aliases: K2K18.5, K2K18_5	3.6	3.4	0.2	0.9	100.0%	-4.7
7955	AT2G37550.2   Symbol: ASP1   similar to ARF GAP-like zinc finger-containing protein ZIGA2 (ZIGA2) [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g53710.1); similar to CG4237-PA [ <i>Drosophila melanogaster</i> ] (GB:NP_524040.2); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164)	6.1	5.8	0.3	0.9	100.0%	-4.6
7956	AT5G18230.1   transcription regulator NOT2/NOT3/NOT5 family protein, contains Pfam domain PF04153: NOT2 / NOT3 / NOT5 family   chr5:6021450-6027215 REVERSE   Aliases: MRG7.19, MRG7_19	5.0	5.3	-0.3	-0.9	100.0%	-4.6
7957	AT2G32850.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:13942263-13945054 REVERSE   Aliases: T21L14.21, T21L14_21	5.6	5.9	-0.3	-0.9	100.0%	-4.9
7958	AT5G01690.1   Symbol: ATCHX27   cation/hydrogen exchanger, putative (CHX27), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr5:257407-260342 FORWARD   Aliases: CHX27, F7A7.210, F7A7_210	3.0	2.7	0.2	0.9	100.0%	-4.7
7959	AT2G40830.3   Symbol: RHC1A   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:17049810-17051935 FORWARD   Aliases: RING H2 FINGER PROTEIN RHC1A, T20B5.3, T20B5_3	7.5	6.9	0.6	0.9	100.0%	-4.1
7960	AT4G15720.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:8949458-8951926 FORWARD   Aliases: DL3900W, FCAALL.369	3.4	3.8	-0.4	-0.9	100.0%	-4.4
7961	AT3G45590.1   Symbol: ATSEN1	7.6	7.9	-0.3	-0.9	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7962	AT1G76800.1   nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313   chr1:28834202-28835171 FORWARD   Aliases: F28O16.17, F28O16_17	5.9	5.6	0.3	0.9	100.0%	-4.7
7963	AT1G26860.1   expressed protein   chr1:9304969-9305787 REVERSE   Aliases: T2P11.5, T2P11_5	2.6	2.7	-0.1	-0.9	100.0%	-5.4
7964	AT1G71695.1   peroxidase 12 (PER12) (P12) (PRXR6), identical to SP:Q96520 Peroxidase 12 precursor (EC 1.11.1.7) (Atperox P12) (PRXR6) (ATP4a) {Arabidopsis thaliana}   chr1:26967967-26970350 FORWARD   Aliases: F14O23.6, F14O23_6	4.0	3.3	0.7	0.9	100.0%	-4.3
7965	AT3G52510.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr3:19480630-19481163 REVERSE   Aliases: F22O6.110	3.1	3.3	-0.1	-0.9	100.0%	-5.1
7966	AT5G48760.1   60S ribosomal protein L13A (RPL13aD)   chr5:19788364-19789948 REVERSE   Aliases: K24G6.9, K24G6_9	6.6	7.1	-0.4	-0.9	100.0%	-4.3
7967	AT5G61360.1   expressed protein   chr5:24688240-24689464 FORWARD   Aliases: MFB13.14, MFB13_14	3.4	3.2	0.2	0.9	100.0%	-4.7
7968	AT4G17230.1   scarecrow-like transcription factor 13 (SCL13)   chr4:9660996-9663782 REVERSE   Aliases: DL4650C, FCAALL.225	4.3	3.9	0.4	0.9	100.0%	-4.2
7969	AT4G22220.1   Symbol: ISU1   iron-sulfur cluster assembly complex protein, putative, similar to iron-sulfur cluster assembly complex ISCU1 (GI:11545705) (Homo sapiens); nifU protein homolog YPL135w (GI:15619823) (Saccharomyces cerevisiae) PIR2:S69049   chr4:11759173-11760943 REVERSE   Aliases: ATISU1, T10I14.50, T10I14_50	7.1	6.4	0.7	0.9	100.0%	-4.1
7970	AT3G01040.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr3:8964-12429 FORWARD   Aliases: T4P13.28, T4P13_28	4.7	4.5	0.2	0.9	100.0%	-4.5
7971	AT5G51930.1   glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:P52707); contains Pfam profile PF00732 GMC oxidoreductase   chr5:21118349-21120794 FORWARD   Aliases: MSG15.1, MSG15_1	2.2	2.1	0.1	0.9	100.0%	-5.4
7972	AT5G42310.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:16933011-16936156 FORWARD   Aliases: K5J14.11, K5J14_11	5.6	6.0	-0.4	-0.9	100.0%	-4.1
7973	AT2G43990.1   expressed protein   chr2:18219000-18220998 FORWARD   Aliases: F6E13.12	3.6	3.7	-0.1	-0.9	100.0%	-5.1
7974	AT2G38560.1   transcription factor S-II (TFIIS) domain-containing protein, similar to SP:P49373 Transcription elongation factor S-II (TFIIS) {Schizosaccharomyces pombe}; contains Pfam profile PF01096: Transcription factor S-II (TFIIS)   chr2:16141717-16143773 FORWARD   Aliases: T6A23.24, T6A23_24	7.5	7.0	0.5	0.9	100.0%	-4.3
7975	AT5G64816.2   expressed protein   chr5:25930226-25931229 FORWARD   Aliases: None	8.7	9.0	-0.3	-0.9	100.0%	-4.4
7976	AT1G67030.1   Symbol: ZFP6   zinc finger (C2H2 type) family protein (ZFP6), identical to zinc finger protein, ZFP6 gi:790683:gb:AAA87302; contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:25020206-25021175 FORWARD   Aliases: F1O19.8, F1O19_8, ZFP6, ZINC FINGER PROTEIN 6	5.7	5.9	-0.2	-0.9	100.0%	-4.6
7977	AT3G62880.2   similar to mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein [Arabidopsis thaliana] (TAIR:At2g28900.1); similar to B1146F03.20 [Oryza sativa (japonica cultivar-group)] (GB:NP_914110.1); contains InterPro domain Mitochondrial import inner membrane translocase, subunit Tim17/22 (InterPro:IPR003397)	8.7	8.3	0.4	0.9	100.0%	-4.2
7978	AT3G49140.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g24060.1); similar to PPR986-12 [Physcomitrella patens] (GB:BAD67155.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr3:18223047-18228833 REVERSE   Aliases: F2K15.2	5.2	5.6	-0.4	-0.9	100.0%	-4.5
7979	AT4G25600.1   ShTK domain-containing protein, similar to PBCV-1 prolyl 4-hydroxylase (Paramecium bursaria Chlorella virus 1) GI:1131429; contains Pfam profile PF01549: ShTK domain   chr4:13060668-13062604 FORWARD   Aliases: M7J2.30, M7J2_30	7.2	6.9	0.3	0.9	100.0%	-4.3
7980	AT5G45640.1   subtilase family protein, contains Pfam domain, PF00082: Subtilase family; contains Pfam domain, PF02225: protease associated (PA) domain   chr5:18524716-18528843 REVERSE   Aliases: MRA19.4, MRA19_4	2.6	2.8	-0.1	-0.9	100.0%	-5.0
7981	AT3G15730.1   Symbol: PLDALPHA1   phospholipase D alpha 1 / PLD alpha 1 (PLDALPHA1) (PLD1) / choline phosphatase 1, identical to SP:Q38882 Phospholipase D alpha 1 (EC 3.1.4.4) (AtPLDalpha1) (PLD alpha 1) (Choline phosphatase 1) (Phosphatidylcholine-hydrolyzing phospholipase D 1) (PLDalpha) (Arabidopsis thaliana)   chr3:5330344-5333752 FORWARD   Aliases: MSJ11.13, PHOSPHOLIPASE D, PHOSPHOLIPASE D ALPHA 1, PLD	9.0	9.7	-0.6	-0.9	100.0%	-4.5
7982	AT1G43320.1   hypothetical protein   chr1:16359202-16359558 FORWARD   Aliases: F1I21.16, F1I21_16	3.1	2.9	0.1	0.9	100.0%	-5.1
7983	AT5G17480.1   polcalcin, putative / calcium-binding pollen allergen, putative, similar to polcalcin Bra r 2/Bra n 2 (Calcium-binding pollen allergen Bra r 2/Bra n 2) SP:Q39406 from (Brassica napus)   chr5:5762691-5762942 FORWARD   Aliases: K3M16.50, K3M16_50	2.3	2.4	-0.1	-0.9	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
7984	AT3G59910.1   expressed protein   chr3:22141460-22144533 REVERSE   Aliases: F24G16.180	4.1	3.9	0.2	0.9	100.0%	-5.0
7985	AT3G45770.2   oxidoreductase, zinc-binding dehydrogenase family protein, similar to nuclear receptor binding factor-1 NRBF-1 - Rattus norvegicus, EMBL:AB015724; contains Pfam zinc-binding dehydrogenase domain PF00107   chr3:16816547-16818780 REVERSE   Aliases: F16L2.2	10.0	9.5	0.5	0.9	100.0%	-4.4
7986	AT1G36070.1   WD-40 repeat family protein, contains 2 WD-40 repeats (PF0400);similar to guanine nucleotide-binding protein beta subunit GPBA (SP:P36408) (Dictyostelium discoideum (Slime mold)); similar to katanin p80 (WD40-containing) subunit B 1 (GI:12655011) (Homo sapiens)   chr1:13468123-13471888 REVERSE   Aliases: F5J5.6, F5J5_6	3.1	2.9	0.2	0.9	100.0%	-4.6
7987	AT2G03550.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873; contains an esterase/lipase/thioesterase active site serine domain (prosite: PS50187)   chr2:1077033-1078080 FORWARD   Aliases: T4M8.1, T4M8_1	3.3	3.2	0.1	0.9	100.0%	-5.0
7988	AT5G51560.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:20962913-20966080 FORWARD   Aliases: K17N15.11, K17N15_11	2.9	3.1	-0.1	-0.9	100.0%	-5.1
7989	AT4G40050.1   expressed protein   chr4:18560854-18563832 REVERSE   Aliases: T5J17.220, T5J17_220	3.5	3.2	0.3	0.9	100.0%	-4.3
7990	AT3G17730.1   Symbol: ANAC057   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to GRAB1 protein GB:CAA09371 (Triticum sp.)   chr3:6064385-6065819 FORWARD   Aliases: ANAC057, MIG5.2	2.9	2.7	0.1	0.9	100.0%	-5.0
7991	AT1G50040.1   expressed protein   chr1:18545798-18547616 FORWARD   Aliases: F2J10.8, F2J10_8	4.5	4.3	0.2	0.9	100.0%	-4.5
7992	AT4G02720.1   expressed protein, temporary automated functional assignment   chr4:1204303-1205866 REVERSE   Aliases: T5J8.1	8.8	8.4	0.4	0.9	100.0%	-4.4
7993	AT1G06960.2   small nuclear ribonucleoprotein U2B, putative / spliceosomal protein, putative, non-consensus splice donor GC at exon 4; similar to spliceosomal protein (U2B) GI:169588 from (Solanum tuberosum)   chr1:2135850-2137731 FORWARD   Aliases: F10K1.32, F10K1_32	5.5	5.2	0.2	0.9	100.0%	-4.4
7994	AT3G54790.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr3:20291469-20296104 REVERSE   Aliases: T5N23.150	4.1	4.5	-0.4	-0.9	100.0%	-4.3
7995	AT1G43190.1   polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative, similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) from {Rattus norvegicus} SP:Q00438, {Homo sapiens} SP:P26599, (Homo sapiens) GI:35770; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:16277550-16281062 REVERSE   Aliases: F1I21.14, F1I21_14	4.9	5.3	-0.4	-0.9	100.0%	-4.4
7996	AT1G12680.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:4319884-4322943 REVERSE   Aliases: T12C24.32, T12C24_32	5.5	5.2	0.3	0.9	100.0%	-4.4
7997	AT5G50260.1   cysteine proteinase, putative, similar to cysteine endopeptidase precursor CysEP GI:2944446 from (Ricinus communis)   chr5:20472543-20474255 FORWARD   Aliases: K6A12.12, K6A12_12	2.8	2.6	0.2	0.9	100.0%	-4.8
7998	AT3G48600.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr3:18021106-18022361 REVERSE   Aliases: T8P19.110	4.7	4.4	0.3	0.9	100.0%	-4.3
7999	AT2G35450.1   expressed protein, similar to conserved hypothetical protein [Streptomyces coelicolor A3(2)] (GB:CAB55712.1); contains InterPro domain Amidohydrolase 2 (InterPro:IPR006992)   chr2:14910124-14912451 REVERSE   Aliases: AT2G35440, T32F12.17, T32F12_17	4.5	4.7	-0.2	-0.9	100.0%	-4.5
8000	AT3G28100.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575   chr3:10457372-10462202 FORWARD   Aliases: MMG15.28	2.4	2.3	0.1	0.9	100.0%	-5.3
8001	AT2G47230.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr2:19394090-19397302 FORWARD   Aliases: T8I13.7	3.3	3.4	-0.1	-0.9	100.0%	-4.9
8002	AT1G30200.2   F-box family protein, contains Pfam PF00646: F-box domain; similar to hypothetical protein GI:2832643 from (Arabidopsis thaliana)   chr1:10625013-10626998 FORWARD   Aliases: F12P21.1, F12P21_1	6.1	5.8	0.2	0.9	100.0%	-4.9
8003	AT3G28210.1   Symbol: PMZ   zinc finger (AN1-like) family protein, contains Pfam profile: PF01428 AN1-like zinc finger   chr3:10521758-10522769 FORWARD   Aliases: T19D11.2	3.7	3.4	0.3	0.9	100.0%	-4.4
8004	AT3G14640.1   Symbol: CYP72A10   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4919863-4921794 FORWARD   Aliases: MIE1.14	2.9	2.7	0.2	0.9	100.0%	-5.0
8005	ATCG01080.1   Symbol: NDHG   NADH dehydrogenase ND6   chrC:118377-118907 REVERSE   Aliases: NDHG	4.2	4.9	-0.7	-0.9	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8006	AT5G25940.1   early nodulin-related, contains weak similarity to Swiss-Prot:Q02921 early nodulin 93 (N-93) (Glycine max)   chr5:9053704-9055217 REVERSE   Aliases: T1N24.3, T1N24_3	9.6	10.0	-0.4	-0.9	100.0%	-4.2
8007	AT1G73940.1   expressed protein   chr1:27801974-27803248 REVERSE   Aliases: F2P9.19, F2P9_19	10.0	10.3	-0.4	-0.9	100.0%	-4.5
8008	AT5G22730.1   F-box family protein, contains F-box domain Pfam:PF00646	4.0	3.8	0.2	0.9	100.0%	-5.1
8009	AT2G23300.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:9921688-9924210 FORWARD   Aliases: T20D16.7, T20D16_7	3.2	3.6	-0.4	-0.9	100.0%	-4.1
8010	AT5G25630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:8947392-8949602 FORWARD   Aliases: T14C9.170, T14C9_170	8.2	7.9	0.3	0.9	100.0%	-4.3
8011	AT5G67560.1   Symbol: ATARLA1D   ADP-ribosylation factor, putative, identical to GP:15450888 ADP-ribosylation factor-like protein {Arabidopsis thaliana}   chr5:26967580-26969410 FORWARD   Aliases: ATARLA1D, K9I9.13, K9I9_13	7.0	6.7	0.3	0.9	100.0%	-4.6
8012	AT5G59610.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9UXR9 Chaperone protein dnaJ (Heat shock protein 40 Methanosarcina thermophila, SP:Q9QYI6 DnaJ homolog subfamily B member 9 Mus musculus; contains Pfam profile PF00226 DnaJ domain	4.9	4.6	0.3	0.9	100.0%	-4.5
8013	AT3G48890.1   Symbol: ATMP2   cytochrome b5 domain-containing protein, similar to SP:O00264 Membrane associated progesterone receptor component (mPR) {Homo sapiens}; contains Pfam profile PF00173: Heme/Steroid binding domain   chr3:18140586-18142558 FORWARD   Aliases: T21J18.160	7.7	7.2	0.5	0.9	100.0%	-4.5
8014	AT1G68940.1   armadillo/beta-catenin repeat protein-related / U-box domain-containing protein, ; contains Pfam profile PF04564: U-box domain   chr1:25925664-25929037 REVERSE   Aliases: T6L1.12, T6L1_12	3.8	4.2	-0.4	-0.9	100.0%	-3.9
8015	AT3G45880.1   expressed protein   chr3:16879974-16882529 REVERSE   Aliases: F16L2.90	3.0	2.9	0.2	0.9	100.0%	-5.0
8016	AT1G32630.1   expressed protein   chr1:11797344-11798537 FORWARD   Aliases: F6N18.3, F6N18_3	7.0	6.4	0.6	0.9	100.0%	-4.1
8017	AT2G31790.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:13525288-13527441 FORWARD   Aliases: F20M17.17, F20M17_17	6.3	6.0	0.3	0.9	100.0%	-4.5
8018	AT2G43800.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr2:18152798-18155974 FORWARD   Aliases: F18O19.9	6.1	6.5	-0.4	-0.9	100.0%	-4.1
8019	AT2G21580.2   similar to 40S ribosomal protein S25 (RPS25E) [Arabidopsis thaliana] (TAIR:At4g39200.1); similar to PREDICTED P0562A06.14 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_507607.1); contains InterPro domain S25 ribosomal protein (InterPro:IPR004977)   chr2:9243633-9244891 FORWARD   Aliases: F2G1.15, F2G1_15	10.6	11.1	-0.4	-0.9	100.0%	-4.2
8020	AT4G22800.1   hypothetical protein   chr4:11978016-11983082 REVERSE   Aliases: T12H17.190, T12H17_190	2.5	2.6	-0.1	-0.9	100.0%	-5.6
8021	AT1G26210.1   expressed protein, similar to hypothetical protein GI:6524175 from (Arabidopsis thaliana)   chr1:9067026-9068194 FORWARD   Aliases: F28B23.12, F28B23_12	3.1	3.0	0.2	0.9	100.0%	-5.1
8022	AT5G49210.2   expressed protein   chr5:19967069-19968910 FORWARD   Aliases: K21P3.8, K21P3_8	6.6	6.9	-0.3	-0.9	100.0%	-4.3
8023	AT5G48630.1   cyclin family protein, similar to SP:P55168 Cyclin C {Gallus gallus}; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr5:19738776-19740460 REVERSE   Aliases: K15N18.10, K15N18_10	6.3	6.7	-0.4	-0.9	100.0%	-4.4
8024	AT1G77930.2   DNAJ heat shock N-terminal domain-containing protein, similar to J-Domain (Residues 1-77) Of The Escherichia Coli N-Terminal Fragment (Residues 1-104) Of The Molecular Chaperone DnaJ GI:5542126; contains Pfam profile PF00226 DnaJ domain   chr1:29305906-29308464 FORWARD   Aliases: F28K19.14, F28K19_14	7.7	7.4	0.3	0.9	100.0%	-4.5
8025	AT5G16180.1   hypothetical protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578)   chr5:5279887-5282901 FORWARD   Aliases: T21H19.100, T21H19_100	4.4	4.7	-0.3	-0.9	100.0%	-4.6
8026	AT4G36660.1   expressed protein   chr4:17286711-17287285 REVERSE   Aliases: AP22.12, AP22_12	7.3	6.9	0.4	0.9	100.0%	-4.5
8027	AT4G34180.1   cyclase family protein, contains Pfam profile: PF04199 putative cyclase   chr4:16369361-16371434 REVERSE   Aliases: F10M10.6	8.9	8.3	0.6	0.9	100.0%	-4.2
8028	AT2G24370.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:10377059-10380143 REVERSE   Aliases: T28I24.10, T28I24_10	2.8	3.0	-0.2	-0.9	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8029	AT1G41900.1   myosin heavy chain-related, similar to Myosin heavy chain, skeletal muscle, extraocular (MyHC-eo) (SP:Q9UKX3) {Homo sapiens}   chr1:15673379-15675592 REVERSE   Aliases: F5A13.10, F5A13_10	3.0	2.8	0.2	0.9	100.0%	-4.8
8030	AT1G26360.1   hydrolase, alpha/beta fold family protein, similar to SP:Q40708 PIR7A protein {Oryza sativa}, ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile PF00561: alpha/beta hydrolase fold   chr1:9118935-9121204 REVERSE   Aliases: T1K7.26, T1K7_26	2.1	2.0	0.1	0.9	100.0%	-5.3
8031	AT1G06840.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase GB:BAA11869 GI:1389566 from (Arabidopsis thaliana)   chr1:2097746-2103478 REVERSE   Aliases: F4H5.8, F4H5_8	4.4	4.7	-0.3	-0.9	100.0%	-4.8
8032	AT5G04640.1   MADS-box family protein, SLM3 MADS-box protein, S.latifolia, EMBL:SLSLM3	2.7	2.6	0.1	0.9	100.0%	-5.5
8033	AT5G37210.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.8	3.6	0.2	0.9	100.0%	-4.6
8034	AT5G16260.1   RNA recognition motif (RRM)-containing protein, similar to Tat-SF1 - Homo sapiens, GI:1667611; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	6.9	7.4	-0.5	-0.9	100.0%	-4.2
8035	AT2G36290.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (Rhodococcus sp. RHA1) GI:8978311; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:15215706-15217918 REVERSE   Aliases: F2H17.10, F2H17_10	8.5	8.8	-0.4	-0.9	100.0%	-5.0
8036	AT5G28130.1   expressed protein   chr5:10114437-10114784 REVERSE   Aliases: T24G3.60, T24G3_60	2.9	3.0	-0.2	-0.9	100.0%	-4.9
8037	AT3G19420.1   expressed protein   chr3:6731463-6735629 FORWARD   Aliases: MLD14.22	7.2	6.9	0.3	0.9	100.0%	-4.5
8038	AT4G34150.1   C2 domain-containing protein, similar to calcium-dependent protein kinase (Dunaliella tertiolecta) GI:6644464; contains Pfam profile PF00168: C2 domain   chr4:16354978-16357297 FORWARD   Aliases: F28A23.90, F28A23_90	3.6	3.3	0.3	0.9	100.0%	-4.4
8039	AT1G59730.1   thioredoxin, putative, similar to SP:Q38879 Thioredoxin H-type 2 (TRX-H-2) {Arabidopsis thaliana}; contains Pfam profile: PF00085 Thioredoxin   chr1:21956299-21957121 REVERSE   Aliases: F23H11.5, F23H11_5	4.0	4.3	-0.3	-0.9	100.0%	-4.5
8040	AT1G01040.1   Symbol: DCL1   DEAD/DEAH box helicase carpel factory / CAF, identical to RNA helicase/RNaseIII CAF protein GB:AAF03534 GI:6102610 from (Arabidopsis thaliana)   chr1:23146-31164 FORWARD   Aliases: ABNORMAL SUSPENSOR 1, ASU1, CAF, CARPEL FACTORY, DICER LIKE1, EMB60, EMB76, EMBRYO DEFECTIVE 60, EMBRYO DEFECTIVE 76, SHORT INTEGUMENTS 1, SIN1, SUS1, SUSPENSOR 1, T25K16.4, T25K16_4	6.9	7.3	-0.4	-0.9	100.0%	-4.8
8041	AT1G78510.1   solanesyl diphosphate synthase (SPS), identical to solanesyl diphosphate synthase (Arabidopsis thaliana) GI:19911233; contains Pfam profile PF00348: Polyprenyl synthetase   chr1:29540178-29542310 REVERSE   Aliases: T30F21.15, T30F21_15	6.7	6.5	0.2	0.9	100.0%	-4.9
8042	AT5G02850.1   hydroxyproline-rich glycoprotein family protein   chr5:652108-653671 FORWARD   Aliases: F9G14.160, F9G14_160	3.7	4.0	-0.3	-0.9	100.0%	-4.8
8043	AT4G08180.3   oxysterol-binding family protein, similar to SP:Q969R2 Oxysterol-binding protein 2 {Homo sapiens}; contains Pfam profiles PF00169: PH domain, PF01237: Oxysterol-binding protein	4.1	3.6	0.5	0.9	100.0%	-4.3
8044	AT5G14320.1   30S ribosomal protein S13, chloroplast (CS13), ribosomal protein S13 precursor, chloroplast Arabidopsis thaliana, PIR:S59594; identical to cDNA ribosomal protein S13 GI:1515106	9.2	9.5	-0.4	-0.9	100.0%	-4.4
8045	AT3G32080.1   expressed protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	3.8	3.9	-0.2	-0.9	100.0%	-5.1
8046	AT3G08490.1   expressed protein   chr3:2574111-2575131 REVERSE   Aliases: T8G24.9	3.3	3.5	-0.3	-0.9	100.0%	-4.4
8047	NA	2.8	2.7	0.1	0.9	100.0%	-5.3
8048	AT3G17590.1   Symbol: BSH   transcription regulatory protein SNF5, putative (BSH), identical to SNF5 homolog BSH GI:1843628 from (Arabidopsis thaliana)   chr3:6017216-6019671 REVERSE   Aliases: MKP6.15	4.5	4.3	0.2	0.9	100.0%	-4.8
8049	AT3G19210.1   DNA repair protein RAD54, putative, similar to RAD54 GB:CAA71278 from (Drosophila melanogaster) (Mol. Cell. Biol.(1997) 17 (10), 6097-6104)   chr3:6652805-6658882 REVERSE   Aliases: MVI11.15	3.2	3.4	-0.1	-0.9	100.0%	-5.2
8050	AT1G08540.1   Symbol: SIGB   RNA polymerase sigma subunit SigB (sigB) / sigma factor 2 (SIG2), identical to sigma factor SigB (Arabidopsis thaliana) GI:5478446, plastid RNA polymerase sigma-subunit (Arabidopsis thaliana) GI:2879922, sigma factor (Arabidopsis thaliana) GI:2597831, sigma factor 2 (SIG2) (Arabidopsis thaliana) GI:2353173; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2   chr1:2703342-2706848 FORWARD   Aliases: PUTATIVE PLASTID RNA POLYMERASE SIGMA SUBUNIT, SIG1, SIG2, SIGA, SIGMA FACTOR B, T27G7.22	5.5	5.8	-0.3	-0.9	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8051	AT1G44318.1   porphobilinogen synthase, putative / delta-aminolevulinic acid dehydratase, putative, similar to delta-aminolevulinic acid dehydratase (Alad) GI:493019 (SP:P43210) from Glycine max, SP:P24493 from Spinacia oleracea, SP:P30124 from Pisum sativum   chr1:16833456-16836356 FORWARD   Aliases: T18F15.10, T18F15_10	2.6	2.5	0.1	0.9	100.0%	-5.2
8052	AT1G66510.3   AAR2 protein family, contains Pfam profile PF05282: AAR2 protein	2.8	2.7	0.1	0.9	100.0%	-5.1
8053	AT3G54860.1   Symbol: ATVPS33   vacuolar protein sorting protein, putative, similar to Swiss-Prot:Q63615 vacuolar protein sorting 33A (r-vps33a) (Rattus norvegicus); contains Pfam domain, PF00995: Sec1 family   chr3:20335068-20340828 REVERSE   Aliases: F28P10.160, VPS33	3.9	4.3	-0.4	-0.9	100.0%	-4.4
8054	AT5G58330.3   malate dehydrogenase (NADP), chloroplast, putative, strong similiarity to chloroplast NADP-dependent malate dehydrogenase (EC 1.1.1.82) SP:O48902 {Medicago sativa}, SP:P21528 {Pisum sativum}, SP:Q05145 {Mesembryanthemum crystallinum}, SP:P46489 {Flaveria bidentis}, (Flaveria trinervia) GI:726334, SP:P176061 {Sorghum bicolor}; contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr5:23596427-23599521 REVERSE   Aliases: MCK7.20, MCK7_20	7.8	8.4	-0.6	-0.9	100.0%	-4.0
8055	AT1G66080.1   expressed protein   chr1:24603881-24604820 REVERSE   Aliases: F15E12.12, F15E12_12	3.5	3.7	-0.2	-0.9	100.0%	-4.6
8056	AT1G15570.1   Symbol: CYCA2;3   cyclin, putative, similar to cyclin A2 (Lycopersicon esculentum) GI:5420276, cyclin (Medicago sativa) GI:1050559; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:5362015-5365544 FORWARD   Aliases: CYCA2;3, Cyclin A2;3, T16N11.8, T16N11_8	3.3	3.5	-0.2	-0.9	100.0%	-4.7
8057	AT1G75900.1   family II extracellular lipase 3 (EXL3), EXL3 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 (Arabidopsis thaliana)   chr1:28502723-28504799 FORWARD   Aliases: T4O12.13, T4O12_13	2.9	3.1	-0.2	-0.9	100.0%	-5.1
8058	AT4G14060.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr4:8107332-8108302 FORWARD   Aliases: DL3070W, FCAALL.193	5.5	6.0	-0.5	-0.9	100.0%	-3.9
8059	AT3G60100.1   citrate synthase, mitochondrial, putative, strong similarity to SP:Q43175 Citrate synthase, mitochondrial precursor {Solanum tuberosum}; contains Pfam profile PF00285: Citrate synthase	3.5	3.7	-0.2	-0.9	100.0%	-4.8
8060	AT1G71390.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-5B (Lycopersicon esculentum) gi:3894391:gb:AAC78595   chr1:26910115-26912469 FORWARD   Aliases: F3I17.31, F3I17_31	3.6	3.7	-0.1	-0.9	100.0%	-5.3
8061	AT4G25160.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr4:12903308-12907348 REVERSE   Aliases: F24A6.13	3.1	3.3	-0.2	-0.9	100.0%	-4.6
8062	AT5G13900.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:4481234-4481879 REVERSE   Aliases: MAC12.14, MAC12_14	2.5	2.9	-0.4	-0.9	100.0%	-4.0
8063	AT1G61640.2   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr1:22750066-22752849 REVERSE   Aliases: T25B24.1, T25B24_1	4.3	4.5	-0.3	-0.9	100.0%	-4.5
8064	AT1G19300.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 Glycosyl transferase family 8   chr1:6671128-6672644 REVERSE   Aliases: F18O14.2, F18O14_2	3.4	3.2	0.2	0.9	100.0%	-4.8
8065	AT4G00910.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.2	3.0	0.2	0.9	100.0%	-4.8
8066	AT3G08820.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:2677124-2679185 REVERSE   Aliases: T16O11.25	4.7	5.2	-0.5	-0.9	100.0%	-4.3
8067	AT1G06040.2   Symbol: STO   zinc finger (B-box type) family protein / salt-tolerance protein (STO), identical to SP:Q96288 Salt-tolerance protein (Arabidopsis thaliana); contains Pfam profile PF00643: B-box zinc finger   chr1:1828412-1829889 REVERSE   Aliases: SALT TOLERANCE, T21E18.9, T21E18_9	8.5	8.0	0.4	0.9	100.0%	-4.3
8068	AT3G22480.2   prefoldin-related KE2 family protein, similar to Swiss-Prot:Q9UHV9 prefoldin subunit 2 (Protein HSPC231) (Homo sapiens); contains Pfam domain, PF01920: KE2 family protein   chr3:7968184-7969636 FORWARD   Aliases: F16J14.4	8.6	8.1	0.5	0.9	100.0%	-4.3
8069	AT3G01540.4   Symbol: DRH1   similar to DEAD box RNA helicase, putative [Arabidopsis thaliana] (TAIR:At5g14610.1); similar to DEAD box RNA helicase, putative [Arabidopsis thaliana] (TAIR:At3g06480.1); similar to putative p68 RNA helicase [Oryza sativa (japonica cultivar-group)] (GB:XP_550286.1); similar to putative RNA helicase, DRH1 [Oryza sativa (japonica cultivar-group)] (GB:XP_462826.1); similar to putative RNA helicase, DRH1 [Oryza sativa (japonica cultivar-group)] (GB:NP_918275.1); similar to P72 DEAD box protein [Pisum sativum] (GB:AAF04377.1); similar to putative ATP-dependent RNA helicase DB10 [Oryza sativa (japonica cultivar-group)] (GB:BAD88050.1); contains InterPro domain WW/Rsp5/WWP domain (InterPro:IPR001202); contains InterPro domain ATP-dependent helicase, DEAD-box (InterPro:IPR000629); contains InterPro domain Helicase, C-terminal (InterPro:IPR001650); contains InterPro domain DEAD/DEAH box helicase (InterPro:IPR001410)   chr3:212525-216678 REVERSE   Aliases: ATDRH1, F4P13.9, F4P13_9, RNA HELICASE DRH1	9.4	9.1	0.3	0.9	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8070	AT5G60610.1   F-box family protein, contains F-box domain Pfam:PF00646	2.9	2.7	0.2	0.9	100.0%	-4.8
8071	AT1G64710.1   alcohol dehydrogenase, putative, similar to alcohol dehydrogenase Gl:551257 from (Nicotiana tabacum)   chr1:24048233-24050215 FORWARD   Aliases: F13O11.3, F13O11_3	3.2	3.1	0.2	0.9	100.0%	-4.8
8072	AT1G21080.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein (Saccharomyces cerevisiae); contains Pfam profile PF00226 DnaJ domain;   chr1:7378581-7382451 REVERSE   Aliases: T22I11.9, T22I11_9	8.2	7.6	0.6	0.9	100.0%	-4.6
8073	AT1G65690.1   harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, similar to hin1 homolog (Gl:13122296) (Arabidopsis thaliana); similar to hin1 (Gl:22830759) (Nicotiana tabacum); contains 1 transmembrane domain;   chr1:24435096-24436616 REVERSE   Aliases: F1E22.7, F1E22_7	3.3	3.4	-0.2	-0.9	100.0%	-4.7
8074	AT1G02070.1   expressed protein   chr1:370257-370967 REVERSE   Aliases: T7I23.30, T7I23_30	3.2	3.1	0.1	0.9	100.0%	-5.1
8075	AT4G08230.1   glycine-rich protein   chr4:5187853-5189637 REVERSE   Aliases: T12G13.70, T12G13_70	8.0	7.7	0.3	0.9	100.0%	-4.5
8076	AT1G47340.1   F-box family protein, contains F-box domain Pfam:PF00646	5.8	6.4	-0.6	-0.9	100.0%	-4.3
8077	AT5G11570.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:3715944-3718277 REVERSE   Aliases: F15N18.160, F15N18_160	2.8	2.5	0.2	0.9	100.0%	-4.6
8078	AT5G04460.1   expressed protein   chr5:1260010-1263846 FORWARD   Aliases: T19N18.3	4.0	3.7	0.3	0.9	100.0%	-4.3
8079	AT5G19120.1   expressed protein, low similarity to extracellular dermal glycoprotein EDGP precursor (Daucus carota) Gl:285741, SP:P13917 Basic 7S globulin precursor {Glycine max}   chr5:6414564-6415807 FORWARD   Aliases: T24G5.20, T24G5_20	6.3	6.7	-0.4	-0.9	100.0%	-4.3
8080	AT1G48210.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 (Lycopersicon esculentum) gi:3668069:gb:AAC61805; contains protein kinase domain, Pfam:PF00069   chr1:17802134-17805655 FORWARD   Aliases: F21D18.32	6.5	5.8	0.7	0.9	100.0%	-4.2
8081	AT4G29330.1   Der1-like family protein / degradation in the ER-like family protein, contains Pfam profile: PF04511 Der1-like family   chr4:14444828-14447121 FORWARD   Aliases: F17A13.150, F17A13_150	5.0	5.4	-0.4	-0.9	100.0%	-4.6
8082	AT1G07060.1   expressed protein   chr1:2167106-2168396 REVERSE   Aliases: F10K1.23, F10K1_23	3.4	3.6	-0.2	-0.9	100.0%	-4.8
8083	AT5G43930.3   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g04140.1); similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g04140.2); similar to transducin family protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD33212.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr5:17694050-17698309 FORWARD   Aliases: MRH10.2, MRH10_2	4.4	4.1	0.3	0.9	100.0%	-4.4
8084	AT3G62860.1   esterase/lipase/thioesterase family protein, similar to monoglyceride lipase from (Homo sapiens) Gl:14594904, (Mus musculus) Gl:2632162; contains Interpro entry IPR000379   chr3:23250421-23253226 REVERSE   Aliases: F26K9.290	4.7	5.0	-0.3	-0.9	100.0%	-4.3
8085	AT3G45910.1   expressed protein   chr3:16887323-16888060 REVERSE   Aliases: F16L2.120	2.1	2.3	-0.1	-0.9	100.0%	-5.1
8086	AT1G53910.2   Symbol: RAP2.12   similar to AP2 domain-containing protein RAP2.2 (RAP2.2) [Arabidopsis thaliana] (TAIR:At3g14230.2); similar to AP2 domain-containing protein RAP2.2 (RAP2.2) [Arabidopsis thaliana] (TAIR:At3g14230.3); similar to AP2 domain-containing protein RAP2.2 (RAP2.2) [Arabidopsis thaliana] (TAIR:At3g14230.1); similar to ethylene transcription factor [Fagus sylvatica] (GB:CAE54591.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr1:20138781-20140609 FORWARD   Aliases: RAP2.12, T18A20.14, T18A20_14	4.9	4.2	0.7	0.9	100.0%	-4.2
8087	AT3G30730.1   hypothetical protein   chr3:12359875-12360078 REVERSE   Aliases: T4A2.2	2.6	2.5	0.1	0.9	100.0%	-5.6
8088	AT2G03870.2   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to U6 snRNA-associated Sm-like protein LSm7 (Homo sapiens) SWISS-PROT:Q9UK45	11.6	11.4	0.2	0.9	100.0%	-5.4
8089	AT5G65220.1   ribosomal protein L29 family protein, contains Pfam profile PF00831: ribosomal protein L29   chr5:26078455-26079888 FORWARD   Aliases: MQN23.16, MQN23_16	6.5	6.8	-0.3	-0.9	100.0%	-4.3
8090	AT1G29195.1   expressed protein   chr1:10202522-10203382 REVERSE   Aliases: None	2.8	2.9	-0.1	-0.9	100.0%	-5.0
8091	AT4G14640.1   Symbol: CAM8   calmodulin-8 (CAM8), identical to calmodulin 8 Gl:5825600 from (Arabidopsis thaliana)   chr4:8397764-8400069 FORWARD   Aliases: CALMODULIN 8, DL3360W, FCAALL.157	2.5	2.5	-0.1	-0.9	100.0%	-5.6
8092	AT5G17570.1   tatD-related deoxyribonuclease family protein, contains Pfam profile PF01026: TatD related DNase	4.6	4.4	0.3	0.9	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8093	AT5G38530.1   tryptophan synthase-related, low similarity to tryptophan synthases, beta subunit, from <i>Lactococcus lactis</i> (SP:Q01998), <i>Pyrococcus kodakaraensis</i> (SP:Q9YGB0), <i>Thermus thermophilus</i> (SP:P16609); contains Pfam pyridoxal-phosphate dependent enzyme domain PF00291   chr5:15441269-15443700 FORWARD   Aliases: MBB18.6, MBB18_6	9.1	9.7	-0.5	-0.9	100.0%	-4.6
8094	AT2G42400.1   expressed protein   chr2:17661310-17663908 REVERSE   Aliases: MHK10.12, MHK10_12	3.2	3.0	0.2	0.9	100.0%	-4.7
8095	AT1G79720.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr1:30002020-30003938 REVERSE   Aliases: F19K16.30, F19K16_30	3.5	3.7	-0.2	-0.9	100.0%	-4.7
8096	AT3G08010.1   expressed protein   chr3:2555988-2557511 FORWARD   Aliases: F17A17.35	8.1	7.8	0.3	0.9	100.0%	-4.1
8097	AT5G41340.1   Symbol: UBC4   ubiquitin-conjugating enzyme 4 (UBC4), E2; identical to gi:431265, SP:P42748   chr5:16555351-16557358 REVERSE   Aliases: ATUBC4, MYC6.5, MYC6_5, UBIQUITIN CONJUGATING ENZYME 4	8.4	7.9	0.6	0.9	100.0%	-4.4
8098	AT4G02670.1   zinc finger (C2H2 type) family protein, similar to potato PCP1 zinc finger protein, GenBank accession number X82328 contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr4:1176190-1178489 REVERSE   Aliases: T10P11.4, T10P11_4	2.7	2.9	-0.3	-0.9	100.0%	-4.6
8099	AT5G33390.1   glycine-rich protein, similar to nuclear antigen EBNA-1 (GI:3342234) {Cercopithecine herpesvirus 15}   chr5:12679019-12680050 FORWARD   Aliases: None	5.6	5.3	0.3	0.9	100.0%	-4.3
8100	AT1G66720.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 ( <i>Brassica carinata</i> )(GI:14009292)(Mol Plant Pathol (2001) 2(3):159-169)   chr1:24884843-24886143 FORWARD   Aliases: F4N21.15, F4N21_15	3.2	3.4	-0.2	-0.9	100.0%	-4.8
8101	AT2G03160.1   Symbol: ASK19   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At19), putative, E3 ubiquitin ligase; similar to Skp1 GI:4959710 from ( <i>Medicago sativa</i> )   chr2:959642-960244 FORWARD   Aliases: ARABIDOPSIS SKP1 LIKE 19, ASK19, T18E12.17, T18E12_17	2.9	2.7	0.1	0.9	100.0%	-4.9
8102	AT1G14530.2   tobamovirus multiplication protein 3, putative / TOM3, putative (THH1), identical to THH1 (GI:15706301) ( <i>Arabidopsis thaliana</i> ); supporting cDNA gi:15706300:dbj:AB057678.1:   chr1:4971199-4973717 REVERSE   Aliases: F14L17.31, F14L17_31, THH1, TOM THREE HOMOLOG	5.1	4.9	0.2	0.9	100.0%	-4.5
8103	AT3G47840.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:17662897-17665017 FORWARD   Aliases: T23J7.170	3.5	3.7	-0.2	-0.9	100.0%	-4.6
8104	AT5G43190.1   F-box family protein (FBX6), contains similarity to unusual floral organs (UFO) GI:4376159 from ( <i>Arabidopsis thaliana</i> )   chr5:17357367-17358740 REVERSE   Aliases: MNL12.1, MNL12_1	5.6	5.4	0.2	0.9	100.0%	-4.8
8105	AT3G21800.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:7680113-7681692 REVERSE   Aliases: MSD21.16	4.2	4.1	0.2	0.9	100.0%	-4.9
8106	AT5G62480.2   Symbol: ATGSTU9   glutathione S-transferase, putative   chr5:25105944-25106819 REVERSE   Aliases: GLUTATHIONE S TRANSFERASE 14, GLUTATHIONE S TRANSFERASE 14B, GLUTATHIONE S TRANSFERASE TAU 9, GST14, GST14B, K19B1.9, K19B1_9	4.9	4.5	0.4	0.9	100.0%	-3.9
8107	AT2G19000.1   expressed protein   chr2:8248186-8248866 FORWARD   Aliases: T20K24.1, T20K24_1	2.7	2.8	-0.1	-0.9	100.0%	-5.4
8108	NA	5.2	4.8	0.4	0.9	100.0%	-4.7
8109	AT3G17100.2   expressed protein   chr3:5831279-5832425 FORWARD   Aliases: K14A17.17	5.6	5.4	0.2	0.9	100.0%	-4.7
8110	AT5G37680.1   Symbol: ATARLA1A   ADP-ribosylation factor, putative, ADP-ribosylation factor, <i>Leishmania major</i> , EMBL:LMFP1421 and ADP-ribosylation factor-like protein 1 (ARL1) (SP:P40616) <i>Homo sapiens</i> ; contains PF00025: ADP-ribosylation factor family   chr5:14986826-14988458 REVERSE   Aliases: ATARLA1A, K12B20.130, K12B20_130	5.9	5.7	0.2	0.9	100.0%	-4.6
8111	AT1G08720.1   Symbol: EDR1   mitogen-activated protein kinase kinase kinase (MAPKKK) (EDR1), identical to EDR1, a MAP kinase kinase kinase ( <i>Arabidopsis thaliana</i> ) gi:11127925:gb:AAG31143   chr1:2774033-2779300 FORWARD   Aliases: ENHANCED DISEASE RESISTANCE 1, F22O13.20, F22O13_20, MAPKK KINASE EDR1	4.2	4.0	0.2	0.9	100.0%	-4.8
8112	AT1G70180.2   sterile alpha motif (SAM) domain-containing protein, contains Pfam profile PF00536: SAM domain (Sterile alpha motif)   chr1:26430109-26433024 FORWARD   Aliases: F20P5.10, F20P5_10	3.4	3.2	0.2	0.9	100.0%	-4.4
8113	AT1G20430.1   expressed protein   chr1:7083186-7083825 REVERSE   Aliases: F5M15.30, F5M15_30	6.1	6.5	-0.4	-0.9	100.0%	-4.2
8114	AT3G32150.1   hypothetical protein   chr3:13147340-13148538 FORWARD   Aliases: F1M23.27	2.4	2.3	0.1	0.9	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8115	AT3G47680.1   expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr3:17588468-17589376 REVERSE   Aliases: T23J7.10	4.2	3.7	0.5	0.9	100.0%	-4.2
8116	AT3G15640.1   cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb   chr3:5299117-5301752 FORWARD   Aliases: MSJ11.5	9.9	10.2	-0.3	-0.9	100.0%	-4.7
8117	AT1G55545.1   nucleoporin-related, similar to nucleoporin CAN (Xenopus laevis) gi:5764080:emb:CAB53357	2.8	2.7	0.1	0.9	100.0%	-5.3
8118	AT3G01810.1   expressed protein   chr3:288580-292762 FORWARD   Aliases: F28J7.14, F28J7_14	4.7	5.1	-0.4	-0.9	100.0%	-4.4
8119	AT5G55640.1   expressed protein   chr5:22550385-22551304 REVERSE   Aliases: MDF20.8, MDF20_8	8.9	9.2	-0.2	-0.9	100.0%	-4.5
8120	AT4G28520.3   Symbol: CRU3   12S seed storage protein, putative / cruciferin, putative, strong similarity to SP:P33525 Cruciferin CRU1 precursor (11S globulin) (12S storage protein) from Brassica napus; contains Pfam profile PF00190 Cupin and Prosite 11-S plant seed storage proteins signature PS00305 isoform contains non-consensus AC acceptor splice site at intron 3   chr4:14087573-14089802 FORWARD   Aliases: CRC, CRUCIFERIN 3, CRUCIFERIN C, F2009.210, F2009_210	2.6	2.8	-0.2	-0.9	100.0%	-4.7
8121	AT2G31990.1   exostosin family protein, contains Pfam profile: PF03016	4.1	3.7	0.4	0.9	100.0%	-4.2
8122	AT1G30880.1   expressed protein, similar to ESTs gb:R30049 and gb:T46176   chr1:10993215-10994100 REVERSE   Aliases: F17F8.25	9.0	8.5	0.5	0.9	100.0%	-4.1
8123	AT1G53350.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.3	2.4	-0.1	-0.9	100.0%	-5.3
8124	AT5G64960.1   Symbol: CDKC;2	5.9	6.2	-0.2	-0.9	100.0%	-4.6
8125	AT1G48660.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr1:17999616-18001640 REVERSE   Aliases: F11I4.15, F11I4_15	3.1	3.2	-0.1	-0.9	100.0%	-5.4
8126	ATMG01240.1   Symbol: ORF100C   hypothetical protein   chrM:309338-309640 REVERSE   Aliases: ORF100C	2.4	2.1	0.3	0.9	100.0%	-4.5
8127	AT1G26710.1   expressed protein   chr1:9232315-9233131 REVERSE   Aliases: T24P13.9, T24P13_9	2.4	2.3	0.1	0.9	100.0%	-5.4
8128	AT3G03600.1   Symbol: RPS2   ribosomal protein S2, mitochondrial (RPS2), identical to SP:Q9GCB9 Mitochondrial ribosomal protein S2 {Arabidopsis thaliana}; contains Pfam profile PF00318: ribosomal protein S2   chr3:867669-868585 REVERSE   Aliases: RIBOSOMAL PROTEIN S2, T12J13.12, T12J13_12	6.5	6.8	-0.3	-0.9	100.0%	-4.3
8129	AT1G80030.3   DNAJ heat shock protein, putative, similar to SP:Q05646 Chaperone protein dnaJ {Erysipelothrix rhusiopathiae}; contains Pfam profiles PF00226: DnaJ domain, PF01556: DnaJ C terminal region, PF00684: DnaJ central domain (4 repeats)   chr1:30109917-30113859 REVERSE   Aliases: F18B13.12, F18B13_12	4.2	4.0	0.2	0.9	100.0%	-5.0
8130	AT2G25970.1   KH domain-containing protein   chr2:11078729-11082747 REVERSE   Aliases: F17H15.1, F17H15_1	6.6	6.1	0.5	0.9	100.0%	-4.4
8131	AT5G39785.2   expressed protein   chr5:15946416-15949504 FORWARD   Aliases: AT5G39780	4.3	4.1	0.2	0.9	100.0%	-4.9
8132	AT2G45150.3   phosphatidate cytidyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidyltransferase   chr2:18620495-18622792 FORWARD   Aliases: T14P1.4	2.8	3.0	-0.2	-0.9	100.0%	-4.8
8133	AT1G25260.1   acidic ribosomal protein P0-related, contains similarity to 60S acidic ribosomal protein GI:5815233 from (Homo sapiens)   chr1:8853946-8855847 REVERSE   Aliases: F4F7.35, F4F7_35	9.5	10.0	-0.5	-0.9	100.0%	-4.3
8134	AT1G52230.1   photosystem I reaction center subunit VI, chloroplast, putative / PSI-H, putative (PSAH2), identical to SP:Q9SUI6; similar to PSI-H precursor (Nicotiana sylvestris) GI:407355; contains Pfam profile PF03244: Photosystem I reaction centre subunit VI   chr1:19458505-19459337 FORWARD   Aliases: F9I5.11, F9I5_11	7.0	6.5	0.5	0.9	100.0%	-3.9
8135	AT1G80230.1   cytochrome c oxidase family protein, contains Pfam domain, PF01215: Cytochrome c oxidase subunit Vb   chr1:30174352-30175988 REVERSE   Aliases: F18B13.29, F18B13_29	8.1	7.9	0.2	0.9	100.0%	-4.6
8136	AT2G19130.1   S-locus lectin protein kinase family protein, contains Pfam domains PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain and PF01453: Lectin (probable mannose binding)   chr2:8300815-8303357 FORWARD   Aliases: T20K24.15, T20K24_15	5.0	5.4	-0.4	-0.9	100.0%	-4.2
8137	AT4G19460.1   glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1   chr4:10610320-10612016 REVERSE   Aliases: F24J7.20, F24J7_20	6.3	6.5	-0.3	-0.9	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8138	AT5G42080.2   Symbol: ADL1   GTP-binding protein / phragmoplastin, putative, strong similarity to GTP-binding protein (Arabidopsis thaliana) GI:807577, phragmoplastin SDL5A (Glycine max) GI:1218004; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family   chr5:16838532-16841981 REVERSE   Aliases: ADL1A, AG68, ARABIDOPSIS DYNAMIN LIKE PROTEIN, DRP1A, DYNAMIN RELATED PROTEIN 1A, MJC20.19, MJC20_19	4.5	4.3	0.2	0.9	100.0%	-4.7
8139	AT3G58200.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:21570870-21572429 REVERSE   Aliases: F9D24.110	5.3	5.9	-0.6	-0.9	100.0%	-4.1
8140	AT3G58830.1   haloacid dehalogenase (HAD) superfamily protein, contains TIGRfam TIGR01668: HAD superfamily (subfamily IIIA) phosphatase, TIGR01668 and TIGR01662: hydrolase, HAD-superfamily, subfamily IIIA   chr3:21766033-21767615 REVERSE   Aliases: T20N10.180	4.8	5.1	-0.3	-0.9	100.0%	-4.3
8141	AT4G29080.1   Symbol: PAP2   auxin-responsive AUX/IAA family protein, similar to SP:Q38826 Auxin-responsive protein IAA8, SP:Q38827 Auxin-responsive protein IAA9 from Arabidopsis thaliana; contains Pfam profile: PF02309: AUX/IAA family   chr4:14323367-14325224 REVERSE   Aliases: F19B15.110, F19B15_110, IAA27, PHYTOCHROME ASSOCIATED PROTEIN 2	6.9	7.1	-0.2	-0.9	100.0%	-4.8
8142	AT1G35710.1   leucine-rich repeat transmembrane protein kinase, putative, similar to many predicted protein kinases   chr1:13222152-13225893 FORWARD   Aliases: F14D7.1, F14D7_1	2.7	2.8	-0.1	-0.9	100.0%	-5.1
8143	AT3G02700.1   NC domain-containing protein, contains Pfam domain, PF04970: NC domain   chr3:581548-582952 REVERSE   Aliases: F16B3.33, F16B3_33	7.1	6.8	0.4	0.9	100.0%	-4.8
8144	AT3G57420.1   expressed protein, contains Pfam domain PF03385: Protein of unknown function, DUF288   chr3:21263396-21266253 REVERSE   Aliases: T8H10.20	3.3	3.6	-0.3	-0.9	100.0%	-4.4
8145	AT3G13470.1   chaperonin, putative, similar SWISS-PROT:P21240- RuBisCO subunit binding-protein beta subunit, chloroplast precursor (60 kDa chaperonin beta subunit, CPN-60 beta) (Arabidopsis thaliana); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr3:4389692-4392762 FORWARD   Aliases: MRP15.11	11.6	12.2	-0.6	-0.9	100.0%	-4.5
8146	AT1G78390.1   Symbol: nced9   9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, similar to 9-cis-epoxycarotenoid dioxygenase (Phaseolus vulgaris)(GI:6715257); similar to neoxanthin cleavage enzyme GI:9857290 from (Vigna unguiculata)   chr1:29495788-29497768 REVERSE   Aliases: ATNCED9, F3F9.10, F3F9_10	2.6	2.5	0.1	0.9	100.0%	-5.5
8147	AT3G20810.3   similar to transcription factor jumonji (jmc) domain-containing protein [Arabidopsis thaliana] (TAIR:At5g19840.1); similar to hypothetical protein LOC77035 [Mus musculus] (GB:NP_084118.1); contains InterPro domain Transcription factor jumonji, jmc (InterPro:IPR003347)   chr3:7275712-7278326 FORWARD   Aliases: MOE17.12	4.9	4.6	0.3	0.9	100.0%	-4.4
8148	AT3G57320.1   expressed protein   chr3:21221008-21221827 FORWARD   Aliases: F28O9.170	8.0	7.6	0.4	0.9	100.0%	-4.1
8149	AT4G22490.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:11849715-11850342 REVERSE   Aliases: F7K2.70, F7K2_70	2.2	2.1	0.1	0.9	100.0%	-5.3
8150	AT1G26370.1   RNA helicase, putative, similar to SP:Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr1:9121479-9125544 REVERSE   Aliases: T1K7.25, T1K7_25	4.8	5.1	-0.2	-0.9	100.0%	-4.5
8151	AT3G50630.1   Symbol: ICK2   kip-related protein 2 (KRP2) / cyclin-dependent kinase inhibitor 2 (ICK2) / cdc2a-interacting protein, identical to Cdc2a-interacting protein (ICK2) (cyclin-dependent kinase inhibitor) (Arabidopsis thaliana) GI:7160669   chr3:18811382-18812568 FORWARD   Aliases: KRP2, Kip related protein 2, T3A5.10	5.5	5.1	0.4	0.9	100.0%	-4.5
8152	AT1G72270.1   expressed protein   chr1:27203395-27214784 REVERSE   Aliases: T9N14.23, T9N14_23	3.1	2.9	0.1	0.9	100.0%	-4.9
8153	AT3G04860.1   expressed protein   chr3:1339114-1340629 REVERSE   Aliases: T9J14.19, T9J14_19	5.6	5.9	-0.3	-0.9	100.0%	-4.2
8154	AT3G20250.1   pumilio/Puf RNA-binding domain-containing protein, contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 copies at C-terminus)   chr3:7058964-7063246 REVERSE   Aliases: MAL21.29	6.8	6.5	0.3	0.9	100.0%	-4.4
8155	AT1G02330.1   expressed protein, contains similarity to hepatocellular carcinoma-associated antigen 59 GI:7158847 from (Homo sapiens)   chr1:462081-463612 REVERSE   Aliases: T6A9.2, T6A9_2	8.5	8.8	-0.3	-0.9	100.0%	-4.4
8156	AT1G19220.1   Symbol: ARF19   transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related, contains Pfam profile: PF02309 AUX/IAA family   chr1:6628059-6632770 REVERSE   Aliases: ARF11, IAA22, T29M8.9, T29M8_9	3.4	3.6	-0.2	-0.9	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8157	AT3G57520.3   alkaline alpha galactosidase, putative, similar to alkaline alpha galactosidase II (Cucumis melo) GI:29838631; contains Pfam profile PF05691: Raffinose synthase or seed imbibition protein Sip1	7.2	6.8	0.4	0.9	100.0%	-4.3
8158	AT2G28950.1   Symbol: ATEXPA6   expansin, putative (EXP6), similar to expansin GI:2828241 from (Brassica napus); contains Pfam profile PF01357: Pollen allergen   chr2:12438418-12440672 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A6, ATEXP6, ATHEXP ALPHA 1.8, EXPANSIN 6, T9I4.3, T9I4_3	9.0	8.5	0.5	0.9	100.0%	-4.4
8159	AT1G54115.1   cation exchanger, putative   chr1:20205786-20207720 FORWARD   Aliases: None	7.0	6.8	0.3	0.9	100.0%	-4.6
8160	AT5G47250.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	4.8	5.1	-0.3	-0.9	100.0%	-4.4
8161	AT3G02590.1   delta 7-sterol-C5-desaturase, putative, similar to delta7 sterol C-5 desaturase GI:5031219 from (Arabidopsis thaliana)   chr3:549347-550560 FORWARD   Aliases: F16B3.22, F16B3_22	2.5	2.6	-0.1	-0.9	100.0%	-5.2
8162	AT3G18740.1   60S ribosomal protein L30 (RPL30C), similar to 60S RIBOSOMAL PROTEIN L30 GB:O49884 from (Lupinus luteus)	11.1	11.3	-0.2	-0.9	100.0%	-4.8
8163	AT3G11490.1   rac GTPase activating protein, putative, similar to rac GTPase activating protein 1 GB:AAC62624 GI:3695059 (Lotus japonicus); contains Pfam profile PF00620: RhoGAP domain   chr3:3617529-3619573 REVERSE   Aliases: F24K9.16	5.0	5.4	-0.4	-0.9	100.0%	-4.5
8164	ATCG00710.1   Symbol: PSBH   Encodes a 8 kD phosphoprotein that is a component of the photosystem II oxygen evolving core. Its exact molecular function has not been determined but it may play a role in mediating electron transfer between the secondary quinone acceptors, QA and QB, associated with the acceptor side of PSII.   chrC:74485-74706 FORWARD   Aliases: PSBH	6.1	6.6	-0.4	-0.9	100.0%	-4.5
8165	AT3G01550.1   triose phosphate/phosphate translocator, putative, similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator (Cauliflower){Brassica oleracea}	2.6	2.7	-0.1	-0.9	100.0%	-5.2
8166	AT1G08510.1   Symbol: FATB   acyl-(acyl carrier protein) thioesterase / acyl-ACP thioesterase / oleoyl-(acyl-carrier protein) hydrolase / S-acyl fatty acid synthase thioesterase, identical to acyl-(acyl carrier protein) thioesterase (Arabidopsis thaliana) GI:804948   chr1:2691083-2694380 REVERSE   Aliases: T27G7.19, T27G7_19	8.8	8.2	0.5	0.9	100.0%	-4.6
8167	AT1G07220.1   expressed protein   chr1:2217072-2219378 REVERSE   Aliases: F10K1.7, F10K1_7	5.2	5.5	-0.3	-0.9	100.0%	-4.3
8168	AT1G22200.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g36050.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475457.1)   chr1:7837580-7840777 REVERSE   Aliases: F16L1.7, F16L1_7	7.9	8.2	-0.3	-0.9	100.0%	-4.8
8169	AT2G21590.2   Symbol: APL4   similar to glucose-1-phosphate adenylyltransferase large subunit 2 (APL2) / ADP-glucose pyrophosphorylase [Arabidopsis thaliana] (TAIR:At1g27680.1); similar to glucose-1-phosphate adenylyltransferase large subunit 3 (APL3) / ADP-glucose pyrophosphorylase [Arabidopsis thaliana] (TAIR:At4g39210.1); similar to ADP-glucose pyrophosphorylase large subunit 1 [Lycopersicon esculentum] (GB:AAC49941.1); similar to ADP-glucose pyrophosphorylase large subunit PvAGPL1 [Phaseolus vulgaris] (GB:BAC66692.1); similar to ADP-glucose pyrophosphorylase large subunit [Solanum tuberosum] (GB:CAA43490.1); similar to ADP-glucose pyrophosphorylase large subunit [Citrus unshiu] (GB:AAD56042.1); similar to ADP-glucose pyrophosphorylase large subunit 1 [Citrullus lanatus] (GB:AAB91467.1); contains InterPro domain Nucleotidyl transferase (InterPro:IPR005835); contains InterPro domain ADP-glucose pyrophosphorylase (InterPro:IPR005836)   chr2:9245827-9249520 FORWARD   Aliases: F2G1.14, F2G1_14	2.9	3.1	-0.2	-0.9	100.0%	-4.9
8170	AT3G18720.1   F-box family protein, contains Pfam PF00646: F-box domain   chr3:6444373-6445765 REVERSE   Aliases: MVE11.8	2.7	2.6	0.1	0.9	100.0%	-5.3
8171	AT2G43900.1   endonuclease/exonuclease/phosphatase family protein, belongs to Pfam:PF03372: Endonuclease/Exonuclease/phosphatase family; contains 3 WD-40 repeats (PF00400); similar to Type II inositol-1,4,5-trisphosphate 5-phosphatase EC 3.1.3.56 (5PTASE) (INPP5B) (SP:P32019) (Homo sapiens)   chr2:18185756-18190899 REVERSE   Aliases: F6E13.3	4.7	4.9	-0.3	-0.9	100.0%	-4.4
8172	AT5G16860.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:5543837-5546389 FORWARD   Aliases: F2K13.10, F2K13_10	2.7	2.8	-0.1	-0.9	100.0%	-5.3
8173	AT3G16760.2   tetratricopeptide repeat (TPR)-containing protein, low similarity to TPR-containing protein involved in spermatogenesis TPIS (Mus musculus) GI:6272682; contains Pfam profile PF00515: tetratricopeptide repeat (TPR) domain   chr3:5703019-5705319 FORWARD   Aliases: MGL6.23	6.9	7.2	-0.3	-0.9	100.0%	-4.6
8174	AT4G12340.1   expressed protein   chr4:7321276-7322448 REVERSE   Aliases: T4C9.180, T4C9_180	9.6	10.0	-0.3	-0.9	100.0%	-4.2
8175	AT1G10522.1   expressed protein   chr1:3469637-3471880 FORWARD   Aliases: None	4.7	5.0	-0.3	-0.9	100.0%	-4.2
8176	AT2G26070.1   expressed protein   chr2:11112750-11114233 REVERSE   Aliases: T19L18.12, T19L18_12	7.7	8.0	-0.4	-0.9	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8177	AT1G55240.1   expressed protein, contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)   chr1:20608666-20610066 FORWARD   Aliases: F7A10.18, F7A10_18	3.0	2.8	0.1	0.9	100.0%	-5.0
8178	AT3G28710.1   H <sup>+</sup> -transporting two-sector ATPase, putative, similar to SP:P54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14) (Vacuolar proton pump d subunit) (V-ATPase 41 kDa accessory protein) {Dictyostelium discoideum}; contains Pfam profile PF01992: ATP synthase (C/AC39) subunit   chr3:10774141-10776964 REVERSE   Aliases: MZN14.4, MZN14_4	7.5	8.2	-0.7	-0.9	100.0%	-4.1
8179	AT3G28715.1   H <sup>+</sup> -transporting two-sector ATPase, putative, similar to SP:P54641 Vacuolar ATP synthase subunit d (EC 3.6.3.14) (Vacuolar proton pump d subunit) (V-ATPase 41 kDa accessory protein) {Dictyostelium discoideum}; contains Pfam profile PF01992: ATP synthase (C/AC39) subunit   chr3:10779262-10781587 FORWARD   Aliases: MZN14.21	7.5	8.2	-0.7	-0.9	100.0%	-4.1
8180	AT4G19220.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:10505277-10508132 REVERSE   Aliases: T18B16.190, T18B16_190	3.1	3.4	-0.3	-0.9	100.0%	-4.7
8181	AT1G17930.1   expressed protein, similar to hypothetical protein GI:4559351 from (Arabidopsis thaliana)   chr1:6166213-6168832 REVERSE   Aliases: F2H15.15, F2H15_15	5.2	5.6	-0.4	-0.9	100.0%	-4.2
8182	AT2G19380.1   RNA recognition motif (RRM)-containing protein, similar to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); contains Pfam profile PF00096: Zinc finger, C2H2 type   chr2:8390938-8393686 FORWARD   Aliases: F27F23.27	3.2	3.5	-0.2	-0.9	100.0%	-4.9
8183	AT1G23330.1   expressed protein   chr1:8279700-8281880 REVERSE   Aliases: F26F24.20, F26F24_20	4.7	5.1	-0.4	-0.9	100.0%	-4.6
8184	AT4G02350.1   exocyst complex subunit Sec15-like family protein, contains Pfam profile PF04091: Exocyst complex subunit Sec15-like   chr4:1038114-1040774 FORWARD   Aliases: T14P8.16, T14P8_16	5.0	5.4	-0.5	-0.9	100.0%	-4.3
8185	AT1G49520.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr1:18333364-18335537 FORWARD   Aliases: F13F21.4, F13F21_4	3.6	3.9	-0.3	-0.9	100.0%	-4.7
8186	AT3G47070.1   expressed protein   chr3:17348050-17348718 REVERSE   Aliases: F13I12.120	7.7	8.1	-0.4	-0.9	100.0%	-4.0
8187	AT3G09090.1   Symbol: DEX1   defective in exine formation protein (DEX1), identical to defective in exine formation (Arabidopsis thaliana) gi:11138669:gb:AAG31444; contains Pfam domain PF01839: FG-GAP repeat   chr3:2782138-2787809 REVERSE   Aliases: DEFECTIVE IN EXINE FORMATION 1, MZB10.12	6.3	6.7	-0.4	-0.9	100.0%	-4.3
8188	AT5G64970.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:25975251-25977870 REVERSE   Aliases: MXK3.20, MXK3_20	4.3	4.1	0.2	0.9	100.0%	-4.7
8189	AT1G72920.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27441608-27442709 FORWARD   Aliases: F3N23.12, F3N23_12	5.7	5.2	0.5	0.9	100.0%	-4.2
8190	AT1G13280.1   Symbol: AOC4   allene oxide cyclase family protein, similar to ERD12 (GI:15320414), allene oxide cyclase GI:8977961 from (Lycopersicon esculentum); contains Pfam profile PF06351: Allene oxide cyclase	5.5	5.9	-0.4	-0.9	100.0%	-4.5
8191	AT1G21230.1   Symbol: WAK5   wall-associated kinase, putative, similar to wall-associated kinase 1 (Arabidopsis thaliana) GI:3549626; expressed in leaves and stems & induced by salicylic acid or INA (PMID:10380805)   chr1:7429969-7432335 FORWARD   Aliases: F16F4.9, F16F4_9, WALL ASSOCIATED KINASE 5	2.7	2.8	-0.1	-0.9	100.0%	-5.3
8192	AT3G17750.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr3:6073814-6078728 FORWARD   Aliases: MIG5.5	4.0	4.2	-0.2	-0.9	100.0%	-4.6
8193	AT3G46590.3   Symbol: TRFL1   similar to telomere repeat-binding protein 1 (TRP1) [Arabidopsis thaliana] (TAIR:At5g59430.2); similar to telomere repeat-binding protein 1 (TRP1) [Arabidopsis thaliana] (TAIR:At5g59430.1); similar to BPF-1 [Petroselinum crispum] (GB:CAA48413.1)   chr3:17163760-17167212 FORWARD   Aliases: F12A12.110, TRF LIKE 1	4.9	4.5	0.4	0.9	100.0%	-4.2
8194	AT1G26350.1   expressed protein   chr1:9115997-9116768 REVERSE   Aliases: F28B23.28	2.6	2.7	-0.1	-0.9	100.0%	-5.1
8195	AT2G17980.1   sec1 family protein, similar to SWISS-PROT:P22213 SLY1 protein (Saccharomyces cerevisiae); contains Pfam domain, PF00995: Sec1 family   chr2:7831256-7833679 FORWARD   Aliases: T27K22.15, T27K22_15	6.4	6.2	0.3	0.9	100.0%	-4.8
8196	AT1G63740.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:23649092-23652636 FORWARD   Aliases: F24D7.7, F24D7_7	3.8	3.6	0.3	0.9	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8197	AT3G17420.1   Symbol: GPK1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	5.8	6.2	-0.4	-0.9	100.0%	-4.3
8198	AT5G53940.1   yippee family protein, similar to mdgl-1 (Mus musculus) GI:10441648, Yippee protein (Drosophila melanogaster) GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein   chr5:21914227-21915836 REVERSE   Aliases: K19P17.11, K19P17_11	7.3	7.0	0.3	0.9	100.0%	-4.4
8199	AT3G58530.1   F-box family protein-related, contains weak similarity to F-box protein FBL2 (GI:6010699) (Rattus norvegicus)   chr3:21656524-21659340 FORWARD   Aliases: F14P22.120	6.7	6.4	0.3	0.9	100.0%	-4.4
8200	AT4G27250.1   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family, similar to dihydrokaempferol 4-reductase, Ipomoea purpurea (GI:4239849), Medicago sativa, PIR2:S61416	3.1	3.2	-0.2	-0.9	100.0%	-4.9
8201	AT3G51620.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g61690.1); similar to GLP_548_4539_3001 [Giardia lamblia ATCC 50803] (GB:EAA36999.1); contains InterPro domain PAP/25A core domain (InterPro:IPR001201)   chr3:19154631-19159031 FORWARD   Aliases: T18N14.7	5.9	5.6	0.3	0.9	100.0%	-4.7
8202	AT3G25250.1   Symbol: AGC2 1	4.4	4.1	0.3	0.9	100.0%	-4.4
8203	AT5G64090.1   expressed protein   chr5:25665253-25666846 FORWARD   Aliases: MHJ24.7, MHJ24_7	4.7	5.0	-0.3	-0.9	100.0%	-4.8
8204	AT2G29460.1   Symbol: ATGSTU4   glutathione S-transferase, putative   chr2:12633624-12634755 REVERSE   Aliases: F16P2.16, F16P2_16, GLUTATHIONE S TRANSFERASE 22, GST22	7.4	7.9	-0.5	-0.9	100.0%	-4.1
8205	AT3G61440.1   Symbol: ATCYSC1   encodes a cysteine synthase isomer. The isomer is however less effective in cysteine biosynthesis. It is involved in beta-cyanoalanine biosynthesis, a intermediate of cyanide detoxification pathway.   chr3:22746722-22748953 FORWARD   Aliases: ARATH;BSAS3;1, CYSTEINE SYNTHASE, F2A19.40	11.2	11.6	-0.3	-0.9	100.0%	-4.8
8206	AT3G49930.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr3:18521231-18521948 FORWARD   Aliases: F3A4.10	3.9	3.6	0.3	0.9	100.0%	-4.4
8207	AT3G12150.1   expressed protein   chr3:3876414-3878907 REVERSE   Aliases: T21B14.3	4.2	4.0	0.2	0.9	100.0%	-4.6
8208	AT3G47650.1   bundle-sheath defective protein 2 family / bsd2 family, similar to bundle sheath defective protein 2 (Zea mays) GI:4732091   chr3:17580523-17581539 FORWARD   Aliases: F1P2.200	8.0	7.6	0.4	0.9	100.0%	-4.0
8209	AT1G24120.1   Symbol: ARL1   DNAJ heat shock protein, putative, similar to Altered Response to Gravity (Arabidopsis thaliana) GI:4249662; contains Pfam profile PF00226 DnaJ domain   chr1:8529132-8532183 REVERSE   Aliases: ARG1 LIKE 1, F3I6.4, F3I6_4	7.3	7.6	-0.3	-0.9	100.0%	-4.4
8210	AT5G40290.1   metal-dependent phosphohydrolase HD domain-containing protein, similar to SP:Q60710 Interferon-gamma inducible protein MG11 {Mus musculus}; contains Pfam profile PF01966: HD domain   chr5:16122487-16125729 REVERSE   Aliases: MSN9.190, MSN9_190	2.2	2.3	-0.1	-0.9	100.0%	-5.7
8211	AT1G07290.1   nucleotide-sugar transporter family protein, similar to SP:Q941R4 GDP-mannose transporter {Arabidopsis thaliana}	4.1	3.9	0.2	0.9	100.0%	-4.6
8212	AT4G21140.1   expressed protein, ; expression supported by MPSS   chr4:11277546-11278232 REVERSE   Aliases: F7J7.80, F7J7_80	6.1	6.3	-0.3	-0.9	100.0%	-4.4
8213	AT2G41280.1   Symbol: M10   late embryogenesis abundant protein (M10) / LEA protein M10, identical to GB:AF076979   chr2:17216775-17217501 FORWARD   Aliases: ATM10, F13H10.17, F13H10_17	4.6	4.3	0.3	0.9	100.0%	-4.5
8214	AT5G58760.1   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); damage-specific DNA binding protein 2 (GI:10798819) (Homo sapiens)   chr5:23747726-23750848 REVERSE   Aliases: MZN1.20, MZN1_20	3.1	2.8	0.2	0.9	100.0%	-4.6
8215	AT1G79160.1   expressed protein   chr1:29784614-29785599 REVERSE   Aliases: YUP8H12R.23, YUP8H12R_23	4.3	4.1	0.2	0.9	100.0%	-4.6
8216	AT3G24750.1   expressed protein   chr3:9036275-9037731 FORWARD   Aliases: K7P8.4	2.3	2.2	0.1	0.9	100.0%	-5.6
8217	AT4G02485.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr4:1092681-1094595 FORWARD   Aliases: None	3.9	3.7	0.2	0.9	100.0%	-4.8
8218	AT5G62100.2   BAG domain-containing protein, similar to BAG domain containing proteins (At5g07220, At5g52060)   chr5:24957622-24959200 FORWARD   Aliases: MTG10.13, MTG10_13	3.2	2.9	0.3	0.9	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8219	AT2G47170.1   Symbol: ARF1   Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct.   chr2:19373694-19375870 FORWARD   Aliases: ADP RIBOSYLATION FACTOR, ADP RIBOSYLATION FACTOR 1, T8I13.1	12.3	12.0	0.4	0.9	100.0%	-4.9
8220	AT2G33330.1   33 kDa secretory protein-related, contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa secretory proteins   chr2:14129967-14132214 REVERSE   Aliases: F4P9.10, F4P9_10	3.6	3.8	-0.1	-0.9	100.0%	-4.8
8221	AT1G55870.1   CAF1 family ribonuclease, contains Pfam domain, PF04857: CAF1 family ribonuclease   chr1:20899271-20902087 FORWARD   Aliases: F14J16.11, F14J16_11	3.7	4.0	-0.2	-0.9	100.0%	-4.7
8222	AT1G33790.1   jacalin lectin family protein, similar to myrosinase binding protein homolog GI:2997767 from (Arabidopsis thaliana); contains contains Pfam profile PF01419 jacalin-like lectin domain   chr1:12256644-12260537 FORWARD   Aliases: F14M2.9, F14M2_9	6.4	6.1	0.3	0.9	100.0%	-4.3
8223	AT1G48070.1   expressed protein   chr1:17734160-17734791 REVERSE   Aliases: T2J15.15	2.6	2.8	-0.1	-0.9	100.0%	-5.2
8224	AT5G24470.1   Symbol: APRR5   pseudo-response regulator 5 (APRR5), identical to pseudo-response regulator 5 GI:10281006 from (Arabidopsis thaliana)   chr5:8355985-8358876 REVERSE   Aliases: PRR5, PSEUDO RESPONSE REGULATOR 5, T31K7.5, T31K7_5	5.1	4.8	0.2	0.9	100.0%	-4.5
8225	AT1G49010.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr1:18136313-18137593 FORWARD   Aliases: F27J15.20	3.9	3.7	0.2	0.9	100.0%	-4.7
8226	AT1G26620.1   expressed protein, ; expression supported by MPSS   chr1:9195825-9198706 REVERSE   Aliases: T1K7.1, T1K7_1	3.2	3.6	-0.4	-0.9	100.0%	-4.4
8227	AT1G16480.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:5625696-5628562 REVERSE   Aliases: F3O9.28, F3O9_28	3.2	3.4	-0.2	-0.9	100.0%	-4.8
8228	AT3G25410.1   bile acid:sodium symporter family protein, low similarity to SP:Q14973 Sodium/bile acid cotransporter (Na(+))/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family   chr3:9215576-9217727 REVERSE   Aliases: MWL2.2	5.4	5.2	0.2	0.9	100.0%	-4.7
8229	AT5G22740.1   Symbol: ATCSLA02   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	10.0	9.4	0.6	0.9	100.0%	-4.3
8230	AT1G80870.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr1:30397025-30399275 FORWARD   Aliases: F23A5.23, F23A5_23	5.4	5.7	-0.4	-0.9	100.0%	-4.5
8231	AT4G05390.1   ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative, strong similarity to SP:P41345 Ferredoxin--NADP reductase, root isozyme, chloroplast precursor (EC 1.18.1.2) (FNR) {Oryza sativa}, ferredoxin-NADP reductase precursor (Zea mays) GI:500751   chr4:2738712-2740562 REVERSE   Aliases: C6L9.70, C6L9_70	10.3	10.0	0.3	0.9	100.0%	-4.5
8232	AT1G44970.1   peroxidase, putative, similar to peroxidase GI:993004 from (Mercurialis annua)   chr1:17004652-17006124 FORWARD   Aliases: F27F5.6, F27F5_6	2.2	2.6	-0.4	-0.9	100.0%	-4.0
8233	AT1G14210.1   ribonuclease T2 family protein, contains similarity to RNase GI:7768564 from (Nicotiana tabacum); contains Pfam profile PF00445: Ribonuclease T2 family   chr1:4856773-4857959 REVERSE   Aliases: F7A19.31, F7A19_31	7.1	7.7	-0.6	-0.9	100.0%	-4.4
8234	AT1G74010.1   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088   chr1:27835819-27837774 REVERSE   Aliases: F2P9.12, F2P9_12	7.1	7.7	-0.6	-0.9	100.0%	-3.8
8235	AT5G20590.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr5:6963440-6966607 FORWARD   Aliases: F7C8.180, F7C8_180	6.9	7.1	-0.3	-0.9	100.0%	-4.5
8236	AT5G10660.1   calmodulin-binding protein-related, contains weak similarity to calmodulin-binding proteins   chr5:3370554-3371777 FORWARD   Aliases: MAJ23.20, MAJ23_20	3.1	3.2	-0.1	-0.9	100.0%	-5.2
8237	AT5G58270.1   Symbol: STA1   mitochondrial half-ABC transporter (STA1), identical to half-molecule ABC transporter ATM3 GI:9964121 from (Arabidopsis thaliana); almost identical to mitochondrial half-ABC transporter STA1 GI:9187883 from (Arabidopsis thaliana); identical to cDNA mitochondrial half-ABC transporter (STA1 gene)GI:9187882   chr5:23579368-23584416 FORWARD   Aliases: ATATM3, ATM3, HALF MOLECULE ABC TRANSPORTER ATM3, MCK7.14, MCK7_14, STARIK, STARIK 1	7.4	7.7	-0.3	-0.9	100.0%	-4.5
8238	AT1G09250.1   expressed protein   chr1:2989380-2990352 FORWARD   Aliases: T12M4.4, T12M4_4	4.3	4.1	0.3	0.9	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8239	AT3G57950.1   expressed protein, hypothetical protein T24P15.9 - Arabidopsis thaliana, PIR:T00927; expression supported by MPSS   chr3:21471400-21471945 FORWARD   Aliases: T10K17.160	2.6	2.7	-0.1	-0.9	100.0%	-5.2
8240	AT1G51900.1   hypothetical protein   chr1:19283553-19286564 REVERSE   Aliases: T14L22.11, T14L22_11	2.2	2.3	-0.1	-0.9	100.0%	-5.6
8241	AT2G36550.1   expressed protein   chr2:15334626-15335881 FORWARD   Aliases: F1O11.18, F1O11_18	3.1	2.9	0.1	0.9	100.0%	-5.1
8242	AT2G40240.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:16818104-16819306 FORWARD   Aliases: T7M7.22	3.7	3.6	0.1	0.9	100.0%	-4.8
8243	AT3G58510.3   similar to DEAD box RNA helicase, putative [Arabidopsis thaliana] (TAIR:At3g58570.1); similar to DEAD box RNA helicase, putative [Arabidopsis thaliana] (TAIR:At2g42520.1); similar to putative DEAD-box RNA helicase DEAD3(i:6753620) [Oryza sativa (japonica cultivar-group)] (GB:XP_477035.1); contains InterPro domain Helicase, C-terminal (InterPro:IPR001650); contains InterPro domain DEAD/DEAH box helicase (InterPro:IPR001410)   chr3:21650987-21654772 FORWARD   Aliases: F14P22.100	6.4	6.0	0.4	0.9	100.0%	-4.4
8244	AT4G17640.1   Symbol: CKB2   casein kinase II beta chain, putative, similar to casein kinase II beta' chain (CK II) (Arabidopsis thaliana) SWISS-PROT:P40229   chr4:9825210-9827285 FORWARD   Aliases: CASEIN KINASE II BETA SUBUNIT CKB2, DL4855W, FCAALL.14	8.2	7.9	0.3	0.9	100.0%	-4.5
8245	AT5G25960.1   expressed protein, various predicted proteins, Arabidopsis thaliana contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr5:9062920-9065014 REVERSE   Aliases: T1N24.5, T1N24_5	2.2	2.1	0.1	0.9	100.0%	-5.4
8246	AT3G22231.1   Symbol: PCC1   expressed protein   chr3:7845879-7846612 REVERSE   Aliases: PATHOGEN AND CIRCADIAN CONTROLLED 1	3.0	3.1	-0.1	-0.9	100.0%	-4.9
8247	AT5G60550.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:24356455-24359719 FORWARD   Aliases: MUF9.13, MUF9_13	7.0	6.5	0.5	0.9	100.0%	-4.2
8248	AT2G03150.1   Symbol: EMB1579   ATP/GTP-binding protein family, contains ATP/GTP-binding site motif A (P-loop), PROSITE:PS00017   chr2:951930-959162 FORWARD   Aliases: EMB1579, EMBRYO DEFECTIVE 1579, T18E12.18, T18E12_18	8.7	9.3	-0.6	-0.9	100.0%	-4.4
8249	AT5G45900.1   Symbol: APG7   autophagy 7 (APG7), nearly identical to autophagy 7 (Arabidopsis thaliana) GI:19912147; contains Pfam profile PF00899: ThiF family   chr5:18632449-18635787 FORWARD   Aliases: ATAPG7, AUTOPHAGY 7, K15I22.10, K15I22_10	5.9	6.5	-0.6	-0.9	100.0%	-4.3
8250	AT3G02100.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:368847-370491 REVERSE   Aliases: F1C9.11, F1C9_11	3.5	3.3	0.2	0.9	100.0%	-4.7
8251	AT4G16170.1   expressed protein   chr4:9165289-9167452 REVERSE   Aliases: DL4125C, FCAALL.293	7.9	8.1	-0.3	-0.9	100.0%	-4.8
8252	AT2G03320.1   hypothetical protein   chr2:1007379-1007942 FORWARD   Aliases: T4M8.25, T4M8_25	2.7	2.6	0.1	0.9	100.0%	-5.3
8253	AT1G80380.2   phosphoribulokinase/uridine kinase-related   chr1:30222157-30224863 FORWARD   Aliases: F5I6.13, F5I6_13	8.0	7.7	0.3	0.9	100.0%	-4.2
8254	AT1G59670.1   Symbol: ATGSTU15   glutathione S-transferase, putative, similar to glutathione S-transferase GB:AAF29773 GI:6856103 from (Gossypium hirsutum)   chr1:21933675-21935031 FORWARD   Aliases: T30E16.25, T30E16_25	3.3	3.1	0.2	0.9	100.0%	-5.0
8255	AT1G64040.1   Symbol: TOPP3   serine/threonine protein phosphatase PP1 isozyme 3 (TOPP3) / phosphoprotein phosphatase 1, identical to SP:P48483 Serine/threonine protein phosphatase PP1 isozyme 3 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GB:AAA32838 GI:166799 from (Arabidopsis thaliana)   chr1:23761946-23764212 REVERSE   Aliases: None	8.0	7.5	0.5	0.9	100.0%	-4.5
8256	AT4G15840.1   expressed protein   chr4:8997042-9001045 FORWARD   Aliases: DL3960W, FCAALL.399	6.4	6.2	0.2	0.9	100.0%	-4.7
8257	AT3G02885.1   Symbol: GASAS5   gibberellin-regulated protein 5 (GASAS5) / gibberellin-responsive protein 5, identical to GASAS5 (Arabidopsis thaliana) GI:1289320   chr3:638111-639059 REVERSE   Aliases: GASAS5	4.2	4.4	-0.2	-0.9	100.0%	-4.4
8258	AT3G04960.1   expressed protein, low similarity to SP:P32380 NUF1 protein (Spindle poly body spacer protein SPC110) {Saccharomyces cerevisiae}	3.6	3.4	0.2	0.9	100.0%	-4.6
8259	AT4G24750.1   similar to rhodanese-like domain-containing protein [Arabidopsis thaliana] (TAIR:At3g08920.1); similar to rhodanese family protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_450481.1); contains InterPro domain Rhodanese-like (InterPro:IPR001763)   chr4:12758224-12760892 REVERSE   Aliases: F22K18.50, F22K18_50	6.6	6.9	-0.3	-0.9	100.0%	-4.3
8260	AT5G24660.1   expressed protein   chr5:8443282-8443837 REVERSE   Aliases: MXC17.2, MXC17_2	11.6	12.2	-0.6	-0.9	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8261	AT1G34130.1   Symbol: STT3B   oligosaccharyl transferase STT3 subunit, putative, similar to SP:P39007 Oligosaccharyl transferase STT3 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF02516: Oligosaccharyl transferase STT3 subunit   chr1:12429868-12433165 FORWARD   Aliases: F12G12.5, F12G12_5, STAUROSPORIN AND TEMPERATURE SENSITIVE 3 LIKE B	6.0	6.7	-0.7	-0.9	100.0%	-3.9
8262	AT1G04380.1   2-oxoglutarate-dependent dioxygenase, putative, Strong similarity to Arabidopsis 2A6 (gb:X83096), tomato ethylene synthesis regulatory protein E8 (SP:P10967)   chr1:1176920-1178396 REVERSE   Aliases: F19P19.18, F19P19_18	3.1	3.0	0.1	0.9	100.0%	-5.1
8263	AT2G33030.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr2:14024761-14025417 REVERSE   Aliases: T21L14.3, T21L14_3	2.3	2.3	0.1	0.9	100.0%	-5.8
8264	AT3G12660.1   fasciclin-like arabinogalactan family protein, similar to fasciclin-like arabinogalactan-protein 1 (Arabidopsis thaliana) gi:13377776:gb:AAK20857;   chr3:4019067-4019834 FORWARD   Aliases: T2E22.3	2.4	2.5	-0.2	-0.9	100.0%	-5.2
8265	AT3G10030.1   aspartate/glutamate/uridylate kinase family protein, low similarity to SP:Q9Z5K8 Uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase) (UMP kinase) {Lactococcus lactis}; contains Pfam profile PF00696: Amino acid kinase family   chr3:3092035-3094950 REVERSE   Aliases: T22K18.15	4.6	4.3	0.3	0.9	100.0%	-5.0
8266	AT2G28640.1   exocyst subunit EXO70 family protein, contains HEAT repeat and Pfam domain PF03081:exocyst subunit EXO70	3.2	3.4	-0.1	-0.9	100.0%	-5.3
8267	AT4G17380.1   Symbol: MSH4   similar to DNA mismatch repair protein MSH2 (MSH2) [Arabidopsis thaliana] (TAIR:At3g18524.1); similar to MutS homolog 4 [Homo sapiens] (GB:AAH33030.1); similar to mutS-like 4 [synthetic construct] (GB:AAX29894.1); contains InterPro domain MutS III (InterPro:IPR007696); contains InterPro domain DNA mismatch repair protein MutS, C-terminal (InterPro:IPR000432); contains InterPro domain MutS IV (InterPro:IPR007861)   chr4:9708696-9714666 FORWARD   Aliases: DL4725W, FCAALL.423, MUTS LIKE PROTEIN 4	2.4	2.4	-0.1	-0.9	100.0%	-5.3
8268	AT2G47580.1   Symbol: U1A   small nuclear ribonucleoprotein U1A / spliceosomal protein U1A / U1snRNP-specific protein, identical to GB:Z49991 U1snRNP-specific protein (Arabidopsis thaliana)	7.7	8.2	-0.5	-0.9	100.0%	-4.5
8269	AT2G48160.1   PWWP domain-containing protein   chr2:19696484-19703891 REVERSE   Aliases: F11L15.11, F11L15_11	3.3	3.5	-0.2	-0.9	100.0%	-4.8
8270	AT1G64650.1   expressed protein   chr1:24027161-24030058 REVERSE   Aliases: F1N19.22, F1N19_22	5.8	6.1	-0.3	-0.9	100.0%	-4.4
8271	AT1G17910.1   wall-associated kinase, putative, contains similarity to wall-associated kinase 4 GI:3355308 from (Arabidopsis thaliana)	3.1	2.9	0.2	0.9	100.0%	-5.0
8272	AT3G15670.1   late embryogenesis abundant protein, putative / LEA protein, putative, similar to SP:P13934 Late embryogenesis abundant protein 76 (LEA 76) {Brassica napus}; contains Pfam profile PF02987: Late embryogenesis abundant protein	2.5	2.4	0.1	0.9	100.0%	-5.4
8273	AT3G13065.1   leucine-rich repeat transmembrane protein kinase, putative, leucine-rich repeat transmembrane protein kinase 1 GB:AAC27894 from (Zea mays)   chr3:4187768-4190870 FORWARD   Aliases: MGH6.19	2.2	2.3	-0.1	-0.9	100.0%	-5.5
8274	AT1G10400.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:3414853-3416285 REVERSE   Aliases: F14N23.30, F14N23_30	4.8	4.5	0.3	0.9	100.0%	-4.7
8275	AT5G11150.1   Symbol: ATVAMP713   synaptobrevin / vesicle-associated membrane protein 713 (VAMP713), identified as AtVAMP713 by Sanderfoot, A.A., et al. in Plant Physiol. 124: 1558-69 (2000); similar to Vesicle-associated membrane protein 722 (AtVAMP722) Synaptobrevin-related protein 1 (SP:P47192) {Arabidopsis thaliana}; synaptobrevin-like protein Syb11, Mus musculus, EMBL:MMU133536   chr5:3546355-3548112 REVERSE   Aliases: F2I11.40, F2I11_40, VAMP713	6.0	5.7	0.2	0.9	100.0%	-4.5
8276	AT3G17980.1   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr3:6152386-6153440 FORWARD   Aliases: MEB5.20	2.6	2.5	0.1	0.9	100.0%	-5.2
8277	AT4G24200.1   expressed protein, hypothetical protein - Arabidopsis thaliana,PIR2:T06677   chr4:12556666-12560883 REVERSE   Aliases: T22A6.30, T22A6_30	3.3	3.6	-0.3	-0.9	100.0%	-4.3
8278	AT1G01560.1   Symbol: ATMPK11   mitogen-activated protein kinase, putative / MAPK, putative (MPK11), similar to MAP kinase 5 GI:4239889 from (Zea mays); mitogen-activated protein kinase (MAPK)(AtMPK11), PMID:12119167   chr1:202267-204335 FORWARD   Aliases: F22L4.10, F22L4_10	3.0	3.1	-0.1	-0.9	100.0%	-5.1
8279	AT1G09920.1   TRAF-type zinc finger-related, contains Pfam PF02176: TRAF-type zinc finger; similar to TNF receptor associated factor 4 (GI:7274404) (Mus musculus) (GI:7274404); similar to Cysteine rich motif Associated to Ring and Traf domains protein (mCART1)(GI:1041446) (Mus musculus)   chr1:3224686-3227068 REVERSE   Aliases: F21M12.31, F21M12_31	6.2	5.9	0.3	0.9	100.0%	-4.4
8280	AT4G16850.1   expressed protein   chr4:9480100-9481757 FORWARD   Aliases: DL4450W, FCAALL.194	5.0	4.9	0.2	0.9	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8281	AT5G37970.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292), theobromine synthase (Coffea arabica)(GI:13365751), SAM:jasmonic acid carboxyl methyltransferase (GI:13676829)   chr5:15140319-15141914 REVERSE   Aliases: K18L3.130, K18L3_130	2.4	2.5	-0.1	-0.9	100.0%	-5.3
8282	AT5G58370.2   expressed protein   chr5:23610343-23613252 FORWARD   Aliases: MCK7.24, MCK7_24	3.8	4.0	-0.2	-0.9	100.0%	-4.9
8283	AT5G40830.2   Symbol: ATRAD3	5.6	5.0	0.6	0.9	100.0%	-4.2
8284	AT5G38070.1   zinc finger (C3HC4-type RING finger) family protein, contains InterPro Entry IPR001841 Zn-finger, RING; contains PROSITE PS00190: Cytochrome c family heme-binding site signature   chr5:15207484-15208919 FORWARD   Aliases: F16F17.8, F16F17_8	2.7	2.9	-0.2	-0.9	100.0%	-4.6
8285	AT2G17500.4   similar to auxin efflux carrier family protein [Arabidopsis thaliana] (TAIR:At5g65980.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAW56872.1); contains InterPro domain Auxin Efflux Carrier (InterPro:IPR004776)   chr2:7613997-7616360 FORWARD   Aliases: MJB20.6, MJB20_6	3.4	3.8	-0.4	-0.9	100.0%	-4.4
8286	AT5G17630.1   glucose-6-phosphate/phosphate translocator, putative, similar to glucose-6-phosphate/phosphate-translocator precursor (Solanum tuberosum) gi:2997593:gb:AAC08526	6.0	6.7	-0.7	-0.9	100.0%	-4.3
8287	AT3G19840.1   FF domain-containing protein / WW domain-containing protein, weak similarity to transcription factor CA150b (Mus musculus) GI:6329166; contains Pfam profiles PF01846: FF domain, PF00397: WW domain   chr3:6891135-6897233 FORWARD   Aliases: MPN9.8	6.1	6.4	-0.3	-0.9	100.0%	-4.6
8288	AT5G26260.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr5:9200479-9202403 FORWARD   Aliases: T19G15.110, T19G15_110	3.5	3.7	-0.2	-0.9	100.0%	-4.7
8289	AT5G27940.1   MFP1 attachment factor, putative, similar to MFP1 attachment factor 1 (Glycine max) gi:7546729:gb:AAF63659 similar to MFP1 attachment factor 1 (Glycine max) gi:7546729:gb:AAF63659   chr5:9974415-9975075 FORWARD   Aliases: F15F15.4	3.3	3.1	0.2	0.9	100.0%	-4.8
8290	AT3G18350.1   expressed protein, contains Pfam profile: PF04842 plant protein of unknown function (DUF639)   chr3:6296856-6300679 FORWARD   Aliases: MYF24.7	5.4	5.7	-0.3	-0.9	100.0%	-4.4
8291	AT4G37940.1   Symbol: AGL21   MADS-box family protein, MADS-box protein AGL17 - Arabidopsis thaliana, PID:g862648; identical to cDNA MADS-box protein AGL21 GI:18478602   chr4:17835689-17838615 REVERSE   Aliases: F20D10.60, F20D10_60	7.6	7.2	0.4	0.9	100.0%	-4.3
8292	AT1G23840.1   expressed protein   chr1:8424286-8425365 REVERSE   Aliases: F5O8.40, F5O8_40	4.7	4.5	0.3	0.9	100.0%	-4.9
8293	AT2G24410.1   hypothetical protein   chr2:10386239-10386487 REVERSE   Aliases: T28I24.14, T28I24_14	2.6	2.7	-0.1	-0.9	100.0%	-5.5
8294	AT3G12810.1   Symbol: PIE1   SNF2 domain-containing protein / helicase domain-containing protein, similar to transcriptional activator SRCAP (Homo sapiens) GI:5106572; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr3:4065586-4074085 FORWARD   Aliases: MBK21.24, PHOTOPERIOD INDEPENDENT EARLY FLOWERING 1	2.2	2.3	-0.1	-0.9	100.0%	-5.3
8295	AT5G19170.1   expressed protein, predicted proteins, Arabidopsis thaliana contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr5:6445247-6447421 FORWARD   Aliases: T24G5.70, T24G5_70	3.1	2.9	0.2	0.9	100.0%	-5.0
8296	AT1G20816.1   expressed protein   chr1:7233757-7235117 FORWARD   Aliases: F2D10.33, F2D10_33	4.7	5.2	-0.5	-0.9	100.0%	-3.9
8297	AT2G14750.1   Symbol: APK   adenylylsulfate kinase 1 (AKN1), identical to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:Q43295   chr2:6321178-6322848 FORWARD   Aliases: ADENOSINE PHOSPHOSULFATE KINASE, APS KINASE, F26C24.11, F26C24_11	9.2	9.5	-0.3	-0.9	100.0%	-4.6
8298	AT1G70200.1   RNA recognition motif (RRM)-containing protein, contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain   chr1:26435960-26438063 REVERSE   Aliases: F20P5.8, F20P5_8	4.6	5.0	-0.5	-0.9	100.0%	-4.5
8299	AT1G49650.1   cell death associated protein-related, similar to PrMC3 (Pinus radiata) GI:5487873; weak similarity to cell death associated protein (Nicotiana tabacum) GI:7417008, hsr203j (Nicotiana tabacum) GI:22830761   chr1:18380923-18382302 REVERSE   Aliases: F14J22.21, F14J22_21	5.6	5.8	-0.3	-0.9	100.0%	-4.4
8300	AT3G12460.1   expressed protein   chr3:3954702-3955430 REVERSE   Aliases: T2E22.22	2.1	2.0	0.1	0.9	100.0%	-5.5
8301	AT3G54280.1   SNF2 domain-containing protein / helicase domain-containing protein, similar to SP:O14981 TBP-associated factor 172 (TAF-172) (TAF(II)170) {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr3:20103339-20115133 FORWARD   Aliases: F24B22.240	5.2	5.0	0.2	0.9	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8302	AT2G38610.2   KH domain-containing protein   chr2:16154191-16156841 REVERSE   Aliases: T6A23.19, T6A23_19	4.3	4.1	0.2	0.9	100.0%	-4.6
8303	AT2G38780.1   expressed protein, similar to hypothetical protein [Lotus corniculatus var. japonicus] (GB:BAC41325.1)   chr2:16217935-16221707 FORWARD   Aliases: T6A23.2, T6A23_2	6.0	5.7	0.3	0.9	100.0%	-4.6
8304	AT2G24960.1   expressed protein, ; expression supported by MPSS   chr2:10624342-10627113 FORWARD   Aliases: F27C12.12, F27C12_12	4.5	4.7	-0.3	-0.9	100.0%	-4.8
8305	AT5G11300.1   Symbol: CYC3B   cyclin, putative (CYC3b), similar to cyclin 3a (Arabidopsis thaliana) GI:509425; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain; identical to cDNA cyc3b mRNA for cyclin 3b protein GI:728520   chr5:3601518-3605260 REVERSE   Aliases: CYC2BAT, CYCA2;2, CYCLIN, CYCLIN A2;2, MITOTIC LIKE CYCLIN 3B FROM ARABIDOPSIS	3.0	3.2	-0.2	-0.9	100.0%	-4.8
8306	AT1G15120.1   ubiquinol-cytochrome C reductase complex 7.8 kDa protein, putative / mitochondrial hinge protein, putative, similar to SP:P48504 Ubiquinol-cytochrome C reductase complex 7.8 kDa protein (EC 1.10.2.2) (Mitochondrial hinge protein) (CR7) {Solanum tuberosum}; contains Pfam profile PF02320: Ubiquinol-cytochrome C reductase hinge protein   chr1:5202849-5204188 FORWARD   Aliases: F9L1.5, F9L1_5	10.7	10.9	-0.2	-0.9	100.0%	-5.3
8307	AT3G53180.1   glutamine synthetase, putative, similar to glutamine synthetase (glutamate--ammonia ligase) (Bacillus subtilis) SWISS-PROT:P12425   chr3:19717872-19722393 FORWARD   Aliases: T4D2.110	5.5	5.7	-0.3	-0.9	100.0%	-4.6
8308	AT3G24900.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr3:9099190-9101844 REVERSE   Aliases: K7P8.27	4.3	4.8	-0.5	-0.9	100.0%	-4.4
8309	AT2G44745.1   WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain   chr2:18454348-18456084 REVERSE   Aliases: None	3.0	2.9	0.1	0.9	100.0%	-5.1
8310	AT1G27910.1   U-box domain-containing protein, contains Pfam profile PF04564: U-box domain   chr1:9720727-9724701 REVERSE   Aliases: F13K9.2, F13K9_2	3.6	3.5	0.1	0.9	100.0%	-4.8
8311	AT2G04000.1   expressed protein   chr2:1267759-1268334 REVERSE   Aliases: F3C11.11, F3C11_11	2.9	2.7	0.1	0.9	100.0%	-4.9
8312	AT4G15480.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr4:8848849-8850514 REVERSE   Aliases: DL3780C, FCAALL.304	3.8	3.7	0.2	0.9	100.0%	-4.8
8313	AT5G58480.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr5:23658368-23660079 REVERSE   Aliases: MQJ2.10, MQJ2_10	7.0	7.4	-0.5	-0.9	100.0%	-4.0
8314	AT3G14110.2   Symbol: FLU   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr3:4675712-4677665 REVERSE   Aliases: FLUORESCENT IN BLUE LIGHT, MAG2.7	7.3	7.6	-0.3	-0.9	100.0%	-4.2
8315	AT5G38080.1   expressed protein   chr5:15208945-15209875 REVERSE   Aliases: F16F17.9, F16F17_9	2.1	2.2	-0.1	-0.9	100.0%	-5.7
8316	AT5G66560.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr5:26581465-26584079 FORWARD   Aliases: K1F13.23, K1F13_23	3.3	3.5	-0.2	-0.9	100.0%	-4.7
8317	AT5G18550.1   similar to zinc finger (CCCH-type) family protein [Arabidopsis thaliana] (TAIR:At3g06410.1); similar to putative floral homeotic protein HUA1 [Oryza sativa (japonica cultivar-group)] (GB:BAD81393.1); contains InterPro domain Zn-finger, C-x8-C-x5-C-x3-H type (InterPro:IPR000571)   chr5:6160180-6163132 FORWARD   Aliases: T28N17.30, T28N17_30	3.2	3.3	-0.1	-0.9	100.0%	-4.9
8318	AT5G48880.3   Symbol: PKT2   similar to acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana] (TAIR:At2g33150.1); similar to acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana] (TAIR:At1g04710.1); similar to acetyl-CoA C-acyltransferase (EC 2.3.1.16) precursor - cucurbit (GB:S72532); contains InterPro domain Thiolase (InterPro:IPR002155)	4.8	5.0	-0.2	-0.9	100.0%	-4.8
8319	AT2G05370.1   expressed protein, similar to SGS2 (GI:8164028) (Arabidopsis thaliana); similar to RNA-dependent RNA polymerase (GI:8248473) (Arabidopsis thaliana)   chr2:1960410-1961422 REVERSE   Aliases: F16J10.8, F16J10_8	2.9	2.7	0.2	0.9	100.0%	-5.1
8320	AT4G24150.1   Symbol: AtGRF8	2.6	2.8	-0.1	-0.9	100.0%	-5.2
8321	AT1G17560.1   Symbol: HLL   ribosomal protein L14 family protein, similar to GB:Z98756 from (Mycobacterium leprae)   chr1:6037457-6038685 REVERSE   Aliases: F1L3.27, F1L3_27, HUELLENLOS	6.7	7.3	-0.6	-0.9	100.0%	-4.0
8322	AT5G51510.1   expressed protein   chr5:20938659-20940204 FORWARD   Aliases: K17N15.6, K17N15_6	7.9	8.1	-0.2	-0.9	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8323	AT5G37660.1   receptor-like protein kinase-related, similar to receptor-like protein kinase 4 (GI:13506745) {Arabidopsis thaliana}; embryonic abundant protein EMB24, white spruce, PIR:T09251; contains Pfam PF01657: Domain of unknown function   chr5:14977027-14978823 FORWARD   Aliases: K12B20.12, K12B20_12	2.7	2.8	-0.1	-0.9	100.0%	-5.0
8324	AT2G35520.2   defender against cell death 2 (DAD2), identical to defender against cell death 2 (DAD-2, AtDAD2) (Arabidopsis thaliana) SWISS-PROT:O22622   chr2:14928572-14929920 FORWARD   Aliases: T32F12.10, T32F12_10	8.6	8.1	0.5	0.9	100.0%	-4.3
8325	AT5G63670.1   transcription initiation protein-related, contains weak similarity to Transcription initiation protein SPT4 homolog 1 (Swiss-Prot:Q16550) (Mus musculus)	9.2	8.9	0.3	0.9	100.0%	-4.4
8326	AT1G66130.1   oxidoreductase N-terminal domain-containing protein, similar to AX110P (Daucus carota) GI:285739; contains Pfam profile PF01408: Oxidoreductase family NAD-binding Rossmann fold	2.8	2.7	0.1	0.9	100.0%	-5.4
8327	AT5G22600.1   expressed protein, ; expression supported by MPSS   chr5:7510026-7511635 FORWARD   Aliases: MDJ22.2, MDJ22_2	2.9	3.0	-0.1	-0.9	100.0%	-5.4
8328	AT5G24810.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr5:8516638-8522770 REVERSE   Aliases: F6A4.20, F6A4_20	8.1	7.8	0.3	0.9	100.0%	-4.5
8329	AT3G54150.1   embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531   chr3:20061622-20063759 REVERSE   Aliases: F24B22.110	3.4	3.6	-0.2	-0.9	100.0%	-4.8
8330	AT4G20890.1   Symbol: TUB9   tubulin beta-9 chain (TUB9), nearly identical to SP:P29517 Tubulin beta-9 chain {Arabidopsis thaliana}   chr4:11182103-11184083 FORWARD   Aliases: T13K14.50, T13K14_50	7.8	8.2	-0.4	-0.9	100.0%	-4.6
8331	AT5G45830.1   expressed protein, low similarity to tumor-related protein (Nicotiana glauca x Nicotiana langsdorffii) GI:688423	3.0	3.1	-0.1	-0.9	100.0%	-5.2
8332	AT1G24460.1   myosin-related, contains TIGRFAM TIGR01612: reticulocyte binding protein; similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II) (SP:Q99323) {Drosophila melanogaster} similar to EST gb:T76116	4.3	4.5	-0.2	-0.9	100.0%	-4.6
8333	AT2G03380.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:1028289-1030358 FORWARD   Aliases: T4M8.19, T4M8_19	3.1	3.0	0.1	0.9	100.0%	-5.1
8334	AT1G74220.1   expressed protein, similar to GB:AAD20071 from (Arabidopsis thaliana)   chr1:27916760-27917795 REVERSE   Aliases: F1O17.11, F1O17_11	2.7	2.6	0.1	0.9	100.0%	-5.3
8335	AT5G54570.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) (Prunus serotina)	3.2	3.4	-0.2	-0.9	100.0%	-4.9
8336	AT1G54460.1   expressed protein   chr1:20344267-20347196 REVERSE   Aliases: F20D21.28, F20D21_28	4.9	5.3	-0.3	-0.9	100.0%	-4.4
8337	ATCG00065.1   Symbol: RPS12A	4.6	5.7	-1.1	-0.9	100.0%	-4.2
8338	AT4G08380.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:5311090-5312403 REVERSE   Aliases: T28D5.70, T28D5_70	3.0	3.3	-0.3	-0.9	100.0%	-4.3
8339	AT5G62165.3   similar to MADS-box protein (AGL20) [Arabidopsis thaliana] (TAIR:At2g45660.1); similar to transcription factor SaMADS A (GB:AAB41526.1); contains InterPro domain Transcription factor, MADS-box (InterPro:IPR002100); contains InterPro domain Transcription factor, K-box (InterPro:IPR002487)	4.4	4.8	-0.4	-0.9	100.0%	-4.3
8340	AT1G22275.1   expressed protein   chr1:7867234-7872055 FORWARD   Aliases: None	3.5	3.4	0.1	0.9	100.0%	-5.0
8341	AT1G50280.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr1:18627366-18630063 REVERSE   Aliases: F14I3.11, F14I3_11	2.5	2.6	-0.1	-0.9	100.0%	-5.4
8342	AT5G56850.2   expressed protein   chr5:23002419-23004255 REVERSE   Aliases: MIK19.5, MIK19_5	4.8	5.0	-0.2	-0.9	100.0%	-4.8
8343	AT5G07130.1   laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)   chr5:2210570-2212621 FORWARD   Aliases: T28J14.70, T28J14_70	3.8	4.2	-0.3	-0.9	100.0%	-4.5
8344	AT2G20190.1   CLIP-associating protein (CLASP) -related, similar to CLIP-associating protein CLASP2 (GI:13508651) (Rattus norvegicus)   chr2:8718680-8726090 REVERSE   Aliases: T2G17.1, T2G17_1	4.0	3.8	0.2	0.9	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8345	AT5G59070.1   glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1   chr5:23862424-23864619 FORWARD   Aliases: K18B18.2, K18B18_2	2.7	2.9	-0.2	-0.8	100.0%	-5.0
8346	AT5G46800.1   Symbol: BOU   mitochondrial carnitine/acyl carrier, putative / a bout de souffle (BOU) / CAC-like protein, identical to SP:Q93XM7 Mitochondrial carnitine/acylcarnitine carrier-like protein (A BOUT DE SOUFFLE) (Carnitine/acylcarnitine translocase-like protein) (CAC-like protein) {Arabidopsis thaliana}; contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:19005858-19007991 REVERSE   Aliases: A BOUT DE SOUFFLE, MZA15.23, MZA15_23	8.9	8.0	0.9	0.8	100.0%	-4.2
8347	AT5G61830.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short chain dehydrogenase/reductase SDR family   chr5:24854561-24856196 FORWARD   Aliases: MAC9.11, MAC9_11	6.2	5.9	0.3	0.8	100.0%	-4.3
8348	AT5G17760.2   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr5:5860423-5862424 REVERSE   Aliases: MVA3.110, MVA3_110	3.0	2.9	0.1	0.8	100.0%	-5.1
8349	AT1G34000.2   Symbol: OHP2   light stress-responsive one-helix protein (OHP2), contains similarity to photosystem II 22 kDa protein GI:6006279 from (Arabidopsis thaliana)   chr1:12358350-12359205 REVERSE   Aliases: ONE HELIX PROTEIN 2	6.5	6.4	0.2	0.8	100.0%	-5.0
8350	AT1G77480.2   nucellin protein, putative, similar to nucellin GB:AAB96882 GI:2290202 (Hordeum vulgare) (nucellin: similar to aspartic protease and its specific expression in nucellar cells during degeneration)   chr1:29119452-29122232 REVERSE   Aliases: T5M16.7, T5M16_7	5.3	5.0	0.3	0.8	100.0%	-4.6
8351	AT3G08560.1   Symbol: VHA E2	3.5	3.3	0.2	0.8	100.0%	-4.7
8352	AT5G56570.1   expressed protein, similar to unknown protein (pir :T06019)   chr5:22919962-22921630 FORWARD   Aliases: MIK19.1, MIK19_1	2.4	2.5	-0.1	-0.8	100.0%	-5.5
8353	AT1G15530.1   receptor lectin kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains pfam domains PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr1:5339956-5341926 REVERSE   Aliases: T16N11.4, T16N11_4	4.1	3.9	0.2	0.8	100.0%	-4.8
8354	AT5G65120.1   expressed protein   chr5:26030108-26031866 FORWARD   Aliases: MQN23.5, MQN23_5	3.7	3.8	-0.2	-0.8	100.0%	-4.7
8355	AT1G78610.1   mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, contains Pfam profile PF00924: Mechanosensitive ion channel   chr1:29573923-29577019 REVERSE   Aliases: T30F21.6, T30F21_6	4.2	4.5	-0.3	-0.8	100.0%	-4.8
8356	AT1G02820.1   late embryogenesis abundant 3 family protein / LEA3 family protein, similar to late embryogenesis abundant protein 5 GI:2981167 from (Nicotiana tabacum); contains Pfam profile PF03242: Late embryogenesis abundant protein   chr1:623782-624474 REVERSE   Aliases: F22D16.18, F22D16_18	4.0	3.8	0.2	0.8	100.0%	-4.7
8357	AT3G50550.2   expressed protein, isoform contains a non-consensus AT donor site at intron 1   chr3:18770444-18771420 FORWARD   Aliases: T20E23.150	9.4	9.1	0.3	0.8	100.0%	-4.4
8358	AT4G03450.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr4:1529444-1531734 REVERSE   Aliases: F9H3.7, F9H3_7	3.0	2.9	0.1	0.8	100.0%	-5.1
8359	AT5G02280.1   synbindin, putative, similar to Swiss-Prot:Q9E556 synbindin (TRS23 homolog) (Mus musculus)   chr5:469324-470792 FORWARD   Aliases: T1E22.40, T1E22_40	7.5	7.9	-0.3	-0.8	100.0%	-4.3
8360	AT2G45990.4   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477679.1)   chr2:18926436-18928302 FORWARD   Aliases: F4I18.49	8.9	9.3	-0.4	-0.8	100.0%	-4.3
8361	AT3G18370.1   C2 domain-containing protein, contains Pfam profile: PF00168 C2 domain   chr3:6305981-6310626 FORWARD   Aliases: MYF24.9	5.1	4.7	0.4	0.8	100.0%	-4.4
8362	AT3G44830.1   lecithin:cholesterol acyltransferase family protein / LACT family protein, similar to lecithin:cholesterol acyltransferase (Rattus norvegicus) GI:2306762; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)   chr3:16379875-16383341 FORWARD   Aliases: F28D10.20	2.5	2.4	0.1	0.8	100.0%	-5.3
8363	AT1G14720.1   Symbol: XTR2   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR2), identical to endoxyloglucan transferase (Arabidopsis thaliana) GI:5533311   chr1:5066631-5068629 REVERSE   Aliases: ENDOXYLOGLUCAN TRANSFERASE A2, EXGT A2, F10B6.12, F10B6_12, XYLOGLUCAN ENDOTRANSGLYCOSYLASE 2, XYLOGLUCAN ENDOTRANSGLYCOSYLASE RELATED 2, XYLOGLUCAN ENDOTRANSGLYCOSYLASE RELATED PROTEIN	8.8	9.0	-0.3	-0.8	100.0%	-4.4
8364	AT2G27200.1   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function   chr2:11632527-11635149 FORWARD   Aliases: T22O13.3, T22O13_3	4.8	5.1	-0.3	-0.8	100.0%	-4.7
8365	AT3G61340.1   F-box family protein, contains F-box domain Pfam:PF00646	2.9	2.8	0.1	0.8	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8366	AT4G34270.1   TIP41-like family protein, contains Pfam PF04176: TIP41-like family; identical to cDNA putative cytoskeletal protein mRNA, partial cds GI:5031529   chr4:16403848-16406210 REVERSE   Aliases: F10M10.40, F10M10_40	7.1	6.9	0.1	0.8	100.0%	-5.0
8367	AT3G43300.1   guanine nucleotide exchange family protein, similar to SP:Q9Y6D5 Brefeldin A-inhibited guanine nucleotide-exchange protein 2 {Homo sapiens}; contains Pfam profile PF01369: Sec7 domain   chr3:15244884-15256022 REVERSE   Aliases: F7K15.150	5.3	5.6	-0.4	-0.8	100.0%	-4.7
8368	AT4G27030.1   expressed protein   chr4:13571957-13572928 FORWARD   Aliases: F10M23.370, F10M23_370	4.7	5.0	-0.4	-0.8	100.0%	-4.7
8369	AT1G73950.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr1:27803563-27808265 REVERSE   Aliases: F2P9.18, F2P9_18	5.5	5.3	0.2	0.8	100.0%	-4.5
8370	AT2G44020.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr2:18224635-18226461 REVERSE   Aliases: F6E13.15	5.2	5.4	-0.2	-0.8	100.0%	-4.7
8371	AT1G03180.2   expressed protein   chr1:773411-775344 FORWARD   Aliases: F15K9.21, F15K9_21	3.8	4.0	-0.2	-0.8	100.0%	-4.7
8372	AT1G02870.1   expressed protein   chr1:637214-638677 REVERSE   Aliases: F22D16.13, F22D16_13	6.7	6.1	0.6	0.8	100.0%	-4.3
8373	AT2G46390.1   expressed protein   chr2:19049374-19050133 REVERSE   Aliases: F11C10.8	11.5	11.7	-0.2	-0.8	100.0%	-4.9
8374	AT1G64630.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719; contains serine/threonine protein kinases active-site signature, PROSITE:PS00108   chr1:24023153-24026490 FORWARD   Aliases: F1N19.20, F1N19_20	7.2	7.4	-0.2	-0.8	100.0%	-4.6
8375	AT5G24440.1   Symbol: CID13   RNA-binding protein, putative. Contains PAM2, PABC binding domain.   chr5:8345405-8347779 REVERSE   Aliases: CID13, T31K7.2, T31K7_2	3.2	3.0	0.2	0.8	100.0%	-4.9
8376	AT2G14530.1   expressed protein   chr2:6194503-6197462 FORWARD   Aliases: T13P21.9, T13P21_9	3.9	3.7	0.2	0.8	100.0%	-5.0
8377	AT5G17580.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr5:5795304-5797180 FORWARD   Aliases: K10A8.60, K10A8_60	3.6	4.0	-0.4	-0.8	100.0%	-4.4
8378	AT4G00270.1   DNA-binding storekeeper protein-related, contains similarity to storekeeper protein (Solanum tuberosum) gi:14268476:emb:CAC39398; contains PF04504: Protein of unknown function, DUF573   chr4:117152-118541 REVERSE   Aliases: A_IG005I10.11, A_IG005I10_11, F5I10.11, F5I10_11	5.0	4.8	0.2	0.8	100.0%	-4.9
8379	AT5G23120.1   Symbol: HCF136	8.8	8.4	0.3	0.8	100.0%	-4.3
8380	AT3G60620.1   phosphatidate cytidyltransferase family protein, contains Pfam profile: PF01148 phosphatidate cytidyltransferase   chr3:22417381-22419572 FORWARD   Aliases: T4C21.30	3.7	3.5	0.1	0.8	100.0%	-4.9
8381	AT1G05800.1   lipase class 3 family protein, similar to DEFECTIVE IN ANOTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase   chr1:1741203-1742618 FORWARD   Aliases: T20M3.6	2.7	2.8	-0.1	-0.8	100.0%	-5.1
8382	AT2G22630.1   Symbol: AGL17   MADS-box protein (AGL17), nearly identical to MADS-box protein AGL17 (Arabidopsis thaliana) GI:862648   chr2:9625452-9628961 FORWARD   Aliases: AGAMOUS LIKE 17, T9I22.7, T9I22_7	2.6	2.8	-0.1	-0.8	100.0%	-4.8
8383	AT1G24350.1   expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963   chr1:8638509-8640476 REVERSE   Aliases: F3I6.29, F3I6_29	5.5	5.2	0.3	0.8	100.0%	-4.9
8384	AT4G02770.1   photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD1), similar to SP:P12353 Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) {Spinacia oleracea}; contains Pfam profile PF02531: PsaD	8.3	7.8	0.5	0.8	100.0%	-4.1
8385	AT5G05190.1   expressed protein, similar to unknown protein (emb:CAB88044.1)   chr5:1541522-1544365 FORWARD   Aliases: K2A11.6, K2A11_6	4.8	4.6	0.2	0.8	100.0%	-4.7
8386	AT1G30110.1   diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative, similar to diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase GI:1888557 from (Lupinus angustifolius), (Hordeum vulgare subsp. vulgare) GI:2564253; contains Pfam profile PF00293: NUDIX domain   chr1:10582076-10584052 FORWARD   Aliases: T2H7.9, T2H7_9	5.1	4.8	0.2	0.8	100.0%	-4.7
8387	AT4G11560.1   bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain   chr4:6999890-7003487 REVERSE   Aliases: F25E4.180, F25E4_180	7.0	7.3	-0.4	-0.8	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8388	AT2G28520.1   vacuolar proton ATPase, putative, similar to Swiss-Prot:Q93050 vacuolar proton translocating ATPase 116 kDa subunit A isoform 1 (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit, Vacuolar proton pump subunit 1, Vacuolar adenosine triphosphatase subunit Ac116) (Homo sapiens)   chr2:12216973-12222972 FORWARD   Aliases: T17D12.8, T17D12_8	5.4	5.1	0.2	0.8	100.0%	-4.6
8389	AT1G11840.5   Symbol: ATGLX1	12.0	11.6	0.4	0.8	100.0%	-4.7
8390	AT5G66080.1   protein phosphatase 2C family protein / PP2C family protein, similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain   chr5:26440645-26442632 REVERSE   Aliases: K2A18.16, K2A18_16	3.7	3.5	0.2	0.8	100.0%	-4.9
8391	AT1G34400.1   expressed protein   chr1:12565970-12566593 REVERSE   Aliases: F7P12.11, F7P12_11	4.5	4.3	0.3	0.8	100.0%	-4.4
8392	AT2G24290.1   expressed protein   chr2:10345759-10347201 FORWARD   Aliases: T28I24.2, T28I24_2	5.4	5.0	0.4	0.8	100.0%	-4.4
8393	AT1G34220.2   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292   chr1:12462442-12465978 REVERSE   Aliases: F23M19.10, F23M19_10	5.5	5.2	0.3	0.8	100.0%	-4.7
8394	AT1G61620.1   expressed protein, contains Pfam profile: PF01363 FYVE zinc finger   chr1:22741208-22743095 FORWARD   Aliases: T25B24.3, T25B24_3	8.6	8.1	0.4	0.8	100.0%	-4.4
8395	AT4G27230.1   histone H2A, putative, strong similarity to histone H2A Arabidopsis thaliana GI:7595337, Triticum aestivum GI:536892, Picea abies SP:P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr4:13637345-13638425 REVERSE   Aliases: M4I22.40, M4I22_40	8.7	9.2	-0.6	-0.8	100.0%	-4.3
8396	AT2G42560.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to LEA protein (Glycine max) GI:1389897; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr2:17721716-17723990 REVERSE   Aliases: F14N22.17, F14N22_17	4.3	4.0	0.3	0.8	100.0%	-4.8
8397	AT3G26570.2   Symbol: PHT2;1	7.8	7.3	0.5	0.8	100.0%	-3.9
8398	AT3G15310.1   expressed protein   chr3:5152106-5153649 REVERSE   Aliases: K7L4.11	2.0	2.1	-0.1	-0.8	100.0%	-5.6
8399	AT2G06255.1   expressed protein   chr2:2457570-2459808 FORWARD   Aliases: None	3.7	3.5	0.1	0.8	100.0%	-4.9
8400	AT1G71860.3   Symbol: PTP1   similar to protein tyrosine phosphatase; PTP [Phaseolus vulgaris] (GB:AAT35563.1); contains InterPro domain Protein tyrosine phosphatase, catalytic region (InterPro:IPR003595); contains InterPro domain Tyrosine specific protein phosphatase (InterPro:IPR000242); contains InterPro domain Tyrosine specific protein phosphatase and dual specificity protein phosphatase (InterPro:IPR000387)   chr1:27030373-27032754 FORWARD   Aliases: ATPTP1, F14O23.24, F14O23_24, PROTEIN TYROSINE PHOSPHATASE 1	8.1	8.6	-0.5	-0.8	100.0%	-4.6
8401	AT4G17590.1   nucleolar protein-related, contains weak similarity to Swiss-Prot:P40991 nucleolar protein NOP2 (Saccharomyces cerevisiae)   chr4:9801989-9802604 REVERSE   Aliases: DL4830C, FCAALL.66	2.6	2.5	0.1	0.8	100.0%	-5.0
8402	AT1G13730.1   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein, contains Pfam profiles PF02136: Nuclear transport factor 2 (NTF2) domain, PF00076: RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)   chr1:4709825-4712546 FORWARD   Aliases: F21F23.16, F21F23_16	3.8	4.0	-0.2	-0.8	100.0%	-4.7
8403	AT4G28160.1   hydroxyproline-rich glycoprotein family protein, similar to Putative cell wall protein precursor (Swiss-Prot:P47925) (Arabidopsis thaliana)   chr4:13980385-13981007 FORWARD   Aliases: F26K10.40, F26K10_40	2.9	2.8	0.2	0.8	100.0%	-5.1
8404	AT2G30150.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:12881783-12883199 FORWARD   Aliases: T27E13.11, T27E13_11	8.5	8.8	-0.3	-0.8	100.0%	-4.5
8405	AT1G12410.1   Symbol: CLPR2   ATP-dependent Clp protease proteolytic subunit (ClpP2), identical to nClpP2 GI:5360589 from (Arabidopsis thaliana)   chr1:4223035-4225112 FORWARD   Aliases: CLPP2, F5O11.13, F5O11_13, NCLPP2	8.8	9.2	-0.4	-0.8	100.0%	-4.4
8406	AT5G44850.1   expressed protein, strong similarity to unknown protein (gb AAC79136.1)   chr5:18125531-18126820 FORWARD   Aliases: K21C13.2, K21C13_2	2.6	2.7	-0.2	-0.8	100.0%	-5.0
8407	AT2G13370.1   chromodomain-helicase-DNA-binding family protein / CHD family protein, similar to SP:O14647 Chromodomain-helicase-DNA-binding protein 2 (CHD-2) {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00385: 'chromo' (CHRromatin Organization MOfifier)   chr2:5551263-5563546 REVERSE   Aliases: F14O4.6, F14O4_6	5.9	6.3	-0.4	-0.8	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8408	AT4G02790.1   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function   chr4:1247399-1249588 FORWARD   Aliases: T5J8.11, T5J8_11	6.6	6.9	-0.3	-0.8	100.0%	-4.2
8409	AT3G13570.1   Symbol: SCL30a	6.7	6.4	0.3	0.8	100.0%	-4.3
8410	AT2G04900.1   expressed protein   chr2:1722478-1723828 FORWARD   Aliases: F1O13.3	9.8	9.6	0.2	0.8	100.0%	-4.9
8411	AT3G51280.1   male sterility MS5, putative, similar to male sterility MS5 (Arabidopsis thaliana) GI:3859112; contains Pfam profile PF00515 TPR Domain   chr3:19048142-19049930 FORWARD   Aliases: F24M12.320	3.7	3.5	0.2	0.8	100.0%	-4.4
8412	AT4G15093.1   catalytic LigB subunit of aromatic ring-opening dioxygenase family, contains Pfam PF02900: Catalytic LigB subunit of aromatic ring-opening dioxygenase   chr4:8618370-8619643 FORWARD   Aliases: None	9.6	9.2	0.3	0.8	100.0%	-4.8
8413	AT4G17860.1   hypothetical protein, predicted protein, Arabidopsis thaliana, PATCHX:E327543 contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr4:9924711-9927155 REVERSE   Aliases: T6K21.40, T6K21_40	2.8	2.6	0.1	0.8	100.0%	-5.0
8414	AT1G10240.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr1:3356682-3359840 REVERSE   Aliases: F14N23.12, F14N23_12	5.4	5.6	-0.2	-0.8	100.0%	-4.5
8415	AT1G75340.1   zinc finger (CCCH-type) family protein, weak similarity to Nucleoporin NUP42 (Nuclear pore protein NUP42) (Swiss-Prot:P49686) (Saccharomyces cerevisiae); contains Pfam profile PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:28272631-28275609 REVERSE   Aliases: F1B16.12, F1B16_12	4.5	4.8	-0.2	-0.8	100.0%	-4.4
8416	AT5G45510.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr5:18461884-18466673 FORWARD   Aliases: MFC19.18, MFC19_18	5.6	5.9	-0.4	-0.8	100.0%	-4.3
8417	AT4G03940.1   expressed protein   chr4:1873622-1875231 FORWARD   Aliases: T24M8.7, T24M8_7	4.9	4.6	0.3	0.8	100.0%	-4.6
8418	AT2G01680.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr2:306384-308629 FORWARD   Aliases: T8O11.15, T8O11_15	7.1	6.8	0.3	0.8	100.0%	-4.6
8419	AT1G43170.3   Symbol: ARP1   similar to 60S ribosomal protein L3 (RPL3B) [Arabidopsis thaliana] (TAIR:At1g61580.1); similar to ribosomal protein L3 [Triticum aestivum] (GB:AAQ62076.1); similar to ribosomal protein L3 [Triticum aestivum] (GB:AAQ62074.1); similar to ribosomal protein L3 [Lycopersicon esculentum] (GB:AAR17783.1); similar to ribosomal protein L3A [Nicotiana tabacum] (GB:AAQ96335.1); similar to ribosomal protein L3 [Triticum aestivum] (GB:AAQ21399.1); contains InterPro domain Ribosomal protein L3 (InterPro:IPR000597)   chr1:16269213-16271310 FORWARD   Aliases: ARABIDOPSIS RIBOSOMAL PROTEIN 1, EMB2207, EMBRYO DEFECTIVE 2207, F1I21.1, F1I21_1, RPL3A	11.8	12.0	-0.3	-0.8	100.0%	-4.9
8420	AT3G01580.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:223536-225461 REVERSE   Aliases: F4P13.34, F4P13_34	2.3	2.4	-0.1	-0.8	100.0%	-5.6
8421	AT2G27960.1   Symbol: CKS1   cyclin-dependent kinase / CDK (CKS1), identical to Cks1 protein (Arabidopsis thaliana) gi:2274859:emb:CAA03859   chr2:11917803-11918703 REVERSE   Aliases: CATALYTIC SUBUNIT OF CYCLIN DEPENDENT KINASE, CDK subunit 1, CKS1, CKS1AT, P10CKS1AT, SUC1, T1E2.12, T1E2_12	9.9	9.5	0.4	0.8	100.0%	-4.5
8422	AT5G43740.2   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.2	3.0	0.2	0.8	100.0%	-4.9
8423	AT4G36630.2   Symbol: EMB2754   expressed protein   chr4:17271834-17276622 REVERSE   Aliases: AP22.59, AP22_59, EMB2754, EMBRYO DEFECTIVE 2754	5.0	5.2	-0.2	-0.8	100.0%	-4.7
8424	AT3G14290.1   Symbol: PAE2   20S proteasome alpha subunit E2 (PAE2), identical to 20S proteasome subunit PAE2 GB:AAC32061 from (Arabidopsis thaliana)	10.1	10.3	-0.2	-0.8	100.0%	-4.8
8425	AT3G23840.1   transferase family protein, low similarity to hypersensitivity-related gene (Nicotiana tabacum) GI:1171577, acetyl-CoA:benzylalcohol acetyltransferase (Clarkia concinna) GI:6166330; contains Pfam profile PF02458: Transferase family   chr3:8611133-8612697 FORWARD   Aliases: F14O13.22	5.0	4.7	0.3	0.8	100.0%	-4.3
8426	AT1G63490.1   transcription factor jumonji (jmc) domain-containing protein, similar to PLU-1 protein (GI:4902724) (Homo sapiens) and PLU1 (GI:22726257) (Mus musculus); similar to Retinoblastoma-binding protein 2 (RBBP-2) (SP:P29375) {Homo sapiens}; contains Pfam PF02373: jmc domain   chr1:23548321-23555695 REVERSE   Aliases: F2K11.14, F2K11_14	4.2	4.5	-0.3	-0.8	100.0%	-4.4
8427	AT1G77140.1   Symbol: VPS45   vacuolar protein sorting protein 45, putative / VPS45p, putative, identical to vacuolar protein sorting homolog VPS45p (Arabidopsis thaliana) gi:2921406:gb:AAC39472   chr1:28988919-28992877 FORWARD   Aliases: ATVPS45, T14N5.2, T14N5_2, VACUOLAR PROTEIN SORTING 45, VPS45	4.4	4.6	-0.2	-0.8	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8428	AT5G05030.1   expressed protein, contains similarity to carboxyl-terminal proteinase contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr5:1484178-1486066 REVERSE   Aliases: MUG13.11, MUG13_11	3.1	2.9	0.2	0.8	100.0%	-4.9
8429	AT5G61980.1   ARF GTPase-activating domain-containing protein, similar to GCN4-complementing protein (GCP1) GI:6465806 from (Arabidopsis thaliana)   chr5:24911698-24916404 FORWARD   Aliases: K22G18.9, K22G18_9	2.9	2.8	0.1	0.8	100.0%	-5.2
8430	AT4G01720.1   Symbol: WRKY47	2.6	2.9	-0.3	-0.8	100.0%	-4.1
8431	AT5G05210.1   nucleolar matrix protein-related, contains Pfam domain, PF04935: Surfeit locus protein 6	8.6	9.0	-0.5	-0.8	100.0%	-4.5
8432	AT2G22180.1   hydroxyproline-rich glycoprotein family protein   chr2:9436049-9436924 FORWARD   Aliases: T26C19.16, T26C19_16	2.8	2.7	0.1	0.8	100.0%	-5.3
8433	AT1G30100.1   Symbol: NCED5   9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, similar to 9-cis-epoxycarotenoid dioxygenase GI:6715257 from (Phaseolus vulgaris)   chr1:10571367-10573136 FORWARD   Aliases: ATNCED5, T2H7.10, T2H7_10	2.3	2.2	0.1	0.8	100.0%	-5.6
8434	AT3G46630.1   expressed protein, contains similarity to defective chloroplasts and leaves protein SP:Q42463 from (Lycopersicon esculentum)   chr3:17191919-17193414 REVERSE   Aliases: F12A12.150	7.2	6.9	0.3	0.8	100.0%	-4.6
8435	AT5G49290.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077.gb:AAC15780   chr5:19997421-20001095 FORWARD   Aliases: K21P3.17, K21P3_17	2.9	3.0	-0.1	-0.8	100.0%	-5.2
8436	AT2G20585.2   expressed protein   chr2:8872180-8873848 FORWARD   Aliases: None	6.4	6.8	-0.4	-0.8	100.0%	-4.2
8437	AT3G02740.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr3:590517-593174 FORWARD   Aliases: F13E7.32, F13E7_32	9.3	9.1	0.2	0.8	100.0%	-4.9
8438	AT4G37040.1   Symbol: MAP1D   metalloproteinase M24 family protein, similar to SP:O33343 Methionine aminopeptidase (EC 3.4.11.18) (Peptidase M) {Mycobacterium tuberculosis}; contains Pfam profile PF00557: metalloproteinase family M24   chr4:17455133-17457351 FORWARD   Aliases: METHIONINE AMINOPEPTIDASE 1D	6.5	6.9	-0.4	-0.8	100.0%	-4.4
8439	AT3G57240.1   Symbol: BG3   similar to glycosyl hydrolase family 17 protein [Arabidopsis thaliana] (TAIR:At3g57260.1); similar to beta-1,3-glucanase (GB:AAA32756.1); contains InterPro domain Glycoside hydrolase, family 17 (InterPro:IPR000490)   chr3:21192721-21194053 REVERSE   Aliases: BETA 1,3 GLUCANASE 3, F28O9.90	2.9	3.0	-0.1	-0.8	100.0%	-5.2
8440	AT1G29850.2   double-stranded DNA-binding family protein, contains Pfam profile: PF01984 double-stranded DNA-binding domain   chr1:10447747-10449930 FORWARD   Aliases: F1N18.11, F1N18_11	11.7	11.4	0.4	0.8	100.0%	-5.0
8441	AT4G17090.1   Symbol: CT BMY	3.4	3.3	0.2	0.8	100.0%	-4.8
8442	AT5G58530.1   glutaredoxin family protein   chr5:23677612-23678575 FORWARD   Aliases: MQJ2.15, MQJ2_15	4.5	4.6	-0.1	-0.8	100.0%	-5.1
8443	AT1G15950.1   Symbol: CCR1   cinnamoyl-CoA reductase, putative, nearly identical to CCR1 (GI:12034897), similar to cinnamoyl CoA reductase GI:2058310 from (Eucalyptus gunnii)   chr1:5478748-5482159 FORWARD   Aliases: CINNAMOYL COA REDUCTASE, CINNAMOYL COA REDUCTASE 1, IRREGULAR XYLEM 4, IRX4, T24D18.5, T24D18_5	10.7	11.2	-0.5	-0.8	100.0%	-4.8
8444	AT5G09730.1   Symbol: BXL3   glycosyl hydrolase family 3 protein, beta-xylosidase, Hypocrea jecorina, EMBL:Z69257   chr5:3015248-3018263 REVERSE   Aliases: ATBXL3, BETA XYLOSIDASE 3, F17I14.80, F17I14_80	2.8	3.0	-0.2	-0.8	100.0%	-4.9
8445	AT2G30170.1   expressed protein   chr2:12886757-12888575 REVERSE   Aliases: T27E13.9, T27E13_9	6.6	6.3	0.3	0.8	100.0%	-4.4
8446	AT5G07810.1   SNF2 domain-containing protein / helicase domain-containing protein / HNH endonuclease domain-containing protein, similar to HepA-related protein HARP (Homo sapiens) GI:6693791; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF01844: HNH endonuclease   chr5:2491284-2498485 REVERSE   Aliases: MXM12.5, MXM12_5	2.5	2.7	-0.2	-0.8	100.0%	-4.7
8447	AT1G52310.1   protein kinase family protein / C-type lectin domain-containing protein, contains protein kinase domain, Pfam:PF00069, PF00059 Lectin C-type domain   chr1:19481793-19484279 FORWARD   Aliases: F19K6.8, F19K6_8	5.7	5.8	-0.2	-0.8	100.0%	-4.8
8448	AT3G11100.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189   chr3:3476220-3477411 REVERSE   Aliases: F11B9.6	3.6	3.4	0.2	0.8	100.0%	-4.8
8449	AT1G43660.1   hypothetical protein   chr1:16452800-16453084 FORWARD   Aliases: F2J6.16, F2J6_16	2.6	2.6	-0.1	-0.8	100.0%	-5.8
8450	AT4G31870.1   Symbol: ATGPX7	3.9	3.7	0.2	0.8	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8451	AT2G18160.1   Symbol: GBF5   bZIP transcription factor family protein, contains a bZIP transcription factor basic domain signature (PDOC00036)   chr2:7905094-7906324 REVERSE   Aliases: F8D23.6, F8D23_6, TRANSCRIPTION FACTOR GBF5	8.3	7.9	0.4	0.8	100.0%	-4.9
8452	AT3G62940.2   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr3:23273925-23275646 REVERSE   Aliases: T20O10.40	8.5	8.7	-0.2	-0.8	100.0%	-4.5
8453	AT3G59290.1   epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain;	5.8	6.2	-0.5	-0.8	100.0%	-4.6
8454	AT4G39980.1   Symbol: DHS1   2-dehydro-3-deoxyphosphoheptonate aldolase 1 / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 1 / DAHP synthetase 1 (DHS1), nearly identical to SP:P29965   chr4:18539575-18542087 FORWARD   Aliases: 3 DEOXY D ARABINO HEPTULOSONATE 7 PHOSPHATE SYNTHASE 1, 3 DEOXY D ARABINO HEPTULOSONATE Y PHOSPHATE SYNTHASE, T5J17.150, T5J17_150	10.4	10.7	-0.3	-0.8	100.0%	-5.0
8455	AT5G56620.1   Symbol: ANAC099   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr5:22935747-22938365 REVERSE   Aliases: ANAC099, MIK19.7, MIK19_7	2.9	2.8	0.1	0.8	100.0%	-5.4
8456	AT4G19490.2   expressed protein   chr4:10615807-10623532 FORWARD   Aliases: F24J7.50, F24J7_50	3.4	3.6	-0.2	-0.8	100.0%	-4.6
8457	AT5G20520.1   Symbol: WAV2   expressed protein   chr5:6943156-6946451 REVERSE   Aliases: F7C8.110, F7C8_110	6.4	6.2	0.2	0.8	100.0%	-4.6
8458	AT5G14440.2   similar to surfeit locus protein 2 family protein / SURF2 family protein [Arabidopsis thaliana] (TAIR:At5g40570.1); similar to hypothetical protein DDB0206414 [Dictyostelium discoideum] (GB:EAL67308.1); contains InterPro domain Surfeit locus 2 (InterPro:IPR008833)	9.9	9.5	0.4	0.8	100.0%	-4.9
8459	AT5G11690.1   Symbol: ATTIM17 3   mitochondrial import inner membrane translocase subunit Tim17, putative, similar to SP:Q9SP35 Mitochondrial import inner membrane translocase subunit TIM17 {Arabidopsis thaliana}; contains Pfam profile PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr5:3761245-3762347 FORWARD   Aliases: T22P22.80, T22P22_80	8.4	8.1	0.3	0.8	100.0%	-4.2
8460	AT4G13380.1   heavy-metal-associated domain-containing protein, low similarity to wound-responsive gene KED (Nicotiana tabacum) GI:8096269; contains Pfam profile PF00403: Heavy-metal-associated domain   chr4:7781778-7782549 FORWARD   Aliases: T9E8.120, T9E8_120	3.1	3.2	-0.1	-0.8	100.0%	-5.3
8461	AT3G56830.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g65420.1); similar to antigen receptor-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD29174.1); contains InterPro domain Protein of unknown function DUF565 (InterPro:IPR007572)   chr3:21053468-21055254 REVERSE   Aliases: T8M16.160	6.0	5.7	0.3	0.8	100.0%	-4.2
8462	AT4G05410.1   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); U3 snoRNP-associated 55-kDa protein, Homo sapiens, gb:NP_004695; Vegetatible incompatibility protein HET-E-1 (SP:Q00808) (Podospora anserina)   chr4:2742929-2745624 REVERSE   Aliases: C6L9.90, C6L9_90	5.9	6.1	-0.2	-0.8	100.0%	-4.5
8463	AT5G66920.1   Symbol: SKS17   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr5:26740076-26742852 FORWARD   Aliases: MUD21.18, MUD21_18, SKS17	5.1	5.6	-0.5	-0.8	100.0%	-4.5
8464	AT3G43740.2   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to somatic embryogenesis receptor-like kinase 2 (Arabidopsis thaliana) gi:14573457;gb:AAK68073   chr3:15655114-15656433 FORWARD   Aliases: T28A8.30	6.3	6.6	-0.3	-0.8	100.0%	-4.3
8465	AT2G02540.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, contains Pfam domain, PF04770: ZF-HD protein dimerisation region   chr2:683646-685308 FORWARD   Aliases: T8K22.16, T8K22_16	2.2	2.3	-0.1	-0.8	100.0%	-5.5
8466	AT5G24030.1   C4-dicarboxylate transporter/malic acid transport family protein, weak similarity to SP:P25396 Tellurite resistance protein tehA. {Escherichia coli}; contains Pfam profile PF03595: C4-dicarboxylate transporter/malic acid transport protein   chr5:8118320-8122755 REVERSE   Aliases: MZF18.9, MZF18_9	3.7	3.4	0.3	0.8	100.0%	-4.3
8467	AT2G45570.1   Symbol: CYP76C2   cytochrome P450 76C2, putative (CYP76C2) (YLS6), identical to SP:O64637 Cytochrome P450 76C2 (EC 1.14.-.-) {Arabidopsis thaliana}, cDNA YLS6 mRNA for cytochrome P450 (CYP76C2), partial cds GI:13122289   chr2:18786867-18789032 REVERSE   Aliases: F17K2.10	3.2	3.0	0.2	0.8	100.0%	-4.6
8468	AT5G17860.1   cation exchanger, putative (CAX7), contains similarity to SWISS-PROT:Q9HC58 NKX3_HUMAN Sodium/potassium/calcium exchanger 3 precursor {Homo sapiens}; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563   chr5:5902396-5904382 REVERSE   Aliases: MPI7.2	3.9	3.7	0.1	0.8	100.0%	-5.0
8469	AT4G30280.1   Symbol: ATXTH18   putative xyloglucan endotransglycosylase/hydrolase, expressed in the mature or basal regions of both the main and lateral roots, but not in the tip of these roots where cell division occurs.   chr4:14825814-14827053 REVERSE   Aliases: ATXTH18, F17I23.380, F17I23_380, XYLOGLUCAN ENDOTRANGLUCOSYLASE/HYDROLASE 18	3.1	3.5	-0.4	-0.8	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8470	AT1G21240.1   Symbol: WAK3   wall-associated kinase, putative, similar to wall-associated kinase 1 (Arabidopsis thaliana) GI:3549626; expressed in leaves and stems & induced by salicylic acid or INA (PMID:10380805)   chr1:7434292-7436819 FORWARD   Aliases: F16F4.8, F16F4_8, WALL ASSOCIATED KINASE 3	2.3	2.2	0.1	0.8	100.0%	-5.5
8471	AT3G56860.3   UBP1 interacting protein 2a (UBA2a), identical to UBP1 interacting protein 2a (Arabidopsis thaliana) GI:19682816; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:21059864-21063216 REVERSE   Aliases: T8M16.190	6.2	5.9	0.2	0.8	100.0%	-4.6
8472	AT3G26130.1   glycosyl hydrolase family 5 protein / cellulase family protein, contains Pfam profile: PF00150 cellulase (glycosyl hydrolase family 5)   chr3:9554945-9556848 REVERSE   Aliases: MTC11.2	2.7	2.8	-0.1	-0.8	100.0%	-5.0
8473	AT5G08450.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28770.1); similar to LOC495149 protein [Xenopus laevis] (GB:AAH84352.1); contains domain HIS_RICH (PS50316)   chr5:2727822-2732888 REVERSE   Aliases: F8L15.180, F8L15_180	5.3	5.5	-0.2	-0.8	100.0%	-4.9
8474	AT1G70080.1   terpene synthase/cyclase family protein, similar to (+)-delta-cadinene synthase (Gossypium hirsutum)(GI:8389329), sesquiterpene synthases (GI:11934937)(Lycopersicon hirsutum), (GI:11934933)(Lycopersicon esculentum); contains Pfam profile: PF01397: Terpene synthase family   chr1:26398332-26401228 REVERSE   Aliases: F20P5.19, F20P5_19	2.7	2.6	0.1	0.8	100.0%	-5.1
8475	AT2G19710.1   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292   chr2:8513216-8517163 FORWARD   Aliases: F6F22.26, F6F22_26	4.1	3.9	0.2	0.8	100.0%	-4.6
8476	AT1G43860.1   expressed protein   chr1:16624508-16626909 REVERSE   Aliases: F28H19.11, F28H19_11	7.4	7.7	-0.2	-0.8	100.0%	-4.5
8477	AT1G62340.1   Symbol: ALE1   subtilisin-like serine protease / abnormal leaf shape1 (ALE1), identical to subtilisin-like serine protease (Arabidopsis thaliana) GI:16444944   chr1:23054667-23059337 REVERSE   Aliases: ABNORMAL LEAF SHAPE, ABNORMAL LEAF SHAPE 1, ALE, F24O1.36, F24O1_36	2.3	2.4	-0.1	-0.8	100.0%	-5.3
8478	AT5G53590.1   auxin-responsive family protein, similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) (Vigna radiata)   chr5:21789047-21790020 FORWARD   Aliases: MNC6.13, MNC6_13	6.3	6.0	0.4	0.8	100.0%	-4.5
8479	ATCG00630.1   Symbol: PSAJ   PSI J protein   chrC:66929-67063 FORWARD   Aliases: PSAJ	5.4	4.6	0.9	0.8	100.0%	-4.3
8480	AT1G15960.1   Symbol: NRAMP6	3.0	2.9	0.1	0.8	100.0%	-5.1
8481	AT2G41490.1   Symbol: GPT   UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase, identical to GI:5804772   chr2:17308773-17311289 FORWARD   Aliases: T26J13.8, T26J13_8, UDP GLCNAC:DOLICHOL PHOSPHATE GLCNAC 1 P TRANSFERASE	7.4	7.7	-0.3	-0.8	100.0%	-4.3
8482	AT1G32020.1   F-box family protein, similar to heat shock transcription factor HSF30-like protein GI:9759202 from (Arabidopsis thaliana) ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:11512532-11513047 REVERSE   Aliases: T12O21.8, T12O21_8	2.7	2.8	-0.1	-0.8	100.0%	-5.1
8483	AT5G38360.1   similar to hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] (TAIR:At1g33990.1); similar to hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] (TAIR:At1g26360.1); similar to hypothetical protein LIC11465 [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130] (GB:YP_001426.1); similar to Predicted hydrolases or acyltransferases, alpha/beta hydrolase superfamily [Leptospira interrogans serovar Lai str. 56601] (GB:NP_712682.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr5:15348941-15350797 REVERSE   Aliases: MXI10.2, MXI10_2	3.8	4.0	-0.2	-0.8	100.0%	-4.6
8484	AT4G35230.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:16755123-16758096 REVERSE   Aliases: F23E12.210, F23E12_210	9.4	9.7	-0.2	-0.8	100.0%	-4.8
8485	AT4G30650.1   hydrophobic protein, putative / low temperature and salt responsive protein, putative, similar to SP:Q9ZNQ7 Hydrophobic protein RCI2A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}; contains Pfam profile PF01679: Uncharacterized protein family   chr4:14954326-14954974 FORWARD   Aliases: F17I23.10, F17I23_10	7.6	8.0	-0.4	-0.8	100.0%	-4.5
8486	AT1G20200.1   Symbol: EMB2719   26S proteasome regulatory subunit S3, putative (RPN3), similar to SP:Q06364 from (Daucus carota)   chr1:7001192-7004409 REVERSE   Aliases: EMB2719, EMBRYO DEFECTIVE 2719, T20H2.3, T20H2_3	7.9	8.6	-0.7	-0.8	100.0%	-4.4
8487	AT3G61200.1   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein   chr3:22668430-22669365 REVERSE   Aliases: T20K12.100	9.1	8.8	0.3	0.8	100.0%	-4.7
8488	AT5G09250.1   Symbol: KIWI   transcriptional coactivator p15 (PC4) family protein, similar to SP:P11031 Activated RNA polymerase II transcriptional coactivator p15 precursor (PC4) (p14) (Single-stranded DNA binding protein p9) {Mus musculus}; contains Pfam profile PF02229: Transcriptional Coactivator p15 (PC4)   chr5:2875233-2876576 REVERSE   Aliases: T2K12.10	5.5	5.3	0.2	0.8	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8489	AT1G04170.1   Symbol: EIF2 GAMMA   eukaryotic translation initiation factor 2 subunit 3, putative / eIF2S3, putative / eIF-2-gamma, putative, similar to gb:U37354 from <i>S. pombe</i> . ESTs gb:T41979, gb:N37284 and gb:N37529 come from this gene	6.6	7.1	-0.6	-0.8	100.0%	-4.4
8490	AT5G06130.2   chaperone protein dnaJ-related, similar to unknown protein (pir::T00468); contains Pfam PF00684 : DnaJ central domain (4 repeats)   chr5:1853450-1855873 REVERSE   Aliases: K16F4.10, K16F4_10	8.2	7.8	0.4	0.8	100.0%	-4.4
8491	AT4G10040.1   cytochrome c, putative, similar to cytochrome c (Pumpkin, Winter squash) SWISS-PROT:P00051   chr4:6276995-6278501 FORWARD   Aliases: F28M11.5	10.1	10.5	-0.3	-0.8	100.0%	-4.5
8492	AT4G27380.1   expressed protein   chr4:13701262-13703156 FORWARD   Aliases: F27G19.4	8.5	8.9	-0.4	-0.8	100.0%	-4.2
8493	AT1G31680.1   copper amine oxidase family protein, contains similarity to amine oxidase (copper-containing) precursor ( <i>Pisum sativum</i> ) SWISS-PROT:Q43077   chr1:11343961-11344746 FORWARD   Aliases: F27M3.12, F27M3_12	2.8	2.9	-0.2	-0.8	100.0%	-5.0
8494	AT5G57100.1   transporter-related, low similarity to GDP-fucose transporter ( <i>Caenorhabditis elegans</i> ) GI:13940504, phosphoenolpyruvate/phosphate translocator precursor ( <i>Mesembryanthemum crystallinum</i> ) GI:9295275   chr5:23123528-23125824 REVERSE   Aliases: MUL3.4, MUL3_4	6.5	6.2	0.3	0.8	100.0%	-4.4
8495	AT3G58230.1   hypothetical protein   chr3:21577837-21578373 REVERSE   Aliases: F9D24.140	2.7	2.8	-0.1	-0.8	100.0%	-5.1
8496	AT5G16510.2   reversibly glycosylated polypeptide, putative, similar to reversibly glycosylatable polypeptide (RGP1) ( <i>Pisum sativum</i> ) GI:2130521; contains Pfam profile PF03214: Reversibly glycosylated polypeptide   chr5:5392642-5394567 FORWARD   Aliases: MQK4.26, MQK4_26	7.3	7.7	-0.4	-0.8	100.0%	-4.3
8497	AT4G32270.1   UDP-sugar transporter-related, contains weak similarity to Swiss-Prot:Q95YI5 UDP-sugar transporter UST74c ( <i>Drosophila melanogaster</i> )   chr4:15575021-15579695 REVERSE   Aliases: F10M6.90, F10M6_90	4.9	4.6	0.2	0.8	100.0%	-4.8
8498	AT5G61770.3   brix domain-containing protein, contains Pfam domain, PF04427: Brix domain   chr5:24832863-24834869 FORWARD   Aliases: MAC9.8, MAC9_8	5.6	6.0	-0.4	-0.8	100.0%	-4.3
8499	AT2G20440.1   RabGAP/TBC domain-containing protein, similar to SP:P09379 GTPase-activating protein GYP7 (Fragment) { <i>Yarrowia lipolytica</i> }; contains Pfam profile PF00566: TBC domain   chr2:8817857-8820604 REVERSE   Aliases: T13C7.3, T13C7_3	4.7	4.3	0.3	0.8	100.0%	-4.2
8500	AT1G21540.1   AMP-binding protein, putative, strong similarity to AMP-binding protein GI:1903034 from ( <i>Brassica napus</i> ); contains Pfam AMP-binding domain PF00501; identical to cDNA adenosine monophosphate binding protein 9 AMPBP9 (AMPBP9) GI:20799726   chr1:7548603-7550554 REVERSE   Aliases: F24J8.14, F24J8_14	4.1	3.9	0.2	0.8	100.0%	-4.9
8501	AT1G21780.1   BTB/POZ domain-containing protein. Contains similarity to gb:AJ000644 SPOP (speckle-type POZ protein) from <i>Homo sapiens</i> and contains a PF:00651 BTB/POZ domain. ESTs gb:T75841, gb:R89974, gb:R30221, gb:N96386, gb:T76457, gb:AI100013 and gb:T76456 come from this gene; supported by full-length. Interacts with CUL3A and CUL3B.   chr1:7652431-7654003 FORWARD   Aliases: F8K7.22, F8K7_22	4.2	3.9	0.3	0.8	100.0%	-4.6
8502	AT3G60220.1   Symbol: ATL4   zinc finger (C3HC4-type RING finger) family protein (ATL4), contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)	2.9	2.7	0.1	0.8	100.0%	-5.2
8503	AT5G48010.1   Encodes an oxidosqualene cyclase involved in the	3.0	3.2	-0.2	-0.8	100.0%	-4.8
8504	AT3G13225.1   similar to PREDICTED: similar to mKIAA1014 protein [ <i>Gallus gallus</i> ] (GB:XP_424260.1); contains InterPro domain WW/Rsp5/WWP domain (InterPro:IPR001202)   chr3:4258777-4262903 REVERSE   Aliases: MJH23.2	2.9	2.7	0.2	0.8	100.0%	-5.0
8505	AT5G24830.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:8530981-8534210 FORWARD   Aliases: F6A4.40, F6A4_40	4.1	4.0	0.2	0.8	100.0%	-4.7
8506	AT3G24070.1   zinc knuckle (CCHC-type) family protein, contains Pfam profile: PF00098 zinc knuckle   chr3:8693092-8694716 FORWARD   Aliases: F14O13.27	4.7	4.4	0.3	0.8	100.0%	-4.6
8507	AT2G45780.1   expressed protein   chr2:18861265-18862162 REVERSE   Aliases: F4I18.24	4.5	4.3	0.2	0.8	100.0%	-4.9
8508	AT5G11360.1   expressed protein   chr5:3625575-3626701 REVERSE   Aliases: F2I11.250, F2I11_250	3.7	3.5	0.3	0.8	100.0%	-4.5
8509	AT5G13010.1   Symbol: EMB3011   RNA helicase, putative, similar to DEAH-box RNA helicase ( <i>Chlamydomonas reinhardtii</i> ) GI:12044832; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr5:4122581-4128864 FORWARD   Aliases: EMB3011, EMBRYO DEFECTIVE 3011, T24H18.180, T24H18_180	8.3	8.8	-0.5	-0.8	100.0%	-4.9
8510	AT3G56340.1   40S ribosomal protein S26 (RPS26C), several 40S ribosomal protein S26   chr3:20903116-20904395 REVERSE   Aliases: T5P19.4	11.4	11.7	-0.4	-0.8	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8511	AT1G11540.1   expressed protein, contains Pfam profile: PF01925 domain of unknown function DUF81   chr1:3875160-3877155 REVERSE   Aliases: T23J18.20, T23J18_20	5.1	4.8	0.3	0.8	100.0%	-4.4
8512	AT3G61860.1   Symbol: ATRSP31   arginine/serine-rich splicing factor RSP31 (RSP31), identical to SP:P92964 Arginine/serine-rich splicing factor RSP31 {Arabidopsis thaliana}   chr3:22911047-22913309 REVERSE   Aliases: ARGININE/SERINE RICH SPLICING FACTOR, F21F14.30	10.0	9.7	0.2	0.8	100.0%	-5.2
8513	AT1G09570.1   Symbol: PHYA   phytochrome A (PHYA), identical to SP:P14712 Phytochrome A {Arabidopsis thaliana}   chr1:3095258-3100327 REVERSE   Aliases: ELONGATED HYPOCOTYL 8, F14J9.23, F14J9_23, FAR RED ELONGATED 1, FHY2, FRE1, HY8, PHYTOCHROME 2, PHYTOCHROME A	6.7	7.1	-0.3	-0.8	100.0%	-4.6
8514	AT1G63720.1   expressed protein, similar to putative protein GB:CAA18164 (Arabidopsis thaliana)   chr1:23639519-23641178 REVERSE   Aliases: F24D7.9, F24D7_9	3.8	3.7	0.2	0.8	100.0%	-4.7
8515	AT4G31980.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr4:15464911-15469210 FORWARD   Aliases: F11C18.13	3.4	3.8	-0.4	-0.8	100.0%	-4.6
8516	AT5G43430.2   expressed protein, similar to hypothetical protein DDB0204353 [Dictyostelium discoideum] (GB:EAL68168.1); contains InterPro domain Electron transfer flavoprotein beta-subunit (InterPro:IPR000049)   chr5:17470826-17472918 FORWARD   Aliases: MWF20.14, MWF20_14	6.2	6.6	-0.4	-0.8	100.0%	-4.2
8517	AT1G64090.1   reticulon family protein (RTNLB3), weak similarity to SP:O95197 Reticulon protein 3 (Neuroendocrine-specific protein-like) {Homo sapiens}; contains Pfam profile PF02453: Reticulon   chr1:23792977-23794585 FORWARD   Aliases: F22C12.15, F22C12_15	8.3	7.6	0.7	0.8	100.0%	-4.6
8518	AT3G26190.1   Symbol: CYP71B21   cytochrome P450 71B21, putative (CYP71B21), identical to Cytochrome P450 71B21 (SP:Q9LTM2) (Arabidopsis thaliana); similar to cytochrome P450 GB:O65784 (Arabidopsis thaliana)   chr3:9584702-9586346 REVERSE   Aliases: MTC11.13	2.8	2.7	0.1	0.8	100.0%	-5.1
8519	AT3G15680.1   zinc finger (Ran-binding) family protein, contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others   chr3:5315008-5316471 FORWARD   Aliases: MSJ11.28	2.6	2.8	-0.2	-0.8	100.0%	-4.9
8520	AT2G16190.1   expressed protein   chr2:7027576-7028683 REVERSE   Aliases: F7H1.21, F7H1_21	2.8	2.9	-0.1	-0.8	100.0%	-5.1
8521	AT5G03450.1   zinc finger (C3HC4-type RING finger) family protein   chr5:858768-862296 REVERSE   Aliases: F12E4.210, F12E4_210	3.6	3.7	-0.1	-0.8	100.0%	-5.2
8522	AT5G64630.3   Symbol: FAS2   transducin family protein / WD-40 repeat family protein, Similar to (SP:Q13112) Chromatin assembly factor 1 subunit B (CAF-1 subunit B) (CAF-lp60) (Homo sapiens)   chr5:25850486-25853610 FORWARD   Aliases: FASCIATA 2, MUB3, MUB3.15, MUB3_15, NFB01, NFB1	3.1	3.3	-0.3	-0.8	100.0%	-4.5
8523	AT1G63260.3   similar to senescence-associated family protein [Arabidopsis thaliana] (TAIR:At3g45600.1); similar to senescence-associated protein DH [Zea mays] (GB:AAV31120.1); contains InterPro domain CD9/CD37/CD63 antigen (InterPro:IPR000301)   chr1:23470425-23472855 REVERSE   Aliases: F9N12.12, F9N12_12	4.9	5.1	-0.2	-0.8	100.0%	-4.6
8524	AT1G21870.1   glucose-6-phosphate/phosphate translocator-related, similar to glucose 6 phosphate/phosphate translocators from Pisum sativum) GI:2997591, (Mesembryanthemum crystallinum) GI:9295277, (Solanum tuberosum) GI:2997593; contains Pfam profile PF00892: Integral membrane protein   chr1:7678197-7679686 FORWARD   Aliases: T26F17.9, T26F17_9	2.6	2.5	0.1	0.8	100.0%	-5.1
8525	AT3G59470.1   far-red impaired responsive family protein / FAR1 family protein, weak similarity to far-red impaired response protein (Arabidopsis thaliana) GI:5764395; contains Pfam profile PF03101: FAR1 family   chr3:21989938-21991521 REVERSE   Aliases: T16L24.20	5.1	4.9	0.3	0.8	100.0%	-4.5
8526	AT1G75230.2   HhH-GPD base excision DNA repair family protein, contains Pfam domain PF00730: HhH-GPD superfamily base excision DNA repair protein   chr1:28238010-28239445 FORWARD   Aliases: F22H5.5, F22H5_5	5.6	5.8	-0.2	-0.8	100.0%	-4.6
8527	AT5G09230.6   transcriptional regulator Sir2 family protein, contains Pfam domain PF02146: transcriptional regulator, Sir2 family;   chr5:2871379-2873785 FORWARD   Aliases: T2K12.8	8.2	8.0	0.1	0.8	100.0%	-5.0
8528	AT1G75020.2   Symbol: LPAT4   phospholipid/glycerol acyltransferase family protein, contains Pfam profile: PF01553 Acyltransferase   chr1:28174786-28177087 FORWARD   Aliases: F25A4.2, F25A4_2, LPAT4	6.6	6.1	0.4	0.8	100.0%	-4.4
8529	AT1G16010.1   magnesium transporter CorA-like family protein (MRS2-1), low similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg2+ transporter protein   chr1:5495367-5497714 REVERSE   Aliases: T24D18.11, T24D18_11	8.4	8.1	0.4	0.8	100.0%	-4.6
8530	AT3G06540.1   GDP dissociation inhibitor family protein / Rab GTPase activator family protein, similar to SP:P26374 Rab proteins geranylgeranyltransferase component A 2 (Rab escort protein 2) {Homo sapiens}; contains Pfam profile PF00996: GDP dissociation inhibitor   chr3:2035010-2037794 REVERSE   Aliases: F5E6.13, F5E6_13	4.8	5.1	-0.2	-0.8	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8531	AT5G43750.1   expressed protein   chr5:17597193-17598449 REVERSE   Aliases: MQD19.9, MQD19_9	4.7	4.3	0.4	0.8	100.0%	-4.4
8532	AT4G38490.1   expressed protein   chr4:18006282-18007366 FORWARD   Aliases: F20M13.50, F20M13_50	8.8	8.6	0.2	0.8	100.0%	-4.6
8533	AT4G03510.2   Symbol: RMA1   zinc finger (C3HC4-type RING finger) family protein (RMA1), identical to RING zinc finger protein RMA1 gi:3164222   chr4:1557766-1559374 REVERSE   Aliases: F9H3.14, F9H3_14	4.2	3.9	0.3	0.8	100.0%	-4.2
8534	AT5G23650.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:7969815-7971022 FORWARD   Aliases: MQM1.9, MQM1_9	2.6	2.5	0.1	0.8	100.0%	-5.3
8535	AT5G57970.2   similar to methyladenine glycosylase family protein [Arabidopsis thaliana] (TAIR:At1g80850.1); similar to OSJNBa0029H02.18 [Oryza sativa (japonica cultivar-group)] (GB:XP_473062.1); contains InterPro domain Methyladenine glycosylase (InterPro:IPR005019)   chr5:23484171-23486241 FORWARD   Aliases: MTI20.23, MTI20_23	5.2	5.7	-0.4	-0.8	100.0%	-4.3
8536	AT3G25680.1   expressed protein   chr3:9350863-9353664 FORWARD   Aliases: T5M7.13	3.1	3.3	-0.1	-0.8	100.0%	-4.9
8537	AT2G41830.1   cyclin-related, contains Pfam profile PF02984: Cyclin, C-terminal domain	3.0	3.2	-0.1	-0.8	100.0%	-5.0
8538	AT5G15870.1   glycosyl hydrolase family 81 protein, similar to beta-glucan-elicitor receptor GI:1752734 from (Glycine max)   chr5:5182644-5184881 REVERSE   Aliases: F1N13.10, F1N13_10	5.9	6.5	-0.6	-0.8	100.0%	-4.4
8539	AT1G55610.1   Symbol: BRL1   protein kinase family protein, contains Prosite:PS00107: Protein kinases ATP-binding region signature   chr1:20783540-20787040 REVERSE   Aliases: BRI 1 LIKE, F20N2.4	4.0	3.8	0.2	0.8	100.0%	-4.6
8540	AT1G17960.1   threonyl-tRNA synthetase, putative / threonine--tRNA ligase, putative, similar to SP:O04630 Threonyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS) {Arabidopsis thaliana}; contains Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF03129: Anticodon binding domain, PF02824: TGS domain   chr1:6181008-6183730 REVERSE   Aliases: F2H15.18, F2H15_18	3.6	3.3	0.3	0.8	100.0%	-4.4
8541	AT3G13900.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Homo sapiens (SP:Q9Y2Q0), Mus musculus (SP:P70704); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr3:4586158-4590688 FORWARD   Aliases: MDC16.2	2.6	2.5	0.1	0.8	100.0%	-5.3
8542	AT2G40770.1   SNF2 domain-containing protein / helicase domain-containing protein / zinc finger (C3HC4 type RING finger) family protein, low similarity to SP:P36607 DNA repair protein rad8 {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00628: PHD-finger, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:17020347-17028393 REVERSE   Aliases: T7D17.5, T7D17_5	3.1	3.3	-0.2	-0.8	100.0%	-4.5
8543	AT1G62520.1   expressed protein   chr1:23148077-23149174 FORWARD   Aliases: T3P18.8, T3P18_8	4.9	5.0	-0.2	-0.8	100.0%	-4.9
8544	AT2G15290.1   expressed protein   chr2:6649408-6651117 REVERSE   Aliases: F27O10.6, F27O10_6	9.0	8.6	0.5	0.8	100.0%	-4.3
8545	AT3G14300.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:4766912-4769905 REVERSE   Aliases: ATPMEPCRC, MLN21.8	2.7	2.5	0.1	0.8	100.0%	-5.0
8546	AT3G12960.1   expressed protein, similar to seed maturation protein PM28 GB:AAD30427 from (Glycine max)   chr3:4136553-4136834 FORWARD   Aliases: MGH6.8	3.0	2.8	0.1	0.8	100.0%	-5.2
8547	AT2G22540.1   Symbol: SVP   short vegetative phase protein (SVP), identical to cDNA short vegetative phase protein (SVP) GI:10944319;	8.0	7.8	0.2	0.8	100.0%	-4.5
8548	AT2G39760.2   Symbol: ATBPM3	5.2	5.8	-0.7	-0.8	100.0%	-4.4
8549	AT2G37400.1   chloroplast lumen common family protein, very similar to GI:6729507 (At5g02590) and GI:7413648 (At3g53560) (Arabidopsis thaliana)   chr2:15703234-15704481 REVERSE   Aliases: F3G5.19, F3G5_19	5.8	6.2	-0.4	-0.8	100.0%	-4.3
8550	AT1G48730.1   expressed protein   chr1:18024005-18025945 REVERSE   Aliases: F11I4.10, F11I4_10	3.0	2.8	0.1	0.8	100.0%	-5.0
8551	AT3G54340.1   Symbol: AP3   floral homeotic protein APETALA3 (AP3)   chr3:20130152-20132101 REVERSE   Aliases: APETALA 3, FLORAL HOMEOTIC PROTEIN APETALA 3, T12E18.30	2.6	2.4	0.1	0.8	100.0%	-5.3
8552	AT2G24440.1   expressed protein   chr2:10398169-10400326 FORWARD   Aliases: T28I24.17, T28I24_17	5.1	5.4	-0.3	-0.8	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8553	AT1G52150.2   Symbol: ATHB 15   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to to HD-zip transcription factor (athb-8) (GI:7270235) (Arabidopsis thaliana); contains Pfam profiles PF01852: START domain, PF00046: Homeobox domain   chr1:19413380-19418347 REVERSE   Aliases: ATHB15, CNA, CORONA, F5F19.21, F5F19_21, ICU4, INCURVATA 4, INCURVATA4	6.9	7.4	-0.5	-0.8	100.0%	-4.5
8554	AT3G27380.1   Symbol: SDH2 1	8.8	8.4	0.4	0.8	100.0%	-4.8
8555	AT5G38380.2   expressed protein   chr5:15362890-15365657 FORWARD   Aliases: MXI10.5, MXI10_5	4.9	4.7	0.2	0.8	100.0%	-4.6
8556	AT2G31940.1   expressed protein   chr2:13587677-13588189 FORWARD   Aliases: F20M17.26	2.8	2.6	0.2	0.8	100.0%	-4.9
8557	AT4G03520.1   Symbol: ATHM2   thioredoxin M-type 2, chloroplast (TRX-M2), nearly identical to SP:Q9SEU8 Thioredoxin M-type 2, chloroplast precursor (TRX-M2) {Arabidopsis thaliana}   chr4:1562357-1564164 REVERSE   Aliases: F9H3.15, F9H3_15, T5L23.1	10.4	10.0	0.4	0.8	100.0%	-4.6
8558	AT3G55960.1   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr3:20771436-20774012 REVERSE   Aliases: F27K19.140	7.4	6.9	0.5	0.8	100.0%	-4.4
8559	AT1G16830.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:5758870-5762612 FORWARD   Aliases: F17F16.24	3.9	4.1	-0.2	-0.8	100.0%	-4.9
8560	AT5G52190.1   sugar isomerase (SIS) domain-containing protein, similar to 6-phospho-3-hexuloisomerase (Mycobacterium gastri) GI:6899860; contains Pfam profile PF01380: SIS domain   chr5:21218956-21219769 REVERSE   Aliases: F17P19.9, F17P19_9	4.9	4.6	0.4	0.8	100.0%	-4.0
8561	AT5G48970.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:19873702-19876989 REVERSE   Aliases: K19E20.10, K19E20_10	6.4	6.1	0.3	0.8	100.0%	-4.6
8562	AT4G35905.1   expressed protein, contains Pfam domain PF03966: Protein of unknown function (DUF343)   chr4:17007031-17008157 REVERSE   Aliases: None	6.1	5.8	0.2	0.8	100.0%	-4.7
8563	AT2G27500.3   similar to glycosyl hydrolase family 17 protein [Arabidopsis thaliana] (TAIR:At1g32860.1); similar to putative beta-1,3-glucanase [Oryza sativa (japonica cultivar-group)] (GB:NP_915593.1); similar to putative elicitor inducible beta-1,3-glucanase NtEIG-E76 [Oryza sativa (japonica cultivar-group)] (GB:BAD82640.1); similar to OSJNBa0073L04.8 [Oryza sativa (japonica cultivar-group)] (GB:XP_472401.1); contains InterPro domain Glycoside hydrolase, family 17 (InterPro:IPR000490)   chr2:11759248-11760845 REVERSE   Aliases: F10A12.18, F10A12_18	4.7	4.4	0.3	0.8	100.0%	-4.6
8564	AT2G28240.1   hydroxyproline-rich glycoprotein family protein   chr2:12046289-12049220 FORWARD   Aliases: T3B23.9, T3B23_9	4.4	4.9	-0.4	-0.8	100.0%	-4.7
8565	AT5G54750.1   transport protein particle (TRAPP) component Bet3, putative, similar to SP:P36149 Transport protein particle 22 kDa subunit (TRAPP 22 kDa subunit) {Saccharomyces cerevisiae}; contains Pfam profile PF04051: Transport protein particle (TRAPP) component, Bet3	8.8	9.1	-0.3	-0.8	100.0%	-4.7
8566	AT4G26140.2   Symbol: BGAL12	2.4	2.8	-0.4	-0.8	100.0%	-4.1
8567	AT2G18770.1   expressed protein   chr2:8141726-8143642 FORWARD   Aliases: MSF3.15, MSF3_15	5.7	5.5	0.2	0.8	100.0%	-4.5
8568	AT1G16770.1   expressed protein   chr1:5737893-5739103 FORWARD   Aliases: F17F16.12, F17F16_12	3.5	3.4	0.2	0.8	100.0%	-5.0
8569	AT4G35040.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr4:16680419-16682098 FORWARD   Aliases: M4E13.100, M4E13_100	8.4	8.1	0.3	0.8	100.0%	-4.8
8570	AT3G06600.1   expressed protein, ; expression supported by MPSS   chr3:2059564-2060464 REVERSE   Aliases: F5E6.7, F5E6_7	3.3	3.1	0.2	0.8	100.0%	-4.8
8571	AT3G10370.1   mitochondrial FAD-dependent glycerol-3-phosphate dehydrogenase, possibly involved in storage lipid catabolism and glycerol assimilation, and in glycerol-3-phosphate shuttle which transports reducing power from cytosol to mitochondrion.   chr3:3216374-3219275 FORWARD   Aliases: F14P13.3	6.7	7.0	-0.3	-0.8	100.0%	-4.6
8572	AT1G11850.2   expressed protein   chr1:3999201-3999875 FORWARD   Aliases: F12F1.31, F12F1_31	4.2	4.0	0.2	0.8	100.0%	-5.0
8573	AT3G54320.3   Symbol: WRI1   similar to ovule development protein, putative [Arabidopsis thaliana] (TAIR:At1g16060.1); similar to AP2 DNA-binding domain protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD68772.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr3:20125708-20129617 FORWARD   Aliases: ASML1, T12E18.10, WRI, WRINKLED 1	3.3	3.5	-0.2	-0.8	100.0%	-4.9
8574	AT1G58080.1   Symbol: ATATP PRT1   ATP phosphoribosyl transferase 1 (ATP-PRT1), identical to ATP phosphoribosyl transferase GI:6683617 from (Arabidopsis thaliana)   chr1:21507979-21511118 REVERSE   Aliases: ATP PHOSPHORIBOSYL TRANSFERASE, T15M6.9, T15M6_9	7.0	7.4	-0.4	-0.8	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8575	AT5G14760.1   L-aspartate oxidase family protein, similar to L-aspartate oxidase, Escherichia coli (SP:P10902); contains Pfam profiles PF00890 FAD binding domain, PF02910 Fumarate reductase/succinate dehydrogenase flavoprotein C-terminal domain   chr5:4768472-4772156 FORWARD   Aliases: T9L3.60, T9L3_60	7.5	7.9	-0.4	-0.8	100.0%	-4.2
8576	AT3G15220.1   protein kinase, putative, similar to serine/threonine protein kinase 24 (Homo sapiens) SWISS-PROT:Q9Y6E   chr3:5126605-5132313 REVERSE   Aliases: K7L4.2	5.2	4.9	0.3	0.8	100.0%	-4.5
8577	AT3G48700.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr3:18049633-18050861 REVERSE   Aliases: T8P19.210	2.9	3.1	-0.2	-0.8	100.0%	-4.8
8578	AT2G13430.1   expressed protein   chr2:5597134-5598504 FORWARD   Aliases: T26C18.2, T26C18_2	2.6	2.5	0.1	0.8	100.0%	-5.3
8579	AT2G36070.1   Symbol: ATTIM44 2   mitochondrial import inner membrane translocase subunit TIM44, putative, contains similarity to Swiss-Prot:O35857 import inner membrane translocase subunit TIM44, mitochondrial precursor (Mus musculus); contains Pfam domain PF04280: Mitochondrial import inner membrane, translocase subunit TIM44   chr2:15151926-15155169 REVERSE   Aliases: F11F19.2, F11F19_2	5.2	5.7	-0.5	-0.8	100.0%	-4.3
8580	AT4G13940.3   Symbol: HOG1   similar to adenosylhomocysteinase, putative / S-adenosyl-L-homocysteine hydrolase, putative / AdoHcyase, putative [Arabidopsis thaliana] (TAIR:At3g23810.1); similar to adenosylhomocysteinase (EC 3.3.1.1) - wheat (GB:T06764); similar to S-adenosyl-L-homocystein hydrolase [Nicotiana sylvestris] (GB:BAA03709.1); similar to adenosylhomocysteinase [Medicago truncatula] (GB:AAO89238.1); similar to S-adenosyl-L-homocysteinase [Lupinus luteus] (GB:AAD56048.1); similar to wheat adenosylhomocysteinase-like protein [Oryza sativa (japonica cultivar-group)] (GB:AAO72664.1); contains InterPro domain S-adenosyl-L-homocysteine hydrolase (InterPro:IPR000043)   chr4:8054856-8057176 FORWARD   Aliases: DL3010W, EMB1395, EMBRYO DEFECTIVE 1395, FCAALL.35, HOMOLOGY DEPENDENT GENE SILENCING 1, S ADENOSYL L HOMOCYSTEINE HYDROLASE, SAHH, SAHH1	9.1	9.6	-0.5	-0.8	100.0%	-4.5
8581	AT5G48670.1   MADS-box family protein, contains similarity to MADS-box DNA-binding protein   chr5:19756051-19757016 REVERSE   Aliases: K15N18.16, K15N18_16	4.7	4.5	0.2	0.8	100.0%	-4.4
8582	ATCG00780.1   Symbol: RPL14   encodes a chloroplast ribosomal protein L14, a constituent of the large subunit of the ribosomal complex   chrC:80696-81064 REVERSE   Aliases: RPL14	8.7	9.5	-0.8	-0.8	100.0%	-4.7
8583	AT1G50950.1   thioredoxin-related, contains weak hit to Pfam PF00085: Thioredoxin; contains 2 predicted transmembrane domains   chr1:18883988-18887893 FORWARD   Aliases: F8A12.17, F8A12_17	3.5	3.8	-0.2	-0.8	100.0%	-4.6
8584	AT5G61570.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:24775573-24777878 FORWARD   Aliases: K11J9.21, K11J9_21	2.4	2.5	-0.1	-0.8	100.0%	-5.1
8585	AT1G52910.1   expressed protein   chr1:19711729-19712991 FORWARD   Aliases: F14G24.18, F14G24_18	4.3	4.6	-0.3	-0.8	100.0%	-4.2
8586	AT1G31480.1   Symbol: SGR2   shoot gravitropism 2 (SGR2), Plant Cell 2002 Jan;14:33-46 PMID:11826297; similar to phospholipase (Homo sapiens) GI:4760647; identical to cDNA PF02862: DDHD domain   chr1:11265898-11271682 FORWARD   Aliases: SHOOT GRAVITROPISM 2, T8E3.1, T8E3_1	5.0	5.2	-0.3	-0.8	100.0%	-4.6
8587	AT1G02100.3   leucine carboxyl methyltransferase family protein, contains Pfam PF04072: Leucine carboxyl methyltransferase domain; similar to Leucine carboxyl methyltransferase (Protein-leucine O- methyltransferase) (CGI-68) (SP:Q9UIC8) {Homo sapiens}   chr1:389823-392811 FORWARD   Aliases: T7I23.16, T7I23_16	3.5	3.3	0.3	0.8	100.0%	-4.6
8588	AT4G25000.1   Symbol: AMY3   alpha-amylase, putative / 1,4-alpha-D-glucan glucanohydrolase, putative, similar to alpha-amylase from Vigna mungo SP:P17859, Ipomoea nil GI:21670851; contains Pfam profile PF00128: Alpha amylase, catalytic domain. Predicted to be secreted protein based on signalP prediction. Involved in starch mobilization.   chr4:12851979-12853855 REVERSE   Aliases: ALPHA AMYLASE LIKE, ATAMY1, F13M23.140, F13M23_140	4.3	4.1	0.3	0.8	100.0%	-4.6
8589	AT5G05670.2   expressed protein   chr5:1695731-1698105 REVERSE   Aliases: MJJ3.7, MJJ3_7	5.7	5.3	0.3	0.8	100.0%	-4.3
8590	AT1G64600.1   expressed protein, similar to Hypothetical 72.2 kDa protein in RPS27A-GPM1 intergenic region (Swiss-Prot:P36056) (Saccharomyces cerevisiae)   chr1:23999634-24002383 FORWARD   Aliases: F1N19.17, F1N19_17	5.5	5.9	-0.4	-0.8	100.0%	-4.2
8591	AT1G54940.1   glycogenin glucosyltransferase (glycogenin)-related, contains similarity to glycogenin-1 from Mus musculus (SP:Q9R062), Rattus norvegicus (SP:O08730), Homo sapiens (SP:P46976)   chr1:20485357-20488208 FORWARD   Aliases: F14C21.47, F14C21_47	2.2	2.3	-0.1	-0.8	100.0%	-5.2
8592	AT2G34540.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g34530.1)   chr2:14557737-14559308 FORWARD   Aliases: T31E10.12, T31E10_12	3.0	2.9	0.1	0.8	100.0%	-5.1
8593	AT5G17650.1   glycine/proline-rich protein, glycine/proline-rich protein GPRP - Arabidopsis thaliana, EMBL:X84315   chr5:5816700-5818349 REVERSE   Aliases: K10A8.130, K10A8_130	5.6	5.4	0.2	0.8	100.0%	-4.6
8594	AT1G07420.2   Symbol: SMO2 2	4.9	4.4	0.5	0.8	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8595	AT5G20710.1   Symbol: BGAL7   similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At2g28470.1); similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At4g36360.2); similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At4g36360.1); similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At3g13750.1); similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At1g31740.1); similar to beta-galactosidase [Fragaria x ananassa] (GB:CAC44501.1); similar to beta-galactosidase [Sandersonia aurantiaca] (GB:AAQ21371.2); similar to beta-D-galactosidase [Pyrus pyrifolia] (GB:BAD91083.1); similar to putative beta-galactosidase [Lycopersicon esculentum] (GB:AAF70824.1); similar to beta-galactosidase [Raphanus sativus] (GB:BAD20774.2); contains InterPro domain Glycoside hydrolase, family 35 (InterPro:IPR001944); contains InterPro domain D-galactoside/L-rhamnose binding SUEL lectin domain (InterPro:IPR000922)   chr5:7010524-7014251 FORWARD   Aliases: T1M15.110, T1M15_110	2.9	2.7	0.1	0.8	100.0%	-5.1
8596	AT5G59760.1   expressed protein   chr5:24092854-24093519 REVERSE   Aliases: MTH12.3, MTH12_3	2.9	2.8	0.1	0.8	100.0%	-5.4
8597	AT2G23400.1   dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076; this may be a pseudogene.   chr2:9971058-9972309 REVERSE   Aliases: F26B6.5, F26B6_5	2.8	2.7	0.1	0.8	100.0%	-5.4
8598	AT4G30160.1   Symbol: VLN4   villin, putative, similar to villin 2 (VLN2) (Arabidopsis thaliana) GI:3415115, villin 3 (VLN3) (Arabidopsis thaliana) GI:3415117; contains Pfam profiles PF00626: Gelsolin repeat, PF02209: Villin headpiece domain   chr4:14753563-14760189 FORWARD   Aliases: ARABIDOPSIS THALIANA VILLIN 4, ATVLN4, F9N11.10, F9N11_10	4.2	5.0	-0.8	-0.8	100.0%	-4.1
8599	AT1G32980.1   subtilisin-like serine protease-related, similar to subtilase SP1 (Oryza sativa) GI:9957714   chr1:11954258-11955342 REVERSE   Aliases: F9L11.33, F9L11_33	2.8	2.9	-0.1	-0.8	100.0%	-4.9
8600	AT2G16900.1   expressed protein   chr2:7330697-7333303 REVERSE   Aliases: F12A24.8, F12A24_8	5.5	5.7	-0.2	-0.8	100.0%	-4.8
8601	AT1G16760.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:5734227-5737300 FORWARD   Aliases: F19K19.25	2.3	2.2	0.1	0.8	100.0%	-5.6
8602	AT3G04200.1   germin-like protein, putative, contains Pfam profile: PF01072 germin family; similar to germin type2 GB:CAA63023 (SP:P92996) (Arabidopsis thaliana)   chr3:1103623-1104608 REVERSE   Aliases: T6K12.18, T6K12_18	2.9	3.0	-0.1	-0.8	100.0%	-5.1
8603	AT1G01340.1   Symbol: ATCNGC10   cyclic nucleotide-regulated ion channel (CNGC10) (ACBK1), almost identical to CaM-regulated potassium ion channel (ACBK1) GI:8515883 from (Arabidopsis thaliana); contains Pfam domain, PF00520: Ion transport protein   chr1:132332-135322 REVERSE   Aliases: ACBK1, CNGC10, F6F3.13, F6F3_13	4.6	4.1	0.5	0.8	100.0%	-4.3
8604	AT4G01680.2   Symbol: MYB55   similar to myb family transcription factor (MYB61) [Arabidopsis thaliana] (TAIR:At1g09540.1); similar to MYB2 [Dendrobium sp. XMW-2002-2] (GB:AAO49411.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)	2.3	2.2	0.1	0.8	100.0%	-5.1
8605	AT4G39460.1   mitochondrial substrate carrier family protein   chr4:18355987-18358887 REVERSE   Aliases: F23K16.90, F23K16_90	6.0	6.4	-0.5	-0.8	100.0%	-4.1
8606	AT1G72680.1   cinnamyl-alcohol dehydrogenase, putative, similar to cinnamyl-alcohol dehydrogenase GB:AAC35846 (Medicago sativa), SP:Q08350 (Picea abies)   chr1:27362894-27364678 REVERSE   Aliases: F28P22.13, F28P22_13	9.4	10.1	-0.7	-0.8	100.0%	-4.5
8607	AT3G14090.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr3:4669260-4671560 REVERSE   Aliases: MAG2.5	4.1	4.4	-0.2	-0.8	100.0%	-4.3
8608	AT5G04010.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g03920.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD68285.1)   chr5:1080104-1081073 REVERSE   Aliases: F8F6.220, F8F6_220	4.1	3.9	0.3	0.8	100.0%	-4.4
8609	AT5G13490.2   Symbol: AAC2   similar to ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1) [Arabidopsis thaliana] (TAIR:At3g08580.2); similar to ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1) [Arabidopsis thaliana] (TAIR:At3g08580.1); similar to ADT1_GOSHI ADP,ATP carrier protein 1, mitochondrial precursor (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (GB:O22342); contains InterPro domain Mitochondrial substrate carrier (InterPro:IPR001993); contains InterPro domain Adenine nucleotide translocator 1 (InterPro:IPR002113); contains InterPro domain Mitochondrial carrier protein (InterPro:IPR002067)   chr5:4335642-4337683 FORWARD   Aliases: T6I14.20, T6I14_20	6.8	7.3	-0.5	-0.8	100.0%	-4.2
8610	AT4G27435.1   expressed protein   chr4:13723824-13725143 FORWARD   Aliases: None	2.9	2.7	0.2	0.8	100.0%	-4.5
8611	AT1G13110.1   Symbol: CYP71B7   cytochrome P450 71B7 (CYP71B7), identical to (SP:Q96514) cytochrome P450 71B7 (Arabidopsis thaliana);	2.8	3.1	-0.3	-0.8	100.0%	-4.3
8612	AT2G38450.1   expressed protein   chr2:16109115-16109993 FORWARD   Aliases: T19C21.6, T19C21_6	7.9	7.6	0.2	0.8	100.0%	-4.5
8613	AT2G28090.1   heavy-metal-associated domain-containing protein, similar to farnesylated protein ATPF3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain   chr2:11979475-11981084 REVERSE   Aliases: F24D13.12, F24D13_12	4.0	3.7	0.3	0.8	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8614	AT4G14790.1   Symbol: ATSUV3	3.2	3.3	-0.1	-0.8	100.0%	-5.1
8615	AT1G80245.2   expressed protein   chr1:30179070-30180434 FORWARD   Aliases: None	4.2	3.9	0.3	0.8	100.0%	-4.7
8616	AT5G53620.2   expressed protein   chr5:21798226-21802438 FORWARD   Aliases: MNC6.16, MNC6_16	4.7	5.1	-0.4	-0.8	100.0%	-4.4
8617	AT3G24170.2   similar to glutathione reductase, chloroplast [Arabidopsis thaliana] (TAIR:At3g54660.1); similar to glutathione reductase [Mesembryanthemum crystallinum] (GB:CAC13956.1); similar to glutathione-disulfide reductase (EC 1.8.1.7) - turnip (GB:T14394); similar to glutathione reductase [Pisum sativum] (GB:CAA66924.1); similar to Glutathione Reductase precursor [Spinacia oleracea] (GB:BAA07108.1); similar to glutathione reductase [Brassica oleracea] (GB:BAD14936.1); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase dimerisation domain (InterPro:IPR004099); contains InterPro domain Glutathione reductase, plant (InterPro:IPR006324); contains InterPro domain Mercuric reductase (InterPro:IPR000815); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class I (InterPro:IPR001100); contains InterPro domain FAD-dependent pyridine nucleotide-disulphide oxidoreductase (InterPro:IPR001327); contains InterPro domain Trypanothione reductase (InterPro:IPR001864); contains InterPro domain Pyridine nucleotide-disulphide oxidoreductase, class-II (InterPro:IPR000103)   chr3:8729517-8734548 REVERSE   Aliases: MUJ8.3, MUJ8_3	10.6	11.1	-0.5	-0.8	100.0%	-4.6
8618	AT4G39960.1   DNAJ heat shock family protein, similar to SP:Q9S5A3 Chaperone protein dnaJ {Listeria monocytogenes}; contains Pfam profiles PF00226 DnaJ domain, PF01556 DnaJ C terminal region, PF00684 DnaJ central domain (4 repeats)   chr4:18533775-18536612 FORWARD   Aliases: T5J17.130, T5J17_130	5.8	5.4	0.4	0.8	100.0%	-4.5
8619	AT3G02460.2   plant adhesion molecule, putative, strong similarity to plant adhesion molecule 1 (Arabidopsis thaliana) GI:3511223; contains Pfam profile PF00566: TBC domain   chr3:505441-508410 FORWARD   Aliases: F16B3.9, F16B3_9	5.6	5.4	0.2	0.8	100.0%	-4.7
8620	AT2G23900.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to SP:P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28   chr2:10181613-10183706 FORWARD   Aliases: T29E15.10, T29E15_10	2.1	2.2	-0.1	-0.8	100.0%	-5.7
8621	AT4G35650.1   isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative, strong similarity to NAD+ dependent isocitrate dehydrogenase subunit 1 (Arabidopsis thaliana) GI:1766046   chr4:16908524-16910195 FORWARD   Aliases: F8D20.160, F8D20_160	6.5	6.0	0.5	0.8	100.0%	-4.0
8622	AT3G03240.1   esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379   chr3:746662-748607 REVERSE   Aliases: T17B22.7, T17B22_7	3.5	3.4	0.1	0.8	100.0%	-5.2
8623	AT3G63500.2   expressed protein   chr3:23456858-23461145 REVERSE   Aliases: MAA21.130	6.2	6.8	-0.6	-0.8	100.0%	-4.5
8624	AT4G02050.1   sugar transporter, putative, similar to SP:Q10710 Sugar carrier protein A {Ricinus communis}, glucose transporter (Saccharum hybrid cultivar H65-7052) GI:347855; contains Pfam profile PF00083: major facilitator superfamily protein   chr4:898307-900199 REVERSE   Aliases: T10M13.6, T10M13_6	6.0	6.3	-0.3	-0.8	100.0%	-4.4
8625	AT1G06780.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr1:2083423-2086961 FORWARD   Aliases: F4H5.13, F4H5_13	9.0	9.4	-0.4	-0.8	100.0%	-4.9
8626	AT1G70270.1   expressed protein   chr1:26468063-26468523 FORWARD   Aliases: F17O7.20, F17O7_20	2.9	2.7	0.1	0.8	100.0%	-5.3
8627	AT1G49270.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr1:18231002-18233895 REVERSE   Aliases: F13F21.28, F13F21_28	2.5	2.6	-0.1	-0.8	100.0%	-5.2
8628	AT1G17510.1   expressed protein   chr1:6023497-6024302 REVERSE   Aliases: F1L3.22, F1L3_22	10.6	10.2	0.4	0.8	100.0%	-4.5
8629	AT5G66500.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:26565221-26566903 REVERSE   Aliases: K1F13.16, K1F13_16	3.1	3.2	-0.1	-0.8	100.0%	-5.0
8630	AT3G05510.2   phospholipid/glycerol acyltransferase family protein, similar to SP:Q16635 Tafazzin from Homo sapiens; contains Pfam profile: PF01553 Acyltransferase   chr3:1595375-1598277 FORWARD   Aliases: F22F7.4, F22F7_4	5.5	5.4	0.2	0.8	100.0%	-4.9
8631	AT1G68540.1   oxidoreductase family protein, similar to cinnamoyl CoA reductase (Eucalyptus gunnii, gi:2058311), cinnamyl-alcohol dehydrogenase, E. gunnii (gi:1143445), CPRD14 protein, Vigna unguiculata (gi:1854445)   chr1:25723725-25725028 FORWARD   Aliases: T26J14.11, T26J14_11	6.9	7.3	-0.4	-0.8	100.0%	-4.0
8632	AT1G49245.1   expressed protein   chr1:18222418-18222922 FORWARD   Aliases: None	4.4	4.2	0.2	0.8	100.0%	-4.8
8633	AT2G04230.1   F-box family protein, contains F-box domain Pfam:PF00646	4.3	4.1	0.2	0.8	100.0%	-4.5
8634	AT2G24790.2   zinc finger (B-box type) family protein   chr2:10573977-10574702 FORWARD   Aliases: F27A10.10	7.1	6.8	0.3	0.8	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8635	AT2G45910.1   protein kinase family protein / U-box domain-containing protein, contains Pfam profiles PF00069 Eukaryotic protein kinase domain, PF04564: U-box domain; supported by tandem duplication of (GI:3386604) (TIGR_Ath1:At2g45920) (Arabidopsis thaliana)   chr2:18901148-18905601 FORWARD   Aliases: F4I18.11	3.6	3.4	0.3	0.8	100.0%	-4.7
8636	AT3G15140.1   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr3:5099539-5101788 REVERSE   Aliases: F4B12.5	3.7	3.9	-0.2	-0.8	100.0%	-4.9
8637	AT2G28390.1   SAND family protein, similar to Sand (GI:3928166) (Takifugu rubripes); contains Pfam PF03164: SAND family protein   chr2:12146660-12150542 REVERSE   Aliases: T1B3.9, T1B3_9	5.9	5.5	0.4	0.8	100.0%	-4.3
8638	AT1G62850.1   expressed protein, similar to Immature colon carcinoma transcript 1 (Digestion subtraction 1) (DS- 1) (Swiss-Prot:Q14197) (Homo sapiens)   chr1:23276139-23277071 REVERSE   Aliases: F23N19.20, F23N19_20	6.3	6.6	-0.3	-0.8	100.0%	-4.6
8639	AT1G80410.1   Symbol: EMB2753   acetyltransferase-related, low similarity to acetyltransferase Tubedown-1 (Mus musculus) GI:8497318, N-TERMINAL ACETYLTRANSFERASE GB:P12945 from (Saccharomyces cerevisiae); contains Pfam profile PF00515 TPR Domain	3.5	3.9	-0.4	-0.8	100.0%	-4.5
8640	AT4G02410.1   lectin protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain, PF00139: Legume lectins beta domain and PF00138: Legume lectins alpha domain   chr4:1059889-1062153 REVERSE   Aliases: T14P8.3, T14P8_3	5.1	5.4	-0.3	-0.8	100.0%	-4.3
8641	AT4G13800.1   permease-related, contains 9 predicted transmembrane domains; contains Pfam PF05653: Protein of unknown function (DUF803); identified as COG0697, Permeases of the drug/metabolite transporter (DMT) superfamily	3.3	3.2	0.1	0.8	100.0%	-5.1
8642	AT2G24360.1   serine/threonine/tyrosine kinase, putative, similar to serine/threonine/tyrosine kinase (Arachis hypogaea) gi:13124865:gb:AAK11734   chr2:10371531-10373971 REVERSE   Aliases: T28I24.9, T28I24_9	8.8	8.6	0.2	0.8	100.0%	-4.7
8643	AT3G61410.1   similar to protein kinase family protein / U-box domain-containing protein [Arabidopsis thaliana] (TAIR:At2g45910.1); similar to putative protein kinase [Oryza sativa (japonica cultivar-group)] (GB:AAP51741.1)   chr3:22732013-22733626 FORWARD   Aliases: F2A19.10	3.3	3.7	-0.3	-0.8	100.0%	-4.3
8644	AT1G15180.1   MATE efflux family protein, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:5224385-5226697 FORWARD   Aliases: F9L1.12, F9L1_12	2.5	2.4	0.1	0.8	100.0%	-5.3
8645	AT2G17410.1   ARID/BRIGHT DNA-binding domain-containing protein, contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain	4.8	4.9	-0.1	-0.8	100.0%	-4.9
8646	AT5G52000.1   importin alpha-1 subunit, putative, similar to importin alpha-1 subunit (Karyopherin alpha-1 subunit, KAP alpha) (Arabidopsis thaliana) SWISS-PROT:Q96321   chr5:21136250-21138345 REVERSE   Aliases: MSG15.24, MSG15_24	2.8	2.9	-0.1	-0.8	100.0%	-5.4
8647	AT3G02750.3   similar to protein phosphatase 2C, putative / PP2C, putative [Arabidopsis thaliana] (TAIR:At5g36250.1); similar to putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] (GB:XP_465582.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr3:593214-595762 REVERSE   Aliases: F13E7.31, F13E7_31	4.5	4.2	0.3	0.8	100.0%	-4.5
8648	AT1G71040.1   multi-copper oxidase type I family protein, similar to SP:P07788 Spore coat protein A {Bacillus subtilis}; contains Pfam profile PF00394: Multicopper oxidase   chr1:26800628-26803984 REVERSE   Aliases: F23N20.3, F23N20_3	7.0	6.7	0.3	0.8	100.0%	-4.4
8649	AT3G12090.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr3:3852151-3853726 REVERSE   Aliases: T21B14.9	7.9	7.7	0.2	0.8	100.0%	-4.8
8650	AT5G12380.1   annexin, putative, similar to annexin (Fragaria x ananassa) GI:6010777, annexin p33 (Zea mays) GI:6272285; contains Pfam profile PF00191: Annexin   chr5:4009224-4010688 FORWARD   Aliases: None	2.4	2.3	0.1	0.8	100.0%	-5.5
8651	AT3G04990.1   hypothetical protein   chr3:1384002-1384685 REVERSE   Aliases: T9J14.6, T9J14_6	2.6	2.7	-0.1	-0.8	100.0%	-5.6
8652	AT2G32630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:13851911-13853785 FORWARD   Aliases: T26B15.19, T26B15_19	3.1	3.3	-0.2	-0.8	100.0%	-5.0
8653	AT5G11730.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr5:3780312-3782714 FORWARD   Aliases: T22P22.120, T22P22_120	5.3	5.0	0.2	0.8	100.0%	-4.6
8654	AT4G27240.1   zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	5.2	5.7	-0.5	-0.8	100.0%	-4.2
8655	AT5G44920.2   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr5:18156002-18157410 FORWARD   Aliases: K21C13.10, K21C13_10	6.6	6.2	0.3	0.8	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8656	AT4G31850.1   Symbol: PGR3   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:15403026-15406364 FORWARD   Aliases: F11C18.50, F11C18_50, PROTON GRADIENT REGULATION 3	4.1	4.4	-0.3	-0.8	100.0%	-4.3
8657	AT2G43940.1   thiol methyltransferase, putative, similar to thiol methyltransferase 2 GI:14583121 from (Brassica oleracea)   chr2:18203029-18204763 REVERSE   Aliases: F6E13.7	4.6	5.0	-0.4	-0.8	100.0%	-4.4
8658	AT2G37990.1   ribosome biogenesis regulatory protein (RRS1) family protein, contains Pfam profile PF04939: Ribosome biogenesis regulatory protein (RRS1); similar to Ribosome biogenesis regulatory protein homolog (Swiss-Prot:Q15050) (Homo sapiens)	9.5	9.9	-0.4	-0.8	100.0%	-4.2
8659	AT2G27375.1   hypothetical protein   chr2:11717752-11718402 FORWARD   Aliases: None	2.2	2.3	-0.1	-0.8	100.0%	-5.3
8660	AT1G56290.1   Cwfj-like family protein, contains Pfam profiles PF04677: Protein similar to Cwfj N terminus 1, PF04676: Protein similar to Cwfj N terminus 2   chr1:21078951-21082443 FORWARD   Aliases: F14G9.10, F14G9_10	5.0	4.9	0.1	0.8	100.0%	-4.9
8661	AT4G17695.1   myb family transcription factor (KAN3), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA GARP-like putative transcription factor KANADI3 (KAN3) GI:15723596   chr4:9848142-9850717 REVERSE   Aliases: None	3.5	3.4	0.2	0.8	100.0%	-4.8
8662	AT3G58590.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:21677059-21679464 FORWARD   Aliases: F14P22.180	3.3	3.5	-0.2	-0.8	100.0%	-4.8
8663	AT1G27650.1   U2 snRNP auxiliary factor small subunit, putative, Strong similarity to gb:Y18349 U2 snRNP auxiliary factor, small subunit from Oryza sativa. ESTs gb:AA586295 and gb:AA597332 come from this gene   chr1:9614562-9616344 FORWARD   Aliases: T22C5.30	3.5	3.3	0.2	0.8	100.0%	-4.8
8664	AT1G22810.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr1:8074040-8075026 REVERSE   Aliases: T22J18.2, T22J18_2	2.2	2.3	-0.1	-0.8	100.0%	-5.3
8665	AT5G12910.1   histone H3, putative, similar to histone H3 from Mus musculus GI:51301, Gallus gallus GI:211859, Medicago sativa GI:166384, Pisum sativum SP:P02300; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr5:4077165-4077560 FORWARD   Aliases: T24H18.80, T24H18_80	2.9	2.7	0.1	0.8	100.0%	-4.9
8666	AT4G24490.1   similar to geranylgeranyl transferase alpha subunit-related / RAB geranylgeranyltransferase alpha subunit-related [Arabidopsis thaliana] (TAIR:At5g41820.1); similar to Rab geranylgeranyl transferase, a subunit [Rattus norvegicus] (GB:NP_113842.1); contains InterPro domain Protein prenyltransferase, alpha subunit (InterPro:IPR002088); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr4:12655069-12658344 REVERSE   Aliases: F22K18.310	4.2	4.4	-0.2	-0.8	100.0%	-4.6
8667	AT3G12670.1   Symbol: EMB2742   CTP synthase, putative / UTP--ammonia ligase, putative, similar to SP:P17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) {Homo sapiens}; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr3:4020127-4024275 REVERSE   Aliases: EMB2742, EMBRYO DEFECTIVE 2742, T2E22.2	7.5	8.0	-0.5	-0.8	100.0%	-4.7
8668	AT3G28155.1   expressed protein, weak similarity to microtubule organization 1 protein (Arabidopsis thaliana) GI:14317953   chr3:10486538-10487228 REVERSE   Aliases: MMG15.26	3.0	2.9	0.1	0.8	100.0%	-5.2
8669	AT5G48780.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr5:19794737-19796830 FORWARD   Aliases: K24G6.11, K24G6_11	3.3	3.4	-0.1	-0.8	100.0%	-5.0
8670	AT5G52280.1   protein transport protein-related, low similarity to SP:P25386 Intracellular protein transport protein USO1 {Saccharomyces cerevisiae}   chr5:21244185-21247359 FORWARD   Aliases: F17P19.19, F17P19_19	6.5	7.1	-0.6	-0.8	100.0%	-4.4
8671	AT5G35530.1   40S ribosomal protein S3 (RPS3C)	11.7	11.9	-0.2	-0.8	100.0%	-5.0
8672	AT4G23060.1   similar to calmodulin-binding family protein [Arabidopsis thaliana] (TAIR:At5g62070.1); similar to P0710E05.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_914546.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048)   chr4:12087214-12090586 FORWARD   Aliases: F7H19.250, F7H19_250	3.8	3.6	0.1	0.8	100.0%	-5.1
8673	AT1G13670.1   expressed protein   chr1:4688173-4688875 FORWARD   Aliases: F21F23.11, F21F23_11	3.7	3.6	0.1	0.8	100.0%	-5.1
8674	AT1G13870.1   Symbol: DRL1   expressed protein, similar to KTI12 protein (SP:P34253) {Saccharomyces cerevisiae}; contains Prosite PS00070: Aldehyde dehydrogenases cysteine active site   chr1:4747262-4748639 REVERSE   Aliases: DEFORMED ROOTS AND LEAVES 1, F16A14.8, F16A14_8	4.5	4.3	0.2	0.8	100.0%	-4.7
8675	AT1G75960.1   AMP-binding protein, putative, similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam profile: PF00501 AMP-binding enzyme; identical to cDNA adenosine monophosphate binding protein 8 AMPBP8 (AMPBP8) GI:20799724   chr1:28521694-28523535 FORWARD   Aliases: T4O12.18, T4O12_18	4.0	3.7	0.3	0.8	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8676	AT2G24610.1   Symbol: ATCNGC14   cyclic nucleotide-regulated ion channel, putative (CNGC14), similar to cyclic nucleotide and calmodulin-regulated ion channel (GI:4581205) (Arabidopsis thaliana)   chr2:10464124-10467587 FORWARD   Aliases: CNGC14, F25P17.9, F25P17_9	2.6	2.9	-0.3	-0.8	100.0%	-4.4
8677	AT1G62730.1   expressed protein   chr1:23232724-23234401 REVERSE   Aliases: F23N19.9, F23N19_9	5.1	5.5	-0.3	-0.8	100.0%	-4.5
8678	AT5G43760.1   beta-ketoacyl-CoA synthase, putative, similar to beta-ketoacyl-CoA synthase (Simmondsia chinensis)(GI:1045614)   chr5:17602990-17605824 FORWARD   Aliases: MQD19.11, MQD19_11	3.6	3.9	-0.3	-0.8	100.0%	-4.4
8679	AT4G29650.1   cytidine deaminase 4 (CDA4) (desH) / cytidine aminohydrolase, identical to cytidine deaminase homolog DesH (Arabidopsis thaliana) GI:4836450, cytidine deaminase 4 (CDA4) (Arabidopsis thaliana) GI:3818579; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14528593-14529348 FORWARD   Aliases: T16L4.160, T16L4_160	2.8	2.7	0.1	0.8	100.0%	-5.1
8680	AT1G31420.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profile: PF00069: Eukaryotic protein kinase domain   chr1:11249634-11253860 FORWARD   Aliases: T8E3.2, T8E3_2	5.9	5.6	0.3	0.8	100.0%	-4.7
8681	AT5G10350.2   polyadenylate-binding protein family protein / PABP family protein, contains weak similarity to poly(A) binding protein II from (Mus musculus) GI:2351846, (Xenopus laevis) GI:11527140; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:3255439-3257774 REVERSE   Aliases: F12B17.300, F12B17_300	8.1	7.8	0.3	0.8	100.0%	-4.3
8682	AT5G08400.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g29400.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD87659.1)   chr5:2706459-2708946 REVERSE   Aliases: F8L15.130, F8L15_130	6.4	6.0	0.4	0.8	100.0%	-4.1
8683	AT1G18810.1   phytochrome kinase substrate-related, contains weak similarity to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 (Arabidopsis thaliana)   chr1:6485587-6487021 REVERSE   Aliases: F6A14.9, F6A14_9	3.3	3.2	0.2	0.8	100.0%	-4.9
8684	AT1G66400.1   calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced from SP:P25070 (Arabidopsis thaliana); contains Pfam profile: PF00036 EF hand (4 copies)   chr1:24774238-24775034 REVERSE   Aliases: T27F4.15, T27F4_15	4.2	4.0	0.2	0.8	100.0%	-4.4
8685	AT1G79810.2   Symbol: TED3   Pex2/Pex12 N-terminal domain-containing protein / zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles PF00097: zinc finger C3HC4 type (RING finger), PF04757: Pex2/Pex12 amino terminal region   chr1:30024637-30027655 FORWARD   Aliases: F20B17.23, F20B17_23, PEX2, PEX2P, REVERSAL OF THE DET PHENOTYPE	5.5	5.8	-0.2	-0.8	100.0%	-4.7
8686	AT1G07170.1   expressed protein, contains Pfam domain PF03660: Uncharacterised protein family (UPF0123)   chr1:2200133-2201139 FORWARD   Aliases: F10K1.35	9.2	9.0	0.2	0.8	100.0%	-4.8
8687	AT3G05610.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:1625678-1628179 REVERSE   Aliases: F18C1.12, F18C1_12	2.5	2.4	0.1	0.8	100.0%	-5.1
8688	AT1G75140.1   expressed protein   chr1:28205827-28207940 REVERSE   Aliases: F22H5.14, F22H5_14	4.2	4.3	-0.2	-0.8	100.0%	-4.8
8689	AT4G23940.1   FtsH protease, putative, contains similarity to zinc dependent protease GI:7650138 from (Arabidopsis thaliana)   chr4:12437118-12441978 FORWARD   Aliases: T32A16.110, T32A16_110	4.5	4.9	-0.4	-0.8	100.0%	-4.3
8690	AT4G17740.2   C-terminal processing protease, putative, similar to C-terminal protease precursor (Spinacia oleracea) GI:999435; similar to SP:Q44879: (Bartonella bacilliformis)   chr4:9866990-9869765 REVERSE   Aliases: DL4905C, FCAALL.169	5.7	5.9	-0.3	-0.8	100.0%	-4.8
8691	AT2G35530.1   bZIP transcription factor family protein, contains Pfam domain PF00170: bZIP transcription factor; similar to G-Box binding protein 2 (GI:5381313) (Catharanthus roseus).   chr2:14930041-14933652 REVERSE   Aliases: T32F12.9, T32F12_9	3.0	3.1	-0.1	-0.8	100.0%	-5.1
8692	AT1G10520.1   DNA polymerase lambda (POLL), identical to DNA polymerase lambda GI:12053869 from (Arabidopsis thaliana)	2.7	2.6	0.1	0.8	100.0%	-5.1
8693	AT2G19500.1   Symbol: CKX2   FAD-binding domain-containing protein / cytokinin oxidase family protein, similar to cytokinin oxidase, Zea mays (SP:Q9T0N8) (gi:3441978)   chr2:8451286-8454437 REVERSE   Aliases: CYTOKININ OXIDASE 2, F3P11.10, F3P11_10	2.7	2.8	-0.1	-0.8	100.0%	-5.0
8694	AT4G28490.1   Symbol: HAESA   leucine-rich repeat transmembrane protein kinase, putative   chr4:14077863-14081177 FORWARD   Aliases: F20O9.180, F20O9_180, RECEPTOR LIKE PROTEIN KINASE 5, RLK5	5.0	5.3	-0.3	-0.8	100.0%	-4.1
8695	AT3G18480.1   CCAAT displacement protein-related / CDP-related, similar to CCAAT displacement protein (CDP) (Cut-like 1) (Swiss-Prot:P39880) (Homo sapiens); contains Pfam:PF00904 Involucrin repeat   chr3:6336754-6341794 FORWARD   Aliases: MYF24.37	7.2	7.4	-0.2	-0.8	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8696	AT1G76760.1   thioredoxin family protein, similar to thioredoxin CH2, M-type, chloroplast precursor GB:P23400 SP:P23400 (Chlamydomonas reinhardtii); contains Pfam profile: PF00085 Thioredoxin   chr1:28816584-28817945 REVERSE   Aliases: F28O16.13, F28O16_13	7.0	6.6	0.3	0.8	100.0%	-4.6
8697	AT1G18160.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:6248786-6254032 FORWARD   Aliases: T10F20.16	7.1	6.8	0.3	0.8	100.0%	-4.3
8698	AT3G51260.2   Symbol: PAD1   similar to 20S proteasome alpha subunit D2 (PAD2) (PRS1) (PRC6) [Arabidopsis thaliana] (TAIR:At5g66140.1); similar to proteasome alpha subunit [Oryza sativa (japonica cultivar-group)] (GB:XP_483663.1); similar to proteasome alpha subunit [Lycopersicon esculentum] (GB:CAA74725.1); contains InterPro domain Proteasome subunit, A-type (InterPro:IPR000426); contains InterPro domain Multispecific proteasome protease (InterPro:IPR001353)   chr3:19041974-19044043 FORWARD   Aliases: 20S PROTEASOME ALPHA SUBUNIT PAD1, F24M12.300	9.5	8.8	0.7	0.8	100.0%	-4.4
8699	AT5G51960.1   expressed protein   chr5:21127929-21128574 FORWARD   Aliases: MSG15.4, MSG15_4	6.1	6.4	-0.4	-0.8	100.0%	-4.5
8700	AT5G09780.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:3036957-3038485 REVERSE   Aliases: F17I14.30, F17I14_30	3.2	2.9	0.3	0.8	100.0%	-4.7
8701	AT5G42070.1   expressed protein, similar to unknown protein (dbj:BAA92898.1)   chr5:16836215-16837423 REVERSE   Aliases: MJC20.18, MJC20_18	5.1	4.7	0.4	0.8	100.0%	-4.2
8702	AT3G18630.1   uracil DNA glycosylase family protein, contains Pfam profile: PF03167 uracil DNA glycosylase superfamily	2.9	3.0	-0.1	-0.8	100.0%	-5.0
8703	AT3G01175.1   expressed protein   chr3:59478-60852 FORWARD   Aliases: None	2.2	2.3	-0.1	-0.8	100.0%	-5.5
8704	AT2G46900.1   expressed protein, contains Pfam profile PF04910: Protein of unknown function, DUF654   chr2:19276646-19279236 FORWARD   Aliases: F14M4.27	7.2	6.9	0.3	0.8	100.0%	-4.5
8705	AT4G23700.1   Symbol: ATCHX17   cation/hydrogen exchanger, putative (CHX17), similar to Na <sup>+</sup> /H <sup>+</sup> -exchanging protein slr1595 - Synechocystis sp., EMBL:D90902; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563	3.5	3.9	-0.4	-0.8	100.0%	-4.2
8706	AT5G55520.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g26660.1); similar to kinesin heavy chain, putative [Oryza sativa (japonica cultivar-group)] (GB:AAV35794.1)   chr5:22505300-22508477 REVERSE   Aliases: MTE17.24, MTE17_24	3.4	3.2	0.2	0.8	100.0%	-4.8
8707	AT1G07050.1   CONSTANS-like protein-related, contains similarity to photoperiod sensitivity quantitative trait locus (Hd1) GI:11094203 from (Oryza sativa); similar to Zinc finger protein constans-like 15 (SP:Q9FHH8) {Arabidopsis thaliana}	2.3	2.2	0.1	0.8	100.0%	-5.6
8708	AT1G24540.1   Symbol: CYP86C1   cytochrome P450, putative, similar to GB:AAB87111, similar to ESTs dbj:D41610, gb:T20562 and emb:Z26058   chr1:8699738-8701408 FORWARD   Aliases: F21J9.20	3.4	3.2	0.2	0.8	100.0%	-5.2
8709	AT1G56440.1   serine/threonine protein phosphatase-related, similar to SP:Q60676 Serine/threonine protein phosphatase 5 (EC 3.1.3.16) (PP5) (Protein phosphatase T) (PPT) Mus musculus, Tetratricopeptide Repeats Of Protein Phosphatase 5 (Homo sapiens) GI:3212250; contains Pfam profile: PF00515: TPR Domain   chr1:21142195-21145234 REVERSE   Aliases: F13N6.2, F13N6_2	3.3	4.0	-0.7	-0.8	100.0%	-4.8
8710	AT1G07025.1   mitochondrial substrate carrier family protein, contains similarity to mitochondrial carrier proteins   chr1:2157657-2158157 REVERSE   Aliases: None	2.6	2.7	-0.1	-0.8	100.0%	-5.0
8711	AT2G22680.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF00092: von Willebrand factor type A domain	4.2	4.5	-0.4	-0.8	100.0%	-4.2
8712	AT5G42140.1   zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein, similar to zinc finger protein (Arabidopsis thaliana) gi:15811367:gb:AAL08940   chr5:16854608-16858868 REVERSE   Aliases: MJC20.25, MJC20_25	4.9	5.1	-0.2	-0.8	100.0%	-4.6
8713	AT5G44160.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:17790168-17792913 FORWARD   Aliases: MLN1.8, MLN1_8	3.6	3.5	0.1	0.8	100.0%	-5.2
8714	AT1G68370.1   Symbol: ARG1   gravity-responsive protein / altered response to gravity protein (ARG1), identical to Altered Response to Gravity (Arabidopsis thaliana) GI:4249662; contains Pfam profile PF00226 Dnaj domain   chr1:25635408-25638401 REVERSE   Aliases: ALTERED RESPONSE TO GRAVITY 1, T22E19.25, T22E19_25	4.3	4.5	-0.3	-0.8	100.0%	-4.6
8715	AT4G21640.1   subtilase family protein, similar to subtilase SP1 (Oryza sativa) GI:9957714   chr4:11496846-11500630 REVERSE   Aliases: F17L22.100, F17L22_100	1.7	1.9	-0.1	-0.8	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8716	ATCG00640.1   Symbol: RPL33   encodes a chloroplast ribosomal protein L33, a constituent of the large subunit of the ribosomal complex   chrC:67488-67688 FORWARD   Aliases: RPL33	8.2	9.0	-0.9	-0.8	100.0%	-4.5
8717	AT1G17110.1   Symbol: UBP15   ubiquitin-specific protease 15 (UBP15), almost identical to ubiquitin-specific protease 15 GI:11993475 (Arabidopsis thaliana), 7 amino acid difference   chr1:5845668-5850038 REVERSE   Aliases: F20D23.20, F20D23_20, UBIQUITIN SPECIFIC PROTEASE 15	4.0	4.5	-0.4	-0.8	100.0%	-4.5
8718	AT1G12480.1   C4-dicarboxylate transporter/malic acid transport family protein, contains Pfam profile PF03595: C4-dicarboxylate transporter/malic acid transport protein   chr1:4257137-4259298 REVERSE   Aliases: F5O11.23, F5O11_23	2.8	2.7	0.1	0.8	100.0%	-5.5
8719	AT2G20570.1   Symbol: GPRI1   golden2-like transcription factor (GLK1), identical to golden2-like transcription factor GI:13311003 from (Arabidopsis thaliana); contains Pfam profile: PF00249 Myb-like DNA-binding domain   chr2:8862439-8864837 FORWARD   Aliases: GLK1, GOLDEN2 LIKE 1, T13C7.1	3.6	3.5	0.1	0.8	100.0%	-4.9
8720	AT1G26500.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:9158367-9159884 FORWARD   Aliases: T1K7.14, T1K7_14	4.3	4.7	-0.4	-0.8	100.0%	-4.4
8721	AT1G80770.1   Symbol: PDE318	5.4	5.6	-0.2	-0.8	100.0%	-4.9
8722	AT2G32190.1   expressed protein   chr2:13681594-13682362 FORWARD   Aliases: F22D22.6, F22D22_6	2.2	2.1	0.1	0.8	100.0%	-5.9
8723	AT5G26630.1   MADS-box protein (AGL35), homeotic protein boi1AP3, Brassica oleracea, EMBL:U67453; contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr5:9350818-9351474 FORWARD   Aliases: None	3.7	3.8	-0.2	-0.8	100.0%	-4.8
8724	AT3G59440.1   calcium-binding protein, putative, similar to calcium-binding protein (Lotus japonicus) GI:18413495   chr3:21981332-21982099 FORWARD   Aliases: F25L23.300	3.3	3.1	0.2	0.8	100.0%	-4.8
8725	AT3G01990.1   Symbol: ACR6   ACT domain-containing protein (ACR6), contains Pfam ACT domain PF01842; similar to uridylyl transferase-like proteins GB:AAD20075, GB:AAC00631 (Arabidopsis thaliana)   chr3:330144-332269 FORWARD   Aliases: F1C9.23, F1C9_23	4.0	3.8	0.2	0.8	100.0%	-4.9
8726	AT3G57150.1   Symbol: NAP57   dyskerin, putative / nucleolar protein NAP57, putative, similar to SP:P40615 Dyskerin (Nucleolar protein NAP57) {Rattus norvegicus}; contains Pfam profiles PF01509: TruB family pseudouridylate synthase (N terminal domain), PF01472: PUA domain; supporting cDNA gi:8901185:gb:AF234984.2:AF234984   chr3:21164952-21166988 REVERSE   Aliases: ATNAP57, F24I3.230	10.6	10.9	-0.4	-0.8	100.0%	-4.9
8727	AT3G48950.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to SP:P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) {Agrobacterium tumefaciens}; contains PF00295: Glycosyl hydrolases family 28   chr3:18159002-18160972 FORWARD   Aliases: T2J13.210	3.7	3.9	-0.2	-0.8	100.0%	-4.8
8728	ATMG00510.1   Symbol: NAD7   NADH dehydrogenase subunit 7   chrM:132071-138153 FORWARD   Aliases: NAD7	3.5	3.2	0.3	0.8	100.0%	-4.6
8729	AT5G63410.1   leucine-rich repeat transmembrane protein kinase, putative, contains similarity to receptor-like protein kinase   chr5:25412211-25415379 REVERSE   Aliases: MLE2.4, MLE2_4	4.3	4.0	0.3	0.8	100.0%	-4.2
8730	AT3G14360.1   lipase class 3 family protein, low similarity to Chain A, Lipase li From Rhizopus Niveus GI:1942798; contains Pfam profile PF01764: Lipase   chr3:4791596-4794445 FORWARD   Aliases: MLN21.14	5.3	5.5	-0.2	-0.8	100.0%	-5.1
8731	AT1G32300.1   FAD-binding domain-containing protein, strong similarity to At5g56490, At2g46740, At2g46750, At2g46760; contains PF01565: FAD binding domain   chr1:11651322-11653345 FORWARD   Aliases: F27G20.8	3.0	3.1	-0.2	-0.8	100.0%	-4.8
8732	AT3G13350.1   high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein, low similarity to Dead Ringer Protein Chain A Dna-Binding Domain (GI:6573608), Arid-Dna Complex (GI:20150982) from (Drosophila melanogaster); contains Pfam profiles PF00505: HMG (high mobility group) box, PF01388: ARID/BRIGHT DNA binding domain   chr3:4335502-4337846 REVERSE   Aliases: MDC11.15	2.7	2.9	-0.1	-0.8	100.0%	-5.1
8733	AT4G39910.1   Symbol: ATUBP3	5.9	5.5	0.4	0.8	100.0%	-4.5
8734	AT5G57040.1   lactoylglutathione lyase family protein / glyoxalase I family protein, contains Pfam PF00903: glyoxalase family protein   chr5:23101131-23102472 REVERSE   Aliases: MHM17.18, MHM17_18	9.0	8.8	0.2	0.8	100.0%	-4.4
8735	AT3G51480.1   Symbol: ATGLR3.6   glutamate receptor family protein (GLR3.6), plant glutamate receptor family, PMID:11379626   chr3:19111655-19115804 FORWARD   Aliases: F26O13.120, GLR3.6	5.0	5.3	-0.3	-0.8	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8736	AT1G08135.1   cation/hydrogen exchanger (CHX6b), Note: CHX6a and CHX6b were originally 1 gene but were split based on alignments with other family members; may be a pseudogene and requires further investigation; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr1:2548816-2551470 REVERSE   Aliases: None	3.3	3.4	-0.1	-0.8	100.0%	-5.1
8737	AT1G61850.1   patatin family protein, similar to membrane-associated calcium-independent phospholipase A2 gamma; IPLA2 gamma (Homo sapiens) GI:8453174; contains Patatin domain PF01734, PF00514: Armadillo/beta-catenin-like repeat   chr1:22859982-22865890 FORWARD   Aliases: F8K4.6, F8K4_6	4.8	5.2	-0.4	-0.8	100.0%	-4.5
8738	AT1G19080.1   Symbol: TTN10   expressed protein   chr1:6584257-6586426 FORWARD   Aliases: F14D16.33, TITAN 10	7.1	7.4	-0.3	-0.8	100.0%	-4.5
8739	AT2G36460.1   fructose-bisphosphate aldolase, putative, similar to PIR:S65073 fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic (Oryza sativa); contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I   chr2:15303780-15305593 REVERSE   Aliases: F1O11.9, F1O11_9	8.0	7.1	0.9	0.8	100.0%	-4.3
8740	AT2G18930.1   hypothetical protein   chr2:8205860-8206154 FORWARD   Aliases: F19F24.13, F19F24_13	2.9	2.8	0.1	0.8	100.0%	-5.3
8741	AT3G52950.1   CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein, contains Pfam profiles: PF00571 CBS domain, PF00564: PB1 domain   chr3:19645474-19647797 FORWARD   Aliases: F8J2.120	7.1	6.9	0.2	0.8	100.0%	-5.0
8742	AT2G26800.3   hydroxymethylglutaryl-CoA lyase, putative / 3-hydroxy-3-methylglutarate-CoA lyase, putative / HMG-CoA lyase, putative, similar to SP:P35915 Hydroxymethylglutaryl-CoA lyase (EC 4.1.3.4) (HMG-CoA lyase) {Gallus gallus}; contains Pfam profile PF00682: HMGL-like   chr2:11436888-11439810 REVERSE   Aliases: F12C20.16, F12C20_16	9.2	8.8	0.4	0.8	100.0%	-4.5
8743	AT1G61140.1   SNF2 domain-containing protein / helicase domain-containing protein / zinc finger protein-related, similar to ATPase (Homo sapiens) GI:531196; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:22538391-22544275 REVERSE   Aliases: F11P17.13, F11P17_13	7.7	8.1	-0.4	-0.8	100.0%	-4.7
8744	AT2G31240.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr2:13324492-13326637 REVERSE   Aliases: F16D14.8, F16D14_8	6.0	6.3	-0.3	-0.8	100.0%	-4.3
8745	AT2G19410.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr2:8411983-8416094 REVERSE   Aliases: F27F23.21, F27F23_21	2.7	2.5	0.2	0.8	100.0%	-4.7
8746	AT3G10800.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor; contains similarity to TGACG-sequence specific DNA-binding protein TGA-1B (HSBF) GB:P14233 (Nicotiana tabacum)   chr3:3379259-3381618 FORWARD   Aliases: T7M13.12	6.0	5.7	0.3	0.8	100.0%	-4.5
8747	AT4G25580.1   stress-responsive protein-related, contains weak similarity to Low-temperature-induced 65 kDa protein (Desiccation-responsive protein 29B) (Swiss-Prot:Q04980) (Arabidopsis thaliana)   chr4:13056201-13058811 FORWARD   Aliases: M7J2.50, M7J2_50	3.6	3.2	0.4	0.8	100.0%	-4.3
8748	AT1G20510.2   4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein, similar to SP:P14912 and SP:P14913 from Petroselinum crispum; contains Pfam AMP-binding enzyme domain PF00501   chr1:7103449-7105859 REVERSE   Aliases: F5M15.17, F5M15_17	7.7	7.6	0.2	0.8	100.0%	-4.6
8749	AT5G17680.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:5823001-5827155 FORWARD   Aliases: MVA3.30, MVA3_30	3.3	3.4	-0.1	-0.8	100.0%	-5.0
8750	AT3G27785.1   Symbol: MYB118	3.4	3.3	0.1	0.8	100.0%	-5.5
8751	AT1G69360.1   expressed protein   chr1:26075947-26079917 REVERSE   Aliases: F10D13.5, F10D13_5	5.0	5.3	-0.3	-0.8	100.0%	-4.5
8752	AT3G52030.1   F-box family protein / WD-40 repeat family protein   chr3:19312850-19315205 FORWARD   Aliases: F4F15.140	6.6	6.8	-0.3	-0.8	100.0%	-5.0
8753	AT2G14910.2   expressed protein   chr2:6413558-6416234 REVERSE   Aliases: T26I20.7, T26I20_7	9.3	8.7	0.7	0.8	100.0%	-4.4
8754	AT5G19300.1   expressed protein, contains Pfam profile PF02598: Uncharacterized ACR, COG2106   chr5:6495581-6498216 FORWARD   Aliases: F7K24.50, F7K24_50	5.6	5.2	0.4	0.8	100.0%	-4.0
8755	AT1G18530.1   calmodulin, putative, similar to calmodulin GI:1565285 from (Toxoplasma gondii)   chr1:6376776-6377249 FORWARD   Aliases: F25I16.13, F25I16_13	2.6	2.5	0.1	0.8	100.0%	-5.5
8756	AT1G04550.2   Symbol: IAA12   auxin-responsive protein / indoleacetic acid-induced protein 12 (IAA12), identical to SP:Q38830 Auxin-responsive protein IAA12 (Indoleacetic acid-induced protein 12) {Arabidopsis thaliana}   chr1:1240413-1242119 FORWARD   Aliases: AUXIN INDUCED PROTEIN 12, BDL, BODENLOS, T1G11.20, T1G11_20	5.3	5.6	-0.3	-0.8	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8757	AT4G14170.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:8176319-8178124 REVERSE   Aliases: DL3125C, FCAALL.113	3.1	3.2	-0.1	-0.8	100.0%	-4.9
8758	AT1G56600.1   galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 GI:5608497 from (Ajuga reptans)   chr1:21211202-21213261 FORWARD   Aliases: F25P12.95, F25P12_95	3.4	3.0	0.4	0.8	100.0%	-4.3
8759	AT5G04600.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:1323641-1325614 FORWARD   Aliases: T1E3.1	7.0	7.4	-0.3	-0.8	100.0%	-4.3
8760	AT3G48460.1   GDSL-motif lipase/hydrolase family protein, similar to lipase (Arabidopsis thaliana) GI:1145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr3:17960430-17962180 FORWARD   Aliases: T29H11.20	2.3	2.5	-0.1	-0.8	100.0%	-5.3
8761	AT5G63135.1   expressed protein   chr5:25342205-25343705 REVERSE   Aliases: None	3.7	3.4	0.4	0.8	100.0%	-4.6
8762	AT3G15630.1   expressed protein   chr3:5296854-5297606 REVERSE   Aliases: MSJ11.3	3.9	3.6	0.3	0.8	100.0%	-4.2
8763	AT1G78410.1   VQ motif-containing protein, contains PF05678: VQ motif   chr1:29507475-29508134 FORWARD   Aliases: F3F9.8, F3F9_8	2.7	2.8	-0.1	-0.8	100.0%	-5.4
8764	AT5G11290.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr5:3599002-3600473 FORWARD   Aliases: F2I11.180, F2I11_180	2.7	2.6	0.1	0.8	100.0%	-5.1
8765	AT2G27220.1   homeodomain-containing protein   chr2:11644384-11646615 REVERSE   Aliases: T22O13.1, T22O13_1	4.0	3.8	0.1	0.8	100.0%	-5.1
8766	AT1G03680.1   Symbol: ATHM1   thioredoxin M-type 1, chloroplast (TRX-M1), nearly identical to SP:O48737 Thioredoxin M-type 1, chloroplast precursor (TRX-M1) {Arabidopsis thaliana}; similar to ESTs gb:T13714, gb:H76398, gb:N37762, gb:AA042639, gb:T21104, emb:Z30901   chr1:916845-918001 REVERSE   Aliases: None	8.6	8.1	0.6	0.8	100.0%	-4.1
8767	AT4G28460.1   expressed protein   chr4:14066004-14066550 FORWARD   Aliases: F20O9.140, F20O9_140	5.2	5.6	-0.4	-0.8	100.0%	-4.5
8768	AT1G20650.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr1:7158234-7162548 REVERSE   Aliases: F5M15.3	6.4	6.6	-0.2	-0.8	100.0%	-4.5
8769	AT3G05280.1   integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain   chr3:1503764-1505648 REVERSE   Aliases: T12H1.25, T12H1_25	7.4	7.0	0.4	0.8	100.0%	-4.3
8770	AT1G09900.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3218135-3219931 FORWARD   Aliases: F21M12.38, F21M12_38	3.5	3.6	-0.1	-0.8	100.0%	-4.9
8771	AT2G06960.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to ripening protein E8, Lycopersicon esculentum (PIR:S01642); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr2:2867669-2870349 REVERSE   Aliases: T4E14.7, T4E14_7	3.1	3.3	-0.2	-0.8	100.0%	-4.9
8772	AT4G34870.1   Symbol: ROC5   peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP1) / rotamase, identical to cyclophilin (CYP1) gi:992643:gb:AAA75512; similar to peptidyl-prolyl cis-trans isomerase, PPIase (cyclophilin, cyclosporin A-binding protein) (Catharanthus roseus) SWISS-PROT:Q39613   chr4:16614332-16615318 FORWARD   Aliases: ATCYP1, CYCLOPHILIN, F11I11.110, F11I11_110, ROTAMASE CYP	10.3	10.9	-0.5	-0.8	100.0%	-4.2
8773	AT1G21760.1   F-box family protein, Contains PF:00646 F-box domain. ESTs gb:Z37267, gb:R90412, gb:Z37268 and gb:T88189 come from this gene similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:7649215-7652226 FORWARD   Aliases: F8K7.20, F8K7_20	8.1	7.7	0.4	0.8	100.0%	-4.5
8774	AT2G37975.1   expressed protein   chr2:15898931-15900717 REVERSE   Aliases: None	8.7	8.2	0.4	0.8	100.0%	-4.6
8775	AT1G60560.2   SWIM zinc finger family protein, contains Pfam domain PF04434: SWIM zinc finger   chr1:22312214-22315015 REVERSE   Aliases: F8A5.10, F8A5_10	3.9	4.3	-0.4	-0.8	100.0%	-4.4
8776	AT2G37210.1   expressed protein, contains Pfam profile PF03641: decarboxylase family protein   chr2:15631070-15634019 REVERSE   Aliases: T2N18.3, T2N18_3	3.7	3.9	-0.2	-0.8	100.0%	-4.8
8777	AT5G43640.1   40S ribosomal protein S15 (RPS15E)   chr5:17548529-17549597 FORWARD   Aliases: K9D7.14, K9D7_14	3.0	3.0	-0.1	-0.8	100.0%	-5.5
8778	AT1G77130.1   glycogenin glucosyltransferase (glycogenin)-related, contains similarity to glycogenin-1 from Mus musculus (SP:Q9R062), Rattus norvegicus (SP:O08730), Homo sapiens (SP:P46976)   chr1:28983788-28986185 REVERSE   Aliases: T14N5.1, T14N5_1	5.9	6.3	-0.5	-0.8	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8779	AT5G16640.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:5460979-5462548 FORWARD   Aliases: MTG13.9, MTG13_9	3.7	3.9	-0.2	-0.8	100.0%	-5.1
8780	AT4G28370.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:14035616-14041672 FORWARD   Aliases: F2009.50, F2009_50	3.5	3.3	0.2	0.8	100.0%	-4.5
8781	AT2G17070.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function; expression supported by MPSS   chr2:7437945-7438736 REVERSE   Aliases: F6P23.22, F6P23_22	2.7	2.6	0.2	0.8	100.0%	-5.0
8782	AT5G52800.2   expressed protein, similar to hypothetical protein [Homo sapiens] (GB:CAI46079.1)   chr5:21413170-21415862 FORWARD   Aliases: MXC20.1, MXC20_1	3.1	3.2	-0.2	-0.8	100.0%	-4.7
8783	AT5G10130.1   pollen Ole e 1 allergen and extensin family protein, contains similarity to pollen specific protein C13 precursor (Zea mays) SWISS-PROT:P33050   chr5:3171552-3172429 REVERSE   Aliases: T31P16.120, T31P16_120	2.8	2.7	0.1	0.8	100.0%	-5.5
8784	AT3G29350.2   Symbol: AHP2   two-component phosphorelay mediator 1 (HP1), identical to ATHP1 (Arabidopsis thaliana) GI:4156241   chr3:11265868-11266767 REVERSE   Aliases: ATHP1, HISTIDINE CONTAINING PHOSPHOTRANSMITTER 2, MUO10.16	6.2	6.6	-0.4	-0.8	100.0%	-4.4
8785	AT3G18390.1   Symbol: EMB1865   expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578)   chr3:6313491-6317977 FORWARD   Aliases: EMB1865, EMBRYO DEFECTIVE 1865, MYF24.11	5.1	5.4	-0.2	-0.8	100.0%	-4.6
8786	AT5G57900.1   Symbol: SKIP1   SKP1/ASK1 interacting partner 1 (SKIP1) / SCF (Skp1-cullin-F-box) ubiquitin ligase, identical to SKP1 interacting partner 1 GI:10716947 from (Arabidopsis thaliana), PMID:11387208   chr5:23466937-23468159 REVERSE   Aliases: MTI20.16, MTI20_16, SKP1 INTERACTING PARTNER 1	7.2	6.8	0.3	0.8	100.0%	-4.8
8787	AT1G73040.1   jacalin lectin family protein, similar to jacalin Artocarpus heterophyllus GI:289160, SP:P18674 Agglutinin alpha chain (MPA) Maclura pomifera, SP:P18670 Agglutinin alpha chain (Jacalin alpha chain) Artocarpus integrifolia; contains Pfam profile PF01419 jacalin-like lectin domain   chr1:27478236-27479623 REVERSE   Aliases: F3N23.24, F3N23_24	3.0	2.8	0.2	0.8	100.0%	-4.7
8788	AT1G15510.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:5329106-5331706 FORWARD   Aliases: T16N11.2, T16N11_2	4.7	5.0	-0.3	-0.8	100.0%	-4.4
8789	AT4G13610.1   DNA (cytosine-5-)-methyltransferase, putative, similar to cytosine-5 methyltransferase (METII) (Arabidopsis thaliana) GI:6523846; contains Pfam profiles PF01426: BAH domain, PF00145: C-5 cytosine-specific DNA methylase   chr4:7915018-7921227 FORWARD   Aliases: T6G15.160, T6G15_160	2.1	2.3	-0.1	-0.8	100.0%	-5.4
8790	AT5G39980.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:16018264-16020300 REVERSE   Aliases: MYH19.18, MYH19_18	3.5	3.6	-0.1	-0.8	100.0%	-5.0
8791	AT1G19600.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr1:6779015-6781164 FORWARD   Aliases: F14P1.7, F14P1_7	9.4	9.0	0.4	0.8	100.0%	-4.3
8792	AT1G64000.1   Symbol: WRKY56	2.5	2.4	0.1	0.8	100.0%	-5.4
8793	AT5G67500.1   porin, putative, similar to SP:P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin   chr5:26952389-26954709 FORWARD   Aliases: K9I9.6, K9I9_6	7.4	8.1	-0.7	-0.8	100.0%	-4.2
8794	AT1G27900.1   RNA helicase, putative, similar to SP:Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr1:9715440-9720548 REVERSE   Aliases: F13K9.28, F13K9_28	7.1	7.4	-0.4	-0.8	100.0%	-4.5
8795	AT2G35540.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226: DnaJ domain	5.5	5.3	0.1	0.8	100.0%	-5.1
8796	AT4G26570.2   Symbol: ATCBL3	8.4	8.7	-0.3	-0.8	100.0%	-4.8
8797	AT2G01920.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (GI:6492344) (Xenopus laevis)   chr2:426051-426989 FORWARD   Aliases: F23I14.1, F23I14_1	1.9	2.0	-0.1	-0.8	100.0%	-5.7
8798	AT4G17260.1   L-lactate dehydrogenase, putative, strong similarity to L-lactate dehydrogenase from Lycopersicon esculentum (GI:1620970, GI:1620972), Hordeum vulgare (SP:P22988, SP:P22989); contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr4:9674005-9675456 FORWARD   Aliases: DL4665W, FCAALL.172	6.4	5.7	0.7	0.8	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8799	AT4G18270.1   Symbol: ATTRANS11   glycosyl transferase family 4 protein, contains Pfam profile PF00953: Glycosyl transferase   chr4:10099375-10101908 REVERSE   Aliases: T9A21.120, T9A21_120, TRANSLOCASE I	5.1	5.5	-0.3	-0.8	100.0%	-4.4
8800	AT2G34270.1   hypothetical protein, and genscan   chr2:14475831-14476955 REVERSE   Aliases: F13P17.11, F13P17_11	3.4	3.3	0.1	0.8	100.0%	-5.0
8801	AT4G22340.3   similar to phosphatidate cytidyltransferase / CDP-diglyceride synthetase (CDS1) [Arabidopsis thaliana] (TAIR:At1g62430.1); similar to putative CDP-diacylglycerol synthetase [Oryza sativa (japonica cultivar-group)] (GB:BAD87586.1); contains InterPro domain Phosphatidate cytidyltransferase (InterPro:IPR000374)   chr4:11799971-11802840 REVERSE   Aliases: T10I14.170, T10I14_170	6.3	6.0	0.3	0.8	100.0%	-4.5
8802	AT3G09430.1   expressed protein   chr3:2901286-2902300 FORWARD   Aliases: F3L24.32	2.6	2.7	-0.1	-0.8	100.0%	-5.3
8803	AT2G12900.1   expressed protein, similar to transcription factor(bZIP family) VSF-1 GI:3425907 from (Lycopersicon esculentum)   chr2:5300979-5302562 FORWARD   Aliases: T18E17.2	2.8	2.6	0.2	0.8	100.0%	-5.0
8804	AT5G23405.2   high mobility group (HMG1/2) family protein, contains Pfam profile PF00505: HMG (high mobility group) box   chr5:7882851-7884363 REVERSE   Aliases: None	3.6	3.5	0.1	0.8	100.0%	-4.9
8805	AT5G15720.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386) and EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:5124528-5126184 REVERSE   Aliases: F14F8.100, F14F8_100	2.3	2.4	-0.1	-0.8	100.0%	-5.6
8806	AT4G30500.1   expressed protein, contains Pfam PF05620: Protein of unknown function (DUF788)   chr4:14903496-14904923 FORWARD   Aliases: F17I23.160, F17I23_160	5.4	5.6	-0.2	-0.8	100.0%	-4.8
8807	AT1G23830.1   expressed protein   chr1:8422949-8424077 REVERSE   Aliases: F5O8.39, F5O8_39	4.7	5.1	-0.3	-0.8	100.0%	-4.3
8808	AT5G40440.1   Symbol: ATMKK3	4.7	4.5	0.1	0.8	100.0%	-5.3
8809	AT1G22980.1   expressed protein   chr1:8132679-8134154 REVERSE   Aliases: F19G10.7	3.3	3.5	-0.2	-0.8	100.0%	-4.5
8810	AT3G46980.3   similar to transporter-related [Arabidopsis thaliana] (TAIR:At2g38060.1); similar to putative membrane glycoprotein HP59 [Oryza sativa (japonica cultivar-group)] (GB:BAD82655.1); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828)   chr3:17318040-17320923 REVERSE   Aliases: F13I12.30	4.2	3.9	0.3	0.8	100.0%	-4.8
8811	AT5G04660.1   Symbol: CYP77A4   cytochrome P450, putative, cytochrome P450 77A3p, Glycine max., PIR:T05948   chr5:1335996-1337671 FORWARD   Aliases: T1E3.20, T1E3_20	4.3	4.5	-0.2	-0.8	100.0%	-4.6
8812	AT1G22310.2   Symbol: MBD8   DNA-binding protein-related, contains Pfam profiles PF02178: AT hook motif, PF01429: Methyl-CpG binding domain   chr1:7881526-7883731 REVERSE   Aliases: T16E15.7, T16E15_7	4.4	4.7	-0.3	-0.8	100.0%	-4.6
8813	AT3G47420.1   glycerol-3-phosphate transporter, putative / glycerol 3-phosphate permease, putative, similar to cAMP inducible 2 protein (Mus musculus) GI:4580997, glycerol-3-phosphate transporter (glycerol 3-phosphate permease) (Homo sapiens) GI:7543982; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:17483327-17486198 REVERSE   Aliases: T21L8.170	5.2	4.5	0.6	0.8	100.0%	-4.4
8814	AT5G60680.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr5:24403371-24404202 FORWARD   Aliases: MUP24.10, MUP24_10	4.7	5.0	-0.3	-0.8	100.0%	-4.6
8815	AT1G19040.1   expressed protein   chr1:6576886-6577404 FORWARD   Aliases: F14D16.19, F14D16_19	2.3	2.2	0.1	0.8	100.0%	-5.4
8816	AT5G06660.1   expressed protein, contains PF05809: Eukaryotic protein of unknown function (DUF841)   chr5:2046811-2047795 FORWARD   Aliases: F15M7.19, F15M7_19	5.2	5.4	-0.2	-0.8	100.0%	-4.8
8817	AT4G34390.1   extra-large guanine nucleotide binding protein, putative / G-protein, putative, similar to extra-large G-protein (XLG) (Arabidopsis thaliana) GI:3201680; contains Pfam profile PF00503: G-protein alpha subunit	4.3	4.0	0.3	0.8	100.0%	-4.6
8818	AT3G42090.1   hypothetical protein   chr3:14285208-14285685 FORWARD   Aliases: F4M19.50	2.2	2.3	-0.1	-0.8	100.0%	-6.1
8819	AT1G73030.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr1:27477487-27478783 FORWARD   Aliases: F3N23.23, F3N23_23	8.8	8.4	0.4	0.8	100.0%	-4.4
8820	AT4G38960.2   similar to zinc finger (B-box type) family protein [Arabidopsis thaliana] (TAIR:At2g21320.1); similar to OSJNBa0011L07.9 [Oryza sativa (japonica cultivar-group)] (GB:XP_473353.1); contains InterPro domain Zn-finger, B-box (InterPro:IPR000315)   chr4:18161508-18163300 FORWARD   Aliases: F19H22.60, F19H22_60	3.4	3.3	0.2	0.8	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8821	AT1G72420.1   chaperone-related, similar to Complex I intermediate-associated protein 30, mitochondrial precursor (CGI-65) (Swiss-Prot:Q9Y375) (Homo sapiens); similar to Probable complex I intermediate-associated protein 30 (Swiss-Prot:Q9LQI7) (Arabidopsis thaliana)   chr1:27265029-27266676 REVERSE   Aliases: T10D10.11, T10D10_11	5.3	5.6	-0.3	-0.8	100.0%	-4.7
8822	AT4G13860.1   glycine-rich RNA-binding protein, putative, similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor (AtGRP2) (Swiss-Prot:Q9SVM8) (Arabidopsis thaliana) ; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr4:8022597-8023158 FORWARD   Aliases: F18A5.250, F18A5_250	7.0	7.2	-0.3	-0.8	100.0%	-4.2
8823	AT3G55630.3   Symbol: ATDFD   dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS4), nearly identical to folylpolyglutamate-dihydrofolate synthetase (Arabidopsis thaliana) GI:17976761	4.3	4.5	-0.3	-0.8	100.0%	-4.9
8824	AT1G01860.1   Symbol: PFC1   dimethyladenosine transferase (PFC1), identical to dimethyladenosine transferase GB:AAC09322 GI:3005590 from (Arabidopsis thaliana)   chr1:304439-306275 REVERSE   Aliases: DIMETHYLADENOSINE TRANSFERASE, F22M8.1, PALEFACE 1	3.6	3.5	0.1	0.8	100.0%	-4.9
8825	AT1G65760.1   F-box family protein, contains F-box domain Pfam:PF00646	2.9	2.7	0.2	0.8	100.0%	-5.2
8826	AT1G20310.1   expressed protein   chr1:7032280-7033198 FORWARD   Aliases: F14O10.9, F14O10_9	2.5	2.4	0.1	0.8	100.0%	-5.2
8827	AT3G05090.2   transducin family protein / WD-40 repeat family protein, contains seven G-protein beta WD-40 repeats; similar to uncharacterized KIAA1449 protein (gi:7959157) (Homo sapiens)   chr3:1417899-1423670 REVERSE   Aliases: T12H1.5, T12H1_5	4.9	5.1	-0.3	-0.8	100.0%	-4.3
8828	AT3G18900.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:6517187-6520798 FORWARD   Aliases: MCB22.8	3.2	3.1	0.1	0.8	100.0%	-5.4
8829	AT3G11280.2   myb family transcription factor, contains Pfam profile: PF00249 Myb-like DNA-binding domain   chr3:3533261-3534502 REVERSE   Aliases: F11B9.25	8.0	7.7	0.3	0.8	100.0%	-4.6
8830	AT5G64590.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr5:25839558-25840427 REVERSE   Aliases: MUB3.11, MUB3_11	3.4	3.2	0.2	0.8	100.0%	-5.0
8831	AT3G12070.2   geranylgeranyl transferase type II beta subunit, putative / RAB geranylgeranyltransferase beta subunit, putative, similar to geranylgeranyl transferase type II beta subunit SP:P53611 (GI:1552549) (Homo sapiens)   chr3:3845221-3847550 REVERSE   Aliases: T21B14.11	5.1	5.3	-0.2	-0.8	100.0%	-4.6
8832	AT5G46540.1   ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter; similar to multidrug-resistant protein CjMDR1 GI:14715462 from (Coptis japonica)	3.2	3.0	0.2	0.8	100.0%	-4.9
8833	AT5G01970.1   expressed protein   chr5:372724-374951 REVERSE   Aliases: T7H20.20, T7H20_20	4.4	4.2	0.2	0.8	100.0%	-4.5
8834	AT5G45670.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	2.1	2.2	-0.1	-0.8	100.0%	-5.3
8835	AT4G02160.1   hypothetical protein   chr4:955101-955652 REVERSE   Aliases: T10M13.23, T10M13_23	3.6	3.3	0.2	0.8	100.0%	-4.7
8836	AT5G47350.1   palmitoyl protein thioesterase family protein   chr5:19229916-19231680 FORWARD   Aliases: MQL5.21, MQL5_21	3.3	3.1	0.2	0.8	100.0%	-5.0
8837	AT3G16610.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:5656377-5658341 REVERSE   Aliases: MGL6.8	2.9	3.1	-0.1	-0.8	100.0%	-4.9
8838	AT1G78570.2   Symbol: RHM1   similar to NAD-dependent epimerase/dehydratase family protein [Arabidopsis thaliana] (TAIR:At3g14790.1); similar to NAD-dependent epimerase/dehydratase family protein [Arabidopsis thaliana] (TAIR:At1g53500.1); similar to dTDP-D-glucose 4,6-dehydratase, putative [Entamoeba histolytica HM-1:IMSS] (GB:EAL47103.1); contains InterPro domain NAD-dependent epimerase/dehydratase (InterPro:IPR001509)   chr1:29554543-29557693 FORWARD   Aliases: RHM1, T30F21.10, T30F21_10	4.9	5.4	-0.5	-0.8	100.0%	-4.4
8839	AT5G61740.1   Symbol: ATATH14   ABC transporter family protein, ABC family transporter, Entamoeba histolytica, TREMBL:EH058   chr5:24825710-24829823 FORWARD   Aliases: MAC9.5, MAC9_5	2.4	2.3	0.1	0.8	100.0%	-5.4
8840	AT4G14900.1   hydroxyproline-rich glycoprotein family protein   chr4:8521517-8523700 REVERSE   Aliases: DL3490C, FCAALL.410	5.6	6.0	-0.4	-0.8	100.0%	-4.6
8841	AT2G28260.1   Symbol: ATCNGC15   cyclic nucleotide-regulated ion channel, putative (CNGC15), similar to cyclic nucleotide and calmodulin-regulated ion channel (cngc6) GI:4581207 from (Arabidopsis thaliana)	5.7	5.8	-0.2	-0.8	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8842	AT2G42930.1   glycosyl hydrolase family protein 17, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr2:17867945-17868349 REVERSE   Aliases: F23E6.9, F23E6_9	2.7	2.7	0.1	0.8	100.0%	-5.5
8843	AT5G41270.1   expressed protein   chr5:16524937-16526107 FORWARD   Aliases: K1O13.7, K1O13_7	4.4	4.2	0.2	0.8	100.0%	-4.7
8844	AT5G18390.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:6090956-6092547 FORWARD   Aliases: F20L16.110, F20L16_110	4.3	4.5	-0.2	-0.8	100.0%	-4.9
8845	AT2G30570.2   photosystem II reaction center W (PsbW) protein-related, similar to photosystem II reaction center W protein SP:Q41387 from (Spinacia oleracea)   chr2:13025520-13027271 REVERSE   Aliases: T6B20.8, T6B20_8	12.2	11.9	0.3	0.8	100.0%	-4.2
8846	AT2G17110.1   expressed protein   chr2:7450062-7453147 REVERSE   Aliases: F6P23.12, F6P23_12	4.0	3.7	0.3	0.8	100.0%	-4.4
8847	AT5G03630.1   monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), cucumber, PIR:JU0182   chr5:922165-924676 REVERSE   Aliases: F17C15.50, F17C15_50	8.4	9.3	-0.9	-0.8	100.0%	-4.3
8848	AT4G22670.1   tetratricopeptide repeat (TPR)-containing protein, similar to Hsc70-interacting protein (Hip) from {Homo sapiens} SP:P50502, {Rattus norvegicus} SP:P50503; contains Pfam profile PF00515: tetratricopeptide repeat (TPR) domain	9.6	9.8	-0.2	-0.8	100.0%	-5.0
8849	AT2G33610.1   Symbol: ATSWI3B   SWIRM domain-containing protein / DNA-binding family protein, contains similarity to SWI/SNF complex 170 KDa subunit (Homo sapiens) gi:1549241:gb:AAC50694; contains Pfam domain PF04433: SWIRM domain, PF00249: Myb-like DNA-binding domain   chr2:14236065-14238361 FORWARD   Aliases: AY074306, CHB2, CHROMATIN REMODELING COMPLEX SUBUNIT B, F4P9.38, F4P9_38	3.4	3.6	-0.2	-0.8	100.0%	-4.6
8850	AT3G14610.1   Symbol: CYP72A7   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4912473-4914659 FORWARD   Aliases: MIE1.11	8.0	7.7	0.3	0.8	100.0%	-4.6
8851	AT5G59140.1   SKP1 family protein, similar to elongin C, Drosophila melanogaster, GI:2780365 PIR:JC5794; contains Pfam profile PF01466: Skp1 family, dimerisation domain   chr5:23891676-23892910 REVERSE   Aliases: MNC17.5, MNC17_5	9.4	9.1	0.3	0.8	100.0%	-4.7
8852	AT5G67340.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr5:26881782-26884825 FORWARD   Aliases: K8K14.6, K8K14_6	3.6	3.8	-0.2	-0.8	100.0%	-4.5
8853	AT1G50400.1   porin family protein, low similarity to haymaker protein (Mus musculus) GI:17834089, mitochondrial outer membrane protein MOM35 (Mus musculus) GI:6650562; contains Pfam profile PF01459: Eukaryotic porin   chr1:18671823-18673990 FORWARD   Aliases: F14I3.2, F14I3_2	5.1	4.8	0.3	0.8	100.0%	-4.4
8854	AT4G35920.3   expressed protein, contains Pfam profile PF04749: Protein of unknown function, DUF614; isoform contains AT-acceptor splice site at intron 8   chr4:17011791-17014821 REVERSE   Aliases: T19K4.50	8.4	8.0	0.4	0.8	100.0%	-4.7
8855	AT3G30340.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr3:11959080-11961577 FORWARD   Aliases: T6J22.10	3.6	3.4	0.1	0.8	100.0%	-5.2
8856	AT5G20110.1   dynein light chain, putative, similar to SP:O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassisipina}; contains Pfam profile PF01221: Dynein light chain type 1   chr5:6791489-6793348 REVERSE   Aliases: F28I16.260, F28I16_260	3.9	4.5	-0.6	-0.8	100.0%	-4.2
8857	AT5G15380.1   Symbol: DRM1   cytosine methyltransferase, putative, similar to cytosine methyltransferase (Arabidopsis thaliana) GI:7658293; contains Pfam profile PF00627: UBA/TS-N domain   chr5:4991350-4994829 FORWARD   Aliases: DOMAINS REARRANGED METHYLASE 1, F8M21.270, F8M21_270	3.3	3.2	0.2	0.8	100.0%	-4.9
8858	AT3G45740.1   hydrolase family protein / HAD-superfamily protein, contains TIGRfam domains TIGR01460: HAD-superfamily hydrolase, subfamily IIA and TIGR01456: HAD-superfamily subfamily IIA hydrolase, TIGR01456, CECR5   chr3:16801746-16804519 FORWARD   Aliases: T6D9.70	5.9	6.1	-0.3	-0.8	100.0%	-4.3
8859	AT1G49950.3   DNA-binding protein, putative, contains similarity to DNA-binding protein PcMYB1 (Petroselinum crispum) gi:2224899:gb:AAB61699   chr1:18497832-18500855 REVERSE   Aliases: F2J10.16, F2J10_16	5.8	5.5	0.2	0.8	100.0%	-4.5
8860	AT1G08320.3   similar to bZIP family transcription factor [Arabidopsis thaliana] (TAIR:At5g06839.1); similar to basic leucine zipper protein [Zea mays] (GB:AAC39351.1); similar to bZIP transcription factor [Oryza sativa (japonica cultivar-group)] (GB:AAX94845.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)	3.1	3.3	-0.2	-0.8	100.0%	-4.6
8861	AT1G72700.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Homo sapiens (SP:Q9Y2Q0, SP:O43520); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:27370572-27375395 FORWARD   Aliases: F28P22.11, F28P22_11	4.2	4.5	-0.3	-0.8	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8862	AT5G57330.1   aldose 1-epimerase family protein, contains Pfam profile PF01263 Aldose 1-epimerase   chr5:23235440-23238315 FORWARD   Aliases: MJB24.14, MJB24_14	8.8	9.2	-0.4	-0.8	100.0%	-4.4
8863	AT5G67590.1   Symbol: FRO1   NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 21 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-21KD) (CI-21KD). (Swiss-Prot:P25711) (Neurospora crassa); contains Pfam PF04800: ETC complex I subunit conserved region	10.3	10.8	-0.5	-0.8	100.0%	-4.5
8864	AT1G14240.3   similar to nucleoside phosphatase family protein / GDA1/CD39 family protein [Arabidopsis thaliana] (TAIR:At1g14250.1); similar to putative ectonucleoside triphosphate diphosphohydrolase [Oryza sativa (japonica cultivar-group)] (GB:XP_482576.1); contains InterPro domain GDA1/CD39 family of nucleoside phosphatase (InterPro:IPR000407)   chr1:4865001-4867992 FORWARD   Aliases: F7A19.34, F7A19_34	2.9	3.0	-0.2	-0.8	100.0%	-4.8
8865	AT1G15700.1   Symbol: ATPC2   ATP synthase gamma chain 2, chloroplast (ATPC2), identical to SP:Q01909 ATP synthase gamma chain 2, chloroplast precursor (EC 3.6.3.14) {Arabidopsis thaliana}; contains Pfam profile: PF00231 ATP synthase; similar to ATP synthase gamma-subunit Gl:21241 from (Spinacia oleracea)   chr1:5402564-5403813 REVERSE   Aliases: F7H2.4, F7H2_4	6.6	6.9	-0.3	-0.8	100.0%	-4.3
8866	AT2G43890.1   polygalacturonase, putative / pectinase, putative, similar to SP:P48979 Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) {Prunus persica}; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr2:18184001-18185467 FORWARD   Aliases: F6E13.2	2.9	2.8	0.1	0.8	100.0%	-5.2
8867	AT1G10880.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr1:3624035-3627082 REVERSE   Aliases: T19D16.28, T19D16_28	2.6	2.8	-0.1	-0.8	100.0%	-5.2
8868	AT3G07780.1   expressed protein   chr3:2484476-2487030 FORWARD   Aliases: MLP3.23	8.5	8.1	0.4	0.8	100.0%	-4.7
8869	AT1G12490.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr1:4260781-4261867 FORWARD   Aliases: F5O11.24, F5O11_24	3.1	2.9	0.2	0.8	100.0%	-4.9
8870	AT3G21465.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g15640.1); similar to putative adenylyl cyclase [Oryza sativa (japonica cultivar-group)] (GB:XP_479441.1)   chr3:7560726-7563433 FORWARD   Aliases: MHC9.15	3.1	3.3	-0.2	-0.8	100.0%	-4.6
8871	AT3G53780.2   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr3:19935546-19938004 REVERSE   Aliases: F5K20.80	8.1	7.9	0.2	0.8	100.0%	-4.5
8872	AT5G07460.1   Symbol: PMSR2   peptide methionine sulfoxide reductase, putative, similar to peptide methionine sulfoxide reductase (msr) (Arabidopsis thaliana) Gl:4884033; contains Pfam profile PF01625: Peptide methionine sulfoxide reductase   chr5:2360635-2362014 REVERSE   Aliases: PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 2, T2I1.170, T2I1_170	7.6	7.1	0.6	0.8	100.0%	-4.3
8873	AT1G64160.1   disease resistance-responsive family protein / dirigent family protein, similar to dirigent protein GB:AAF25365 Gl:6694709 from (Thuja plicata); similar to pathogenesis-related protein (Pisum sativum) gi:4585273 gb:AAD25355   chr1:23817726-23818274 FORWARD   Aliases: F22C12.8, F22C12_8	2.5	2.3	0.1	0.8	100.0%	-5.0
8874	AT3G57050.3   Symbol: CBL   cystathionine beta-lyase, chloroplast / beta-cystathionase / cysteine lyase (CBL), identical to SP:P53780 Cystathionine beta-lyase, chloroplast precursor (EC 4.4.1.8) (CBL) (Beta-cystathionase) (Cysteine lyase) {Arabidopsis thaliana}	10.4	10.7	-0.3	-0.8	100.0%	-4.8
8875	AT5G03790.1   homeobox-leucine zipper family protein, similar to homeobox-leucine zipper protein Athb-7 (SP:P46897) (Arabidopsis thaliana); contains Pfam PF00046: Homeobox domain   chr5:1004984-1006372 FORWARD   Aliases: F17C15.210	3.4	3.5	-0.1	-0.8	100.0%	-5.2
8876	AT1G54020.2   myrosinase-associated protein, putative, strong similarity to myrosinase-associated proteins Gl:1769968, Gl:1769970, Gl:1216389, Gl:1216391 from (Brassica napus); contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr1:20165340-20167406 REVERSE   Aliases: F15I1.10, F15I1_10	2.2	2.1	0.1	0.8	100.0%	-5.5
8877	AT1G77405.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:29092039-29093415 FORWARD   Aliases: F2P24.16, F2P24_16	5.2	5.4	-0.2	-0.8	100.0%	-4.8
8878	AT5G57150.3   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.3	4.9	0.4	0.8	100.0%	-4.3
8879	AT3G51120.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr3:18996880-19002989 REVERSE   Aliases: F24M12.160	5.2	5.5	-0.3	-0.8	100.0%	-4.7
8880	AT4G12030.2   bile acid:sodium symporter family protein, low similarity to SP:Q12908 Ileal sodium/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family   chr4:7210913-7212830 FORWARD   Aliases: F16J13.100, F16J13_100	3.7	3.3	0.3	0.8	100.0%	-4.2
8881	AT1G16310.1   cation efflux family protein, contains cation efflux family protein domain, Pfam:PF01545	10.4	9.8	0.6	0.8	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8882	AT1G74510.2   kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain   chr1:28009212-28011400 FORWARD   Aliases: F1M20.19, F1M20_19	6.4	6.2	0.2	0.8	100.0%	-4.8
8883	AT4G12960.1   gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein, similar to SP:P13284 Gamma-interferon inducible lysosomal thiol reductase precursor {Homo sapiens}; contains Pfam profile PF03227: Gamma interferon inducible lysosomal thiol reductase (GILT)   chr4:7583269-7584627 FORWARD   Aliases: F25G13.50, F25G13_50	2.2	2.3	-0.1	-0.8	100.0%	-5.5
8884	AT5G04910.1   expressed protein, ; expression supported by MPSS   chr5:1437696-1438771 FORWARD   Aliases: MUG13.24, MUG13_24	8.8	9.0	-0.2	-0.8	100.0%	-4.8
8885	AT5G58200.1   expressed protein   chr5:23566860-23569278 FORWARD   Aliases: MCK7.7, MCK7_7	7.5	7.2	0.3	0.8	100.0%	-4.7
8886	AT5G18640.1   lipase class 3 family protein, low similarity to Triacylglycerol Acylhydrolase (E.C.3.1.1.3) (Rhizomucor miehei) GI:230348; contains Pfam profile PF01764: Lipase   chr5:6213249-6215496 FORWARD   Aliases: T1A4.20, T1A4_20	5.1	4.8	0.4	0.8	100.0%	-4.1
8887	AT4G39890.1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family   chr4:18505963-18507578 FORWARD   Aliases: T5J17.60, T5J17_60	3.5	3.3	0.2	0.8	100.0%	-4.9
8888	AT2G29180.1   expressed protein   chr2:12550111-12551306 FORWARD   Aliases: F16P2.44, F16P2_44	6.5	6.1	0.4	0.8	100.0%	-4.0
8889	AT4G33360.1   terpene cyclase/mutase-related, low similarity to squalene-hopene cyclase from Zymomonas mobilis (SP:P33990)   chr4:16067675-16069377 REVERSE   Aliases: F17M5.120, F17M5_120	9.4	9.9	-0.5	-0.8	100.0%	-4.4
8890	AT5G01620.2   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr5:232732-234878 FORWARD   Aliases: F7A7.140, F7A7_140	6.6	6.9	-0.3	-0.8	100.0%	-4.7
8891	AT5G44830.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Lycopersicon esculentum) GI:4325090; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:18117355-18119112 REVERSE   Aliases: K23L20.18, K23L20_18	3.0	2.9	0.1	0.8	100.0%	-5.2
8892	AT5G44840.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Persea americana) GI:166951; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:18122078-18124354 REVERSE   Aliases: K21C13.1, K21C13_1	3.0	2.9	0.1	0.8	100.0%	-5.2
8893	AT1G18440.1   peptidyl-tRNA hydrolase family protein, contains Pfam profile PF01195: peptidyl-tRNA hydrolase   chr1:6345969-6347903 FORWARD   Aliases: F15H18.24, F15H18_24	5.7	5.4	0.3	0.8	100.0%	-4.4
8894	AT1G73790.1   expressed protein   chr1:27748333-27749038 FORWARD   Aliases: F25P22.21, F25P22_21	7.5	7.2	0.2	0.8	100.0%	-4.5
8895	AT4G09320.1   Symbol: NDPK1   nucleoside diphosphate kinase 1 (NDK1), identical to identical to Nucleoside diphosphate kinase I (NDK I) (NDP kinase I) (NDPK I) (SP:P39207) (Arabidopsis thaliana); contains Pfam PF00334 : Nucleoside diphosphate kinase domain;   chr4:5923397-5924529 FORWARD   Aliases: T30A10.80, T30A10_80	12.2	12.3	-0.1	-0.8	100.0%	-4.9
8896	AT1G08800.1   expressed protein, weak similarity to SP:Q02455 Myosin-like protein MLP1 {Saccharomyces cerevisiae}; contains Pfam profile PF04576: Protein of unknown function, DUF593   chr1:2813064-2817642 REVERSE   Aliases: F22O13.29, F22O13_29	3.5	3.1	0.4	0.8	100.0%	-4.3
8897	AT3G55100.1   ABC transporter family protein, ATP-binding cassette-sub-family G-member 2, Mus musculus, EMBL:AF140218   chr3:20431267-20433317 REVERSE   Aliases: T15C9.100	3.1	3.3	-0.2	-0.8	100.0%	-4.9
8898	AT2G03090.1   Symbol: ATEXPA15   expansin, putative (EXP15), identical to SWISS-PROT:O80622 alpha-expansin 15 precursor (At-EXP15)(Arabidopsis thaliana); alpha-expansin gene family, PMID:11641069   chr2:916853-918642 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A15, ATEXP15, ATHEXP ALPHA 1.3, EXP15, T17M13.26, T17M13_26	5.6	5.4	0.2	0.8	100.0%	-4.6
8899	AT5G27770.1   60S ribosomal protein L22 (RPL22C), ribosomal protein L22 (cytosolic), Rattus norvegicus, PIR:S52084   chr5:9835890-9837332 FORWARD   Aliases: T1G16.100, T1G16_100	10.2	10.5	-0.3	-0.8	100.0%	-4.4
8900	AT4G31410.2   expressed protein   chr4:15243743-15245767 FORWARD   Aliases: F3L17.5	6.1	5.9	0.2	0.8	100.0%	-4.7
8901	AT3G22970.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g14620.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:AAT76408.1); contains InterPro domain Uncharacterized plant-specific domain 01615 (InterPro:IPR006502)   chr3:8152045-8154113 FORWARD   Aliases: F5N5.17	5.6	6.1	-0.4	-0.8	100.0%	-4.4
8902	AT5G09590.1   Symbol: mtHSC70 2   heat shock protein 70 / HSP70 (HSC70-5), identical to heat shock protein 70 (Arabidopsis thaliana) GI:6746590   chr5:2975576-2978751 FORWARD   Aliases: F17I14.220, F17I14_220, HEAT SHOCK PROTEIN 70, HSC70 5	10.8	11.2	-0.4	-0.8	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8903	AT1G27130.1   Symbol: ATGSTU13   glutathione S-transferase, putative, similar to glutathione S-transferase GB: AAF22517 GI:6652870 from (Papaver somniferum)   chr1:9425447-9426873 FORWARD   Aliases: GLUTATHIONE S TRANSFERASE 12, GST12, T7N9.190, T7N9_190	9.6	9.4	0.2	0.8	100.0%	-4.9
8904	AT5G03140.1   lectin protein kinase family protein, contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr5:737589-740015 REVERSE   Aliases: F15A17.170, F15A17_170	6.2	6.6	-0.4	-0.8	100.0%	-4.3
8905	AT5G24570.1   expressed protein   chr5:8405684-8406135 REVERSE   Aliases: K18P6.10, K18P6_10	4.8	4.3	0.5	0.8	100.0%	-4.6
8906	AT4G02190.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.7	-0.2	-0.8	100.0%	-5.4
8907	AT1G14540.1   anionic peroxidase, putative, similar to lignin forming anionic peroxidase (Nicotiana sylvestris) SWISS-PROT: Q02200   chr1:4974062-4975595 REVERSE   Aliases: F14L17.32, F14L17_32	3.0	3.2	-0.1	-0.8	100.0%	-5.0
8908	AT3G47940.1   DNAJ heat shock protein, putative, similar to SP:O89114 DnaJ homolog subfamily B member 5 (Heat shock protein Hsp40-3) {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr3:17698941-17700534 REVERSE   Aliases: T17F15.190	4.1	4.3	-0.2	-0.8	100.0%	-4.6
8909	AT4G23110.1   expressed protein   chr4:12110955-12111401 FORWARD   Aliases: F7H19.300, F7H19_300	2.2	2.1	0.1	0.8	100.0%	-5.8
8910	AT1G62400.1   protein kinase, putative, similar to protein kinase gi:170047:gb:AAA34002; contains protein kinase domain, Pfam:PF00069   chr1:23093908-23095254 FORWARD   Aliases: F24O1.13, F24O1_13	2.2	2.1	0.1	0.8	100.0%	-5.3
8911	AT4G02120.1   CTP synthase, putative / UTP--ammonia ligase, putative, similar to SP:P17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) {Homo sapiens}; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr4:940841-944284 FORWARD   Aliases: T10M13.13, T10M13_13	4.7	5.2	-0.5	-0.8	100.0%	-4.3
8912	AT1G72950.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27448246-27449641 FORWARD   Aliases: F3N23.15, F3N23_15	3.6	3.8	-0.2	-0.8	100.0%	-4.8
8913	AT5G54380.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:22094318-22097106 REVERSE   Aliases: GA469.3, GA469_3	6.0	5.7	0.2	0.8	100.0%	-4.4
8914	AT4G14330.1   phragmoplast-associated kinesin-related protein 2 (PAKRP2), identical to cDNA phragmoplast-associated kinesin-related protein 2 (PAKRP2) GI:16973450   chr4:8244190-8247437 FORWARD   Aliases: DL3205W, FCAALL.179	3.4	3.7	-0.2	-0.8	100.0%	-4.7
8915	AT4G21780.1   expressed protein   chr4:11567142-11567711 FORWARD   Aliases: F17L22.240, F17L22_240	4.8	4.5	0.3	0.8	100.0%	-4.4
8916	AT3G13940.1   expressed protein, weak similarity to DNA-directed RNA polymerase I 49 kDa polypeptide (EC 2.7.7.6) (A49) (Swiss-Prot:O14086) (Schizosaccharomyces pombe); similar to Nuclear pore complex protein Nup107 (Nucleoporin Nup107) (107 kDa nucleoporin) (p105) (Swiss-Prot:P52590) (Rattus norvegicus)   chr3:4600499-4602493 REVERSE   Aliases: MDC16.6	3.9	4.3	-0.3	-0.8	100.0%	-4.6
8917	AT3G27500.1   similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g27480.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g28650.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g45530.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g42840.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g27473.1); similar to CHP-rich zinc finger protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_479135.1); contains InterPro domain Zn-finger-like, PHD finger (InterPro:IPR001965); contains InterPro domain Protein kinase C, phorbol ester/diacylglycerol binding (InterPro:IPR002219); contains InterPro domain DC1 domain (InterPro:IPR004146)   chr3:10184070-10186318 REVERSE   Aliases: MMJ24.4	2.1	2.2	-0.1	-0.8	100.0%	-5.5
8918	AT4G12350.1   Symbol: MYB42   transcription factor, putative (MYB42), identical to cDNA putative transcription factor (MYB42) GI:5823330   chr4:7324910-7326633 FORWARD   Aliases: T4C9.190, T4C9_190	2.8	2.6	0.1	0.8	100.0%	-4.9
8919	AT4G01897.1   expressed protein   chr4:819957-821484 REVERSE   Aliases: None	8.2	7.9	0.3	0.8	100.0%	-4.4
8920	AT1G62880.1   cornichon family protein, contains Pfam profile: PF03311 cornichon protein   chr1:23295594-23297217 FORWARD   Aliases: F16P17.3, F16P17_3	3.6	3.7	-0.2	-0.8	100.0%	-4.9
8921	AT2G04650.1   ADP-glucose pyrophosphorylase family protein, contains Pfam profile PF00483: Nucleotidyl transferase; low similarity to mannose-1-phosphate guanylyltransferase (Hypocrea jecorina) GI:3323397   chr2:1621785-1624590 REVERSE   Aliases: F28I8.31, F28I8_31	3.1	3.0	0.1	0.8	100.0%	-5.3
8922	AT3G29380.1   transcription factor IIB (TFIIB) family protein, contains Pfam profile: PF00382 transcription factor TFIIB repeat   chr3:11283644-11284761 REVERSE   Aliases: MUO10.22	2.8	2.6	0.2	0.8	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8923	AT5G04840.1   bZIP protein   chr5:1405306-1407935 FORWARD   Aliases: MUK11.16, MUK11_16	4.0	3.8	0.2	0.8	100.0%	-4.3
8924	AT3G19790.1   expressed protein, ; expression supported by MPSS   chr3:6874943-6875446 REVERSE   Aliases: MMB12.25	8.1	8.4	-0.3	-0.8	100.0%	-4.4
8925	AT5G48390.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr5:19629304-19632589 FORWARD   Aliases: MJE7.2, MJE7_2	2.3	2.4	-0.1	-0.8	100.0%	-5.3
8926	AT1G73805.1   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum)   chr1:27751150-27752839 REVERSE   Aliases: None	2.6	2.6	0.1	0.8	100.0%	-5.4
8927	AT5G64170.1   dentin sialophosphoprotein-related, contains weak similarity to Swiss-Prot:Q9NZW4 dentin sialophosphoprotein precursor (Homo sapiens)   chr5:25689692-25693972 REVERSE   Aliases: MHJ24.1, MHJ24_1	5.2	4.8	0.4	0.8	100.0%	-4.4
8928	AT3G58640.2   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:21697718-21704818 REVERSE   Aliases: F14P22.230	6.1	6.2	-0.1	-0.8	100.0%	-4.9
8929	AT3G07650.3   similar to zinc finger (B-box type) family protein [Arabidopsis thaliana] (TAIR:At5g48250.1); similar to CONSTANS-like protein [Ipomoea nil] (GB:AAG24863.1); contains InterPro domain Zn-finger, CONSTANS type (InterPro:IPR002926); contains InterPro domain Zn-finger, B-box (InterPro:IPR000315)   chr3:2441663-2444538 FORWARD   Aliases: MLP3.10	2.6	2.6	0.1	0.8	100.0%	-5.3
8930	AT5G08050.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:2578370-2579164 FORWARD   Aliases: T22D6.3	7.3	7.0	0.4	0.8	100.0%	-4.1
8931	AT1G80350.1   Symbol: ERH3   katanin 1 (KTN1), identical to katanin 1 (KTN1) (Arabidopsis thaliana) GI:14133602   chr1:30210216-30213097 REVERSE   Aliases: AAA1, ATKTN1, BOT1, BOTERO 1, CAD ATPASE, ECTOPIC ROOT HAIR 3, F5I6.10, F5I6_10, FAT ROOT, FRA2, FRAGILE FIBER 2, FRC2, FTR, FURCA2, KATANIN 1, KTN1, LUE1	5.8	6.2	-0.3	-0.8	100.0%	-4.5
8932	AT3G08040.1   Symbol: FRD3   MATE efflux family protein, low similarity to enhanced disease susceptibility 5 (Arabidopsis thaliana) GI:16589070; contains TIGRfam profile: TIGR00797: MATE efflux family protein, Pfam profile PF01554 Uncharacterized membrane protein family   chr3:2566283-2569505 REVERSE   Aliases: FERRIC REDUCTASE DEFECTIVE 3, MAN1, MANGANESE ACCUMULATOR 1, T8G24.8	4.4	4.1	0.3	0.8	100.0%	-4.2
8933	AT5G16590.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:5431684-5434113 FORWARD   Aliases: MTG13.3, MTG13_3	3.4	3.6	-0.2	-0.8	100.0%	-5.0
8934	AT3G62770.3   similar to WD-40 repeat protein family [Arabidopsis thaliana] (TAIR:At3g56440.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_550260.1)   chr3:23229609-23232207 REVERSE   Aliases: F26K9.200	3.7	3.4	0.3	0.8	100.0%	-4.4
8935	AT2G29860.1   kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	2.5	2.6	-0.1	-0.8	100.0%	-5.4
8936	AT1G04590.2   Symbol: EMB2748   expressed protein, isoform contains GG acceptor splice site at intron 7   chr1:1258577-1261424 REVERSE   Aliases: EMB2748, EMBRYO DEFECTIVE 2748, T1G11.16, T1G11_16	9.4	9.0	0.4	0.8	100.0%	-4.5
8937	AT2G12170.1   expressed protein   chr2:4897274-4898273 REVERSE   Aliases: F23M2.37	3.0	3.1	-0.2	-0.8	100.0%	-5.2
8938	AT5G04260.1   thioredoxin family protein, low similarity to SP:P29429 Thioredoxin. (Aspergillus nidulans) {Emericella nidulans}; contains Pfam profile: PF00085 Thioredoxin   chr5:1178645-1180037 REVERSE   Aliases: T19N18.5	6.7	6.6	0.2	0.8	100.0%	-4.9
8939	AT4G30290.1   Symbol: ATXTH19   putative xyloglucan endotransglycosylase/hydrolase, expressed throughout both the main and the lateral root, with intensive expression at the dividing and elongating regions. Is expressed in lateral root primordia but expression ceases after lateral root begins to grow.   chr4:14828718-14830022 REVERSE   Aliases: ATXTH19, F17I23.370, F17I23_370, XYLOGLUCAN ENDOTRANSGLUCOSYLASE/HYDROLASE 19	3.8	4.0	-0.2	-0.8	100.0%	-4.7
8940	AT1G48260.1   Symbol: CIPK17	3.3	3.6	-0.3	-0.8	100.0%	-4.1
8941	AT4G21950.1   expressed protein   chr4:11644230-11644617 FORWARD   Aliases: F1N20.4	2.9	2.8	0.1	0.8	100.0%	-5.2
8942	AT1G71250.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile: PF00657 lipase/acylhydrolase with GDSL-like motif   chr1:26863780-26865332 FORWARD   Aliases: F3I17.10, F3I17_10	2.1	2.0	0.1	0.8	100.0%	-5.6
8943	AT2G25010.1   expressed protein   chr2:10638649-10640736 FORWARD   Aliases: F27C12.7, F27C12_7	4.2	3.7	0.4	0.8	100.0%	-4.2
8944	AT5G50100.1   expressed protein, contains Pfam domain PF04134: Protein of unknown function, DUF393   chr5:20389079-20390667 FORWARD   Aliases: MPF21.11, MPF21_11	5.9	5.7	0.2	0.8	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8945	AT3G03050.1   Symbol: CSLD3   cellulose synthase family protein (CslD3), similar to cellulose synthase catalytic subunit gi:2827143 from (Arabidopsis thaliana), cellulose synthase-7 (gi:9622886) from Zea mays; contains Pfam profile PF03552: Cellulose synthase   chr3:687059-691905 FORWARD   Aliases: ATCSLD3, CELLULOSE SYNTHASE LIKE 3, KJK, KOJAK, T17B22.26, T17B22_26	6.8	6.5	0.3	0.8	100.0%	-4.7
8946	AT1G51460.1   ABC transporter family protein, similar to SP:Q9UNQ0 ATP-binding cassette, sub-family G, member 2 (Placenta-specific ATP- binding cassette transporter) (Breast cancer resistance protein) {Homo sapiens}; contains Pfam profile PF00005: ABC transporter   chr1:19080650-19085101 REVERSE   Aliases: F5D21.8, F5D21_8	3.4	3.2	0.2	0.8	100.0%	-4.8
8947	AT4G02370.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr4:1042338-1043206 FORWARD   Aliases: T14P8.18, T14P8_18	7.8	8.2	-0.4	-0.8	100.0%	-4.5
8948	AT5G01870.1   lipid transfer protein, putative, similar to lipid transfer protein 6 from Arabidopsis thaliana (gi:8571927); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:337174-337812 FORWARD   Aliases: T20L15.140, T20L15_140	3.1	3.6	-0.5	-0.8	100.0%	-4.3
8949	AT3G12920.1   expressed protein   chr3:4121890-4123503 REVERSE   Aliases: MGH6.3	9.7	9.8	-0.1	-0.8	100.0%	-4.9
8950	AT1G49910.1   WD-40 repeat family protein / mitotic checkpoint protein, putative, contains 5 WD-40 repeats (PF00400) (1 weak); similar to testis mitotic checkpoint protein BUB3 (GB:AAC28439,SP:O43684)(Homo sapiens)	3.6	3.7	-0.1	-0.8	100.0%	-5.0
8951	AT1G29240.1   expressed protein, contains Pfam profile: PF05097 protein of unknown function (DUF688)   chr1:10216785-10219816 REVERSE   Aliases: F28N24.8, F28N24_8	4.6	4.4	0.2	0.8	100.0%	-4.8
8952	AT3G48200.1   expressed protein   chr3:17843758-17848499 REVERSE   Aliases: T24C20.80	3.2	3.1	0.1	0.8	100.0%	-5.3
8953	AT4G24100.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr4:12515086-12519851 FORWARD   Aliases: T19F6.90, T19F6_90	3.1	2.8	0.3	0.8	100.0%	-4.4
8954	AT4G01690.2   Symbol: PPOX   protoporphyrinogen oxidase (PPOX), identical to SP:P55826   chr4:729892-732734 FORWARD   Aliases: PROTOPORPHYRINOGEN OXIDASE, T15B16.13, T15B16_13	8.3	7.9	0.4	0.8	100.0%	-4.4
8955	AT1G28590.1   lipase, putative, similar to lipase (Arabidopsis thaliana) GI:1145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr1:10047262-10049286 REVERSE   Aliases: F1K23.17, F1K23_17	3.1	2.9	0.1	0.8	100.0%	-4.8
8956	AT3G22690.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:8020764-8024541 REVERSE   Aliases: MWI23.6	3.1	3.3	-0.1	-0.8	100.0%	-4.9
8957	AT5G65810.1   expressed protein, similar to unknown protein (emb CAB66910.1)   chr5:26354895-26356963 REVERSE   Aliases: K22J17.2, K22J17_2	8.1	7.7	0.4	0.8	100.0%	-4.4
8958	AT3G45510.1   zinc finger (C3HC4-type RING finger) family protein, contains a zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr3:16701775-16702713 REVERSE   Aliases: F9K21.90	2.6	2.7	-0.1	-0.8	100.0%	-5.4
8959	AT2G46220.1   expressed protein   chr2:18986544-18987843 FORWARD   Aliases: T3F17.13	7.0	6.6	0.4	0.8	100.0%	-4.2
8960	AT1G72820.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:27406540-27408335 FORWARD   Aliases: F3N23.2, F3N23_2	9.2	8.9	0.3	0.8	100.0%	-4.7
8961	AT3G47610.1   expressed protein   chr3:17560106-17562405 FORWARD   Aliases: F1P2.160	6.7	7.1	-0.4	-0.8	100.0%	-4.3
8962	AT1G63690.2   protease-associated (PA) domain-containing protein, contains protease associated (PA) domain, Pfam:PF02225   chr1:23622041-23626059 FORWARD   Aliases: F24D7.12, F24D7_12	7.5	7.3	0.2	0.8	100.0%	-4.6
8963	AT3G19160.1   Symbol: ATIPT8	3.0	2.9	0.1	0.8	100.0%	-5.3
8964	AT3G09300.1   oxysterol-binding family protein, similar to SP:P22059 Oxysterol-binding protein 1 {Homo sapiens}; contains Pfam profile PF01237: Oxysterol-binding protein   chr3:2857883-2860674 FORWARD   Aliases: F3L24.17	10.5	10.7	-0.2	-0.8	100.0%	-4.6
8965	AT1G65470.1   Symbol: FAS1   chromatin assembly factor-1 (FASCIATA1) (FAS1), identical to FAS1 (Arabidopsis thaliana) GI:4887626   chr1:24323411-24327542 REVERSE   Aliases: FAS1, FASCIATA 1, NFB2, NUCLEOSOME/CHROMATIN ASSEMBLY FACTOR GROUP B, T8F5.24	3.1	3.3	-0.2	-0.8	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8966	AT1G74330.1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g39420.1); similar to putative CRK1 protein [Oryza sativa (japonica cultivar-group)] (GB:NP_913178.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:27947279-27950770 REVERSE   Aliases: F1M20.1, F1M20_1	3.4	3.2	0.1	0.8	100.0%	-4.9
8967	AT5G20510.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr5:6939594-6942895 REVERSE   Aliases: F7C8.100, F7C8_100	5.8	5.6	0.2	0.8	100.0%	-4.8
8968	AT5G49410.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g73940.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470431.1)   chr5:20049713-20051152 FORWARD   Aliases: K7J8.8, K7J8_8	3.0	3.1	-0.1	-0.8	100.0%	-5.1
8969	AT1G33350.1   pentatricopeptide (PPR) repeat-containing protein, contains multiple Pfam domains: PF01535: PPR repeat   chr1:12089383-12091667 REVERSE   Aliases: F10C21.4	3.6	3.8	-0.2	-0.8	100.0%	-4.9
8970	AT2G32970.1   expressed protein   chr2:13998661-14002826 REVERSE   Aliases: T21L14.9, T21L14_9	3.7	4.0	-0.3	-0.8	100.0%	-4.5
8971	AT5G02380.1   Symbol: MT2B   metallothionein protein 2B (MT-2B), identical to SWISS-PROT:Q38805 metallothionein-like protein 2B (MT-2B) (Arabidopsis thaliana)   chr5:506545-507242 REVERSE   Aliases: METALLOTHIONEIN 2B, T1E22.140, T1E22_140	14.1	13.9	0.2	0.8	100.0%	-5.4
8972	AT2G43260.1   F-box family protein / S locus-related, weak similarity to S locus F-box (SLF)-S2 protein (Antirrhinum hispanicum) GI:13161526; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr2:17990768-17992181 REVERSE   Aliases: F14B2.20	6.2	6.4	-0.2	-0.8	100.0%	-4.5
8973	AT3G20620.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; similar to F-box protein family, AtFBX8 (GI:20197464) (Arabidopsis thaliana)   chr3:7198460-7202495 REVERSE   Aliases: K10D20.16	5.2	5.0	0.2	0.8	100.0%	-4.6
8974	AT1G04620.1   coenzyme F420 hydrogenase family / dehydrogenase, beta subunit family, contains Pfam PF04432: Coenzyme F420 hydrogenase/dehydrogenase, beta domain; similar to Coenzyme F420 hydrogenase beta subunit (SP:Q00391) {Methanobacterium thermoautotrophicum}	4.5	4.3	0.2	0.8	100.0%	-4.6
8975	AT2G34090.2   expressed protein, similar to GP:1301832:gnl:PID:e239862:Z71287	3.9	3.7	0.2	0.8	100.0%	-4.6
8976	AT4G09810.1   transporter-related, low similarity to UDP-sugar transporter (Drosophila melanogaster) GI:14971008, UDP-glucuronic acid transporter (Homo sapiens) GI:11463949   chr4:6175178-6177269 REVERSE   Aliases: F17A8.160, F17A8_160	4.6	4.7	-0.2	-0.8	100.0%	-4.8
8977	AT2G44920.2   thylakoid lumenal 15 kDa protein, chloroplast, identical to SP:O22160 Thylakoid lumenal 15 kDa protein, chloroplast precursor (p15) {Arabidopsis thaliana}; contains 8 pentapeptide repeats   chr2:18531480-18533902 FORWARD   Aliases: T13E15.7	5.3	5.0	0.3	0.8	100.0%	-4.2
8978	AT1G05170.1   galactosyltransferase family protein   chr1:1491110-1494218 REVERSE   Aliases: YUP8H12.22, YUP8H12_22	3.1	2.9	0.2	0.8	100.0%	-4.7
8979	AT5G14670.1   Symbol: ATARFA1B   Gene encoding ADP-ribosylation factor and similar to ADP-ribosylation factor DcARF1 (GI:965483) (Daucus carota), other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct.   chr5:4729322-4730498 FORWARD   Aliases: ATARFA1B, T15N1.160, T15N1_160	4.4	4.3	0.2	0.8	100.0%	-4.7
8980	AT3G02440.1   expressed protein   chr3:500811-502236 REVERSE   Aliases: F16B3.7, F16B3_7	2.7	2.8	-0.1	-0.8	100.0%	-5.2
8981	AT5G46920.1   intron maturase, type II family protein, similar to SP:Q57005 Group II intron-encoded protein ltrA {Lactococcus lactis subsp}; contains Pfam profiles PF00078: Reverse transcriptase (RNA-dependent DNA polymerase), PF01348: Type II intron maturase   chr5:19070855-19073234 FORWARD   Aliases: MQD22.6, MQD22_6	5.7	5.9	-0.2	-0.8	100.0%	-4.5
8982	AT1G10760.1   Symbol: SEX1   starch excess protein (SEX1), identical to SEX1 (Arabidopsis thaliana) GI:12044358; supporting cDNA gi:12044357:gb:AF312027.1:AF312027   chr1:3581035-3590044 REVERSE   Aliases: GWD1, SEX1, SOP, SOP1, STARCH EXCESS 1 PROTEIN, STARCH EXCESS 1, T16B5.10, T16B5_10	11.1	10.8	0.2	0.8	100.0%	-4.8
8983	AT5G57110.2   Symbol: ACA8   calcium-transporting ATPase 8, plasma membrane-type / Ca(2+)-ATPase isoform 8 (ACA8), identical to calcium-transporting ATPase 8, plasma membrane-type SP:Q9LF79 from (Arabidopsis thaliana)   chr5:23126698-23134770 REVERSE   Aliases: AT ACA8, AUTOINHIBITED CA2+ ATPASE, ISOFORM 8, MUL3.5, MUL3_5	6.4	6.6	-0.2	-0.8	100.0%	-5.2
8984	AT1G13790.1   XH/XS domain-containing protein / XS zinc finger domain-containing protein, contains Pfam domains PF03469: XH domain, PF03468: XS domain and PF03470: XS zinc finger domain   chr1:4727435-4730226 FORWARD   Aliases: F16A14.2, F16A14_2	2.8	2.9	-0.2	-0.8	100.0%	-5.1
8985	AT5G44530.1   subtilase family protein, contains Pfam profiles: PF00082 subtilase family   chr5:17955158-17958420 FORWARD   Aliases: MFC16.21, MFC16_21	5.6	5.3	0.3	0.8	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
8986	AT4G38660.2   similar to pathogenesis-related thaumatin family protein [Arabidopsis thaliana] (TAIR:At4g24180.1); similar to putative thaumatin-like protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52107.1); contains InterPro domain Thaumatin, pathogenesis-related (InterPro:IPR001938)   chr4:18066171-18067867 REVERSE   Aliases: T9A14.6	3.9	4.1	-0.2	-0.8	100.0%	-4.7
8987	AT1G68720.1   cytidine/deoxycytidylate deaminase family protein, contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region   chr1:25808081-25812645 FORWARD   Aliases: F24J5.5, F24J5_5	7.2	7.6	-0.4	-0.8	100.0%	-4.5
8988	AT4G30230.1   expressed protein   chr4:14806382-14807164 FORWARD   Aliases: F9N11.80, F9N11_80	2.2	2.3	-0.1	-0.8	100.0%	-5.4
8989	AT3G30370.1   expressed protein   chr3:11967659-11968198 REVERSE   Aliases: T6J22.16	2.5	2.4	0.1	0.8	100.0%	-5.5
8990	AT1G59580.2   Symbol: ATMPK2	3.8	4.0	-0.2	-0.8	100.0%	-4.4
8991	AT5G57090.1   Symbol: EIR1   auxin transport protein (EIR1), identical to auxin transport protein EIR1 (Arabidopsis thaliana) gi:3377507:gb:AAC39513; identical to root gravitropism control protein (Arabidopsis thaliana) gi:4322486:gb:AAD16060   chr5:23117973-23121948 FORWARD   Aliases: AGR, AGR1, AGRAVITROPIC, AGRAVITROPIC 1, AGRAVITROPIC ROOT 1, ATPIN2, AUXIN TRANSPORT PROTEIN EIR1, ETHYLENE INSENSITIVE ROOT 1, MUL3.3, MUL3_3, PIN FORMED 2, PIN2, POLAR AUXIN TRANSPORT EFFLUX COMPONENT AGRAVITROPIC 1, WAV6, WAVY ROOTS 6	3.7	3.9	-0.3	-0.8	100.0%	-4.5
8992	AT4G36490.1   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus; supporting cDNA gi:23463078:gb:BT000834.1:   chr4:17222001-17225019 FORWARD   Aliases: AP22.26, AP22_26	3.1	2.9	0.1	0.8	100.0%	-5.1
8993	AT3G45090.2   2-phosphoglycerate kinase-related, contains weak similarity to 2-phosphoglycerate kinase (GI:467751) (Methanothermus fervidus)   chr3:16501585-16505696 REVERSE   Aliases: T14D3.30	3.8	4.2	-0.4	-0.8	100.0%	-4.4
8994	AT1G18350.1   Symbol: ATMKK7	2.6	2.5	0.1	0.8	100.0%	-5.2
8995	AT4G30890.2   Symbol: UBP24   ubiquitin-specific protease 24, putative (UBP24), identical to ubiquitin-specific protease 24 (Arabidopsis thaliana) GI:11993488   chr4:15036102-15039239 REVERSE   Aliases: F6I18.200, F6I18_200, UBIQUITIN SPECIFIC PROTEASE 24	5.4	5.8	-0.3	-0.8	100.0%	-4.7
8996	AT5G38880.1   expressed protein   chr5:15580536-15586424 REVERSE   Aliases: K15E6.9, K15E6_9	3.8	4.1	-0.3	-0.8	100.0%	-4.6
8997	ATMG00140.1   Symbol: ORF167	2.4	2.3	0.1	0.8	100.0%	-5.5
8998	AT4G00955.1   expressed protein   chr4:412118-413278 FORWARD   Aliases: None	4.1	3.9	0.2	0.8	100.0%	-4.4
8999	AT3G16980.1   DNA-directed RNA polymerase II, putative, similar to SP:P36958 DNA-directed RNA polymerase II 15.1 kDa polypeptide (EC 2.7.7.6) {Drosophila melanogaster}; contains Pfam profile PF02150: RNA polymerases M/15 Kd subunit   chr3:5794502-5795705 FORWARD   Aliases: K14A17.16	5.9	5.5	0.4	0.8	100.0%	-4.1
9000	AT1G49000.1   expressed protein   chr1:18127227-18127789 REVERSE   Aliases: F27J15.21, F27J15_21	3.3	3.7	-0.4	-0.8	100.0%	-4.3
9001	AT3G48440.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr3:17952387-17954561 FORWARD   Aliases: T29H11.40	4.8	5.0	-0.3	-0.8	100.0%	-4.3
9002	AT2G03510.1   band 7 family protein, contains Pfam profile PF01145: SPFH domain / Band 7 family   chr2:1066639-1069096 FORWARD   Aliases: T4M8.5, T4M8_5	8.3	8.8	-0.5	-0.8	100.0%	-4.5
9003	AT1G56410.1   Symbol: HSP70T 1   heat shock cognate 70 kDa protein, putative / HSC70, putative / HSP70, putative, strong similarity to heat shock cognate 70 kd protein 1 SP:P22953 (Arabidopsis thaliana (Mouse-ear cress))   chr1:21120812-21122906 FORWARD   Aliases: F13N6.9, F13N6_9, HSP70T 1	3.6	3.5	0.1	0.8	100.0%	-5.1
9004	AT5G55160.1   Symbol: SUM2   small ubiquitin-like modifier 2 (SUMO), similar to ubiquitin-like protein SMT3 SP:P55852 from (Arabidopsis thaliana); identical to cDNA small ubiquitin-like modifier 2 (SUMO) GI:22652843; contains Pfam profile PF00240: Ubiquitin family   chr5:22400795-22402151 REVERSE   Aliases: MCO15.11, MCO15_11, SMALL UBIQUITIN LIKE MODIFIER 2, SUMO 2, SUMO2	9.9	9.7	0.2	0.8	100.0%	-4.7
9005	AT3G09940.1   monodehydroascorbate reductase, putative, similar to monodehydroascorbate reductase (NADH) GB:JU0182 (Cucumis sativus)   chr3:3056384-3059153 REVERSE   Aliases: F8A24.20	3.2	3.4	-0.2	-0.8	100.0%	-4.4
9006	AT3G07800.1   thymidine kinase, putative, similar to thymidine kinase (Oryza sativa) SWISS-PROT:O81263	8.5	8.9	-0.4	-0.8	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9007	AT1G30520.1   acyl-activating enzyme 14 (AAE14), identical to acyl-activating enzyme 14 (Arabidopsis thaliana); similar to SP:Q42524 4-coumarate--CoA ligase 1 (EC 6.2.1.12) (4-coumaroyl-CoA synthase 1) {Arabidopsis thaliana}; contains Pfam profile PF00501: AMP-binding enzyme; identical to cDNA acyl-activating enzyme 14 (At1g30520) GI:29893263   chr1:10810966-10813603 FORWARD   Aliases: F26G16.14, F26G16_14	6.1	6.3	-0.2	-0.8	100.0%	-4.5
9008	AT5G44670.1   expressed protein, contains Pfam:PF01697 Domain of unknown function   chr5:18036132-18038612 REVERSE   Aliases: K15C23.12, K15C23_12	7.2	6.9	0.3	0.8	100.0%	-4.4
9009	AT1G44110.1   Symbol: CYCA1;1   cyclin, putative, similar to mitotic cyclin a2-type (Glycine max) GI:857397, cyclin A-like protein (Nicotiana tabacum) GI:1064927; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:16777361-16779679 REVERSE   Aliases: CYCA1;1, Cyclin A1;1, T7O23.18, T7O23_18	3.3	3.5	-0.3	-0.8	100.0%	-4.3
9010	AT2G16280.1   very-long-chain fatty acid condensing enzyme, putative, similar to fatty acid condensing enzyme CUT1 GI:5001734 from (Arabidopsis thaliana)   chr2:7058026-7059979 FORWARD   Aliases: F16F14.22, F16F14_22	5.3	5.4	-0.2	-0.8	100.0%	-4.9
9011	AT3G54210.1   ribosomal protein L17 family protein, contains Pfam profile: PF01196 ribosomal protein L17   chr3:20078525-20079413 REVERSE   Aliases: F24B22.170	8.5	8.9	-0.4	-0.8	100.0%	-4.3
9012	AT5G52510.1   scarecrow-like transcription factor 8 (SCL8)   chr5:21324275-21326528 FORWARD   Aliases: T4M5.2, T4M5_2	5.5	5.2	0.3	0.8	100.0%	-4.6
9013	AT3G21340.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr3:7511793-7515943 REVERSE   Aliases: MHC9.2	2.4	2.5	-0.1	-0.8	100.0%	-4.9
9014	AT5G44250.1   expressed protein, contains Pfam PF05705: Eukaryotic protein of unknown function (DUF829)   chr5:17840972-17842943 REVERSE   Aliases: MLN1.18, MLN1_18	6.2	6.7	-0.5	-0.8	100.0%	-4.5
9015	AT3G01570.1   glycine-rich protein / oleosin, similar to oleosin GB:AAB58402 (Sesamum indicum)	2.6	2.5	0.1	0.8	100.0%	-5.4
9016	AT1G12460.1   leucine-rich repeat transmembrane protein kinase, putative   chr1:4247247-4250628 FORWARD   Aliases: F5O11.21, F5O11_21	4.4	4.6	-0.2	-0.8	100.0%	-4.6
9017	AT5G49150.1   Symbol: GEX2   hypothetical protein   chr5:19942160-19945753 FORWARD   Aliases: GENAMETE EXPRESSED2, K21P3.2, K21P3_2	2.7	2.8	-0.1	-0.8	100.0%	-5.2
9018	AT5G63580.1   flavonol synthase, putative, similar to SP:Q96330; contains PF03171 2OG-Fe(II) oxygenase superfamily   chr5:25471956-25473702 FORWARD   Aliases: MBK5.4, MBK5_4	2.6	2.7	-0.1	-0.8	100.0%	-5.3
9019	AT5G02130.1   Symbol: NDP1   expressed protein, kinesin light chain - Plectonema boryanum, EMBL:U78597   chr5:419655-421972 REVERSE   Aliases: RANDOM POTATO CDNA CLONE, T7H20.180, T7H20_180	5.7	6.0	-0.3	-0.8	100.0%	-4.5
9020	AT4G35300.2   transporter-related, low similarity to hexose transporter (Solanum tuberosum) GI:8347246; contains Pfam profile PF00083: major facilitator superfamily protein   chr4:16796261-16799558 REVERSE   Aliases: F23E12.140, F23E12_140	5.3	5.0	0.3	0.8	100.0%	-4.7
9021	AT4G14210.2   Symbol: PDS3   phytoene dehydrogenase, chloroplast / phytoene desaturase (PDS), identical to SP:Q07356 Phytoene dehydrogenase, chloroplast precursor (EC 1.14.99.-) (Phytoene desaturase){Arabidopsis thaliana}; high similarity to phytoene desaturase (Lycopersicon esculentum)(GI:19287)   chr4:8190256-8195095 REVERSE   Aliases: DL3145C, FCAALL.28, PDE226, PDS, PHYTOENE DESATURASE	8.1	8.5	-0.4	-0.8	100.0%	-4.3
9022	AT5G11520.1   Symbol: ASP3   aspartate aminotransferase, chloroplast / transaminase A (ASP3) (YLS4), identical to SP:P46644 Aspartate aminotransferase, chloroplast precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}; identical to cDNA YLS4 mRNA for aspartate aminotransferase (ASP3), partial cds GI:13122285   chr5:3685090-3687765 REVERSE   Aliases: ASPARTATE AMINOTRANSFERASE 3, ASPARTATE AMINOTRANSFERASE, CHLOROPLAST PRECURSOR, F15N18.110, F15N18_110, YELLOW LEAF SPECIFIC GENE 4, YLS4	11.4	11.9	-0.4	-0.8	100.0%	-4.8
9023	AT2G41980.1   seven in absentia (SINA) family protein, similar to siah-1A protein (Mus musculus) GI:297035; contains Pfam profile PF03145: Seven in absentia protein family   chr2:17530572-17531770 REVERSE   Aliases: T6D20.13, T6D20_13	2.8	2.7	0.2	0.8	100.0%	-5.0
9024	AT5G42390.1   metalloendopeptidase, identical to chloroplast processing enzyme metalloendopeptidase (Arabidopsis thaliana) gi:2827039:gb:AAC39482   chr5:16962479-16970328 FORWARD   Aliases: MDH9.8, MDH9_8	7.0	6.5	0.5	0.8	100.0%	-4.4
9025	AT3G61580.1   delta-8 sphingolipid desaturase (SLD1), identical to delta-8 sphingolipid desaturase GI:3819710 from (Arabidopsis thaliana); contains Pfam profile PF00487: Fatty acid desaturase; contains Pfam profile PF00173: Heme/Steroid binding domain   chr3:22797022-22798947 FORWARD   Aliases: F2A19.180, F2A19_180	7.3	6.8	0.5	0.8	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9026	AT3G49730.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:18453260-18458631 REVERSE   Aliases: T16K5.80	6.8	7.1	-0.3	-0.8	100.0%	-4.3
9027	AT2G18640.1   Symbol: GGPS4   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltransferase, putative, similar to gi:1944371; contains GB:L22347   chr2:8090822-8091970 REVERSE   Aliases: F24H14.2, GERANYLGERANYL PYROPHOSPHATE SYNTHASE 4	2.7	2.6	0.1	0.8	100.0%	-5.2
9028	AT1G17600.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:6053243-6056565 REVERSE   Aliases: F1L3.30, F1L3_30	2.3	2.4	-0.1	-0.8	100.0%	-5.5
9029	AT5G60960.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:24545476-24547237 REVERSE   Aliases: MSL3.8, MSL3_8	8.3	8.8	-0.6	-0.8	100.0%	-4.4
9030	AT4G18290.1   Symbol: KAT2   similar to inward rectifying potassium channel (KAT1) [Arabidopsis thaliana] (TAIR:At5g46240.1); similar to K+ channel protein [Populus tremula x Populus tremuloides] (GB:CAC87141.1); similar to inward rectifying shaker-like K+ channel [Vitis vinifera] (GB:AAL09479.1); similar to K+ channel inward rectifying [Solanum tuberosum] (GB:CAA56175.1); similar to putative inward rectifying shaker K+ channel; ZmK2.1 [Oryza sativa (japonica cultivar-group)] (GB:XP_464796.1); similar to inward rectifying potassium channel [Vitis vinifera] (GB:AAL24466.1); contains InterPro domain EAG/ELK/ERG potassium channel (InterPro:IPR003938); contains InterPro domain Ion transport protein (InterPro:IPR005821); contains InterPro domain Cyclic nucleotide-binding domain (InterPro:IPR000595)   chr4:10115429-10118610 FORWARD   Aliases: T9A21.140, T9A21_140, VOLTAGE GATED POTASSIUM CHANNEL 2	3.1	3.2	-0.1	-0.8	100.0%	-5.2
9031	AT4G21200.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to gibberellin 20-oxidase from A. thaliana (gi:1109699), Phaseolis vulgaris (gi:2262201); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr4:11302761-11306611 FORWARD   Aliases: F7J7.140, F7J7_140	2.7	2.9	-0.2	-0.8	100.0%	-5.2
9032	AT4G28100.1   expressed protein   chr4:13965114-13966837 REVERSE   Aliases: T13J8.210, T13J8_210	2.8	3.0	-0.2	-0.8	100.0%	-4.6
9033	AT3G28680.1   prolylcarboxypeptidase-related, weak similarity to SP:P42785: Lysosomal Pro-X carboxypeptidase precursor (EC 3.4.16.2) (Prolylcarboxypeptidase) (PRCP) (Proline carboxypeptidase) {Homo sapiens}	3.5	3.6	-0.1	-0.8	100.0%	-5.2
9034	AT4G21400.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:11399142-11401720 REVERSE   Aliases: F18E5.20	5.3	4.9	0.4	0.8	100.0%	-4.6
9035	AT3G27200.1   plastocyanin-like domain-containing protein, contains similarity to uclacyanin I GI:3399767 GB:AAC32038 from (Arabidopsis thaliana)   chr3:10044759-10045608 REVERSE   Aliases: K17E12.2	3.8	4.3	-0.5	-0.8	100.0%	-3.9
9036	AT2G31570.1   Symbol: ATGPX2	10.8	10.4	0.4	0.8	100.0%	-5.0
9037	AT4G27150.1   2S seed storage protein 2 / 2S albumin storage protein / NWMU2-2S albumin 2, identical to SP:P15458   chr4:13609347-13610081 FORWARD   Aliases: T24A18.100, T24A18_100	2.7	2.6	0.1	0.8	100.0%	-5.4
9038	AT2G38160.1   expressed protein   chr2:15993864-15995600 REVERSE   Aliases: F16M14.9, F16M14_9	2.2	2.3	-0.1	-0.8	100.0%	-5.3
9039	AT5G20610.1   expressed protein   chr5:6968692-6972997 FORWARD   Aliases: T1M15.10, T1M15_10	5.1	4.7	0.4	0.8	100.0%	-4.7
9040	AT1G73310.1   Symbol: SCPL4   serine carboxypeptidase S10 family protein, similar to serine carboxypeptidase I precursor (SP:P07519) (Hordeum vulgare); glucose acyltransferase GB:AAD01263 (Solanum berthaultii); contains Pfam profile: PF00450 Serine carboxypeptidase   chr1:27566476-27568838 REVERSE   Aliases: SCPL4, T18K17.2, T18K17_2	2.9	3.1	-0.2	-0.8	100.0%	-4.7
9041	AT5G39580.2   similar to peroxidase, putative [Arabidopsis thaliana] (TAIR:At5g64120.1); similar to peroxidase precursor [Lycopersicon esculentum] (GB:CAA64413.1); contains InterPro domain Haem peroxidase (InterPro:IPR002016); contains InterPro domain Plant peroxidase (InterPro:IPR000823)   chr5:15864306-15866336 REVERSE   Aliases: MIJ24.50, MIJ24_50	2.4	2.6	-0.2	-0.8	100.0%	-4.5
9042	AT1G61210.1   WD-40 repeat family protein / katanin p80 subunit, putative, contains 5 WD-40 repeats (PF00400); similar to katanin p80 subunit (GI:3005601) (Strongylocentrotus purpuratus)   chr1:22568177-22575571 FORWARD   Aliases: F11P17.7, F11P17_7	2.7	2.6	0.1	0.8	100.0%	-5.1
9043	AT4G12400.2   similar to stress-inducible protein, putative [Arabidopsis thaliana] (TAIR:At1g12270.1); similar to stress-inducible protein, putative [Arabidopsis thaliana] (TAIR:At1g62740.1); similar to stress inducible protein [Glycine max] (GB:CAA56165.1); similar to stress-induced protein sti1 - soybean (GB:S56658); similar to OSJNBa0091D06.14 [Oryza sativa (japonica cultivar-group)] (GB:XP_473336.1); contains InterPro domain Heat shock chaperonin-binding (InterPro:IPR006636); contains InterPro domain TPR repeat (InterPro:IPR001440)   chr4:7338656-7341358 REVERSE   Aliases: T1P17.2	5.9	5.7	0.2	0.8	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9044	AT1G60990.1   similar to aminomethyltransferase, putative [Arabidopsis thaliana] (TAIR:At1g11860.1); similar to aminomethyltransferase, putative [Arabidopsis thaliana] (TAIR:At1g11860.2); similar to COG0354: Predicted aminomethyltransferase related to GcvT [Trichodesmium erythraeum IMS101] (GB:ZP_00327983.1); contains InterPro domain Glycine cleavage T protein (aminomethyl transferase) (InterPro:IPR006222)   chr1:22466305-22469089 REVERSE   Aliases: T7P1.13, T7P1_13	5.7	5.4	0.3	0.8	100.0%	-4.3
9045	AT5G26150.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:9137464-9140102 REVERSE   Aliases: T1N24.15, T1N24_15	2.2	2.1	0.1	0.8	100.0%	-5.7
9046	AT4G17390.1   60S ribosomal protein L15 (RPL15B)   chr4:9714225-9715624 REVERSE   Aliases: DL4730C, FCAALL.32	10.8	11.1	-0.2	-0.8	100.0%	-4.9
9047	AT2G19740.1   60S ribosomal protein L31 (RPL31A)   chr2:8520599-8521601 FORWARD   Aliases: F6F22.23, F6F22_23	9.1	8.7	0.4	0.8	100.0%	-4.2
9048	AT4G32350.1   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	5.0	5.2	-0.2	-0.8	100.0%	-4.5
9049	AT5G15190.2   expressed protein   chr5:4932823-4933539 REVERSE   Aliases: F8M21.80, F8M21_80	2.9	2.6	0.3	0.8	100.0%	-4.8
9050	AT3G49720.1   expressed protein   chr3:18450988-18453182 REVERSE   Aliases: T16K5.70	9.8	9.5	0.3	0.8	100.0%	-4.6
9051	AT1G31960.1   hypothetical protein   chr1:11479113-11479634 REVERSE   Aliases: F5M6.4	3.3	3.2	0.2	0.8	100.0%	-4.9
9052	AT1G56530.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965;   chr1:21182902-21184553 FORWARD   Aliases: F25P12.22, F25P12_22	3.6	3.9	-0.3	-0.8	100.0%	-5.2
9053	AT2G32750.1   exostosin family protein, contains Pfam profile: PF03016 exostosin family   chr2:13896718-13898247 FORWARD   Aliases: F24L7.11, F24L7_11	2.5	2.4	0.1	0.8	100.0%	-5.3
9054	AT2G38950.1   transcription factor jumonji (jnj) family protein / zinc finger (C5HC2 type) family protein, contains Pfam domains, PF02375: jmjN domain, PF02373: jmjC domain and PF02928: C5HC2 zinc finger   chr2:16267931-16272297 FORWARD   Aliases: T7F6.12, T7F6_12	5.6	5.9	-0.2	-0.8	100.0%	-4.6
9055	AT1G22180.3   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, contains Pfam profile: PF00650 CRAL/TRIO domain; similar to polyphosphoinositide binding protein Ssh1p (Gl::2739044) {Glycine max}; similar to Phosphatidylinositol Transfer Protein Sec14p (Gl:2780955) (Saccharomyces cerevisiae)   chr1:7828315-7830307 REVERSE   Aliases: F16L1.9, F16L1_9	8.0	7.4	0.6	0.8	100.0%	-4.5
9056	AT4G11175.1   translation initiation factor IF-1, chloroplast, putative, similar to Swiss-Prot:P08698 translation initiation factor IF-1, chloroplast (Spinacia oleracea); contains Pfam profile PF00575: S1 RNA binding domain   chr4:6818089-6819038 FORWARD   Aliases: T22B4.1, T22B4_1	4.2	4.4	-0.2	-0.8	100.0%	-4.9
9057	AT4G39620.1   Symbol: EMB2453   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:18395288-18397572 FORWARD   Aliases: EMB2453, EMBRYO DEFECTIVE 2453, F23K16.250, F23K16_250	5.3	5.1	0.2	0.8	100.0%	-4.9
9058	AT1G03100.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to CRP1 (Zea mays) Gl:3289002; contains Pfam profile PF01535: PPR repeat   chr1:744026-746407 REVERSE   Aliases: F10O3.8, F10O3_8	5.2	5.4	-0.2	-0.8	100.0%	-4.5
9059	AT2G29500.1   17.6 kDa class I small heat shock protein (HSP17.6B-CI), contains Pfam PF00011: Hsp20/alpha crystallin family; identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.   chr2:12640180-12640882 REVERSE   Aliases: F16P2.12, F16P2_12	7.2	7.6	-0.4	-0.8	100.0%	-4.0
9060	AT4G27480.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr4:13736841-13738921 REVERSE   Aliases: F27G19.80, F27G19_80	5.9	5.6	0.3	0.8	100.0%	-4.3
9061	AT1G63900.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:23720382-23722923 FORWARD   Aliases: AT1G63890, T12P18.8, T12P18_8	7.5	7.4	0.1	0.8	100.0%	-5.0
9062	AT4G34000.4   Symbol: ABF3   similar to ABA-responsive element-binding protein 2 (AREB2) [Arabidopsis thaliana] (TAIR:At3g19290.1); similar to AREB-like protein [Lycopersicon esculentum] (GB:AAS20434.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr4:16295436-16298248 FORWARD   Aliases: ABSCISIC ACID RESPONSIVE ELEMENTS BINDING FACTOR 3, F17I5.200	4.2	4.6	-0.4	-0.8	100.0%	-4.3
9063	AT1G62950.1   leucine-rich repeat transmembrane protein kinase, putative, contains protein kinase domains   chr1:23318959-23321726 FORWARD   Aliases: F16P17.10, F16P17_10	4.4	4.6	-0.2	-0.8	100.0%	-4.7
9064	AT3G50320.1   hypothetical protein   chr3:18664818-18665665 REVERSE   Aliases: F11C1.160	2.4	2.3	0.1	0.8	100.0%	-5.4
9065	AT4G09300.1   expressed protein   chr4:5898795-5901011 FORWARD   Aliases: T30A10.60, T30A10_60	3.2	3.3	-0.1	-0.8	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9066	AT3G01480.1   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to peptidyl-prolyl cis-trans isomerase, chloroplast precursor (40 kDa thylakoid lumen PPIase, 40 kDa thylakoid lumen rotamase) (Spinacia oleracea) SWISS-PROT:O49939	6.2	6.4	-0.2	-0.8	100.0%	-4.5
9067	AT5G20330.1   Symbol: BETAG4	2.6	2.5	0.1	0.8	100.0%	-5.2
9068	AT4G32500.1   Symbol: AKT5   potassium channel protein, putative, similar to potassium channel (Solanum tuberosum) gi:1514649:emb:CAA60016; similar to AKT1 (Arabidopsis thaliana) gi:563112:gb:AAA96810; member of the 1 pore, 6 transmembrane (1P/6TM- Shaker-type) K+ channel family, PMID:11500563   chr4:15681128-15685220 FORWARD   Aliases: F8B4.200, F8B4_200	3.7	3.8	-0.2	-0.8	100.0%	-4.7
9069	AT5G49555.1   amine oxidase-related, contains Pfam profile PF01593: amine oxidase, flavin-containing   chr5:20124455-20127862 REVERSE   Aliases: None	6.3	6.8	-0.5	-0.8	100.0%	-4.5
9070	AT1G09440.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:3045515-3047395 REVERSE   Aliases: F14J9.10, F14J9_10	3.6	3.9	-0.3	-0.8	100.0%	-4.9
9071	AT3G05660.1   similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:At3g11080.1); similar to disease resistance family protein / LRR family protein [Arabidopsis thaliana] (TAIR:At3g11010.1); similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:At2g15080.2); similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:At5g27060.1); similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:At3g05650.1); similar to Cf-2.1 [Lycopersicon pimpinellifolium] (GB:AAC15779.1); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)	2.8	2.7	0.1	0.8	100.0%	-5.2
9072	AT4G22780.1   Symbol: ACR7   ACT domain-containing protein (ACR7), low similarity to uridylyltransferase SP:P56884 from Rhizobium meliloti; contains Pfam ACT domain PF01842   chr4:11968287-11971158 REVERSE   Aliases: T12H17.170, T12H17_170	3.4	3.1	0.3	0.8	100.0%	-4.3
9073	AT1G52200.1   expressed protein, similar to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr1:19445744-19447094 REVERSE   Aliases: F9I5.19, F9I5_19	2.8	3.3	-0.4	-0.8	100.0%	-4.0
9074	AT4G31170.3   similar to serine/threonine/tyrosine kinase, putative [Arabidopsis thaliana] (TAIR:At2g24360.1); similar to OSJNBa0060N03.16 [Oryza sativa (japonica cultivar-group)] (GB:XP_473833.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:15153188-15155644 REVERSE   Aliases: F6E21.90, F6E21_90	8.0	7.8	0.3	0.8	100.0%	-4.5
9075	AT5G13590.1   expressed protein   chr5:4374721-4378478 REVERSE   Aliases: T6I14.8	3.4	3.1	0.3	0.8	100.0%	-4.7
9076	AT1G79890.1   helicase-related, similar to CHL1 potential helicase protein (GI:2632247) (Homo sapiens); similar to helicase GB:AAB06962 (Homo sapiens)	3.6	3.7	-0.1	-0.8	100.0%	-5.1
9077	AT4G31030.1   expressed protein   chr4:15111223-15111605 REVERSE   Aliases: F6I18.60, F6I18_60	7.3	7.2	0.1	0.8	100.0%	-5.1
9078	AT4G16490.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr4:9293566-9295648 REVERSE   Aliases: DL4270C, FCAALL.59	2.1	2.0	0.1	0.8	100.0%	-5.6
9079	AT4G12000.1   expressed protein   chr4:7193264-7195146 REVERSE   Aliases: F16J13.70, F16J13_70	4.9	4.6	0.3	0.8	100.0%	-4.6
9080	AT4G11745.1   kelch repeat-containing protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profile PF01344: Kelch motif   chr4:7075820-7076674 REVERSE   Aliases: None	2.8	2.7	0.1	0.8	100.0%	-5.3
9081	AT4G03930.1   pectin methylesterase, putative, similar to pectin methylesterase GI:1617588 from (Lycopersicon esculentum)   chr4:1870420-1872528 FORWARD   Aliases: T24M8.6, T24M8_6	3.0	2.7	0.2	0.8	100.0%	-4.7
9082	AT3G51910.1   Symbol: AT HSFA7A   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr3:19276272-19277597 FORWARD   Aliases: F4F15.20, HSFA7A	5.2	4.5	0.7	0.8	100.0%	-4.4
9083	ATCG00340.1   Symbol: PSAB   Encodes the D1 subunit of photosystem I and II reaction centers.   chrC:37375-39579 REVERSE   Aliases: PSAB	11.5	11.2	0.4	0.8	100.0%	-4.7
9084	AT1G62750.1   elongation factor Tu family protein, similar to elongation factor G SP:P34811 (Glycine max (Soybean))   chr1:23237099-23240112 REVERSE   Aliases: F23N19.11, F23N19_11	10.8	10.2	0.5	0.8	100.0%	-4.5
9085	AT2G14210.1   Symbol: ANR1   MADS-box protein (ANR1), identical to ANR1, MADS-box protein (Arabidopsis thaliana) GI:2959320   chr2:6025640-6030945 FORWARD   Aliases: F15N24.5, F15N24_5	2.6	2.5	0.2	0.8	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9086	AT5G45540.1   expressed protein, contains Pfam domain, PF04578: Protein of unknown function, DUF594; expression supported by MPSS   chr5:18475521-18477932 REVERSE   Aliases: MFC19.21, MFC19_21	2.2	2.3	-0.1	-0.8	100.0%	-5.2
9087	AT1G70170.1   Symbol: MMP   matrixin family protein, similar to SP:P29136 Metalloendoproteinase 1 precursor (EC 3.4.24.-) (SMEP1) {Glycine max}; contains InterPro accession IPR001818: Matrixin   chr1:26427581-26428985 FORWARD   Aliases: F20P5.11, F20P5_11, MATRIX METALLOPROTEINASE	3.0	3.2	-0.2	-0.8	100.0%	-4.4
9088	AT4G30680.1   MA3 domain-containing protein, similar to SP:Q03387 Eukaryotic initiation factor (iso)4F subunit P82-34 (eIF-(iso)4F P82-34) {Triticum aestivum}; contains Pfam profile PF02847: MA3 domain   chr4:14958693-14960018 REVERSE   Aliases: T10C21.30, T10C21_30	4.5	4.4	0.2	0.8	100.0%	-4.8
9089	AT5G43810.1   Symbol: ZLL   pinhead protein (PINHEAD) / zwillie protein (ZWILLE), identical to SP:Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain   chr5:17628199-17634024 FORWARD   Aliases: MQD19.17, MQD19_17, PINHEAD, PNH, ZWILLE	5.2	5.6	-0.4	-0.8	100.0%	-4.2
9090	AT2G30210.1   laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)   chr2:12894523-12896904 REVERSE   Aliases: T9D9.2	3.5	4.0	-0.5	-0.8	100.0%	-4.1
9091	AT3G16060.1   kinesin motor family protein, similar to kinesin heavy chain member 2 GB:NP_032468 from (Mus musculus); contains Pfam profile PF00225: Kinesin motor domain   chr3:5447396-5451533 FORWARD   Aliases: MSL1.9	4.7	5.0	-0.3	-0.8	100.0%	-4.7
9092	AT1G21160.1   eukaryotic translation initiation factor 2 family protein / eIF-2 family protein, similar to SP:O60841 Translation initiation factor IF-2 {Homo sapiens}; contains Pfam profiles PF00009: Elongation factor Tu GTP binding domain, PF03144: Elongation factor Tu domain 2   chr1:7407946-7412739 REVERSE   Aliases: T22I11.2, T22I11_2	4.8	4.4	0.4	0.8	100.0%	-4.3
9093	AT1G21670.1   expressed protein, similar to TolB protein precursor (SP:P50601) {Pseudomonas aeruginosa}   chr1:7610387-7612671 FORWARD   Aliases: F8K7.9, F8K7_9	8.5	9.1	-0.6	-0.8	100.0%	-4.4
9094	AT3G58170.1   Symbol: ATBS14A   Bet1-like SNARE 1-1 / Bet1 / Sft1-like SNARE 14a / BS14a (BET11), identical to SP:Q9M2J9 Bet1-like SNARE 1-1 (AtBET11) (Bet1/Sft1-like SNARE 14a) (AtBS14a) (Mouse-ear cress) {Arabidopsis thaliana}; supporting cDNA gi:14030602:gb:AF368175.1:AF368175   chr3:21553344-21554918 REVERSE   Aliases: ATBET11, BET11, F9D24.80	9.2	8.8	0.4	0.8	100.0%	-4.4
9095	AT1G16000.1   expressed protein   chr1:5494530-5495317 FORWARD   Aliases: T24D18.10, T24D18_10	9.7	10.0	-0.3	-0.8	100.0%	-4.2
9096	AT4G04220.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-2A (Lycopersicon pimpinellifolium) gi:3894389:gb:AAC78594   chr4:2033425-2035944 FORWARD   Aliases: T27D20.9, T27D20_9	2.6	2.7	-0.1	-0.8	100.0%	-5.3
9097	AT4G30480.3   expressed protein   chr4:14897352-14899127 FORWARD   Aliases: F17I23.180, F17I23_180	9.4	8.9	0.4	0.8	100.0%	-4.7
9098	AT4G32080.1   expressed protein, ; expression supported by MPSS   chr4:15508439-15508774 REVERSE   Aliases: F10N7.110, F10N7_110	2.2	2.3	-0.1	-0.8	100.0%	-5.6
9099	AT5G47610.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:19318414-19319133 REVERSE   Aliases: MNJ7.20, MNJ7_20	2.0	2.1	-0.1	-0.8	100.0%	-5.6
9100	AT5G11370.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr5:3627850-3629718 FORWARD   Aliases: F2I11.260, F2I11_260	2.9	2.8	0.1	0.8	100.0%	-5.1
9101	AT3G24430.1   Symbol: HCF101	7.4	7.0	0.4	0.8	100.0%	-4.2
9102	AT5G58400.1   peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi:5381253:dbj:BAA82306   chr5:23622428-23624244 REVERSE   Aliases: MCK7.27, MCK7_27	2.2	2.1	0.1	0.8	100.0%	-5.4
9103	AT3G04280.2   Symbol: ARR22   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain   chr3:1129951-1130897 REVERSE   Aliases: ARABIDOPSIS RESPONSE REGULATOR 22, T6K12.10, T6K12_10	2.5	2.6	-0.1	-0.8	100.0%	-5.1
9104	AT2G22870.1   Symbol: EMB2001   expressed protein   chr2:9746537-9748586 FORWARD   Aliases: EMB2001, EMBRYO DEFECTIVE 2001, T20K9.8, T20K9_8	6.2	6.5	-0.3	-0.8	100.0%	-4.4
9105	AT1G20770.1   expressed protein   chr1:7215016-7216693 REVERSE   Aliases: F2D10.26, F2D10_26	7.7	7.2	0.5	0.8	100.0%	-4.4
9106	AT3G52420.1   outer envelope membrane protein, putative, similar to outer envelope membrane protein gi:703236:gb:AAA63414   chr3:19440753-19440947 FORWARD   Aliases: F22O6.200	8.7	8.9	-0.2	-0.8	100.0%	-4.5
9107	AT3G30810.1   expressed protein   chr3:12495302-12498859 FORWARD   Aliases: K11J14.2	4.0	3.8	0.3	0.8	100.0%	-4.7
9108	AT5G06930.1   expressed protein   chr5:2145140-2148040 FORWARD   Aliases: MOJ9.10, MOJ9_10	3.3	3.5	-0.2	-0.8	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9109	AT2G13950.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.4	3.2	0.2	0.8	100.0%	-4.8
9110	AT5G22620.1   phosphoglycerate/bisphosphoglycerate mutase family protein, weak similarity to SP:P15259 Phosphoglycerate mutase, muscle form (EC 5.4.2.1 {Homo sapiens}); contains Pfam profile PF00300: phosphoglycerate mutase family   chr5:7517624-7520242 REVERSE   Aliases: MDJ22.4, MDJ22_4	7.5	7.8	-0.3	-0.8	100.0%	-4.8
9111	AT2G33520.1   expressed protein   chr2:14203828-14204782 FORWARD   Aliases: F4P9.29, F4P9_29	4.6	4.3	0.3	0.8	100.0%	-4.4
9112	AT2G43240.1   nucleotide-sugar transporter family protein, weak similarity to SP:P78382 CMP-sialic acid transporter {Homo sapiens}; contains Pfam profile PF04142: Nucleotide-sugar transporter   chr2:17975775-17982365 REVERSE   Aliases: F14B2.18	4.8	4.7	0.1	0.8	100.0%	-5.1
9113	AT4G28280.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g20700.1); similar to GPI-anchored protein [Vigna radiata] (GB:BAA34247.1)   chr4:14010691-14011564 FORWARD   Aliases: F26K10.160, F26K10_160	3.0	3.2	-0.2	-0.8	100.0%	-4.9
9114	AT5G63630.1   DEAD box RNA helicase, putative, strong similarity to RNA helicase RH25 (Arabidopsis thaliana) GI:3776023; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain; identical to cDNA DEAD box RNA helicase, RH31 GI:3776030   chr5:25489824-25492422 REVERSE   Aliases: MBK5.11, MBK5_11	4.7	5.0	-0.3	-0.8	100.0%	-4.5
9115	AT4G16650.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator like protein' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	4.1	4.5	-0.3	-0.8	100.0%	-4.6
9116	AT5G61920.1   expressed protein   chr5:24882056-24882854 FORWARD   Aliases: K22G18.4, K22G18_4	2.9	2.8	0.1	0.8	100.0%	-5.0
9117	AT5G09700.1   glycosyl hydrolase family 3 protein, contains Pfam profile PF01915: Glycosyl hydrolase family 3 C terminal domain   chr5:3003721-3005129 REVERSE   Aliases: F17I14.110, F17I14_110	2.7	2.9	-0.2	-0.8	100.0%	-4.8
9118	AT4G18395.1   expressed protein   chr4:10169455-10169941 FORWARD   Aliases: None	3.2	3.3	-0.1	-0.8	100.0%	-5.2
9119	AT1G78740.1   similar to F-box family protein [Arabidopsis thaliana] (TAIR:At1g69630.1)   chr1:29615387-29616385 REVERSE   Aliases: F9K20.22, F9K20_22	4.0	3.8	0.2	0.8	100.0%	-4.7
9120	AT4G20880.1   ethylene-responsive nuclear protein / ethylene-regulated nuclear protein (ERT2), identical to ethylene-regulated nuclear protein (Arabidopsis thaliana) gi:2765442:emb:CAA75349   chr4:11179126-11180810 REVERSE   Aliases: T13K14.40, T13K14_40	6.0	5.6	0.4	0.8	100.0%	-4.4
9121	AT2G14630.1   hypothetical protein, contains Pfam profile PF03004: Plant transposase (Ptta/En/Spm family)   chr2:6259574-6260493 REVERSE   Aliases: T6B13.13, T6B13_13	2.3	2.4	-0.1	-0.8	100.0%	-5.7
9122	AT3G20110.1   Symbol: CYP705A20   cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	2.7	2.6	0.1	0.8	100.0%	-5.1
9123	AT3G09200.1   60S acidic ribosomal protein P0 (RPP0B), similar to putative 60S acidic ribosomal protein P0 GB:P50346 (Glycine max)   chr3:2823096-2825096 REVERSE   Aliases: F3L24.7	11.4	11.0	0.4	0.8	100.0%	-4.6
9124	AT1G79640.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:29971806-29975983 REVERSE   Aliases: F20B17.7, F20B17_7	2.7	2.6	0.1	0.8	100.0%	-5.3
9125	AT1G48460.1   expressed protein   chr1:17915014-17916968 FORWARD   Aliases: T1N15.7, T1N15_7	4.9	5.1	-0.3	-0.8	100.0%	-4.3
9126	AT1G15730.1   PRLI-interacting factor L, putative, strong similarity to PRLI-interacting factor L GI:11139268 from (Arabidopsis thaliana); contains Pfam profile PF02492: Cobalamin synthesis protein/P47K   chr1:5407023-5409979 REVERSE   Aliases: F7H2.7, F7H2_7	7.3	7.1	0.3	0.8	100.0%	-4.5
9127	AT1G04800.1   glycine-rich protein   chr1:1348451-1349285 REVERSE   Aliases: F13M7.21, F13M7_21	6.6	6.2	0.4	0.8	100.0%	-4.6
9128	AT3G50880.1   HhH-GPD base excision DNA repair family protein, contains weak similarity to DNA-3-methyladenine glycosylase 1 (EC 3.2.2.21) (3-methyladenine DNA glycosidase 1) (3MEA DNA glycosylase 1) (Swiss-Prot:Q92383) (Schizosaccharomyces pombe); contains Pfam profile PF00730: HhH-GPD superfamily base excision DNA repair protein   chr3:18924467-18925918 FORWARD   Aliases: F18B3.160	4.8	4.7	0.1	0.8	100.0%	-4.8
9129	AT1G30910.1   molybdenum cofactor sulfurase family protein, weak similarity to molybdenum cofactor sulfurase (LOS5/ABA3) (Arabidopsis thaliana) GI:15407262; contains Pfam profiles PF03476: MOSC N-terminal beta barrel domain, PF03473: MOSC domain   chr1:11000864-11002917 FORWARD   Aliases: F17F8.22	7.7	7.2	0.5	0.8	100.0%	-4.4
9130	AT4G14230.1   CBS domain-containing protein-related, contains Pfam profile PF01595: Domain of unknown function	6.6	6.4	0.2	0.8	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9131	AT1G61730.1   DNA-binding storekeeper protein-related, contains Pfam profile: PF04504 protein of unknown function, DUF573; similar to storekeeper protein GI:14268476 (Solanum tuberosum)   chr1:22796884-22798368 REVERSE   Aliases: T13M11.9, T13M11_9	8.7	8.5	0.2	0.8	100.0%	-5.2
9132	AT4G24040.1   Symbol: ATTRE1	10.0	9.7	0.3	0.8	100.0%	-4.4
9133	AT5G53200.1   Symbol: TRY   myb family transcription factor (TRIPTYCHON), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:21600000-21601371 FORWARD   Aliases: MFH8.14, MFH8_14, TRIPTYCHON, TRY	3.1	3.3	-0.1	-0.8	100.0%	-5.0
9134	AT5G62170.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr5:24990209-24992764 REVERSE   Aliases: MTG10.21, MTG10_21	3.1	3.3	-0.1	-0.8	100.0%	-5.2
9135	AT2G17600.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.0	2.9	0.1	0.8	100.0%	-5.2
9136	AT3G06670.1   expressed protein   chr3:2105465-2113421 REVERSE   Aliases: T8E24.10	3.8	3.6	0.2	0.8	100.0%	-4.5
9137	AT1G73020.1   similar to PREDICTED: similar to expressed sequence AI604832 [Rattus norvegicus] (GB:XP_236774.3); contains InterPro domain Protein of unknown function DUF590 (InterPro:IPR007632)   chr1:27473211-27477145 REVERSE   Aliases: F3N23.22, F3N23_22	7.2	7.6	-0.4	-0.8	100.0%	-4.0
9138	AT3G13740.1   URF 4-related, similar to URF 4 (GI:49224) (Swiss-Prot:Q05370)(Synechococcus sp.)   chr3:4504278-4506243 FORWARD   Aliases: MMM17.16	4.9	5.2	-0.2	-0.8	100.0%	-4.4
9139	AT2G40650.1   pre-mRNA splicing factor PRP38 family protein, contains Pfam profile PF03371: PRP38 family   chr2:16970397-16972830 REVERSE   Aliases: T7D17.17, T7D17_17	7.3	8.1	-0.7	-0.8	100.0%	-4.3
9140	AT1G27320.1   Symbol: AHK3   histidine kinase (AHK3), identical to histidine kinase AHK3 (Arabidopsis thaliana) gi:13537198:dbj:BAB40775   chr1:9487767-9492280 FORWARD   Aliases: ARABIDOPSIS HISTIDINE KINASE 3, F17L21.11, F17L21_11	3.8	3.5	0.3	0.8	100.0%	-4.4
9141	AT4G34990.1   myb family transcription factor (MYB32), similar to myb DNA-binding protein GI:19052 from (Hordeum vulgare)   chr4:16661334-16662372 REVERSE   Aliases: M4E13.50, M4E13_50	6.1	6.4	-0.2	-0.8	100.0%	-4.4
9142	AT2G21620.2   Symbol: RD2   universal stress protein (USP) family protein / responsive to desiccation protein (RD2), strong similarity to RD2 protein (Arabidopsis thaliana) GI:15320408; contains Pfam profile PF00582: universal stress protein family; identical to cDNA RD2 GI:15320407   chr2:9255678-9257319 FORWARD   Aliases: F2G1.11, F2G1_11	9.1	8.6	0.5	0.8	100.0%	-4.5
9143	AT2G43680.2   calmodulin-binding family protein, similar to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr2:18115428-18118904 FORWARD   Aliases: F18O19.21	5.6	6.0	-0.3	-0.8	100.0%	-4.5
9144	AT1G47310.1   expressed protein   chr1:17345354-17347242 FORWARD   Aliases: T3F24.7, T3F24_7	8.5	8.2	0.3	0.8	100.0%	-4.4
9145	AT5G63320.1   similar to DNA-binding bromodomain-containing protein [Arabidopsis thaliana] (TAIR:At3g27260.1); similar to kinase-like protein [Oryza sativa] (GB:BAB41205.1)   chr5:25391639-25393813 REVERSE   Aliases: K9H21.12, K9H21_12	6.3	6.9	-0.7	-0.8	100.0%	-4.4
9146	AT1G78990.1   transferase family protein, low similarity to acetyl CoA: benzylalcohol acetyltransferase Clarkia breweri GI:3170250, GI:6166336, Clarkia concinna GI:6166326, anthranilate N-hydroxycinnamoyl/benzoyltransferase Dianthus caryophyllus GI:2239091; contains Pfam profile PF02458 transferase family   chr1:29718424-29719862 REVERSE   Aliases: YUP8H12R.39, YUP8H12R_39	2.5	2.7	-0.2	-0.8	100.0%	-4.5
9147	AT2G17670.2   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:7681433-7683239 FORWARD   Aliases: T17A5.11, T17A5_11	6.9	7.1	-0.2	-0.8	100.0%	-4.6
9148	AT1G44085.1   glycine-rich protein, similar to glycine-rich protein GI:18147 from (Chenopodium rubrum)	3.4	3.3	0.1	0.8	100.0%	-5.1
9149	AT5G20950.2   glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, EMBL:AB017502   chr5:7107378-7111311 REVERSE   Aliases: F22D1.120, F22D1_120	5.7	6.4	-0.7	-0.8	100.0%	-4.2
9150	AT2G38880.6   Symbol: HAP3A   similar to CCAAT-box binding transcription factor subunit B (NF-YB) (HAP3 ) (AHAP3) family [Arabidopsis thaliana] (TAIR:At4g14540.1); similar to CAAT-box DNA binding protein subunit B (NF-YB) [Zea mays] (GB:CAA42234.1); contains InterPro domain Transcription factor CBF/NF-Y/archaeal histone (InterPro:IPR003958); contains InterPro domain Histone-like transcription factor/archaeal histone/topoisomerase (InterPro:IPR003957); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124); contains InterPro domain Histone-like transcription factor CBF/NF-Y/archaeal histone, subunit A (InterPro:IPR003956)   chr2:16245570-16247833 FORWARD   Aliases: ATHAP3, HAP3, T7F6.5, T7F6_5	7.0	7.2	-0.3	-0.8	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9151	AT2G31900.1   Symbol: XIF   myosin family protein, contains Pfam profiles: PF00063 myosin head (motor domain), PF01843 DIL domain, PF00612 IQ calmodulin-binding motif, PF02736 myosin N-terminal SH3-like domain   chr2:13567837-13576700 REVERSE   Aliases: ATMYO5, ATXIF, F20M17.6, F20M17_6, PCR11	2.5	2.6	-0.2	-0.8	100.0%	-5.1
9152	AT5G16190.1   Symbol: ATCSLA11   similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At1g23480.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At1g24070.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At1g23480.2); similar to glucosyltransferase-related [Arabidopsis thaliana] (TAIR:At4g16590.1); similar to glycosyl transferase family 2 protein [Arabidopsis thaliana] (TAIR:At4g13410.1); similar to TPA: cellulose synthase-like A1 [Oryza sativa (japonica cultivar-group)] (GB:DAA01743.1); contains InterPro domain Glycosyl transferase, family 2 (InterPro:IPR001173)   chr5:5283576-5286296 REVERSE   Aliases: CSLA11, T21H19.110, T21H19_110	4.2	4.5	-0.3	-0.8	100.0%	-4.2
9153	AT3G03360.1   F-box family protein, low similarity to ribosomal RNA apurinic site specific lyase (Triticum aestivum) GI:6505722; contains F-box domain Pfam:PF00646   chr3:795225-796925 FORWARD   Aliases: T21P5.22, T21P5_22	5.3	5.6	-0.3	-0.8	100.0%	-4.6
9154	AT5G16840.1   RNA recognition motif (RRM)-containing protein, predicted proteins - Arabidopsis thaliana   chr5:5535923-5538253 FORWARD   Aliases: F5E19.180, F5E19_180	9.7	9.3	0.4	0.8	100.0%	-4.5
9155	AT3G20830.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:7284969-7286266 REVERSE   Aliases: MOE17.13	4.3	4.4	-0.2	-0.8	100.0%	-4.8
9156	AT2G32415.1   3'-5' exonuclease domain-containing protein, similar to SP:Q12149 Exosome complex exonuclease RRP6 (EC 3.1.13.-) (Ribosomal RNA processing protein 6) {Saccharomyces cerevisiae}	3.1	2.9	0.2	0.8	100.0%	-4.9
9157	AT2G33740.2   Symbol: CUTA   copper-binding protein (CUTA), identical to copper-binding protein CUTA GI:12963361 from (Arabidopsis thaliana); contains Pfam profile: PF03091 CutA1 divalent ion tolerance protein   chr2:14276657-14278752 FORWARD   Aliases: T1B8.5, T1B8_5	8.7	8.4	0.3	0.8	100.0%	-4.4
9158	AT1G56150.1   auxin-responsive family protein, similar to SP:P33082 Auxin-induced protein X15. (Soybean) {Glycine max}	5.2	4.9	0.4	0.8	100.0%	-4.0
9159	AT3G50850.1   expressed protein   chr3:18912323-18913334 REVERSE   Aliases: F18B3.130	4.4	4.5	-0.2	-0.8	100.0%	-4.7
9160	AT5G23080.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g53800.1); similar to hypothetical protein [Homo sapiens] (GB:CAD39124.1); contains InterPro domain SWAP/Surp (InterPro:IPR000061)   chr5:7742648-7748931 REVERSE   Aliases: MYJ24.7, MYJ24_7	7.3	6.8	0.5	0.8	100.0%	-4.2
9161	AT3G52750.1   Symbol: FTSZ2 2   chloroplast division protein, putative, strong similarity to plastid division protein FtsZ (Arabidopsis thaliana) GI:14195704, chloroplast division protein AtFtsZ2-1 (Arabidopsis thaliana) GI:15636809   chr3:19560639-19563992 REVERSE   Aliases: F3C22.150	7.9	8.3	-0.5	-0.8	100.0%	-4.3
9162	AT4G15900.1   Symbol: PRL1   PP1/PP2A phosphatases pleiotropic regulator 1 (PRL1), identical to PP1/PP2A phosphatases pleiotropic regulator PRL1 (SP:Q42384) (Arabidopsis thaliana), PRL1 (Arabidopsis thaliana) GI:577733; contains Pfam PF00400: WD domain, G-beta repeat (7 copies)   chr4:9023743-9027681 FORWARD   Aliases: DL3990W, FCAALL.40, PLEIOTROPIC REGULATORY LOCUS 1, PRL1 PROTEIN	4.9	5.2	-0.3	-0.8	100.0%	-4.5
9163	AT3G12760.1   expressed protein, similar to RP42 protein (Homo sapiens) GI:9896486; contains Pfam profile PF00627: UBA/TS-N domain, PF03556: Domain of unknown function (DUF298)   chr3:4054746-4056987 FORWARD   Aliases: MBK21.14	11.9	12.0	-0.2	-0.8	100.0%	-5.1
9164	AT1G04270.2   Symbol: RPS15   similar to 40S ribosomal protein S15 (RPS15D) [Arabidopsis thaliana] (TAIR:At5g09510.1); similar to ribosomal S15 protein [Retama raetam] (GB:AAL32040.1); contains InterPro domain Ribosomal protein S19/S15 (InterPro:IPR002222); contains InterPro domain Ribosomal protein S15, eukaryotic and archaeal form (InterPro:IPR005713)   chr1:1141603-1143050 REVERSE   Aliases: F19P19.29, F19P19_29, RIBOSOMAL PROTEIN S15	11.2	11.4	-0.2	-0.8	100.0%	-4.9
9165	AT2G44730.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189   chr2:18444408-18445640 REVERSE   Aliases: F16B22.22	6.4	5.9	0.5	0.8	100.0%	-4.4
9166	AT3G61460.1   Symbol: BRH1   zinc finger (C3HC4-type RING finger) family protein (BRH1), identical to BRH1 RING finger protein (Arabidopsis thaliana) GI:4689366; identical to cDNA BRH1 RING finger protein, GI:4689365   chr3:22752486-22753259 REVERSE   Aliases: BRASSINOSTEROID RESPONSIVE RING H2, F2A19.60	4.9	4.7	0.3	0.8	100.0%	-4.5
9167	AT2G25000.1   Symbol: WRKY60	3.5	3.3	0.2	0.8	100.0%	-4.6
9168	AT1G05270.1   TraB family protein, contains Pfam domain PF01963: TraB family   chr1:1531640-1534389 REVERSE   Aliases: YUP8H12.12, YUP8H12_12	4.3	4.0	0.3	0.8	100.0%	-4.5
9169	AT1G53240.1   malate dehydrogenase (NAD), mitochondrial, identical to mitochondrial NAD-dependent malate dehydrogenase GI:3929649 SP:Q9ZP06 from (Arabidopsis thaliana); contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr1:19858283-19860605 REVERSE   Aliases: F12M16.14, F12M16_14	11.1	11.5	-0.4	-0.8	100.0%	-4.8
9170	AT3G11780.1   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, weak similarity to phosphatidylglycerol/phosphatidylinositol transfer protein (Aspergillus oryzae) GI:10178615; contains Pfam profile PF02221: ML domain   chr3:3724153-3725595 REVERSE   Aliases: F26K24.7	6.4	6.0	0.5	0.8	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9171	AT2G38580.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g65010.1); similar to putative (GB:AAB00143.1); contains domain GLU_RICH (PS50313)   chr2:16145661-16149666 FORWARD   Aliases: T6A23.22, T6A23_22	5.3	5.5	-0.1	-0.8	100.0%	-5.1
9172	AT3G17640.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; contains some similarity to receptor-like protein kinase INRPK1 (Ipomoea nil) gi:14495542:gb:AAB36558	3.1	3.2	-0.2	-0.8	100.0%	-4.8
9173	AT5G22500.1   acyl CoA reductase, putative / male-sterility protein, putative, similar to acyl CoA reductase (Simmondsia chinensis) GI:5020215; contains Pfam profile PF03015: Male sterility protein; identical to cDNA male sterility 2-like protein GI:1491614   chr5:7470446-7474084 FORWARD   Aliases: MQJ16.4, MQJ16_4	2.1	2.1	-0.1	-0.8	100.0%	-5.8
9174	AT5G11960.1   expressed protein   chr5:3858580-3861516 REVERSE   Aliases: F14F18.130, F14F18_130	6.0	5.3	0.7	0.8	100.0%	-4.2
9175	AT3G60820.2   Symbol: PBF1   similar to 20S proteasome beta subunit C1 (PBC1) (PRCT) [Arabidopsis thaliana] (TAIR:At1g21720.1); similar to beta 6 subunit of 20S proteasome [Oryza sativa (japonica cultivar-group)] (GB:BAA28276.1); contains InterPro domain Proteasome B-type subunit (InterPro:IPR000243); contains InterPro domain Multispecific proteasome protease (InterPro:IPR001353)   chr3:22482730-22484904 REVERSE   Aliases: 20S PROTEASOME BETA SUBUNIT PBF1, T4C21.230	10.1	10.5	-0.5	-0.8	100.0%	-4.5
9176	AT1G79960.1   ovate protein-related, contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568   chr1:30084558-30085442 REVERSE   Aliases: F18B13.4, F18B13_4	3.3	3.1	0.2	0.8	100.0%	-4.7
9177	AT5G01700.2   similar to protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] (TAIR:At3g02750.1); similar to putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] (GB:XP_478745.1); similar to putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] (GB:XP_465582.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr5:260745-262579 REVERSE   Aliases: F7A7.220, F7A7_220	3.6	3.4	0.2	0.8	100.0%	-4.5
9178	AT2G21655.1   expressed protein, contains Pfam PF05617: Arabidopsis thaliana protein of unknown function (DUF784)   chr2:9270617-9271178 FORWARD   Aliases: None	2.6	2.7	-0.2	-0.8	100.0%	-5.1
9179	AT4G18375.2   KH domain-containing protein, contains similarity to RNA-binding KH-domains PF:00013   chr4:10152836-10155167 FORWARD   Aliases: F28J12.2, F28J12_2	2.2	2.2	-0.1	-0.8	100.0%	-5.7
9180	AT4G04040.1   pyrophosphate--fructose-6-phosphate 1-phosphotransferase beta subunit, putative / pyrophosphate-dependent 6-phosphofructose-1-kinase, putative, strong similarity to SP:Q41141 Pyrophosphate--fructose 6-phosphate 1-phosphotransferase beta subunit (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate-dependent) (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPI-PFK) {Ricinus communis}   chr4:1939248-1942952 FORWARD   Aliases: T24H24.15, T24H24_15	8.5	8.7	-0.2	-0.8	100.0%	-4.7
9181	AT3G62100.1   Symbol: IAA30   auxin-responsive protein, putative, similar to SP:O24410 Auxin-responsive protein IAA20 (Indoleacetic acid-induced protein 20) {Arabidopsis thaliana}; contains Pfam profile: PF02309: AUX/IAA family   chr3:23006766-23007736 FORWARD   Aliases: T17J13.60	2.9	3.1	-0.1	-0.8	100.0%	-5.3
9182	AT2G25380.1   zinc finger protein-related, very low similarity to SP:O95376 Ariadne-2 protein homolog (ARI-2) (Triad1 protein) {Homo sapiens}; contains Pfam profile PF01485: IBR (In Between Ring fingers) domain   chr2:10817441-10819226 FORWARD   Aliases: F13B15.4, F13B15_4	2.7	2.9	-0.1	-0.8	100.0%	-5.3
9183	AT4G14320.1   60S ribosomal protein L36a/L44 (RPL36aB)	9.7	10.0	-0.2	-0.8	100.0%	-4.7
9184	AT2G35585.1   expressed protein   chr2:14943745-14945042 FORWARD   Aliases: None	2.9	2.6	0.3	0.8	100.0%	-4.4
9185	AT1G20380.1   prolyl oligopeptidase, putative / prolyl endopeptidase, putative / post-proline cleaving enzyme, putative, similar to SP:P48147 Prolyl endopeptidase (EC 3.4.21.26) (Post-proline cleaving enzyme) {Homo sapiens}; contains Pfam profiles PF00326: prolyl oligopeptidase family, PF02897: Prolyl oligopeptidase, N-terminal beta-propeller domain   chr1:7061655-7065168 FORWARD   Aliases: F14O10.2, F14O10_2	4.7	5.0	-0.3	-0.8	100.0%	-4.2
9186	AT3G49420.1   Got1-like family protein, contains Pfam profile: PF04178 Got1-like family   chr3:18340372-18342416 FORWARD   Aliases: T9C5.20	5.8	5.3	0.5	0.8	100.0%	-3.9
9187	AT5G01430.1   Got1-like family protein, contains Pfam profile: PF04178 Got1-like family   chr5:176446-178598 REVERSE   Aliases: T10O8.140	5.8	5.3	0.5	0.8	100.0%	-3.9
9188	AT4G25120.1   UvrD/REP helicase family protein, contains Pfam PF00580: UvrD/REP helicase   chr4:12890704-12898511 FORWARD   Aliases: F24A6.8	2.9	3.1	-0.1	-0.8	100.0%	-5.0
9189	AT4G33620.1   Ulp1 protease family protein, low similarity to SP:Q9BQF6 SUMO-1-specific protease 2 (EC 3.4.22.-) (Sentrin-specific protease SENP7) {Homo sapiens}; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr4:16147695-16152856 FORWARD   Aliases: T16L1.110, T16L1_110	3.1	3.5	-0.4	-0.8	100.0%	-4.0
9190	AT1G32000.1   expressed protein   chr1:11508265-11508889 REVERSE   Aliases: T12O21.10, T12O21_10	2.0	1.9	0.1	0.8	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9191	AT3G07600.1   heavy-metal-associated domain-containing protein, identical to residues 23 to 179 of farnesylated protein ATPF4 (putative metal-binding protein) GB:AAD09508 (Arabidopsis thaliana); contains Pfam profile PF00403: Heavy-metal-associated domain   chr3:2424123-2425028 REVERSE   Aliases: MLP3.5	3.0	3.4	-0.4	-0.8	100.0%	-4.3
9192	AT5G07040.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:2190345-2190824 FORWARD   Aliases: MOJ9.21, MOJ9_21	2.5	2.3	0.1	0.8	100.0%	-5.0
9193	AT1G42970.1   Symbol: GAPB   glyceraldehyde-3-phosphate dehydrogenase B, chloroplast (GAPB) / NADP-dependent glyceraldehydephosphate dehydrogenase subunit B, identical to SP:P25857 Glyceraldehyde 3-phosphate dehydrogenase B, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit B) {Arabidopsis thaliana}   chr1:16129874-16132283 FORWARD   Aliases: F13A11.3, F13A11_3, GLYCERALDEHYDE 3 PHOSPHATE DEHYDROGENASE B SUBUNIT	9.1	8.6	0.5	0.8	100.0%	-4.0
9194	AT2G25740.1   ATP-dependent protease La (LON) domain-containing protein, low similarity to protease Lon (Pseudomonas fluorescens) GI:7644385; contains Pfam profile PF02190: ATP-dependent protease La (LON) domain   chr2:10987219-10990859 FORWARD   Aliases: F3N11.21	7.3	7.1	0.2	0.8	100.0%	-4.8
9195	AT5G28750.1   thylakoid assembly protein, putative, similar to thylakoid assembly 4 (tha4) protein (Pisum sativum) GI:4929305; contains Pfam profile PF02416: mttA/Hcf106 family   chr5:10784003-10785723 REVERSE   Aliases: T32B20.2, T32B20_2	9.0	9.3	-0.3	-0.8	100.0%	-4.5
9196	AT3G28720.1   expressed protein   chr3:10783513-10785684 FORWARD   Aliases: T19N8.1	8.3	8.7	-0.4	-0.8	100.0%	-4.6
9197	AT5G66330.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-5B (Lycopersicon esculentum) gi:3894391:gb:AAC78595   chr5:26517628-26519181 REVERSE   Aliases: K1L20.11, K1L20_11	2.4	2.5	-0.1	-0.8	100.0%	-5.2
9198	AT5G11720.1   alpha-glucosidase 1 (AGLU1), identical to alpha-glucosidase 1 (Arabidopsis thaliana) GI:2323344   chr5:3776815-3780129 FORWARD   Aliases: T22P22.110, T22P22_110	6.0	6.2	-0.2	-0.8	100.0%	-4.7
9199	AT1G71090.1   auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547   chr1:26815874-26817792 FORWARD   Aliases: F23N20.8, F23N20_8	7.1	6.9	0.3	0.8	100.0%	-4.4
9200	AT2G26620.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to SP:P35339 Exopolygalacturonase precursor (EC 3.2.1.67) (Pectinase) (Galacturan 1,4-alpha-galacturonidase) {Zea mays}; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)	2.5	2.4	0.1	0.8	100.0%	-5.8
9201	AT5G66740.1   hypothetical protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr5:26664956-26665784 FORWARD   Aliases: MSN2.13, MSN2_13	2.9	3.1	-0.1	-0.8	100.0%	-5.3
9202	AT3G18510.1   expressed protein   chr3:6355670-6356159 FORWARD   Aliases: MYF24.41	6.4	6.0	0.4	0.8	100.0%	-4.2
9203	AT3G19930.1   Symbol: STP4   sugar transport protein (STP4), identical to GB:S25009 GI:16524 from (Arabidopsis thaliana)   chr3:6934780-6937120 FORWARD   Aliases: MPN9.19, SUGAR TRANSPORTER	5.9	6.4	-0.6	-0.8	100.0%	-4.5
9204	AT5G53220.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g22795.1); similar to OSJNBb0076A22.19 [Oryza sativa (japonica cultivar-group)] (GB:XP_472168.1); contains domain ASP_RICH (PS50312)   chr5:21613216-21615450 FORWARD   Aliases: K19E1.2, K19E1_2	3.9	3.6	0.3	0.8	100.0%	-4.6
9205	AT1G70730.1   phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative, strong similarity to SP:P93804 Phosphoglucomutase, cytoplasmic 1 (EC 5.4.2.2) (Glucose phosphomutase 1) (PGM 1) {Zea mays}; contains InterPro accession IPR006352: Phosphoglucosamine mutase   chr1:26672527-26676418 REVERSE   Aliases: F5A18.9, F5A18_9	10.5	10.9	-0.4	-0.8	100.0%	-4.7
9206	AT1G01310.1   allergen V5/Tpx-1-related family protein, similar to pathogenesis related protein-1 GB:AAC25629 GI:3290004 from (Zea mays); contains Pfam profile PF00188: SCP-like extracellular protein   chr1:120154-121130 FORWARD   Aliases: F6F3.11, F6F3_11	2.7	2.6	0.1	0.8	100.0%	-5.6
9207	AT5G47380.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr5:19238699-19241698 REVERSE   Aliases: MQL5.24, MQL5_24	2.5	2.6	-0.1	-0.8	100.0%	-5.2
9208	AT1G68700.1   expressed protein   chr1:25796481-25796786 FORWARD   Aliases: F24J5.7, F24J5_7	3.3	3.5	-0.2	-0.8	100.0%	-4.5
9209	AT3G56390.1   hypothetical protein   chr3:20918333-20918676 FORWARD   Aliases: T5P19.40	2.2	2.2	0.1	0.8	100.0%	-5.7
9210	AT3G42530.1   Ulp1 protease family, similar to At5g28170, At1g35110, At1g44880, At4g19320, At5g36020, At4g03970, At3g43010, At2g10350; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr3:14646026-14650769 REVERSE   Aliases: T32A11.100	2.1	2.1	-0.1	-0.8	100.0%	-5.8
9211	AT5G61250.2   glycosyl hydrolase family 79 N-terminal domain-containing protein, similar to beta-glucuronidase GI:8918740 from (Scutellaria baicalensis)   chr5:24649210-24652505 REVERSE   Aliases: MFB13.2, MFB13_2	5.1	4.6	0.5	0.8	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9212	AT3G15990.1   Symbol: SULTR3;4   sulfate transporter, putative, similar to sulfate transporter (Arabidopsis thaliana) GI:2285885; contains Pfam profiles PF00916: Sulfate transporter family, PF01740: STAS domain   chr3:5426993-5430885 FORWARD   Aliases: MSL1.24, sulfate transporter	4.2	4.4	-0.1	-0.8	100.0%	-4.9
9213	AT3G08910.1   DNAJ heat shock protein, putative, similar to SP:P25685 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) {Homo sapiens}; contains Pfam profile PF00226: DnaJ domain   chr3:2710160-2711898 REVERSE   Aliases: T16O11.15	3.2	3.4	-0.2	-0.8	100.0%	-5.0
9214	AT5G46710.1   zinc-binding family protein, similar zinc-binding protein (Pisum sativum) GI:16117799; contains Pfam profile PF04640 : Protein of unknown function, DUF597   chr5:18969564-18971919 REVERSE   Aliases: MZA15.12, MZA15_12	4.4	4.6	-0.2	-0.8	100.0%	-4.6
9215	AT3G61430.1   Symbol: PIP1A   plasma membrane intrinsic protein 1A (PIP1A) / aquaporin PIP1.1 (PIP1.1) (AQ1), identical to plasma membrane intrinsic protein 1A SP:P43285 from (Arabidopsis thaliana)	4.6	4.4	0.3	0.8	100.0%	-4.3
9216	AT1G17390.1   expressed protein   chr1:5958694-5959512 REVERSE   Aliases: F28G4.15	2.0	2.1	-0.1	-0.8	100.0%	-5.9
9217	AT5G21040.1   F-box family protein / WD-40 repeat family protein, contains G-protein beta WD-40 repeats   chr5:7144924-7147128 REVERSE   Aliases: T10F18.1	7.4	7.1	0.3	0.8	100.0%	-4.5
9218	AT5G57690.1   diacylglycerol kinase, putative, contains INTERPRO domain, IPR001206, DAG-kinase catalytic domain   chr5:23389289-23391695 REVERSE   Aliases: MRI1.5, MRI1_5	4.1	3.9	0.2	0.8	100.0%	-4.8
9219	AT2G30070.1   Symbol: ATKT1   potassium transporter (KUP1), identical to potassium transporter (Arabidopsis thaliana) gi:2654088:gb:AAB87687; KUP/HAK/KT Transporter family member, PMID:11500563   chr2:12842132-12845675 FORWARD   Aliases: ATKT1P, ATKUP1, KUP1, POTASSIUM TRANSPORTER KUP1, T27E13.19, T27E13_19	4.3	4.7	-0.4	-0.8	100.0%	-4.3
9220	AT4G19515.1   disease resistance family protein, similar to downy mildew resistance protein RPP5 (Arabidopsis thaliana) GI:6449046; contains Pfam profile PF01582: TIR domain   chr4:10640168-10642205 REVERSE   Aliases: None	2.4	2.2	0.2	0.8	100.0%	-4.8
9221	AT1G53650.2   Symbol: CID8   similar to RNA-binding protein, putative [Arabidopsis thaliana] (TAIR:At3g14450.1); similar to putative RNA-binding protein [Oryza sativa (japonica cultivar-group)] (GB:BAD28276.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr1:20032741-20035115 REVERSE   Aliases: CID8, F22G10.7, F22G10_7	5.1	5.5	-0.4	-0.8	100.0%	-4.6
9222	AT4G00750.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr4:314353-317507 FORWARD   Aliases: F15P23.1, F15P23_1	3.0	2.9	0.1	0.8	100.0%	-5.1
9223	AT2G39950.1   expressed protein   chr2:16683620-16687567 REVERSE   Aliases: T28M21.11, T28M21_11	3.8	3.7	0.1	0.8	100.0%	-4.8
9224	AT2G35605.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr2:14953143-14954355 FORWARD   Aliases: None	7.6	8.1	-0.5	-0.8	100.0%	-4.2
9225	AT1G50920.1   GTP-binding protein-related, similar to GTP-binding protein SP:Q99ME9 from (Mus musculus)   chr1:18873807-18876598 FORWARD   Aliases: F8A12.14, F8A12_14	8.8	9.3	-0.5	-0.8	100.0%	-4.7
9226	AT5G61710.1   expressed protein   chr5:24817271-24817738 FORWARD   Aliases: MAC9.2, MAC9_2	3.0	2.8	0.1	0.8	100.0%	-4.9
9227	AT1G22770.1   Symbol: GI   gigantea protein (GI), identical to gigantea protein SP:Q95QI2 from (Arabidopsis thaliana)	7.3	7.0	0.3	0.8	100.0%	-4.9
9228	AT3G27925.1   Symbol: DEGP   DegP protease, putative, SP:022609; almost identical to DegP protease precursor GB:AF028842 from (Arabidopsis thaliana) (J. Biol. Chem. 273 (12), 7094-7098 (1998))   chr3:10367747-10370101 REVERSE   Aliases: K24A2.12	6.3	6.1	0.3	0.8	100.0%	-4.7
9229	AT3G06680.1   60S ribosomal protein L29 (RPL29B), similar to 60S ribosomal protein L29 GB:P25886 from (Rattus norvegicus)   chr3:2114408-2114885 REVERSE   Aliases: T8E24.9	8.9	9.4	-0.5	-0.8	100.0%	-4.5
9230	AT5G18880.1   expressed protein, ; expression supported by MPSS   chr5:6300537-6301424 REVERSE   Aliases: F17K4.130, F17K4_130	3.0	2.8	0.2	0.8	100.0%	-5.0
9231	AT2G42290.1   leucine-rich repeat family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr2:17623919-17626671 REVERSE   Aliases: MHK10.1, MHK10_1	3.3	3.4	-0.1	-0.8	100.0%	-5.0
9232	AT2G46580.1   pyridoxine 5'-phosphate oxidase-related, similar to pyridoxine 5'-phosphate oxidase (GI:3237304) (Rattus norvegicus); similar to pyridoxamine 5'-phosphate oxidase (GI:22294052) (Thermosynechococcus elongatus BP-1)   chr2:19136313-19137667 REVERSE   Aliases: F13A10.11	5.6	5.7	-0.1	-0.8	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9233	AT5G41790.1   Symbol: CIP1   COP1-interactive protein 1 / CIP1, almost identical to CIP1 (GI:836950) (Arabidopsis thaliana)   chr5:16745606-16750004 FORWARD   Aliases: COP1 INTERACTIVE PROTEIN 1, K16L22.7, K16L22_7	8.8	8.2	0.6	0.8	100.0%	-4.4
9234	AT1G67300.2   hexose transporter, putative, similar to hexose transporters from Solanum tuberosum (GI:8347246), Nicotiana tabacum (GI:8347244), Arabidopsis thaliana (GI:8347250); contains Pfam profile PF00083: major facilitator superfamily protein   chr1:25197367-25200594 REVERSE   Aliases: F1N21.12	6.9	6.7	0.1	0.8	100.0%	-5.0
9235	AT4G21790.1   Symbol: TOM1   transmembrane protein-related (TOM1), contains some similarity to transmembrane protein TOM3 GI:15425641 from (Arabidopsis thaliana); identical to cDNA TOM1 GI:9967414   chr4:11569793-11572561 FORWARD   Aliases: F17L22.250, F17L22_250, TOBAMOVIRUS MULTIPLICATION 1	7.5	7.3	0.2	0.8	100.0%	-4.7
9236	AT5G36190.1   expressed protein, similar to unknown protein (gb:AAD08947.1)   chr5:14260339-14260776 REVERSE   Aliases: MAB16.14, MAB16_14	2.2	2.3	-0.1	-0.8	100.0%	-5.6
9237	AT2G46740.1   FAD-binding domain-containing protein, strong similarity to At1g32300, At5g56490, At2g46750, At2g46760; contains PF01565: FAD binding domain   chr2:19212227-19214525 REVERSE   Aliases: F19D11.2	2.8	3.1	-0.3	-0.8	100.0%	-4.1
9238	AT2G19470.1   casein kinase, putative, similar to casein kinase I, delta isoform (Arabidopsis thaliana) SWISS-PROT:P42158; contains protein kinase domain, Pfam:PF00069   chr2:8440697-8443625 REVERSE   Aliases: F3P11.7, F3P11_7	5.9	6.1	-0.2	-0.8	100.0%	-4.7
9239	AT4G27690.2   similar to vacuolar protein sorting-associated protein 26, putative / VPS26, putative [Arabidopsis thaliana] (TAIR:At5g53530.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG02719.1); contains InterPro domain Vacuolar protein sorting-associated protein 26 (InterPro:IPR005377)   chr4:13823594-13826401 FORWARD   Aliases: T29A15.180, T29A15_180	6.9	6.7	0.3	0.8	100.0%	-4.7
9240	AT4G08750.1   RNA recognition motif (RRM)-containing protein, contains Pfam domain PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr4:5580233-5583141 REVERSE   Aliases: T32A17.60, T32A17_60	3.3	3.0	0.3	0.8	100.0%	-4.5
9241	AT4G08760.1   hypothetical protein   chr4:5584736-5591130 REVERSE   Aliases: T32A17.70, T32A17_70	3.3	3.0	0.3	0.8	100.0%	-4.5
9242	AT1G15290.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g28080.1); similar to tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] (TAIR:At1g01320.1); similar to putative tetratricopeptide repeat (TPR)-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477727.1); contains InterPro domain TPR repeat (InterPro:IPR001440)	4.1	3.9	0.2	0.8	100.0%	-4.9
9243	AT1G52500.2   Symbol: ATMMH 1   formamidopyrimidine-DNA glycolase family protein / mutM, putative (MMH-1), identical to mutM homologue-2 (Arabidopsis thaliana) GP:3550983 PMID:9819050; contains Pfam profile PF01149: Formamidopyrimidine-DNA glycosylase   chr1:19563652-19566782 FORWARD   Aliases: ATFPG 1, ATFPG 2, F6D8.37, F6D8_37, FORMAMIDOPYRIMIDINE DNA GLYCOSYLASE 1, FORMAMIDOPYRIMIDINE DNA GLYCOSYLASE 2, FPG1, FPG2	4.4	4.7	-0.3	-0.8	100.0%	-4.6
9244	AT3G47000.1   glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1   chr3:17324631-17327547 REVERSE   Aliases: F13I12.50	9.5	9.1	0.4	0.8	100.0%	-4.5
9245	AT2G46980.2   expressed protein   chr2:19308936-19311240 REVERSE   Aliases: F14M4.19	2.0	2.1	-0.1	-0.8	100.0%	-5.6
9246	AT5G19070.1   expressed protein   chr5:6375247-6377662 FORWARD   Aliases: T16G12.110, T16G12_110	5.9	5.3	0.6	0.8	100.0%	-4.5
9247	AT1G27960.1   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr1:9742193-9745721 REVERSE   Aliases: F13K9.7, F13K9_7	4.0	4.4	-0.4	-0.8	100.0%	-4.5
9248	AT1G18140.1   laccase family protein / diphenol oxidase family protein, similar to high-pI laccase (LAC2-1) GI:1621460 from (Liriodendron tulipifera)   chr1:6238837-6241429 REVERSE   Aliases: T10F20.14	3.0	3.1	-0.2	-0.8	100.0%	-4.9
9249	AT3G11320.1   similar to phosphate translocator-related [Arabidopsis thaliana] (TAIR:At5g05820.1); similar to Putative phosphate/phosphoenolpyruvate translocator protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470662.1)   chr3:3546652-3548862 REVERSE   Aliases: F11B9.28	4.2	4.5	-0.3	-0.8	100.0%	-4.4
9250	AT3G54350.2   Symbol: EMB1967   forkhead-associated domain-containing protein / FHA domain-containing protein, MSP58 - nucleolar protein, Mus musculus, EMBL:AF015309	6.4	6.6	-0.2	-0.8	100.0%	-4.8
9251	AT5G16620.2   Symbol: PDE120	5.3	5.6	-0.4	-0.8	100.0%	-4.3
9252	AT3G05670.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr3:1653270-1657165 FORWARD   Aliases: F18C1.6, F18C1_6	5.1	5.5	-0.4	-0.8	100.0%	-4.4
9253	AT1G18600.1   rhomboid family protein, contains Pfam profile PF01694: Rhomboid family   chr1:6400396-6402770 FORWARD   Aliases: F25I16.6, F25I16_6	7.9	8.5	-0.6	-0.8	100.0%	-4.6
9254	AT5G54150.1   expressed protein, similar to unknown protein (pir::T05871)   chr5:21993691-21995463 REVERSE   Aliases: K18G13.2, K18G13_2	2.6	2.5	0.1	0.8	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9255	AT4G31550.3   Symbol: WRKY11	4.1	3.9	0.2	0.8	100.0%	-4.3
9256	AT1G07795.1   expressed protein   chr1:2414283-2414964 FORWARD   Aliases: None	4.7	4.4	0.3	0.8	100.0%	-4.5
9257	AT3G54570.1   calmodulin-binding protein-related, contains similarity to potato calmodulin-binding protein PCBP GI:17933110 from (Solanum tuberosum)   chr3:20208927-20210180 REVERSE   Aliases: T14E10.140	3.1	3.0	0.1	0.8	100.0%	-5.3
9258	AT5G58360.1   ovate family protein, 69% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	2.4	2.3	0.1	0.8	100.0%	-5.0
9259	AT3G21840.1   Symbol: ASK7   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At7), putative, E3 ubiquitin ligase; similar to Skp1 homolog GI:3068809, UIP2 GI:3719211 from (Arabidopsis thaliana)   chr3:7695235-7695943 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 7, ASK7, MSD21.21	2.5	2.4	0.1	0.8	100.0%	-5.8
9260	AT5G15770.1   GCN5-related N-acetyltransferase (GNAT) family protein, similar to SP:O93806 Glucosamine-phosphate N-acetyltransferase (EC 2.3.1.4) (Phosphoglucosamine transacetylase) (Phosphoglucosamine acetylase) {Candida albicans}; contains Pfam profile PF00583: acetyltransferase, GNAT family	5.3	5.1	0.3	0.8	100.0%	-4.3
9261	AT5G09480.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; Common family members At5g09530, At5g09520, At1g44222 (Arabidopsis thaliana)   chr5:2950915-2951694 REVERSE   Aliases: T5E8.280, T5E8_280	2.9	3.4	-0.5	-0.8	100.0%	-4.3
9262	AT1G75520.1   lateral root primordium (LRP) protein-related, similar to lateral root primordium 1 (LRP1) (Arabidopsis thaliana) GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702)   chr1:28355440-28356840 REVERSE   Aliases: F1B16.17	2.2	2.2	0.1	0.8	100.0%	-5.5
9263	AT2G20510.1   Symbol: ATTIM44 1   mitochondrial import inner membrane translocase subunit TIM44, putative, contains similarity to Swiss-Prot:O35857 import inner membrane translocase subunit TIM44, mitochondrial precursor (Mus musculus); contains Pfam domain PF04280: Mitochondrial import inner membrane, translocase subunit TIM44   chr2:8843099-8845679 REVERSE   Aliases: T13C7.10, T13C7_10	2.2	2.3	-0.1	-0.8	100.0%	-5.5
9264	AT4G33980.1   expressed protein   chr4:16282801-16285063 REVERSE   Aliases: F17I5.170, F17I5_170	6.5	5.8	0.7	0.8	100.0%	-4.5
9265	AT3G24330.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr3:8830343-8831845 FORWARD   Aliases: K7M2.12	3.3	3.2	0.1	0.8	100.0%	-5.0
9266	AT1G23800.1   Symbol: ALDH2B7   aldehyde dehydrogenase, mitochondrial (ALDH3), nearly identical to mitochondrial aldehyde dehydrogenase ALDH3 (Arabidopsis thaliana) gi:19850249:gb:AAL99612; contains Pfam profile PF00171: aldehyde dehydrogenase (NAD) family protein   chr1:8412041-8414868 REVERSE   Aliases: ALDH2B, F5O8.35, F5O8_35	8.8	9.5	-0.7	-0.8	100.0%	-4.5
9267	AT3G02580.1   Symbol: STE1   delta 7-sterol-C5-desaturase (STE1), identical to sterol-C5-desaturase GB:AAD12944 GI:4234768 from (Arabidopsis thaliana)   chr3:546910-548800 FORWARD   Aliases: BOULE 1, BUL1, DELTA7 STEROL C 5 DESATURASE, DWARF 7, DWF7, F16B3.21, F16B3_21, STEROL 1	7.3	6.6	0.6	0.8	100.0%	-4.4
9268	AT5G01730.1   Symbol: wave3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g38440.1); similar to SCAR2 -like [Oryza sativa (japonica cultivar-group)] (GB:BAD73100.1)	3.8	3.6	0.2	0.8	100.0%	-4.7
9269	AT3G25400.1   expressed protein   chr3:9214469-9215516 FORWARD   Aliases: MWL2.8	8.6	8.4	0.3	0.8	100.0%	-4.4
9270	AT4G35060.1   heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID:9701579); similar to farnesylated proteins GMFP7 (Glycine max)(GI:4097573) and ATPF6 (GI:4097553); contains heavy-metal-associated domain PF00403   chr4:16685725-16686708 REVERSE   Aliases: T12J5.12	3.1	3.4	-0.3	-0.8	100.0%	-4.2
9271	AT3G52150.2   similar to 33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative [Arabidopsis thaliana] (TAIR:At3g52380.1); similar to putative plastid-specific ribosomal protein 2 precursor [Oryza sativa (japonica cultivar-group)] (GB:XP_450482.1); contains InterPro domain Paraneoplastic encephalomyelitis antigen (InterPro:IPR002343); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)	6.7	7.3	-0.6	-0.8	100.0%	-4.1
9272	AT1G19060.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr1:6582057-6583592 REVERSE   Aliases: F14D16.21, F14D16_21	2.8	2.7	0.1	0.8	100.0%	-5.0
9273	AT2G27040.1   Symbol: AGO4   PAZ domain-containing protein / piwi domain-containing protein, similar to SP:Q9QZ81 Eukaryotic translation initiation factor 2C 2 {Rattus norvegicus}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain	6.3	6.7	-0.4	-0.8	100.0%	-4.5
9274	AT4G39730.1   lipid-associated family protein, contains PLAT/LH2 (Polycystin-1, Lipoxygenase, Alpha-Toxin/Lipoxygenase homology) domain Pfam:PF01477   chr4:18432893-18433689 FORWARD   Aliases: T19P19.120, T19P19_120	9.3	9.7	-0.4	-0.8	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9275	AT5G40910.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. Non-consensus TT donor splice site at exon 1   chr5:16412735-16416357 FORWARD   Aliases: MHK7.14, MHK7_14	4.1	4.6	-0.5	-0.8	100.0%	-4.6
9276	AT5G24110.1   Symbol: WRKY30	2.8	2.9	-0.1	-0.8	100.0%	-5.6
9277	AT5G08170.1   Symbol: EMB1873   porphyromonas-type peptidyl-arginine deiminase family protein, contains Pfam PF04371: Porphyromonas-type peptidyl-arginine deiminase   chr5:2628326-2631084 REVERSE   Aliases: EMB1873, EMBRYO DEFECTIVE 1873, T22D6.110, T22D6_110	6.5	6.0	0.5	0.8	100.0%	-4.4
9278	AT5G03880.1   expressed protein   chr5:1038507-1041479 REVERSE   Aliases: MED24.18, MED24_18	8.5	8.1	0.3	0.8	100.0%	-4.4
9279	AT1G65310.1   Symbol: ATXTH17   putative xyloglucan endotransglycosylase/hydrolase, expressed in the mature or basal regions of both the main and lateral roots, but not in the tip of these roots where cell division occurs.   chr1:24260925-24262136 FORWARD   Aliases: ATXTH17, T8F5.9, T8F5_9, XYLOGLUCAN ENDOTRANGLUCOSYLASE/HYDROLASE 17	2.8	2.5	0.3	0.8	100.0%	-4.2
9280	AT1G80590.1   Symbol: WRKY66	2.6	2.7	-0.1	-0.8	100.0%	-5.3
9281	AT5G03310.1   auxin-responsive family protein, similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) (Vigna radiata)   chr5:799301-799645 REVERSE   Aliases: F12E4.40, F12E4_40	2.2	2.3	-0.1	-0.8	100.0%	-5.7
9282	AT5G44120.3   Symbol: CRA1   12S seed storage protein (CRA1), nearly identical to SP:P15455 (Plant Mol Biol 11:805-820 (1988)); contains Pfam profile PF00190 Cupin and Prosite 11-S plant seed storage proteins signature PS00305   chr5:17773491-17775502 REVERSE   Aliases: 12S STORAGE PROTEIN, ATCRA1, CRU1, CRUCIFERINA, MLN1.4, MLN1_4	2.4	2.3	0.1	0.8	100.0%	-5.4
9283	AT4G16760.1   Symbol: ACX1   acyl-CoA oxidase (ACX1), identical to acyl-CoA oxidase (Arabidopsis thaliana) GI:3044214	7.8	8.3	-0.5	-0.8	100.0%	-4.4
9284	AT1G05460.1   Symbol: SDE3   RNA helicase SDE3 (SDE3), identical to RNA helicase SDE3 (Arabidopsis thaliana) GI:13811296   chr1:1601031-1605026 REVERSE   Aliases: SILENCING DEFECTIVE, T25N20.11, T25N20_11	6.3	6.9	-0.7	-0.8	100.0%	-4.7
9285	AT5G55100.2   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein, contains Pfam domain PF01805: Surp module   chr5:22378385-22381985 REVERSE   Aliases: MCO15.5, MCO15_5	6.6	6.2	0.4	0.8	100.0%	-4.6
9286	AT1G17060.1   Symbol: CYP72C1   cytochrome P450, putative, 41% identical to Cytochrome P450 (Catharanthus roseus) (gi:404690)	3.0	3.1	-0.1	-0.8	100.0%	-4.9
9287	AT5G14790.1   expressed protein   chr5:4782949-4785808 FORWARD   Aliases: T9L3.90, T9L3_90	4.1	4.4	-0.2	-0.8	100.0%	-5.1
9288	AT3G25805.1   expressed protein   chr3:9427513-9429426 REVERSE   Aliases: None	4.5	4.3	0.2	0.8	100.0%	-4.5
9289	AT1G32080.1   membrane protein, putative, contains 12 transmembrane domains; similar to yohK (GI:405873) (Escherichia coli)   chr1:11537328-11539780 REVERSE   Aliases: F3C3.12	3.3	3.1	0.2	0.8	100.0%	-4.8
9290	AT5G18630.3   lipase class 3 family protein, low similarity to Triacylglycerol Acylhydrolase (E.C.3.1.1.3) (Rhizomucor miehei) GI:230348; contains Pfam profile PF01764: Lipase   chr5:6202635-6205108 FORWARD   Aliases: T1A4.10, T1A4_10	5.0	4.7	0.3	0.8	100.0%	-4.4
9291	AT1G10030.1   integral membrane family protein, contains Pfam PF03694: Erg28 like protein   chr1:3273863-3275839 FORWARD   Aliases: T27I1.5, T27I1_5	8.1	7.8	0.3	0.8	100.0%	-4.6
9292	AT4G34670.1   40S ribosomal protein S3A (RPS3aB)   chr4:16548651-16550453 FORWARD   Aliases: T4L20.250, T4L20_250	11.3	11.5	-0.2	-0.8	100.0%	-5.0
9293	AT1G56260.1   expressed protein   chr1:21067944-21069242 REVERSE   Aliases: F14G9.13, F14G9_13	4.2	4.4	-0.2	-0.8	100.0%	-4.6
9294	AT4G18640.1   leucine-rich repeat transmembrane protein kinase, putative   chr4:10259695-10263775 FORWARD   Aliases: F28A21.50, F28A21_50	3.8	4.1	-0.3	-0.8	100.0%	-4.4
9295	AT2G40250.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	2.8	2.6	0.1	0.8	100.0%	-5.0
9296	AT3G47950.1   Symbol: AHA4   ATPase, plasma membrane-type, putative / proton pump, putative, strong similarity to P-type H(+)-transporting ATPase from Nicotiana glauca (SP:Q08435, SP:Q08436), Lycopersicon esculentum (GI:5901757, SP:P22180), Solanum tuberosum (GI:435003); contains InterPro accession IPR001757: ATPase, E1-E2 type   chr3:17703687-17709837 FORWARD   Aliases: T17F15.180	3.8	4.0	-0.2	-0.8	100.0%	-4.9
9297	AT5G11240.1   transducin family protein / WD-40 repeat family protein, contains 3 WD-40 repeats (PF00400); similar to uncharacterized protein KIAA0007 (GI:1663708) {Homo sapiens} 1.2e-11   chr5:3582564-3586987 FORWARD   Aliases: F2I11.130, F2I11_130	4.0	4.2	-0.2	-0.8	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9298	AT5G43980.1   receptor-like protein kinase-related, similar to receptor-like protein kinase homolog RK20-1 (GI:4530126) (Phaseolus vulgaris); contains Pfam PF01657: Domain of unknown function   chr5:17711907-17713849 REVERSE   Aliases: MRH10.9, MRH10_9	5.7	5.4	0.3	0.8	100.0%	-4.4
9299	AT4G29370.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:14455608-14456744 FORWARD   Aliases: F17A13.190, F17A13_190	3.9	3.6	0.3	0.8	100.0%	-4.6
9300	AT2G45010.2   expressed protein, weak similarity to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr2:18574998-18576932 FORWARD   Aliases: T14P1.19	7.0	7.2	-0.2	-0.8	100.0%	-4.7
9301	AT5G11340.1   GCN5-related N-acetyltransferase (GNAT) family protein, low similarity to SP:Q03503 L-A virus GAG protein N-acetyltransferase (EC 2.3.1.-) {Saccharomyces cerevisiae}; contains Pfam profile PF00583: acetyltransferase, GNAT family   chr5:3619156-3621232 FORWARD   Aliases: F2I11.230, F2I11_230	9.6	9.8	-0.3	-0.8	100.0%	-4.5
9302	AT1G43770.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr1:16550949-16552991 FORWARD   Aliases: F28H19.3, F28H19_3	4.5	4.3	0.2	0.8	100.0%	-4.6
9303	AT3G42500.1   expressed protein, includes At2g10370, At5g36050, At1g35090, At1g44860, At4g19300, At1g42400, At3g43040, At3g42500   chr3:14642275-14642911 REVERSE   Aliases: T32A11.70	2.4	2.5	-0.1	-0.8	100.0%	-5.7
9304	AT3G53990.2   universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family   chr3:20000315-20002084 REVERSE   Aliases: F5K20.290, F5K20_290	6.5	6.0	0.5	0.8	100.0%	-4.6
9305	AT1G26540.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr1:9167576-9170921 REVERSE   Aliases: T1K7.9, T1K7_9	3.2	3.3	-0.2	-0.8	100.0%	-5.0
9306	AT1G51540.1   kelch repeat-containing protein, contains Pfam profile PF01344: Kelch motif   chr1:19117052-19121734 FORWARD   Aliases: F5D21.24, F5D21_24	6.4	6.6	-0.2	-0.8	100.0%	-4.8
9307	AT4G32640.1   sec23/sec24 transport protein-related   chr4:15742076-15750550 FORWARD   Aliases: F4D11.160, F4D11_160	4.5	4.8	-0.3	-0.8	100.0%	-4.5
9308	AT2G21150.1   XAP5 family protein, contains Pfam profile: PF04921 XAP5 protein	6.6	6.8	-0.2	-0.8	100.0%	-4.7
9309	AT3G27330.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles: PF00097 zinc finger, C3HC4 type (RING finger), PF01697 Domain of unknown function   chr3:10118187-10121882 REVERSE   Aliases: K1G2.5	6.7	6.4	0.3	0.8	100.0%	-4.3
9310	AT4G03820.2   expressed protein   chr4:1771885-1774420 REVERSE   Aliases: T7M24.8, T7M24_8	2.9	3.0	-0.1	-0.8	100.0%	-5.2
9311	AT2G21050.1   amino acid permease, putative, similar to AUX1 (Arabidopsis thaliana) GI:1531758; contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr2:9041171-9043717 FORWARD   Aliases: F26H11.19, F26H11_19	2.5	2.6	-0.1	-0.8	100.0%	-4.9
9312	AT2G02820.2   Symbol: MYB88   similar to myb family transcription factor (MYB115) [Arabidopsis thaliana] (TAIR:At5g40360.1); similar to putative Myb-like DNA-binding protein [Solanum demissum] (GB:AAT40484.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)   chr2:804687-807138 REVERSE   Aliases: MYB88, T20F6.4, T20F6_4	2.8	2.9	-0.1	-0.8	100.0%	-5.4
9313	AT5G66815.1   expressed protein   chr5:26694591-26695091 FORWARD   Aliases: None	2.6	2.9	-0.3	-0.8	100.0%	-4.4
9314	AT1G33860.1   expressed protein   chr1:12294374-12295285 FORWARD   Aliases: T3M13.25	5.0	4.7	0.3	0.8	100.0%	-4.2
9315	AT4G39410.1   Symbol: WRKY13	3.6	3.4	0.2	0.8	100.0%	-5.1
9316	AT1G65120.2   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr1:24195011-24199736 REVERSE   Aliases: T23K8.3, T23K8_3	2.7	2.8	-0.1	-0.8	100.0%	-5.4
9317	AT5G05260.1   Symbol: CYP79A2   cytochrome P450 79A2 (CYP79A2), identical to SP:Q9FLC8 Cytochrome P450 79A2 (EC 1.-.-.-) {Arabidopsis thaliana}   chr5:1559779-1561766 REVERSE   Aliases: CYTOCHROME P450 79A2, K18I23.6, K18I23_6	2.5	2.4	0.2	0.8	100.0%	-5.1
9318	AT5G49550.1   expressed protein   chr5:20123879-20124417 REVERSE   Aliases: K6M13.19	7.7	7.5	0.2	0.8	100.0%	-4.7
9319	AT4G38000.1   Dof-type zinc finger domain-containing protein, Zn finger protein BBF2aO -Nicotiana tabacum,PID:e246547   chr4:17858354-17859316 FORWARD   Aliases: F20D10.120, F20D10_120	3.3	3.2	0.1	0.8	100.0%	-4.9
9320	AT5G24000.1   expressed protein, contains Pfam profile PF05684: Protein of unknown function (DUF819)   chr5:8110316-8112695 REVERSE   Aliases: MZF18.12, MZF18_12	4.0	4.2	-0.2	-0.8	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9321	AT5G13510.1   ribosomal protein L10 family protein, ribosomal protein L10- Nicotiana tabacum, EMBL:AB010879   chr5:4341267-4342098 FORWARD   Aliases: T6I14.40, T6I14_40	7.9	8.3	-0.4	-0.8	100.0%	-4.3
9322	AT1G55890.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:20905011-20906465 FORWARD   Aliases: F14J16.14, F14J16_14	7.9	8.3	-0.4	-0.8	100.0%	-4.6
9323	AT5G37690.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana)   chr5:14990583-14993399 REVERSE   Aliases: AT5G37700, K12B20.140, K12B20_140	4.0	4.4	-0.3	-0.8	100.0%	-4.1
9324	AT3G17140.1   invertase inhibitor-related, weak similarity to tomato invertase inhibitor (Lycopersicon esculentum) GI:3582002   chr3:5846008-5846595 REVERSE   Aliases: K14A17.21	3.5	3.4	0.2	0.8	100.0%	-4.8
9325	AT3G61800.1   expressed protein   chr3:22885530-22887821 REVERSE   Aliases: F21F14.3	5.0	5.2	-0.2	-0.8	100.0%	-4.7
9326	AT4G32400.1   mitochondrial substrate carrier family protein   chr4:15638631-15640471 FORWARD   Aliases: F8B4.100, F8B4_100	7.6	7.1	0.5	0.8	100.0%	-4.4
9327	AT1G23390.1   kelch repeat-containing F-box family protein, similar to hypothetical protein GB:AAF27090 GI:6730669 from (Arabidopsis thaliana); contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:8309101-8310638 REVERSE   Aliases: F26F24.26, F26F24_26	6.8	7.0	-0.2	-0.8	100.0%	-4.8
9328	AT1G06700.2   similar to serine/threonine protein kinase, putative [Arabidopsis thaliana] (TAIR:At2g30740.1); similar to putative protein kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_470385.1); contains InterPro domain Tyrosine protein kinase, active site (InterPro:IPR008266); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:2052480-2055547 REVERSE   Aliases: F4H5.21, F4H5_21	8.4	8.0	0.4	0.8	100.0%	-4.6
9329	AT3G13310.1   DNAJ heat shock N-terminal domain-containing protein, similar to J11 protein (Arabidopsis thaliana) GI:9843641; contains Pfam profile: PF00226 DnaJ domain   chr3:4310615-4311448 REVERSE   Aliases: MDC11.6	6.7	5.8	0.9	0.8	100.0%	-4.1
9330	AT5G46360.1   Symbol: KCO3   outward rectifying potassium channel, putative (KCO3), identical to KCO3 protein (Arabidopsis thaliana) gi:4583550:emb:CAB40380; similar to kco1 (Arabidopsis thaliana) gi:2230761:emb:CAA69158; member of the 2 pore, 4 transmembrane (2P/4TM) K+ channel family, PMID:11500563	4.1	4.3	-0.2	-0.8	100.0%	-5.0
9331	AT1G68080.1   similar to leprecan [Ciona intestinalis] (GB:BAB00631.1); contains InterPro domain Prolyl 4-hydroxylase, alpha subunit (InterPro:IPR006620)   chr1:25521116-25522970 FORWARD   Aliases: T23K23.7, T23K23_7	4.8	4.7	0.2	0.8	100.0%	-4.7
9332	AT5G01190.1   similar to laccase, putative / diphenol oxidase, putative [Arabidopsis thaliana] (TAIR:At5g60020.1); similar to laccase, putative / diphenol oxidase, putative [Arabidopsis thaliana] (TAIR:At5g58910.1); similar to laccase, putative / diphenol oxidase, putative [Arabidopsis thaliana] (TAIR:At5g03260.1); similar to laccase, putative / diphenol oxidase, putative [Arabidopsis thaliana] (TAIR:At2g38080.1); similar to laccase [Pinus taeda] (GB:AAK37829.1); similar to laccase [Pinus taeda] (GB:AAK37830.1); similar to laccase [Populus trichocarpa] (GB:CAA74103.1); similar to laccase (EC 1.10.3.2) precursor - common tobacco [Oryza sativa (japonica cultivar-group)] (GB:AAX95423.1); similar to laccase [Populus trichocarpa] (GB:CAC14719.1); contains InterPro domain Multicopper oxidase, type 1 (InterPro:IPR001117); contains InterPro domain Multicopper oxidase, copper-binding site (InterPro:IPR002355)   chr5:72391-74755 FORWARD   Aliases: F7J8.170, F7J8_170	2.9	3.0	-0.2	-0.8	100.0%	-4.7
9333	AT2G48030.1   endonuclease/exonuclease/phosphatase family protein, contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr2:19654597-19657218 REVERSE   Aliases: T9J23.18	4.6	4.4	0.2	0.8	100.0%	-4.5
9334	AT1G20720.1   helicase-related, similar to BRCA1-binding helicase-like protein BACH1 (GI:13661819) Homo sapiens.;   chr1:7185648-7192784 REVERSE   Aliases: F2D10.21, F2D10_21	2.9	3.1	-0.2	-0.8	100.0%	-4.8
9335	AT5G58860.1   Symbol: CYP86A1   cytochrome P450 86A1 (CYP86) (CYP86A1) / CYPLXXXVI / P450-dependent fatty acid omega-hydroxylase, identical to Cytochrome P450 86A1 (CYPLXXXVI) (P450-dependent fatty acid omega-hydroxylase) (SP:P48422) (Arabidopsis thaliana)   chr5:23783040-23785275 REVERSE   Aliases: CYP86, K19M22.14, K19M22_14	2.5	2.9	-0.3	-0.8	100.0%	-4.2
9336	AT5G08210.1   expressed protein   chr5:2641265-2641761 REVERSE   Aliases: F8L15.6	4.1	3.8	0.2	0.8	100.0%	-4.8
9337	AT1G62180.1   Symbol: APR2   5'-adenylylsulfate reductase 2, chloroplast (APR2) (APSR) / adenosine 5'-phosphosulfate 5'-adenylylsulfate (APS) sulfotransferase 2 / 3'-phosphoadenosine-5'-phosphosulfate (PAPS) reductase homolog 43 (PRH-43), identical to SP:P92981 5'-adenylylsulfate reductase 2, chloroplast precursor (EC 1.8.4.9) (Adenosine 5'-phosphosulfate 5'-adenylylsulfate sulfotransferase 2) (APS sulfotransferase 2) (Thioredoxin independent APS reductase 2) (3'-phosphoadenosine-5'-phosphosulfate reductase homolog 43) (PAPS reductase homolog 43) (Prh-43) {Arabidopsis thaliana}; identical to cDNA PAPS reductase homolog (PRH43) GI:1710115	9.7	10.0	-0.3	-0.7	100.0%	-4.5
9338	AT5G38310.1   expressed protein   chr5:15327911-15328477 REVERSE   Aliases: MSI17.4, MSI17_4	3.2	3.4	-0.2	-0.7	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9339	AT2G33230.1   flavin-containing monooxygenase, putative / FMO, putative, similar to flavin-containing monooxygenase YUCCA3 (Arabidopsis thaliana) GI:16555356   chr2:14087488-14089048 REVERSE   Aliases: F25I18.3, F25I18_3	3.7	3.9	-0.2	-0.7	100.0%	-4.9
9340	AT1G80570.3   F-box family protein (FBL14), contains similarity to F-box protein FBL2 GI:6063090 from (Homo sapiens)   chr1:30295255-30297310 FORWARD   Aliases: T21F11.10, T21F11_10	3.9	3.6	0.3	0.7	100.0%	-4.2
9341	AT1G75980.1   expressed protein   chr1:28526215-28527963 REVERSE   Aliases: T4O12.20, T4O12_20	6.0	6.3	-0.3	-0.7	100.0%	-4.6
9342	AT1G66570.3   similar to sucrose transporter, putative / sucrose-proton symporter, putative [Arabidopsis thaliana] (TAIR:At2g14670.1); similar to sucrose transporter-related / sucrose-proton symporter-related [Arabidopsis thaliana] (TAIR:At5g43610.1); similar to sucrose transporter / sucrose-proton symporter (SUC1) [Arabidopsis thaliana] (TAIR:At1g71880.1); similar to sucrose transporter, putative / sucrose-proton symporter, putative [Arabidopsis thaliana] (TAIR:At5g06170.1); similar to sucrose transporter / sucrose-proton symporter (SUC5) [Arabidopsis thaliana] (TAIR:At1g71890.1); similar to sucrose transporter SUC2 [Brassica oleracea] (GB:AAL58072.1); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sucrose/H+ symporter (InterPro:IPR005989)   chr1:24838972-24840984 REVERSE   Aliases: T12I7.2, T12I7_2	2.5	2.6	-0.1	-0.7	100.0%	-5.6
9343	AT5G58340.1   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At1g15720.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_479635.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)	2.8	3.0	-0.2	-0.7	100.0%	-4.9
9344	AT3G17040.1   Symbol: HCF107	5.3	5.1	0.2	0.7	100.0%	-4.4
9345	AT2G23200.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:9886356-9888988 FORWARD   Aliases: T20D16.17, T20D16_17	3.8	3.6	0.2	0.7	100.0%	-4.7
9346	AT2G39580.1   expressed protein   chr2:16517503-16524151 FORWARD   Aliases: F12L6.24, F12L6_24	3.7	3.4	0.4	0.7	100.0%	-4.7
9347	AT3G06090.1   hypothetical protein   chr3:1840779-1841018 FORWARD   Aliases: F28L1.2, F28L1_2	3.4	3.3	0.1	0.7	100.0%	-5.1
9348	AT2G25840.3   tRNA synthetase class I (W and Y) family protein, contains Pfam profile: PF00579 tRNA synthetases class I (W and Y)   chr2:11028983-11032448 FORWARD   Aliases: F17H15.13, F17H15_13	5.3	5.6	-0.3	-0.7	100.0%	-4.3
9349	AT3G43250.1   cell cycle control protein-related, contains similarity to Swiss-Prot:Q9P7C5 cell cycle control protein cwf16 (Schizosaccharomyces pombe)   chr3:15227701-15228450 FORWARD   Aliases: F7K15.100	2.4	2.3	0.1	0.7	100.0%	-5.7
9350	AT2G39290.1   Symbol: PGP   phosphatidylglycerolphosphate synthase (PGS1), identical to phosphatidylglycerolphosphate synthase GI:13365519 from (Arabidopsis thaliana)   chr2:16414333-16416201 FORWARD   Aliases: PGP1, PGS1, PHOSPHATIDYLGLYCEROLPHOSPHATE SYNTHASE, PHOSPHATIDYLGLYCEROLPHOSPHATE SYNTHASE 1, T16B24.7, T16B24_7	6.4	6.2	0.2	0.7	100.0%	-4.8
9351	AT3G26540.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr3:9745779-9747881 REVERSE   Aliases: MFE16.1	2.6	2.5	0.1	0.7	100.0%	-5.5
9352	AT1G62430.1   Symbol: ATCDS1	4.8	4.3	0.5	0.7	100.0%	-4.7
9353	AT1G07700.3   thioredoxin family protein, low similarity to thioredoxin (Gallus gallus) GI:212766; contains Pfam profile: PF00085 Thioredoxin   chr1:2379644-2381357 FORWARD   Aliases: F24B9.21, F24B9_21	10.5	10.1	0.4	0.7	100.0%	-4.3
9354	AT3G44530.1   transducin family protein / WD-40 repeat family protein, contains 6 (4 significant) WD-40 repeats (PF0400); nuclear protein HIRA, mouse, PIR:S68141   chr3:16127013-16132471 FORWARD   Aliases: F14L2.80	3.2	3.4	-0.2	-0.7	100.0%	-4.7
9355	AT5G19760.1   dicarboxylate/tricarboxylate carrier (DTC), identical to dicarboxylate/tricarboxylate carrier (Arabidopsis thaliana) GI:19913113	11.1	11.5	-0.4	-0.7	100.0%	-4.8
9356	AT5G39510.1   Symbol: VTI11   vesicle transport v-SNARE 11 (VTI11) / vesicle soluble NSF attachment protein receptor VTI1a (VTI1A), identical to SP:Q9SEL6 Vesicle transport v-SNARE 11 (AtVTI11) (Vesicle transport v-SNARE protein VTI1a) (Vesicle soluble NSF attachment protein receptor VTI1a) (AtVTI1a) {Arabidopsis thaliana}   chr5:15838671-15840992 FORWARD   Aliases: ATVTI11, ATVTI1A, MUL8.190, MUL8_190, SGR4, VTI1A, ZIG	9.5	9.1	0.4	0.7	100.0%	-4.9
9357	AT1G06670.1   Symbol: NIH   DEIH-box RNA/DNA helicase, identical to DEIH-box RNA/DNA helicase GB:BAA84364 GI:5881579 (Arabidopsis thaliana)   chr1:2040432-2047611 FORWARD   Aliases: DEIH BOX RNA/DNA HELICASE, F12K11.4, F12K11_4, NUCLEAR DEIH BOXHELICASE	7.6	8.4	-0.8	-0.7	100.0%	-4.3
9358	AT2G29210.1   splicing factor PWI domain-containing protein, contains Pfam profile PF01480: PWI domain	8.5	9.4	-0.8	-0.7	100.0%	-4.4
9359	AT5G12050.1   expressed protein   chr5:3890105-3891514 FORWARD   Aliases: F14F18.220, F14F18_220	2.3	2.4	-0.1	-0.7	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9360	AT2G25310.1   expressed protein   chr2:10784187-10786289 REVERSE   Aliases: T22F11.10, T22F11_10	7.1	6.8	0.3	0.7	100.0%	-4.4
9361	AT1G07610.1   Symbol: MT1C   metallothionein-like protein 1C (MT-1C), identical to Metallothionein-like protein 1C (MT-1C). (SP:Q38804) (Arabidopsis thaliana)   chr1:2341539-2342120 FORWARD   Aliases: F22G5.40	11.2	11.4	-0.2	-0.7	100.0%	-5.3
9362	AT5G67360.1   Symbol: ARA12   cucumisin-like serine protease (ARA12), Asp48; almost identical to cucumisin-like serine protease (ARA12) GI:3176874 from (Arabidopsis thaliana)   chr5:26889117-26891805 REVERSE   Aliases: K8K14.8, K8K14_8	4.2	4.8	-0.6	-0.7	100.0%	-4.5
9363	AT2G02720.1   pectate lyase family protein, similar to pectate lyase P59 SP:P15722 from (Lycopersicon esculentum)   chr2:763010-765026 FORWARD   Aliases: T20F6.14, T20F6_14	2.4	2.4	-0.1	-0.7	100.0%	-5.6
9364	AT1G26650.1   expressed protein   chr1:9210076-9211547 FORWARD   Aliases: T24P13.3, T24P13_3	5.4	5.7	-0.2	-0.7	100.0%	-4.7
9365	AT4G21700.1   expressed protein   chr4:11529968-11532856 FORWARD   Aliases: F17L22.160, F17L22_160	4.3	4.2	0.1	0.7	100.0%	-5.1
9366	AT5G18120.1   Symbol: ATAPRL7   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily. This protein also belongs to the adenosine 5'-phosphosulfate reductase-like (APRL) group.   chr5:5990958-5993938 FORWARD   Aliases: APR LIKE 7, ATAPRL7, MRG7.8, MRG7_8	6.9	6.4	0.5	0.7	100.0%	-4.4
9367	AT1G23260.1   ubiquitin-conjugating enzyme family protein, similar to TRAF6-regulated IKK activator 1 beta Uev1A (Homo sapiens) GI:10880969; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr1:8257017-8258676 REVERSE   Aliases: F26F24.10, F26F24_10	7.9	8.2	-0.3	-0.7	100.0%	-4.5
9368	AT2G26170.2   Symbol: CYP711A1   thromboxane-A synthase, putative / cytochrome P450 family protein, similar to Thromboxane-A synthase (TXA synthase) (TXS) (SP:P47787) (Sus scrofa); contains Pfam profile: PF00067: Cytochrome P450; supported by cDNA: gi_15810029_gb_AY054283.1_   chr2:11147899-11150761 FORWARD   Aliases: MAX1, MORE AXILLARY BRANCHES, MORE AXILLARY BRANCHES 1, T1D16.19, T1D16_19	9.6	9.4	0.3	0.7	100.0%	-4.7
9369	AT1G79750.1   malate oxidoreductase, putative, similar to malate oxidoreductase (NADP-dependent malic enzyme) GB:P34105 (Populus balsamifera subsp. trichocarpa)   chr1:30012219-30016279 REVERSE   Aliases: F19K16.27, F19K16_27	8.9	8.5	0.4	0.7	100.0%	-4.6
9370	AT1G65810.1   tRNA-splicing endonuclease positive effector-related, contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease (Saccharomyces cerevisiae) gi:172574:gb:AAB63976   chr1:24480706-24484391 REVERSE   Aliases: F1E22.16, F1E22_16	2.9	2.8	0.2	0.7	100.0%	-5.1
9371	AT5G40645.1   nitrate-responsive NOI protein, putative, similar to nitrate-induced NOI protein (Zea mays) GI:2642213   chr5:16297511-16298200 REVERSE   Aliases: None	3.0	2.9	0.1	0.7	100.0%	-5.3
9372	AT5G61310.3   similar to cytochrome c oxidase subunit Vc family protein / COX5C family protein [Arabidopsis thaliana] (TAIR:At2g47380.1); similar to cytochrome c oxidase subunit 5c [Helianthus annuus] (GB:AAL67939.1); contains InterPro domain Cytochrome c oxidase subunit Vc (InterPro:IPR008432)   chr5:24670635-24672079 REVERSE   Aliases: MFB13.16, MFB13_16	8.7	9.0	-0.3	-0.7	100.0%	-4.4
9373	AT4G37660.1   ribosomal protein L12 family protein, ribosomal protein L12, Liberobacter africanum, U09675   chr4:17695490-17696264 FORWARD   Aliases: F19F18.150, F19F18_150	4.8	5.2	-0.5	-0.7	100.0%	-4.0
9374	AT5G63680.1   pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Glycine max) SWISS-PROT:Q42806	6.2	6.9	-0.7	-0.7	100.0%	-4.6
9375	AT4G22790.1   MATE efflux family protein, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr4:11975042-11976759 REVERSE   Aliases: T12H17.180, T12H17_180	4.8	5.1	-0.3	-0.7	100.0%	-4.4
9376	AT5G44170.1   expressed protein, low similarity to SP:P40389 Rapid response to glucose protein 1 {Schizosaccharomyces pombe}   chr5:17797605-17798510 FORWARD   Aliases: MLN1.9, MLN1_9	4.1	4.0	0.1	0.7	100.0%	-5.4
9377	AT5G35520.1   kinetochore protein-related, contains Pfam PF05859: Mis12 protein   chr5:13718626-13720719 FORWARD   Aliases: MOK9.12, MOK9_12	4.0	4.2	-0.1	-0.7	100.0%	-4.9
9378	AT2G24530.1   expressed protein, ; expression supported by MPSS   chr2:10430142-10430900 FORWARD   Aliases: F25P17.17, F25P17_17	3.8	3.6	0.2	0.7	100.0%	-4.8
9379	AT1G68530.2   Symbol: CUT1   very-long-chain fatty acid condensing enzyme (CUT1), identical to very-long-chain fatty acid condensing enzyme (CUT1) GB:AF129511 (required for cuticular wax biosynthesis and pollen fertility: Millar,A.A., et al., Plant Cell (1999))	2.3	2.2	0.1	0.7	100.0%	-5.7
9380	AT5G44140.1   prohibitin, putative, similar to SP:P24142 Prohibitin (B-cell receptor associated protein 32) (BAP 32) {Rattus norvegicus}; contains Pfam profile PF01145: SPFH domain / Band 7 family; non-consensus TT acceptor splice site at exon 2   chr5:17779718-17780856 FORWARD   Aliases: MLN1.6, MLN1_6	2.4	2.5	-0.1	-0.7	100.0%	-5.4
9381	AT4G01960.1   expressed protein   chr4:851210-853078 REVERSE   Aliases: T7B11.22, T7B11_22	7.4	7.1	0.3	0.7	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9382	AT2G44270.1   expressed protein, contains Pfam profile PF01171: PP-loop family   chr2:18305154-18307229 REVERSE   Aliases: F4I1.8	6.1	5.9	0.2	0.7	100.0%	-4.8
9383	AT2G45870.1   expressed protein, contains Pfam profile PF05249: Uncharacterised protein family (UPF0187)   chr2:18882968-18884551 FORWARD   Aliases: F4I18.15	2.7	2.9	-0.2	-0.7	100.0%	-4.9
9384	AT4G32700.1   DNA-directed DNA polymerase family protein, similar to DNA helicase HEL308 (Homo sapiens) GI:19110782; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00476: DNA polymerase family A   chr4:15770583-15779051 FORWARD   Aliases: F4D11.100, F4D11_100	2.7	2.8	-0.1	-0.7	100.0%	-5.2
9385	AT1G04910.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator protein' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr1:1387878-1391177 REVERSE   Aliases: F13M7.10, F13M7_10	5.8	6.1	-0.3	-0.7	100.0%	-4.5
9386	AT3G01740.1   expressed protein   chr3:267836-268845 FORWARD   Aliases: F4P13.29	10.8	10.6	0.2	0.7	100.0%	-4.8
9387	AT4G29250.1   transferase family protein, low similarity to CER2 Arabidopsis thaliana GI:1213594, anthocyanin 5-aromatic acyltransferase Gentiana triflora GI:4185599; contains Pfam profile PF02458 transferase family   chr4:14420695-14422287 FORWARD   Aliases: F17A13.70, F17A13_70	3.7	3.5	0.2	0.7	100.0%	-4.8
9388	AT3G18400.1   Symbol: ANAC058   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to GP:1279640 NAM {Petunia x hybrida}   chr3:6318751-6320599 REVERSE   Aliases: ANAC058, MYF24.12	2.6	2.9	-0.3	-0.7	100.0%	-4.4
9389	AT3G09160.1   RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain)   chr3:2805784-2806917 REVERSE   Aliases: F3L24.2	3.0	2.9	0.1	0.7	100.0%	-5.4
9390	AT5G40660.1   ATP12 protein-related, weak similarity to SP:P22135 ATP12 protein, mitochondrial precursor {Saccharomyces cerevisiae}   chr5:16300739-16302554 REVERSE   Aliases: MNF13.22, MNF13_22	7.9	8.3	-0.4	-0.7	100.0%	-4.3
9391	AT5G23260.2   Symbol: TT16   MADS-box protein, putative   chr5:7836099-7838508 FORWARD   Aliases: ABS, ARABIDOPSIS BSISTER, MKD15.12, MKD15_12, TRANSPARENT TESTA16	2.1	2.2	-0.1	-0.7	100.0%	-5.4
9392	AT2G26770.2   plectin-related, contains weak similarity to Swiss-Prot:Q9JI55 plectin 1 (PLTN, PCN, 300-kDa intermediate filament-associated protein, IFAP300)(Cricetulus griseus)   chr2:11411144-11415385 REVERSE   Aliases: F18A8.14, F18A8_14	4.3	4.4	-0.1	-0.7	100.0%	-5.0
9393	AT1G03020.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.7	2.8	-0.1	-0.7	100.0%	-5.1
9394	AT4G31180.2   aspartyl-tRNA synthetase, putative / aspartate--tRNA ligase, putative, similar to Aspartyl-tRNA synthetase (Aspartate--tRNA ligase) (AspRS) (Homo sapiens) GI:20178330   chr4:15155916-15159568 FORWARD   Aliases: F6E21.100, F6E21_100	9.8	10.0	-0.2	-0.7	100.0%	-4.8
9395	AT2G47880.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.7	2.8	-0.1	-0.7	100.0%	-4.9
9396	AT4G10200.1   hAT dimerisation domain-containing protein / transposase-related, low similarity to transposase (Ipomoea purpurea) AB004906 GI:4063770   chr4:6353168-6355587 FORWARD   Aliases: T9A4.11	2.3	2.4	-0.1	-0.7	100.0%	-5.8
9397	AT3G05810.1   expressed protein   chr3:1730982-1732390 REVERSE   Aliases: F10A16.10, F10A16_10	7.6	7.9	-0.4	-0.7	100.0%	-4.1
9398	AT3G12570.4   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g37570.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_550166.1)   chr3:3988721-3991086 FORWARD   Aliases: T2E22.12	7.8	7.6	0.2	0.7	100.0%	-4.8
9399	AT3G02120.1   hydroxyproline-rich glycoprotein family protein   chr3:377104-377720 FORWARD   Aliases: F1C9.2	3.6	3.9	-0.3	-0.7	100.0%	-4.7
9400	AT5G27530.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Lycopersicon esculentum) GI:4325090; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:9717506-9721100 FORWARD   Aliases: F21A20.240	3.9	3.7	0.2	0.7	100.0%	-5.0
9401	AT5G07550.1   Symbol: GRP19   glycine-rich protein (GRP19), oleosin; glycine-rich protein 19 (GRP19) PMID:11431566   chr5:2388325-2389238 REVERSE   Aliases: ATGRP19, T2I1.260, T2I1_260	2.7	2.8	-0.1	-0.7	100.0%	-5.6
9402	AT5G11000.1   expressed protein   chr5:3479030-3480426 REVERSE   Aliases: T30N20.270, T30N20_270	7.0	7.3	-0.3	-0.7	100.0%	-4.7
9403	AT5G66230.1   expressed protein   chr5:26479821-26481357 FORWARD   Aliases: K2A18.31, K2A18_31	3.8	3.6	0.2	0.7	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9404	AT2G43770.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to U5 snRNP-specific 40 kDa protein (GI:3820594) (Homo sapiens)   chr2:18141138-18143057 REVERSE   Aliases: F18O19.12	8.0	8.4	-0.4	-0.7	100.0%	-4.4
9405	AT5G26190.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	2.8	0.2	0.7	100.0%	-4.8
9406	AT1G31820.1   amino acid permease family protein, weak similarity to asc-type amino acid transporter 2 (Mus musculus) GI:18148438; contains Pfam profile PF00324: Amino acid permease   chr1:11416432-11418147 REVERSE   Aliases: None	4.1	3.8	0.3	0.7	100.0%	-4.6
9407	AT5G51950.1   glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:P52707); contains Pfam profile PF00732 GMC oxidoreductase   chr5:21123171-21125831 REVERSE   Aliases: MSG15.3, MSG15_3	2.5	2.4	0.1	0.7	100.0%	-5.5
9408	AT1G44740.1   expressed protein, ; expression supported by MPSS   chr1:16889844-16891595 FORWARD   Aliases: T12C22.1, T12C22_1	3.0	2.9	0.1	0.7	100.0%	-4.9
9409	AT5G49230.1   Symbol: HRB1   drought-responsive family protein, similar to drought-induced mRNA, Di19 (Arabidopsis thaliana) gi:469110:emb:CAA55321   chr5:19976099-19977707 REVERSE   Aliases: HYPERSENSITIVE TO RED AND BLUE, K21P3.11, K21P3_11	7.0	7.3	-0.3	-0.7	100.0%	-4.4
9410	AT2G37810.1   CHP-rich zinc finger protein, putative   chr2:15852428-15853129 REVERSE   Aliases: T8P21.28, T8P21_28	2.4	2.3	0.1	0.7	100.0%	-5.4
9411	AT2G47020.2   peptide chain release factor, putative, similar to peptide chain release factor 1 (Escherichia coli) GI:147567; contains Pfam profiles PF00472: Peptidyl-tRNA hydrolase domain, PF03462: PCR domain   chr2:19326755-19329461 REVERSE   Aliases: F14M4.15	3.5	3.4	0.1	0.7	100.0%	-5.0
9412	AT4G02510.1   Symbol: TOC159	9.9	10.1	-0.2	-0.7	100.0%	-4.8
9413	AT4G33710.1   pathogenesis-related protein, putative, similar to PR-1a protein (Nicotiana tabacum) GI:19944; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:16181015-16181779 FORWARD   Aliases: T16L1.200, T16L1_200	2.5	2.6	-0.1	-0.7	100.0%	-5.0
9414	AT1G18950.1   aminoacyl-tRNA synthetase family, contains aminoacyl-transfer RNA synthetases class-II signature 1, PROSITE:PS00179   chr1:6546390-6551878 FORWARD   Aliases: F14D16.10, F14D16_10	4.3	4.9	-0.7	-0.7	100.0%	-4.4
9415	AT1G30580.1   expressed protein   chr1:10831655-10835520 REVERSE   Aliases: T5I8.3, T5I8_3	7.2	7.9	-0.7	-0.7	100.0%	-4.4
9416	AT1G76360.1   protein kinase, putative, similar to protein kinase APK1B, SWISS-PROT:P46573; contains protein kinase domain, Pfam:PF00069   chr1:28647254-28651489 REVERSE   Aliases: F15M4.14, F15M4_14	4.0	3.7	0.2	0.7	100.0%	-4.5
9417	AT5G55650.1   hypothetical protein   chr5:22553586-22554050 FORWARD   Aliases: MDF20.9, MDF20_9	3.7	3.9	-0.2	-0.7	100.0%	-5.0
9418	AT3G02950.1   expressed protein   chr3:665365-666910 REVERSE   Aliases: F13E7.10, F13E7_10	4.4	4.7	-0.3	-0.7	100.0%	-4.6
9419	AT2G07520.1   hypothetical protein   chr2:3135109-3135777 FORWARD   Aliases: F9A16.11, F9A16_11	2.0	2.1	-0.1	-0.7	100.0%	-5.9
9420	AT1G24735.1   caffeoyl-CoA 3-O-methyltransferase, putative, similar to SP:Q43237 (Vitis vinifera), GI:684942 (Medicago sativa subsp. sativa)   chr1:8758685-8759434 FORWARD   Aliases: F5A9.20, F5A9_20	10.2	9.8	0.4	0.7	100.0%	-4.2
9421	AT5G56350.1   pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Nicotiana tabacum) SWISS-PROT:Q42954   chr5:22837232-22839992 REVERSE   Aliases: MCD7.8, MCD7_8	7.4	8.4	-0.9	-0.7	100.0%	-4.3
9422	AT4G09960.2   Symbol: STK   MADS-box protein (AGL11)   chr4:6236482-6240770 REVERSE   Aliases: AGL11, SEEDSTICK, T5L19.90, T5L19_90	2.9	2.8	0.1	0.7	100.0%	-5.6
9423	AT2G37120.1   DNA-binding S1FA family protein, contains Pfam profile: PF04689 DNA binding protein S1FA	9.4	9.6	-0.2	-0.7	100.0%	-4.9
9424	AT4G11950.1   hypothetical protein   chr4:7173270-7174253 REVERSE   Aliases: F16J13.20, F16J13_20	4.7	4.4	0.3	0.7	100.0%	-4.6
9425	AT2G17750.1   hypothetical protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr2:7716320-7718233 REVERSE   Aliases: T17A5.3, T17A5_3	2.4	2.3	0.1	0.7	100.0%	-5.6
9426	AT4G07500.1   expressed protein   chr4:4300046-4301481 REVERSE   Aliases: T3E15.18, T3E15_18	2.5	2.3	0.1	0.7	100.0%	-5.1
9427	AT1G76270.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr1:28617892-28621633 REVERSE   Aliases: F15M4.23, F15M4_23	6.0	6.6	-0.6	-0.7	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9428	AT1G61280.1   expressed protein, similar to SP:P57054 Down syndrome critical region protein 5 (Down syndrome critical region protein C) {Homo sapiens}; expression supported by MPSS   chr1:22607251-22607746 FORWARD   Aliases: T1F9.23, T1F9_23	3.9	4.1	-0.2	-0.7	100.0%	-4.9
9429	AT1G15390.1   Symbol: PDF1A   peptide deformylase, mitochondrial / polypeptide deformylase 1A (PDF1A), nearly identical to SP:Q9FV53 Peptide deformylase, mitochondrial precursor (EC 3.5.1.88) (PDF) (Polypeptide deformylase) {Arabidopsis thaliana}; contains Pfam profile PF01327: polypeptide deformylase; supporting cDNA gi:11320951:gb:AF250959.1:AF250959   chr1:5294624-5295792 FORWARD   Aliases: PEPTIDE DEFORMYLASE 1A	8.9	9.2	-0.3	-0.7	100.0%	-4.3
9430	AT5G15560.1   hypothetical protein   chr5:5064054-5064892 FORWARD   Aliases: T20K14.170, T20K14_170	2.8	2.9	-0.1	-0.7	100.0%	-5.0
9431	AT5G02640.1   expressed protein, predicted proteins, Arabidopsis thaliana and Oryza sativa   chr5:594177-594865 REVERSE   Aliases: T22P11.230, T22P11_230	3.8	3.9	-0.1	-0.7	100.0%	-4.9
9432	AT4G23496.1   expressed protein   chr4:12257689-12258421 REVERSE   Aliases: None	3.4	3.5	-0.2	-0.7	100.0%	-4.9
9433	AT3G12140.3   similar to emsy N terminus domain-containing protein / ENT domain-containing protein [Arabidopsis thaliana] (TAIR:At5g06780.1); similar to emsy N terminus domain-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_450476.1); contains InterPro domain ENT domain (InterPro:IPR005491)   chr3:3869075-3871707 REVERSE   Aliases: T21B14.4	5.9	5.6	0.2	0.7	100.0%	-4.6
9434	AT4G13980.1   Symbol: AT HSAF5   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr4:8076975-8079284 REVERSE   Aliases: DL3030C, FCAALL.27, HSAF5	3.5	3.6	-0.1	-0.7	100.0%	-5.3
9435	AT1G23180.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr1:8215710-8219573 FORWARD   Aliases: T26J12.19, T26J12_19	4.0	4.2	-0.2	-0.7	100.0%	-4.9
9436	AT1G11270.3   F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.1	0.1	0.7	100.0%	-5.3
9437	AT1G54890.1   late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (EMB7) GI:1350543 from (Picea glauca)   chr1:20466750-20468137 FORWARD   Aliases: F14C21.44, F14C21_44	3.0	3.1	-0.2	-0.7	100.0%	-5.0
9438	AT1G18460.1   lipase family protein, similar to triacylglycerol lipase, gastric precursor (EC 3.1.1.3) {Canis familiaris} (SP:P80035)   chr1:6352463-6356106 FORWARD   Aliases: F15H18.6, F15H18_6	5.8	5.6	0.2	0.7	100.0%	-4.6
9439	AT5G65560.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:26218238-26221004 REVERSE   Aliases: K21L13.7, K21L13_7	3.5	3.8	-0.3	-0.7	100.0%	-4.4
9440	AT1G26530.1   expressed protein, contains Pfam profile: PF04900 protein of unknown function, DUF652; expression supported by MPSS   chr1:9165877-9167349 FORWARD   Aliases: T1K7.10, T1K7_10	2.6	2.5	0.1	0.7	100.0%	-5.6
9441	AT1G31530.1   endonuclease/exonuclease/phosphatase family protein, contains similarity to nocturnin (Homo sapiens) GI:9885288; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr1:11281169-11282449 REVERSE   Aliases: F27M3.24, F27M3_24	2.2	2.2	0.1	0.7	100.0%	-5.4
9442	AT1G51350.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr1:19039423-19043009 FORWARD   Aliases: F11M15.21, F11M15_21	3.6	3.8	-0.2	-0.7	100.0%	-4.8
9443	AT5G59240.1   40S ribosomal protein S8 (RPS8B), 40S ribosomal protein S8, Prunus armeniaca, EMBL:AF071889   chr5:23919697-23920959 REVERSE   Aliases: MNC17.7, MNC17_7	4.8	5.0	-0.2	-0.7	100.0%	-4.9
9444	AT1G77860.1   Symbol: KOM   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr1:29287572-29289352 REVERSE   Aliases: F28K19.7, F28K19_7, KOMPEITO	3.4	3.6	-0.2	-0.7	100.0%	-4.9
9445	AT2G40740.1   Symbol: WRKY55	3.7	3.6	0.1	0.7	100.0%	-5.1
9446	AT5G63990.2   3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP:Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family   chr5:25630548-25633023 FORWARD   Aliases: MBM17.9, MBM17_9	6.5	6.9	-0.4	-0.7	100.0%	-4.4
9447	AT4G38250.1   amino acid transporter family protein, low similarity to lysosomal amino acid transporter 1 (Rattus norvegicus) GI:14571904; contains Pfam profile PF01490: Transmembrane amino acid transporter protein	7.1	6.8	0.3	0.7	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9448	AT2G47810.1   histone-like transcription factor (CBF/NF-Y) family protein, contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to LEC1-like protein (GI:22536010) (Phaseolus coccineus)	3.7	3.5	0.2	0.7	100.0%	-4.9
9449	AT1G74750.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to post-transcriptional control of chloroplast gene expression CRP1 (Zea mays) GI:3289002; contains Pfam profile PF01535: PPR repeat   chr1:28090461-28093028 FORWARD   Aliases: F25A4.28, F25A4_28	3.2	3.1	0.1	0.7	100.0%	-5.0
9450	AT1G20450.2   Symbol: ERD10   dehydrin (ERD10), identical to dehydrin ERD10 (Low-temperature-induced protein LTI45) (Arabidopsis thaliana) SWISS-PROT:P42759   chr1:7087993-7089596 REVERSE   Aliases: ER10, ERD10, F5M15.21, F5M15_21, LTI45	10.4	10.1	0.2	0.7	100.0%	-5.0
9451	NA	2.2	2.2	0.1	0.7	100.0%	-5.5
9452	AT5G62220.1   exostosin family protein, contains Pfam profile: PF03016	5.4	5.2	0.2	0.7	100.0%	-4.7
9453	AT3G45600.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr3:16744740-16746936 REVERSE   Aliases: F9K21.180	4.0	4.3	-0.3	-0.7	100.0%	-4.4
9454	AT5G46630.2   clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	8.5	8.8	-0.3	-0.7	100.0%	-4.8
9455	AT4G29840.2   Symbol: MTO2   threonine synthase, chloroplast, identical to SP:Q9S7B5 Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS) {Arabidopsis thaliana}   chr4:14597716-14601061 REVERSE   Aliases: F27B13.80, F27B13_80, METHIONINE OVER ACCUMULATOR, THREONINE SYNTHASE, TS	9.5	9.8	-0.3	-0.7	100.0%	-4.4
9456	AT4G26640.2   Symbol: WRKY20	6.3	6.5	-0.3	-0.7	100.0%	-4.5
9457	AT4G37400.1   Symbol: CYP81F3   cytochrome P450 family protein, similar to cytochrome P450 monooxygenase CYP91A2, Arabidopsis thaliana, D78607   chr4:17584045-17586354 FORWARD   Aliases: F6G17.50, F6G17_50	4.0	4.3	-0.4	-0.7	100.0%	-4.3
9458	AT2G19780.1   leucine-rich repeat family protein / extensin family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to leucine-rich repeat/extensin 1 (GI:13809918) (Arabidopsis thaliana); contains similarity to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591   chr2:8529760-8531156 REVERSE   Aliases: F6F22.19, F6F22_19	4.6	4.9	-0.3	-0.7	100.0%	-4.2
9459	AT4G11660.1   Symbol: AT HSF2B   heat shock factor protein 7 (HSF7) / heat shock transcription factor 7 (HSTF7), identical to heat shock factor protein 7 (HSF7) SP:Q9T0D3 from (Arabidopsis thaliana)   chr4:7042627-7044702 FORWARD   Aliases: HSF2B, T5C23.90, T5C23_90	4.6	4.4	0.2	0.7	100.0%	-4.9
9460	AT3G11250.1   60S acidic ribosomal protein P0 (RPP0C), similar to 60S acidic ribosomal protein P0 GI:2088654 (Arabidopsis thaliana)   chr3:3521366-3523006 FORWARD   Aliases: F11B9.17	6.8	7.2	-0.4	-0.7	100.0%	-4.2
9461	AT5G42700.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:17139399-17141581 FORWARD   Aliases: MJB21.7, MJB21_7	2.4	2.5	-0.1	-0.7	100.0%	-5.3
9462	AT2G25340.1   Symbol: ATVAMP712   synaptobrevin family protein, similar to Synaptobrevin-like protein 1 (SP:P51809) (Homo sapiens)   chr2:10799743-10800911 REVERSE   Aliases: T22F11.7, T22F11_7, VAMP712	2.9	2.7	0.2	0.7	100.0%	-4.9
9463	AT2G37980.1   expressed protein, similar to axi 1 (Nicotiana tabacum) GI:559921; contains Pfam profile PF03138: Plant protein family   chr2:15901135-15904688 REVERSE   Aliases: T8P21.11, T8P21_11	3.3	3.6	-0.2	-0.7	100.0%	-4.7
9464	AT1G36150.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, low similarity to glucoamylase S1/S2 (Precursor) from Saccharomyces cerevisiae (SP:P08640), proteophosphoglycan from Leishmania major (GI:5420387); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	3.9	3.7	0.2	0.7	100.0%	-4.9
9465	AT2G32640.2   expressed protein   chr2:13853996-13857978 REVERSE   Aliases: T26B15.22	3.0	3.2	-0.1	-0.7	100.0%	-5.0
9466	AT3G13540.1   Symbol: ATMYB5	3.4	3.3	0.1	0.7	100.0%	-5.0
9467	AT5G52330.2   similar to meprin and TRAF homology domain-containing protein / MATH domain-containing protein [Arabidopsis thaliana] (TAIR:At1g04300.1); similar to meprin and TRAF homology domain-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD52955.1); contains InterPro domain Meprin/TRAF-like MATH (InterPro:IPR002083)   chr5:21264822-21267139 REVERSE   Aliases: K24M7.6, K24M7_6	2.5	2.5	0.1	0.7	100.0%	-5.5
9468	AT5G26870.1   MADS-box family protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr5:9457062-9457669 REVERSE   Aliases: F2P16.19, F2P16_19	2.4	2.5	-0.0	-0.7	100.0%	-6.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9469	AT5G01530.1   chlorophyll A-B binding protein CP29 (LHCB4), identical to CP29 (Arabidopsis thaliana) GI:298036; contains Pfam profile: PF00504 chlorophyll A-B binding protein	10.4	10.0	0.4	0.7	100.0%	-4.2
9470	AT4G29030.1   glycine-rich protein, glycine-rich protein - Onobrychis viciifolia,PID:g2565429   chr4:14307255-14307979 FORWARD   Aliases: F19B15.60, F19B15_60	4.9	4.7	0.2	0.7	100.0%	-4.8
9471	AT1G04650.1   expressed protein   chr1:1294892-1298902 REVERSE   Aliases: T1G11.9, T1G11_9	2.9	3.0	-0.1	-0.7	100.0%	-5.2
9472	AT1G05010.1   Symbol: EFE   1-aminocyclopropane-1-carboxylate oxidase / ACC oxidase / ethylene-forming enzyme (ACO) (EAT1), Identical to 1-aminocyclopropane-1-carboxylate oxidase (ACC oxidase) gb:X66719 (EAT1). ESTs gb:T43073, gb:T5714, gb:R90435, gb:R44023, gb:AA597926, gb:AI099676, gb:AA650810 and gb:29725 come from this gene   chr1:1431189-1432857 REVERSE   Aliases: 1 AMINOCYCLOPROPANE 1 CARBOXYLATE OXIDASE, EAT1, ETHYLENE FORMING ENZYME, T7A14.12, T7A14_12	4.1	3.8	0.3	0.7	100.0%	-4.2
9473	AT4G34450.1   coatomer gamma-2 subunit, putative / gamma-2 coat protein, putative / gamma-2 COP, putative, similar to SP:Q9UBF2 Coatomer gamma-2 subunit (Gamma-2 coat protein) (Gamma-2 COP) {Homo sapiens}; contains Pfam profile: PF01602 Adaptin N terminal region	9.5	9.7	-0.2	-0.7	100.0%	-4.6
9474	AT2G16360.1   40S ribosomal protein S25 (RPS25A)   chr2:7083795-7084448 REVERSE   Aliases: F16F14.14, F16F14_14	4.3	4.2	0.2	0.7	100.0%	-4.7
9475	AT5G61410.2   Symbol: RPE   ribulose-phosphate 3-epimerase, chloroplast, putative / pentose-5-phosphate 3-epimerase, putative, strong similarity to SP:Q43157 Ribulose-phosphate 3-epimerase, chloroplast precursor (EC 5.1.3.1) (Pentose-5-phosphate 3-epimerase) (PPE) (RPE) (R5P3E) {Spinacia oleracea}; contains Pfam profile PF00834: Ribulose-phosphate 3 epimerase family   chr5:24700832-24703200 REVERSE   Aliases: D RIBULOSE 5 PHOSPHATE 3 EPIMERASE, EMB2728, EMBRYO DEFECTIVE 2728, MFB13.21, MFB13_21	8.6	8.0	0.6	0.7	100.0%	-4.3
9476	AT3G01280.1   porin, putative, similar to SP:P42055 34 kDa outer mitochondrial membrane protein porin (Voltage-dependent anion-selective channel protein) (VDAC) {Solanum tuberosum}; contains Pfam profile PF01459: Eukaryotic porin   chr3:85619-87865 FORWARD   Aliases: T22N4.9, T22N4_9	10.9	11.5	-0.6	-0.7	100.0%	-4.5
9477	AT3G58860.1   F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.3	-0.1	-0.7	100.0%	-5.3
9478	AT4G13710.1   pectate lyase family protein   chr4:7962428-7966440 FORWARD   Aliases: F18A5.100, F18A5_100	3.5	3.7	-0.2	-0.7	100.0%	-4.6
9479	AT2G17530.1   protein kinase family protein, identical to SRPK2 (Arabidopsis thaliana) gi:9843645:emb:CAC03676; contains protein kinase domain, Pfam:PF00069   chr2:7633478-7636231 FORWARD   Aliases: MJB20.9, MJB20_9	4.6	5.0	-0.4	-0.7	100.0%	-4.5
9480	AT4G14430.1   enoyl-CoA hydratase/isomerase family protein, low similarity to 2-cyclohexenylcarbonyl CoA isomerase (Streptomyces collinus) GI:8133118, enoyl-CoA isomerase (Escherichia coli) GI:2764829; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr4:8304596-8305701 REVERSE   Aliases: DL3255C, FCAALL.43	7.3	7.2	0.2	0.7	100.0%	-4.8
9481	AT1G06440.1   expressed protein   chr1:1963379-1965050 REVERSE   Aliases: F12K11.21, F12K11_21	2.4	2.4	0.1	0.7	100.0%	-5.5
9482	AT3G08960.1   importin beta-2 subunit family protein, low similarity to Lph2p (Saccharomyces cerevisiae) GI:1163089; contains Pfam profile PF03810: Importin-beta N-terminal domain   chr3:2731898-2736767 REVERSE   Aliases: T16O11.8	3.5	3.7	-0.2	-0.7	100.0%	-4.8
9483	AT3G21710.2   expressed protein   chr3:7648366-7649792 FORWARD   Aliases: MSD21.2	5.3	5.6	-0.3	-0.7	100.0%	-4.0
9484	AT2G15320.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr2:6673398-6674786 REVERSE   Aliases: F27O10.3, F27O10_3	3.1	3.0	0.1	0.7	100.0%	-5.3
9485	AT3G16840.1   similar to DEAD/DEAH box helicase, putative (RH10) [Arabidopsis thaliana] (TAIR:At5g60990.1); similar to hypothetical protein DDB0204240 [Dictyostelium discoideum] (GB:EAL66480.1); contains InterPro domain ATP-dependent helicase, DEAD-box (InterPro:IPR000629); contains InterPro domain Bipartite nuclear localization signal (InterPro:IPR001472); contains InterPro domain Helicase, C-terminal (InterPro:IPR001650); contains InterPro domain DEAD/DEAH box helicase (InterPro:IPR001410)   chr3:5737895-5743150 REVERSE   Aliases: K2019.7	6.9	7.4	-0.5	-0.7	100.0%	-4.4
9486	AT1G69700.1   Symbol: ATHVA22C   ABA-responsive protein (HVA22c), identical to AtHVA22c (Arabidopsis thaliana) GI:4884936   chr1:26223901-26225487 FORWARD   Aliases: ATHVA22C, T6C23.10, T6C23_10	6.9	6.5	0.4	0.7	100.0%	-4.1
9487	AT2G28305.1   expressed protein, contains Pfam profile PF03641: decarboxylase family protein   chr2:12088190-12091741 FORWARD   Aliases: T1B3.18	2.6	2.5	0.1	0.7	100.0%	-5.2
9488	AT2G03730.2   Symbol: ACR5   similar to ACT domain containing protein (ACR4) [Arabidopsis thaliana] (TAIR:At1g69040.2); similar to putative ACT domain repeat protein [Oryza sativa (japonica cultivar-group)] (GB:NP_909842.1); contains InterPro domain Amino acid-binding ACT (InterPro:IPR002912)	4.5	4.7	-0.2	-0.7	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9489	AT1G66340.1   Symbol: ETR1   ethylene receptor 1 (ETR1), identical to GB:P49333 from (Arabidopsis thaliana) (Science 262 (5133), 539-544 (1993))   chr1:24737827-24741029 FORWARD   Aliases: EIN1, ETHYLENE INSENSITIVE 1, ETHYLENE RESPONSE 1, ETR, HISTIDINE KINASE ETR1, T27F4.9, T27F4_9	4.0	4.2	-0.2	-0.7	100.0%	-4.6
9490	AT1G16330.1   Symbol: CYCB3;1   cyclin family protein, similar to SP:P25011 G2/mitotic-specific cyclin S13-6 (B-like cyclin) {Glycine max}; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:5582381-5584451 REVERSE   Aliases: CYCLIN B3;1, F3O9.13, F3O9_13	3.3	3.4	-0.1	-0.7	100.0%	-5.0
9491	AT1G66440.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr1:24785834-24788014 FORWARD   Aliases: F28G11.16, F28G11_16	3.3	3.7	-0.4	-0.7	100.0%	-4.1
9492	AT5G59360.1   expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	3.2	3.5	-0.3	-0.7	100.0%	-4.6
9493	AT5G18400.2   expressed protein, contains Pfam profile PF05093: Protein of unknown function (DUF689)   chr5:6092684-6094996 REVERSE   Aliases: F20L16.120, F20L16_120	7.6	7.9	-0.3	-0.7	100.0%	-4.6
9494	AT5G05550.2   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189	2.8	2.9	-0.1	-0.7	100.0%	-5.1
9495	AT5G42765.1   expressed protein   chr5:17166762-17168907 REVERSE   Aliases: None	5.3	5.2	0.2	0.7	100.0%	-4.6
9496	AT1G70190.1   ribosomal protein L12 family protein, contains similarity to ribosomal protein GI:7270590 from (Arabidopsis thaliana)   chr1:26434206-26435240 FORWARD   Aliases: F20P5.9, F20P5_9	3.4	3.2	0.2	0.7	100.0%	-4.9
9497	AT4G38800.1   phosphorylase family protein, contains weak similarity to Swiss-Prot:O51931 nucleosidase (Includes: 5'-methylthioadenosine nucleosidase (EC 3.2.2.16); S-adenosylhomocysteine nucleosidase (Buchnera aphidicola)	11.7	11.5	0.2	0.7	100.0%	-4.9
9498	AT4G24350.1   phosphorylase family protein, contains Pfam PF01048: Phosphorylase family   chr4:12609538-12611477 FORWARD   Aliases: T22A6.180, T22A6_180	2.5	2.4	0.1	0.7	100.0%	-5.4
9499	AT3G16785.1   Symbol: PLDP1   phospholipase D zeta1 / PLDzeta1 (PLDP1), identical to phospholipase D zeta1 (Arabidopsis thaliana) GI:15723315, SP:Q9LRZ5 Phospholipase D p1 (EC 3.1.4.4) (AtPLDp1) (Phospholipase D1 PHOX and PX containing domain) (Phospholipase D zeta 1) (PLDzeta1) {Arabidopsis thaliana}; supported by cDNA gi:15723314; non-consensus splice site (GC) at the beginning of first intron.   chr3:5711088-5718949 FORWARD   Aliases: K20I9.1, PHOSPHOLIPASE D P1, PHOSPHOLIPASE D ZETA 1, PLDZETA1	4.2	4.4	-0.2	-0.7	100.0%	-5.1
9500	AT3G06980.1   DEAD/DEAH box helicase, putative, contains Pfam profile: PF00270 DEAD/DEAH box helicase   chr3:2201473-2204839 FORWARD   Aliases: F17A9.13	5.5	5.3	0.2	0.7	100.0%	-4.9
9501	AT5G64460.5   similar to phosphoglycerate/bisphosphoglycerate mutase family protein [Arabidopsis thaliana] (TAIR:At2g17280.1); similar to phosphoglycerate mutase-like protein [Glycine max] (GB:AAG38145.1)   chr5:25790075-25792761 REVERSE   Aliases: T12B11.5, T12B11_5	10.6	10.9	-0.4	-0.7	100.0%	-4.4
9502	AT5G54460.1   wound-responsive protein-related, contains weak similarity to KED (Nicotiana tabacum) gi:8096269:dbj:BAA95789   chr5:22127651-22128175 REVERSE   Aliases: F24B18.8, F24B18_8	3.7	3.5	0.2	0.7	100.0%	-4.7
9503	AT2G24500.1   Symbol: FZF   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr2:10408115-10409948 REVERSE   Aliases: C2H2 ZINC FINGER PROTEIN FZF, T28I24.23, T28I24_23	8.9	8.8	0.2	0.7	100.0%	-5.0
9504	AT1G74170.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr1:27895155-27899306 REVERSE   Aliases: F9E11.7, F9E11_7	3.3	3.6	-0.3	-0.7	100.0%	-4.8
9505	AT4G08370.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:5301959-5303311 REVERSE   Aliases: T28D5.60, T28D5_60	2.3	2.4	-0.1	-0.7	100.0%	-5.5
9506	AT2G21850.1   similar to CHP-rich zinc finger protein, putative [Arabidopsis thaliana] (TAIR:At2g21840.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At2g21830.1); similar to CHP-rich zinc finger protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_479125.1); contains InterPro domain Zn-finger-like, PHD finger (InterPro:IPR001965); contains InterPro domain Protein kinase C, phorbol ester/diacylglycerol binding (InterPro:IPR002219); contains InterPro domain DC1 domain (InterPro:IPR004146)   chr2:9322298-9325318 FORWARD   Aliases: F7D8.17, F7D8_17	2.7	3.1	-0.4	-0.7	100.0%	-4.0
9507	AT1G67510.1   leucine-rich repeat family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr1:25301140-25303847 REVERSE   Aliases: T1F15.2, T1F15_2	3.4	3.7	-0.2	-0.7	100.0%	-4.5
9508	AT2G31590.1   expressed protein   chr2:13453906-13455210 REVERSE   Aliases: T9H9.11, T9H9_11	4.8	4.6	0.2	0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9509	AT4G29260.1   acid phosphatase class B family protein, similar to acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr4:14422182-14423609 REVERSE   Aliases: F17A13.80, F17A13_80	6.4	6.7	-0.3	-0.7	100.0%	-4.5
9510	AT5G03345.1   expressed protein   chr5:814122-815618 FORWARD   Aliases: None	10.4	10.3	0.1	0.7	100.0%	-5.1
9511	AT1G67850.2   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr1:25441633-25445782 FORWARD   Aliases: F12A21.2, F12A21_2	5.9	6.2	-0.3	-0.7	100.0%	-4.4
9512	AT5G17530.2   phosphoglucosamine mutase family protein, low similarity to phosphoglucomutase/phosphomannomutase (Sphingomonas paucimobilis) GI:6103619; contains InterPro accession IPR006352: Phosphoglucosamine mutase   chr5:5777605-5782150 FORWARD   Aliases: K10A8.10, K10A8_10	6.5	6.7	-0.2	-0.7	100.0%	-4.7
9513	AT2G01650.1   Symbol: pux2   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:284671-286492 REVERSE   Aliases: PLANT UBX DOMAIN CONTAINING PROTEIN 2, T8O11.18, T8O11_18	7.1	7.4	-0.2	-0.7	100.0%	-4.6
9514	AT3G16630.2   kinesin motor family protein, similar to mitotic centromere-associated kinesin GB:AAC27660 from (Homo sapiens); contains Pfam profile PF00225: Kinesin motor domain   chr3:5662390-5667809 REVERSE   Aliases: MGL6.9	6.5	6.9	-0.4	-0.7	100.0%	-4.5
9515	AT2G42080.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QY17 DnaJ homolog subfamily B member 8 (mDJ6) {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr2:17560326-17562565 REVERSE   Aliases: T6D20.3, T6D20_3	5.6	5.8	-0.2	-0.7	100.0%	-4.8
9516	AT3G42430.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr3:14554366-14555496 FORWARD   Aliases: T14K23.140	2.5	2.4	0.1	0.7	100.0%	-5.7
9517	AT2G31945.1   expressed protein   chr2:13588658-13589203 FORWARD   Aliases: None	3.6	3.4	0.2	0.7	100.0%	-4.8
9518	AT2G47500.1   kinesin motor protein-related   chr2:19500065-19505226 FORWARD   Aliases: T30B22.20	3.8	4.0	-0.2	-0.7	100.0%	-4.4
9519	AT1G50410.1   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to transcription factor RUSH-1alpha (Oryctolagus cuniculus) GI:1655930; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:18675831-18681224 FORWARD   Aliases: F11F12.23, F11F12_23	5.3	5.5	-0.2	-0.7	100.0%	-4.5
9520	AT2G05990.2   Symbol: MOD1   enoyl-(acyl-carrier protein) reductase (NADH), chloroplast, putative / NADH-dependent enoyl-ACP reductase, putative, strong similarity to enoyl-(acyl-carrier protein) reductase (NADH) SP:P80030 from (Brassica napus)   chr2:2322219-2325143 FORWARD   Aliases: ENOYL ACP REDUCTASE, ENOYL ACP REDUCTASE 1, ENR1, MOSAIC DEATH 1, T6P5.19, T6P5_19	7.5	8.1	-0.6	-0.7	100.0%	-4.5
9521	AT2G38420.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:16098183-16099628 FORWARD   Aliases: T19C21.9, T19C21_9	4.4	4.5	-0.1	-0.7	100.0%	-4.9
9522	AT5G28810.1   hypothetical protein   chr5:10824437-10826579 FORWARD   Aliases: T32B20.100, T32B20_100	2.9	3.0	-0.1	-0.7	100.0%	-5.4
9523	AT3G54170.1   Symbol: ATFIP37   FKBP12 interacting protein (FIP37), identical to FKBP12 interacting protein (FIP37) GI:3859944 from (Arabidopsis thaliana)   chr3:20067729-20070497 FORWARD   Aliases: ARABIDOPSIS THALIANA FKBP12 INTERACTING PROTEIN 37, F24B22.130, FIP37, FKBP12 INTERACTING PROTEIN 37	4.5	4.8	-0.3	-0.7	100.0%	-4.8
9524	AT1G67855.1   expressed protein, hypothetical protein   chr1:25445809-25447019 REVERSE   Aliases: F12A21.1, F12A21_1	2.3	2.4	-0.1	-0.7	100.0%	-5.7
9525	AT4G15830.1   expressed protein   chr4:8995126-8996614 REVERSE   Aliases: DL3955C, FCAALL.419	8.0	8.3	-0.3	-0.7	100.0%	-4.6
9526	AT1G14760.1   expressed protein   chr1:5084683-5085208 REVERSE   Aliases: F10B6.16, F10B6_16	2.7	2.6	0.1	0.7	100.0%	-5.2
9527	AT3G59380.1   Symbol: FTA   farnesyltransferase alpha subunit, putative / FTA, putative / protein farnesyltransferase, putative, similar to farnesyltransferase alpha subunit (GI:2246442)(Pisum sativum)   chr3:21955170-21956915 FORWARD   Aliases: F25L23.240, FARNESYLTRANSFERASE A, FARNESYLTRANSFERASE SUBUNIT A, PLP, PLURIPETALA	6.4	6.8	-0.4	-0.7	100.0%	-4.6
9528	AT5G57870.2   eukaryotic translation initiation factor 4F, putative / eIF-4F, putative, similar to SP:Q03387 Eukaryotic initiation factor (iso)4F subunit P82-34 (eIF-(iso)4F P82-34) {Triticum aestivum}; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain   chr5:23456724-23461007 FORWARD   Aliases: MTI20.13, MTI20_13	7.2	6.8	0.3	0.7	100.0%	-4.3
9529	AT5G09520.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:2958293-2958857 REVERSE   Aliases: T5E8.1	2.7	2.9	-0.2	-0.7	100.0%	-4.4
9530	AT3G10220.1   tubulin folding cofactor B, identical to tubulin folding cofactor B GI:20514259 from (Arabidopsis thaliana); identical to cDNA tubulin folding cofactor B GI:20514258   chr3:3161815-3164674 FORWARD   Aliases: F14P13.18	4.6	4.8	-0.2	-0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9531	AT2G02590.1   expressed protein   chr2:704936-706667 FORWARD   Aliases: T8K22.11, T8K22_11	4.4	4.3	0.2	0.7	100.0%	-5.0
9532	AT3G49350.1   RabGAP/TBC domain-containing protein, similar to GTPase activating protein (Yarrowia lipolytica) GI:2370595; contains Pfam profile PF00566: TBC domain   chr3:18308178-18311174 REVERSE   Aliases: F2K15.210	5.6	5.8	-0.2	-0.7	100.0%	-4.4
9533	AT2G27030.3   Symbol: CAM2   calmodulin-2/3/5 (CAM5) (TCH1), identical to calmodulin GI:474183 from (Arabidopsis thaliana), SP:P25069 Calmodulin-2/3/5 {Arabidopsis thaliana}	9.1	8.8	0.4	0.7	100.0%	-4.4
9534	AT3G27840.1   Symbol: RPL12 B   50S ribosomal protein L12-2, chloroplast (CL12-B), identical to ribosomal protein L12 GB:X68046 (Arabidopsis thaliana) (J. Biol. Chem. 269 (10), 7330-7336 (1994))   chr3:10324591-10325187 FORWARD   Aliases: K16N12.20, RIBOSOMAL PROTEIN L12 B	2.6	2.5	0.1	0.7	100.0%	-5.5
9535	AT2G25790.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:11007677-11011313 FORWARD   Aliases: F17H15.18, F17H15_18	7.5	7.8	-0.3	-0.7	100.0%	-4.6
9536	AT3G03420.1   Ku70-binding family protein, similar to Ku70-binding protein GB:AAD31085 GI:4867999 (Homo sapiens); contains Prosite PS00142: Neutral zinc metallopeptidases, zinc-binding region signature   chr3:812455-814034 FORWARD   Aliases: T21P5.16, T21P5_16	6.1	6.4	-0.3	-0.7	100.0%	-4.4
9537	AT2G20150.1   expressed protein, and genefinder   chr2:8705280-8705561 FORWARD   Aliases: T2G17.5, T2G17_5	4.1	4.3	-0.2	-0.7	100.0%	-4.9
9538	AT5G63340.1   expressed protein   chr5:25396120-25396900 FORWARD   Aliases: K9H21.7, K9H21_7	2.4	2.3	0.1	0.7	100.0%	-5.4
9539	AT1G23670.2   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8373275-8375857 REVERSE   Aliases: F28C11.25	2.4	2.4	-0.1	-0.7	100.0%	-5.6
9540	AT2G28660.1   copper-binding family protein, similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain   chr2:12302404-12304194 FORWARD   Aliases: T8O18.5, T8O18_5	5.1	4.7	0.4	0.7	100.0%	-4.5
9541	AT1G17000.1   Symbol: ATTPS3	2.3	2.4	-0.1	-0.7	100.0%	-5.6
9542	AT4G01280.2   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At1g01520.1); similar to myb family transcription factor-like [Oryza sativa (japonica cultivar-group)] (GB:BAD29385.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005); contains InterPro domain Myb-like DNA-binding domain, SHAQKYF class (InterPro:IPR006447)   chr4:535245-537307 FORWARD   Aliases: F2N1.20, F2N1_20	3.4	3.3	0.2	0.7	100.0%	-4.7
9543	AT5G22980.1   Symbol: SCPL47	4.1	4.4	-0.2	-0.7	100.0%	-4.8
9544	AT1G62280.1   C4-dicarboxylate transporter/malic acid transport family protein, contains Pfam profile PF03595: C4-dicarboxylate transporter/malic acid transport protein   chr1:23010812-23012250 REVERSE   Aliases: F19K23.20, F19K23_20	3.3	3.2	0.1	0.7	100.0%	-5.3
9545	AT1G51400.1   photosystem II 5 kD protein, 100% identical to GI:4836947 (F5D21.10)   chr1:19055730-19056250 REVERSE   Aliases: F5D21.10, F5D21_10	8.9	8.5	0.4	0.7	100.0%	-4.3
9546	AT5G24450.1   transcription factor-related, low similarity to transcription factor IIC63 (Homo sapiens) GI:5281316   chr5:8348783-8353298 FORWARD   Aliases: T31K7.3, T31K7_3	5.8	6.3	-0.5	-0.7	100.0%	-4.4
9547	AT4G16740.2   Symbol: ATTPS03   similar to myrcene/ocimene synthase, putative [Arabidopsis thaliana] (TAIR:At3g25810.1); similar to terpenoid synthase [Vitis vinifera] (GB:AAS79352.1); contains InterPro domain Terpene synthase metal binding domain (InterPro:IPR005630); contains InterPro domain Terpene synthase-like (InterPro:IPR001906)   chr4:9407790-9409942 FORWARD   Aliases: DL4395W, FCAALL.18	2.4	2.5	-0.1	-0.7	100.0%	-5.1
9548	AT4G13670.1   peptidoglycan-binding domain-containing protein, similar to spore cortex-lytic enzyme prepeptide (GI:1644192) (Bacillus cereus); contains Pfam PF01471: Putative peptidoglycan binding domain; contains Pfam PF00684 : DnaJ central domain (4 repeats)   chr4:7948575-7950881 FORWARD   Aliases: F18A5.60, F18A5_60	9.5	9.0	0.4	0.7	100.0%	-4.7
9549	AT3G20140.1   Symbol: CYP705A23   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr3:7029181-7030793 FORWARD   Aliases: MAL21.2	2.9	3.1	-0.2	-0.7	100.0%	-4.9
9550	AT2G40100.1   Symbol: LHCB4.3   chlorophyll A-B binding protein (LHCB4.3), identical to Lhcb4:3 protein (Arabidopsis thaliana) GI:4741956; contains Pfam profile: PF00504 chlorophyll A-B binding protein   chr2:16752881-16754478 FORWARD   Aliases: F27I1.2, F27I1_2	9.7	9.3	0.4	0.7	100.0%	-4.1
9551	AT2G25880.1   Encodes a member of a family of Ser/Thr kinases whose activities peak during cell division. Transcripts are abundant in tissues rich in dividing cells like roots and flowers but are low or absent in fully expanded leaves and stems.	6.5	6.2	0.3	0.7	100.0%	-4.5
9552	AT5G39950.1   Symbol: ATTRX2	11.2	10.8	0.4	0.7	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9553	AT1G31790.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:11394132-11395999 REVERSE   Aliases: F5M6.20, F5M6_20	3.5	3.7	-0.1	-0.7	100.0%	-4.9
9554	AT5G50930.1   expressed protein, similar to unknown protein (emb:CAB61034.1)   chr5:20739295-20741543 FORWARD   Aliases: K3K7.8, K3K7_8	6.5	6.9	-0.4	-0.7	100.0%	-3.9
9555	AT5G66490.1   expressed protein   chr5:26564453-26564994 REVERSE   Aliases: K1F13.15, K1F13_15	4.3	4.6	-0.3	-0.7	100.0%	-4.4
9556	NA	2.3	2.4	-0.1	-0.7	100.0%	-5.8
9557	AT1G12550.1   oxidoreductase family protein, similar to glyoxylate reductase from Homo sapiens (gi:6002730); contains Pfam D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain PF02826   chr1:4274647-4275829 FORWARD   Aliases: F5O11.29, F5O11_29	5.6	6.0	-0.3	-0.7	100.0%	-4.5
9558	AT5G21100.1   L-ascorbate oxidase, putative, similar to L-ascorbate oxidase (Precursor) SP:Q40588 from (Nicotiana tabacum)   chr5:7168186-7170930 FORWARD   Aliases: T10F18.130, T10F18_130	3.9	3.8	0.1	0.7	100.0%	-5.2
9559	AT2G47760.3   expressed protein, similar to PREDICTED: hypothetical protein XP_535823 [Canis familiaris] (GB:XP_535823.1); contains InterPro domain ALG3 (InterPro:IPR007873)   chr2:19572552-19575335 REVERSE   Aliases: F17A22.15	6.7	6.5	0.2	0.7	100.0%	-4.7
9560	AT4G10910.1   expressed protein   chr4:6696708-6697451 FORWARD   Aliases: F25I24.120, F25I24_120	3.4	3.4	0.1	0.7	100.0%	-5.3
9561	AT3G11740.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g01750.2); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470102.1); contains InterPro domain Protein of unknown function DUF567 (InterPro:IPR007612)   chr3:3712385-3713448 FORWARD   Aliases: F26K24.3	2.8	2.7	0.1	0.7	100.0%	-5.0
9562	AT1G79330.1   Symbol: AMC6/ATMCP2B   Metacaspase AtMCPb2/AMC6. Caspase family protein. Arginine/lysine-specific cysteine protease activity. Induces apoptosis in yeast. Contains Pfam domain, PF00656: ICE-like protease (caspase) p20 domain.   chr1:29843546-29845030 FORWARD   Aliases: AMC6, ATMCP2B, YUP8H12R.5, YUP8H12R_5	2.5	2.4	0.1	0.7	100.0%	-4.8
9563	AT2G25220.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:10749793-10752202 REVERSE   Aliases: T22F11.19	3.3	3.1	0.2	0.7	100.0%	-4.8
9564	AT4G00920.1   COP1-interacting protein-related, similar to COP1-interacting protein 4 (CIP4) (Arabidopsis thaliana) GI:13160646   chr4:393767-395382 FORWARD   Aliases: A_TM018A10.16, A_TM018A10_16, T18A10.22, T18A10_22	2.4	2.3	0.1	0.7	100.0%	-5.4
9565	AT4G20820.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr4:11150171-11151769 FORWARD   Aliases: F21C20.170, F21C20_170	3.0	3.1	-0.2	-0.7	100.0%	-4.7
9566	AT5G02250.1   Symbol: EMB2730   ribonuclease II family protein, contains Pfam profile PF00773: RNB-like protein   chr5:454783-459525 FORWARD   Aliases: EMB2730, EMBRYO DEFECTIVE 2730, T1E22.10, T1E22_10	5.8	5.5	0.3	0.7	100.0%	-4.3
9567	AT4G19910.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, contains Pfam profile PF01582: TIR domain   chr4:10795879-10796697 REVERSE   Aliases: None	2.5	2.4	0.1	0.7	100.0%	-5.3
9568	AT4G33910.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus (GI:212530), Rattus norvegicus (GI:474940), Drosophila melanogaster (GI:4336512); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr4:16256738-16258776 REVERSE   Aliases: F17I5.100, F17I5_100	8.5	8.4	0.1	0.7	100.0%	-4.8
9569	AT2G18915.2   Symbol: LKP2   F-box family protein / LOV kelch protein 2 (LKP2) / adagio 2 (ADO2), E3 ubiquitin ligase SCF complex F-box subunit; identical to Adagio 2 GI:13487070 from (Arabidopsis thaliana); contains Pfam profiles PF01344: Kelch motif and PF00646: F-box domain; identical to cDNA LOV kelch protein 2 GI:18146957; identical to cDNA Adagio 2 (ADO2) GI:13487069   chr2:8201654-8204565 REVERSE   Aliases: ADAGIO 2, ADO2, LOV KELCH PROTEIN 2	4.5	4.3	0.1	0.7	100.0%	-5.0
9570	AT1G10770.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	4.7	4.5	0.2	0.7	100.0%	-4.5
9571	AT5G56280.1   Symbol: CSN6A   COP9 signalosome subunit 6 / CSN subunit 6 (CSN6A), identical to CSN complex subunit 6A (Arabidopsis thaliana) GI:18056665, COP9 complex subunit 6 (Arabidopsis thaliana) GI:15809663; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family; identical to cDNA CSN complex subunit 6A (CSN6A) GI:18056664   chr5:22800610-22802785 REVERSE   Aliases: MXK23.2, MXK23_2	7.8	8.6	-0.8	-0.7	100.0%	-4.4
9572	AT5G16400.1   thioredoxin, putative, similar to SP:P29450 Thioredoxin F-type, chloroplast precursor (TRX-F) {Pisum sativum}; contains Pfam profile: PF00085 Thioredoxin   chr5:5363664-5365319 REVERSE   Aliases: MQK4.13, MQK4_13	6.9	6.6	0.3	0.7	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9573	AT1G49840.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr1:18455738-18458026 FORWARD   Aliases: F10F5.2, F10F5_2	5.3	5.0	0.3	0.7	100.0%	-4.4
9574	AT3G12685.1   expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963   chr3:4029190-4030362 REVERSE   Aliases: None	3.6	3.8	-0.2	-0.7	100.0%	-4.6
9575	AT1G21130.2   O-methyltransferase, putative, similar to GI:2781394   chr1:7399051-7400593 REVERSE   Aliases: T22I11.4, T22I11_4	3.9	3.7	0.2	0.7	100.0%	-5.1
9576	AT1G50260.1   C2 domain-containing protein, low similarity to CLB1 (Lycopersicon esculentum) GI:2789434; contains Pfam profile PF00168: C2 domain   chr1:18621261-18625358 REVERSE   Aliases: F14I3.13, F14I3_13	7.4	7.1	0.2	0.7	100.0%	-4.7
9577	AT3G07400.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr3:2367308-2372721 FORWARD   Aliases: F21O3.11	6.7	6.5	0.2	0.7	100.0%	-4.8
9578	AT5G38460.1   ALG6, ALG8 glycosyltransferase family protein, similar to SP:Q9Y672 Dolichyl pyrophosphate Man9GlcNAc2 alpha-1,3-glycosyltransferase (EC 2.4.1.-) (Dolichyl-P-Glc:Man9GlcNAc2-PP-dolichyl glucosyltransferase) {Homo sapiens}; contains Pfam profile PF03155: ALG6, ALG8 glycosyltransferase family   chr5:15415514-15418256 REVERSE   Aliases: MXI10.19, MXI10_19	3.3	3.1	0.2	0.7	100.0%	-4.8
9579	ATMG01350.1   Symbol: ORF145C   hypothetical protein   chrM:346757-347194 FORWARD   Aliases: ORF145C	2.8	3.0	-0.2	-0.7	100.0%	-5.0
9580	AT4G18030.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr4:10012373-10015688 REVERSE   Aliases: T6K21.210, T6K21_210	7.9	8.2	-0.3	-0.7	100.0%	-4.6
9581	AT5G49690.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:20206881-20208616 REVERSE   Aliases: K2I5.5, K2I5_5	3.6	3.4	0.1	0.7	100.0%	-5.1
9582	AT2G16460.2   expressed protein   chr2:7140559-7142734 REVERSE   Aliases: F16F14.4, F16F14_4	5.6	5.8	-0.1	-0.7	100.0%	-4.9
9583	AT5G24630.1   expressed protein, ; expression supported by MPSS   chr5:8432526-8436173 REVERSE   Aliases: K18P6.17, K18P6_17	5.1	5.6	-0.5	-0.7	100.0%	-4.4
9584	AT3G27980.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:10395141-10397098 FORWARD   Aliases: K24A2.9	2.1	2.0	0.1	0.7	100.0%	-5.9
9585	AT3G15351.2   expressed protein   chr3:5176066-5177644 FORWARD   Aliases: None	5.6	5.9	-0.3	-0.7	100.0%	-4.8
9586	AT5G48030.1   Symbol: GFA2   DNAJ heat shock protein, mitochondrially targeted (GFA2), 99.8% identical to mitochondrially targeted DnaJ protein GFA2 (Arabidopsis thaliana) GI:21429604; contains Pfam profiles PF00226: DnaJ domain, PF01556: DnaJ C terminal region, PF00684: DnaJ central domain (4 repeats)   chr5:19483304-19487128 REVERSE   Aliases: GAMETOPHYTIC FACTOR 2, MDN11.11, MDN11_11	8.1	8.4	-0.3	-0.7	100.0%	-4.4
9587	AT4G18520.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At3g09040.1); similar to PPR986-12 [Physcomitrella patens] (GB:BAD67155.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr4:10215132-10217114 REVERSE   Aliases: F28J12.180, F28J12_180	3.8	3.6	0.2	0.7	100.0%	-4.6
9588	AT3G48190.1   Symbol: ATM   ataxia-telangiectasia mutated protein (Atm), identical to ataxia-telangiectasia mutated protein (Atm) (Arabidopsis thaliana) GI:7529272; contains Pfam profile PF00855: PWWP domain; contains GA donor splice site at exon 73   chr3:17808319-17839576 FORWARD   Aliases: ATATM, ATAXIA TELANGIECTASIA MUTATED, T24C20.1	5.1	5.5	-0.4	-0.7	100.0%	-4.5
9589	AT4G34910.1   DEAD/DEAH box helicase, putative (RH16), identical to cDNA DEAD box RNA helicase, RH16 GI:3776006   chr4:16631538-16635154 FORWARD   Aliases: F11I11.150, F11I11_150	4.8	4.6	0.2	0.7	100.0%	-4.9
9590	AT5G35100.1   similar to peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein [Arabidopsis thaliana] (TAIR:At1g74070.1); similar to P0439B06.15 [Oryza sativa (japonica cultivar-group)] (GB:NP_908419.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_549879.1); contains InterPro domain Peptidyl-prolyl cis-trans isomerase, cyclophilin type (InterPro:IPR002130)   chr5:13377513-13378619 REVERSE   Aliases: F7N22.3, F7N22_3	5.5	5.4	0.2	0.7	100.0%	-4.7
9591	AT3G52360.1   expressed protein   chr3:19423098-19423896 FORWARD   Aliases: T25B15.130	6.9	6.7	0.3	0.7	100.0%	-4.6
9592	AT5G37870.1   seven in absentia (SINA) family protein, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr5:15090994-15092081 REVERSE   Aliases: K18L3.4, K18L3_4	3.2	3.0	0.2	0.7	100.0%	-4.9
9593	AT3G16120.1   dynein light chain, putative, similar to SP:O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassispina}; contains Pfam profile PF01221: Dynein light chain type 1   chr3:5464775-5465537 FORWARD   Aliases: MSL1.16	2.8	2.7	0.1	0.7	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9594	AT1G50340.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:18651044-18651517 REVERSE   Aliases: F14I3.26, F14I3_26	2.3	2.3	-0.1	-0.7	100.0%	-5.6
9595	AT4G34740.1   Symbol: ATASE2	4.5	4.3	0.2	0.7	100.0%	-4.6
9596	AT2G38040.2   Symbol: CAC3   acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit family, contains Pfam profile: PF03255: Acetyl co-enzyme A carboxylase carboxyltransferase alpha subunit   chr2:15924196-15928247 FORWARD   Aliases: CARBOXYLTRANSFERASE ALPHA SUBUNIT, T8P21.5, T8P21_5	8.0	8.2	-0.3	-0.7	100.0%	-5.0
9597	AT1G05300.2   Symbol: ZIP5   metal transporter, putative (ZIP5), identical to putative metal transporter ZIP5 (Arabidopsis thaliana) gi:17385784:gb:AAL38432; similar to zinc transporter protein ZIP1 (Glycine max) gi:15418778:gb:AAK37761; member of the Zinc (Zn <sup>2+</sup> )-Iron (Fe <sup>2+</sup> ) permease (ZIP) family, PMID:11500563   chr1:1545215-1547797 REVERSE   Aliases: YUP8H12.8, YUP8H12_8	3.8	4.2	-0.4	-0.7	100.0%	-4.0
9598	AT5G13050.2   similar to putative 5-formyltetrahydrofolate cycloligase [Oryza sativa (japonica cultivar-group)] (GB:XP_478853.1)   chr5:4136208-4138724 REVERSE   Aliases: T19L5.10, T19L5_10	5.6	5.4	0.2	0.7	100.0%	-4.7
9599	AT2G18420.1   gibberellin-responsive protein, putative, similar to SP:P46689 Gibberellin-regulated protein 1 precursor {Arabidopsis thaliana}; contains Pfam profile PF02704: Gibberellin regulated protein   chr2:8000943-8001724 FORWARD   Aliases: T30D6.7, T30D6_7	2.9	2.7	0.1	0.7	100.0%	-5.0
9600	AT1G74900.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr1:28137594-28139042 FORWARD   Aliases: F25A4.13, F25A4_13	4.9	5.1	-0.2	-0.7	100.0%	-4.8
9601	AT2G47060.4   similar to serine/threonine protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g62220.1); similar to Pto kinase interactor 1 [Lycopersicon esculentum] (GB:AAC61805.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr2:19339974-19342041 REVERSE   Aliases: F14M4.11	5.7	5.4	0.2	0.7	100.0%	-4.5
9602	AT3G02010.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:337972-340449 FORWARD   Aliases: F1C9.21	4.1	4.3	-0.2	-0.7	100.0%	-4.9
9603	AT2G11910.2   expressed protein   chr2:4812767-4814399 REVERSE   Aliases: F23M2.7, F23M2_7	7.9	8.3	-0.3	-0.7	100.0%	-4.6
9604	AT4G32250.3   similar to protein kinase family protein / ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At5g13530.1); similar to NIMA-related kinase 2 [Chlamydomonas reinhardtii] (GB:AAQ64683.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:15570050-15573329 REVERSE   Aliases: F10M6.110, F10M6_110	6.5	6.7	-0.2	-0.7	100.0%	-4.5
9605	AT3G26030.1   Symbol: ATB' DELTA   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative, similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)	5.3	5.6	-0.3	-0.7	100.0%	-4.7
9606	AT3G22500.1   Symbol: ATECP31   late embryogenesis abundant protein (ECP31) / LEA protein, identical to LEA protein in group 5 (AtECP31) (Arabidopsis thaliana) GI:1526422; contains Pfam profile PF04927: Seed maturation protein   chr3:7971632-7972900 REVERSE   Aliases: F16J14.1	2.4	2.3	0.1	0.7	100.0%	-5.4
9607	AT5G19540.1   expressed protein   chr5:6595704-6597891 FORWARD   Aliases: T20D1.60, T20D1_60	8.0	7.6	0.4	0.7	100.0%	-4.5
9608	AT3G29600.1   hypothetical protein   chr3:11409888-11410546 REVERSE   Aliases: MTO24.7	2.3	2.3	0.1	0.7	100.0%	-5.8
9609	AT5G43380.3   Symbol: TOPP6   similar to serine/threonine protein phosphatase PP1 isozyme 4 (TOPP4) / phosphoprotein phosphatase 1 [Arabidopsis thaliana] (TAIR:At2g39840.1); similar to protein phosphatase 1, catalytic beta subunit [Medicago sativa] (GB:CAA05491.1); contains InterPro domain Metallo-phosphoesterase (InterPro:IPR004843); contains InterPro domain Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase (InterPro:IPR006186)   chr5:17437047-17439210 REVERSE   Aliases: None	2.6	2.5	0.1	0.7	100.0%	-5.2
9610	AT5G16230.1   acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative, similar to Acyl-(acyl-carrier protein) desaturase from Spinacia oleracea SP:P28645, Ricinus communis SP:P22337; contains Pfam profile PF03405 Fatty acid desaturase   chr5:5303351-5306071 FORWARD   Aliases: T21H19.150, T21H19_150	4.3	4.1	0.2	0.7	100.0%	-4.7
9611	AT3G06290.1   SAC3/GANP family protein, contains Pfam profile: PF03399 SAC3/GANP family   chr3:1899048-1907303 REVERSE   Aliases: F28L1.23, F28L1_23	3.2	3.1	0.2	0.7	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9612	AT5G51060.1   Symbol: RHD2   respiratory burst oxidase protein C (RbohC) / NADPH oxidase, nearly identical to respiratory burst oxidase protein C from Arabidopsis thaliana (gi:3242785)   chr5:20774510-20779657 REVERSE   Aliases: A. THALIANA RESPIRATORY BURST OXIDASE HOMOLOG C, ATRBOHC, K3K7.25, K3K7_25, RBOHC, ROOT HAIR DEFECTIVE 2	5.5	5.9	-0.4	-0.7	100.0%	-4.3
9613	AT2G40140.2   similar to zinc finger (CCCH-type) family protein [Arabidopsis thaliana] (TAIR:At3g55980.1); similar to putative finger transcription factor [Oryza sativa (japonica cultivar-group)] (GB:AAU10743.1); contains InterPro domain Zn-finger, C-x8-C-x5-C-x3-H type (InterPro:IPR000571); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr2:16779294-16781735 FORWARD   Aliases: T7M7.3, T7M7_3	5.7	5.5	0.2	0.7	100.0%	-4.6
9614	AT1G54100.2   Symbol: ALDH7B4   aldehyde dehydrogenase, putative / antiquitin, putative, strong similarity to SP:Q41247 Aldehyde dehydrogenase family 7 member A1 (EC 1.2.1.3) (Antiquitin 1) (Brassica turgor-responsive/drought-induced gene 26 protein) (Btg-26) {Brassica napus}; similar to turgor-responsive protein 26G (aldehyde dehydrogenase family 7 member A1) (Pisum sativum) SWISS-PROT:P25795   chr1:20198932-20202640 REVERSE   Aliases: F15I1.19, F15I1_19	11.4	11.6	-0.2	-0.7	100.0%	-5.1
9615	AT4G27520.1   plastocyanin-like domain-containing protein, similar to PIR:JC7196 phytoecyanin-related protein Pn14 {Ipomoea nil}; contains Pfam profile PF02298: Plastocyanin-like domain   chr4:13750446-13751911 REVERSE   Aliases: T29A15.10, T29A15_10	4.9	5.2	-0.3	-0.7	100.0%	-4.4
9616	AT2G32280.1   expressed protein   chr2:13720137-13721086 FORWARD   Aliases: T32F6.20, T32F6_20	3.4	3.6	-0.2	-0.7	100.0%	-4.6
9617	AT5G45550.1   mob1/phocein family protein, contains Pfam profile: PF03637 Mob1/phocein family   chr5:18479444-18482248 FORWARD   Aliases: MFC19.22, MFC19_22	7.9	7.1	0.8	0.7	100.0%	-4.2
9618	AT3G52930.1   fructose-bisphosphate aldolase, putative, similar to SP:O65735:ALF_CICAR Fructose-bisphosphate aldolase, cytoplasmic isozyme {Cicer arietinum}, cytosolic aldolase (Fragaria x ananassa) GI:10645188; contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I   chr3:19637726-19639920 REVERSE   Aliases: F8J2.100	10.2	10.8	-0.6	-0.7	100.0%	-4.7
9619	AT3G59730.1   receptor lectin kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains pfam domains PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr3:22075285-22076856 REVERSE   Aliases: T16L24.280	2.8	2.9	-0.1	-0.7	100.0%	-5.2
9620	AT4G28590.1   expressed protein   chr4:14125286-14126841 REVERSE   Aliases: T5F17.40, T5F17_40	3.0	3.1	-0.1	-0.7	100.0%	-5.1
9621	AT4G21240.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.5	-0.1	-0.7	100.0%	-5.5
9622	AT3G04000.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to SP:Q08632 Short-chain type dehydrogenase/reductase (EC 1.-.-.-) {Picea abies}; contains Pfam:PF00106 oxidoreductase, short chain dehydrogenase/reductase family   chr3:1035507-1036679 FORWARD   Aliases: T11I18.11, T11I18_11	7.7	7.3	0.4	0.7	100.0%	-4.0
9623	AT2G07560.1   ATPase, plasma membrane-type, putative / proton pump, putative, similar to P-type H(+)-transporting ATPase from (Phaseolus vulgaris) GI:758250, (Lycopersicon esculentum) GI:1621440, SP:Q03194 {Nicotiana plumbaginifolia}, (Solanum tuberosum) GI:435001; contains InterPro accession IPR001757: ATPase, E1-E2 type   chr2:3169969-3174009 REVERSE   Aliases: F9A16.7, F9A16_7	2.4	2.5	-0.1	-0.7	100.0%	-5.3
9624	AT4G19160.3   expressed protein   chr4:10477307-10480150 FORWARD   Aliases: T18B16.130, T18B16_130	5.5	5.9	-0.3	-0.7	100.0%	-4.4
9625	AT1G49620.1   Symbol: ICK5   kip-related protein 7 (KRP7) / cyclin-dependent kinase inhibitor 7 (ICK7), identical to cyclin-dependent kinase inhibitor 7 (krp7) (Arabidopsis thaliana) GI:14422297   chr1:18369360-18370227 REVERSE   Aliases: F14J22.14, F14J22_14, ICN6, KRP7, Kip related protein 7	3.1	3.4	-0.3	-0.7	100.0%	-4.6
9626	AT2G23080.2   casein kinase II alpha chain, putative, identical to probable casein kinase II, alpha chain (Arabidopsis thaliana) SWISS-PROT:O64817; similar to casein kinase II, alpha chain 1 (Arabidopsis thaliana) SWISS-PROT:Q08467   chr2:9834201-9836535 FORWARD   Aliases: F21P24.14, F21P24_14	6.9	7.4	-0.5	-0.7	100.0%	-4.4
9627	AT5G24240.1   phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain, Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase   chr5:8231113-8232928 REVERSE   Aliases: MOP9.5, MOP9_5	3.6	3.5	0.2	0.7	100.0%	-4.9
9628	AT1G77400.1   expressed protein   chr1:29090705-29091737 FORWARD   Aliases: F2P24.15, F2P24_15	3.0	3.2	-0.1	-0.7	100.0%	-4.8
9629	AT3G07860.1   expressed protein   chr3:2507886-2509515 FORWARD   Aliases: F17A17.20	4.6	4.4	0.2	0.7	100.0%	-4.7
9630	AT1G75710.1   zinc finger (C2H2 type) family protein, contains zinc finger, C2H2 type, domain, PROSITE:PS00028	5.3	4.9	0.3	0.7	100.0%	-4.4
9631	AT1G13040.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:4447645-4449198 FORWARD   Aliases: F3F19.6, F3F19_6	2.2	2.3	-0.1	-0.7	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9632	AT5G40300.1   integral membrane protein, putative, MtN24 gene, Medicago truncatula, EMBL:MTY15290; contains Pfam PF04535 : Domain of unknown function (DUF588); contains 4 transmembrane domains; similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)   chr5:16128006-16130106 FORWARD   Aliases: MPO12.1, MPO12_1	7.0	6.8	0.2	0.7	100.0%	-4.7
9633	AT2G37820.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.9	-0.2	-0.7	100.0%	-4.5
9634	AT3G53840.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:19956549-19958697 FORWARD   Aliases: F5K20.140	4.2	4.0	0.2	0.7	100.0%	-4.8
9635	AT2G41310.1   Symbol: ATRR3   two-component responsive regulator / response reactor 3 (RR3), identical to response reactor 3 GI:3273200 from (Arabidopsis thaliana); contains Pfam profile: PF00072 response regulator receiver domain   chr2:17229011-17231505 FORWARD   Aliases: ARR8, RESPONSE REGULATOR 3	3.1	3.3	-0.2	-0.7	100.0%	-4.8
9636	AT3G13380.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr3:4346564-4350930 FORWARD   Aliases: MRP15.1	4.4	4.6	-0.2	-0.7	100.0%	-5.0
9637	AT1G14200.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:4854379-4855195 REVERSE   Aliases: F7A19.29, F7A19_29	5.6	5.3	0.3	0.7	100.0%	-4.6
9638	AT3G62140.1   similar to P0426D06.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_908670.1)	8.5	8.2	0.3	0.7	100.0%	-4.6
9639	AT1G48040.1   similar to protein phosphatase 2C-related / PP2C-related [Arabidopsis thaliana] (TAIR:At3g17250.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAT94045.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932); contains InterPro domain Protein phosphatase 2C subfamily (InterPro:IPR000222)   chr1:17723409-17725510 REVERSE   Aliases: T2J15.5	2.5	2.4	0.1	0.7	100.0%	-5.3
9640	AT3G63310.1   expressed protein, low similarity to N-methyl-D-aspartate receptor-associated protein (Drosophila melanogaster) GI:567104; contains Pfam profile PF01027: Uncharacterized protein family UPF0005	9.5	9.1	0.4	0.7	100.0%	-4.6
9641	AT2G26900.1   bile acid:sodium symporter family protein, low similarity to SP:Q12908 Ileal sodium/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family   chr2:11482034-11485022 REVERSE   Aliases: F12C20.6, F12C20_6	6.4	7.1	-0.6	-0.7	100.0%	-4.3
9642	AT5G03610.1   GDSL-motif lipase/hydrolase family protein, low similarity to SP:P40602 Anther-specific proline-rich protein APG precursor {Arabidopsis thaliana}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	6.9	7.1	-0.2	-0.7	100.0%	-4.9
9643	AT5G58110.1   expressed protein, predicted proteins, Homo sapiens and Drosophila melanogaster   chr5:23532412-23533860 FORWARD   Aliases: K21L19.11, K21L19_11	10.2	10.1	0.2	0.7	100.0%	-4.6
9644	AT5G45310.1   expressed protein   chr5:18376502-18378245 REVERSE   Aliases: K9E15.9, K9E15_9	4.1	3.9	0.2	0.7	100.0%	-4.8
9645	AT4G09510.2   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr4:6021271-6023815 REVERSE   Aliases: T15G18.70, T15G18_70	4.8	5.0	-0.2	-0.7	100.0%	-4.4
9646	AT5G18360.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:6080051-6083029 REVERSE   Aliases: F20L16.80, F20L16_80	2.9	2.7	0.2	0.7	100.0%	-5.0
9647	ATCG01040.1   Symbol: YCF5   hypothetical protein   chrC:114461-115447 FORWARD   Aliases: YCF5	10.1	10.7	-0.6	-0.7	100.0%	-4.8
9648	AT1G78815.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr1:29636636-29637638 REVERSE   Aliases: None	4.8	5.0	-0.2	-0.7	100.0%	-4.8
9649	AT4G25020.1   KOW domain-containing protein / D111/G-patch domain-containing protein, contains Pfam profiles PF01585: G-patch domain, PF00467: KOW motif   chr4:12860644-12861985 REVERSE   Aliases: F13M23.160, F13M23_160	6.7	6.3	0.3	0.7	100.0%	-4.2
9650	AT3G44370.1   expressed protein, weak similarity to AtOXA1 (Arabidopsis thaliana) GI:6624207   chr3:16044274-16046134 REVERSE   Aliases: T22K7.50	3.0	3.1	-0.1	-0.7	100.0%	-5.1
9651	AT3G22570.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:8000522-8001245 REVERSE   Aliases: F16J14.13	4.4	4.0	0.3	0.7	100.0%	-4.1
9652	AT3G62820.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Arabidopsis thaliana SP:Q43867, Lycopersicon esculentum SP:Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr3:23240724-23241476 FORWARD   Aliases: F26K9.250	2.1	2.1	-0.1	-0.7	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9653	AT4G02390.1   Symbol: APP   poly (ADP-ribose) polymerase / NAD(+) ADP-ribosyltransferase / poly(ADP-ribose) synthetase (APP), identical to SP:Q11207 Poly (ADP-ribose) polymerase (EC 2.4.2.30) (PARP) (ADPRT) (NAD(+) ADP- ribosyltransferase) (Poly(ADP-ribose) synthetase) {Arabidopsis thaliana}	4.9	5.0	-0.2	-0.7	100.0%	-4.6
9654	AT4G39130.1   dehydrin family protein, contains Pfam domain, PF00257: Dehydrin	2.4	2.3	0.1	0.7	100.0%	-5.1
9655	AT5G45820.1   Symbol: CIPK20	3.0	2.8	0.2	0.7	100.0%	-5.0
9656	AT5G44780.1   expressed protein, low similarity to SP:Q38732 DAG protein, chloroplast precursor {Antirrhinum majus}   chr5:18085327-18087868 FORWARD   Aliases: K23L20.12, K23L20_12	3.7	3.9	-0.2	-0.7	100.0%	-4.6
9657	AT5G28040.1   expressed protein, contains Pfam profile: PF04504 protein of unknown function, DUF573   chr5:10037273-10039005 REVERSE   Aliases: F15F15.110, F15F15_110	6.0	5.7	0.3	0.7	100.0%	-4.7
9658	NA	2.3	2.2	0.1	0.7	100.0%	-5.8
9659	AT2G02730.2   expressed protein   chr2:764546-767429 REVERSE   Aliases: T20F6.13, T20F6_13	4.2	4.4	-0.2	-0.7	100.0%	-5.1
9660	AT5G07730.1   expressed protein   chr5:2457348-2458431 REVERSE   Aliases: MBK20.19, MBK20_19	4.6	4.4	0.2	0.7	100.0%	-4.7
9661	AT1G74540.1   Symbol: CYP98A8   cytochrome P450, putative, similar to cytochrome P450 GB:O48922 (Glycine max); contains Pfam profile: PF00067 cytochrome P450	2.7	2.6	0.1	0.7	100.0%	-5.4
9662	AT2G03370.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At2g03360.1); similar to HGA1-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73716.1); contains InterPro domain Protein of unknown function DUF563 (InterPro:IPR007657)   chr2:1024707-1027042 REVERSE   Aliases: T4M8.20, T4M8_20	3.3	3.5	-0.2	-0.7	100.0%	-5.0
9663	AT2G39960.1   microsomal signal peptidase 25 kDa subunit, putative (SPC25), identical to Probable microsomal signal peptidase 25 kDa subunit (EC 3.4.-.-) (SPase 25 kDa subunit) (SPC25) (Swiss-Prot:P58684) (Arabidopsis thaliana); contains non-consensus AT-AC splice sites; contains 1 transmembrane domain;   chr2:16688609-16690718 REVERSE   Aliases: T28M21.12, T28M21_12	8.0	8.3	-0.3	-0.7	100.0%	-4.5
9664	AT1G23350.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.5	2.7	-0.1	-0.7	100.0%	-5.3
9665	AT5G55290.1   ATP synthase subunit H family protein, contains weak similarity to Vacuolar ATP synthase subunit H (EC 3.6.3.14) (V-ATPase H subunit) (Vacuolar proton pump H subunit) (V-ATPase M9.2 subunit) (V-ATPase 9.2 kDa membrane accessory protein) (Swiss-Prot:P81103) (Bos taurus); contains Pfam profile PF05493: ATP synthase subunit H   chr5:22440263-22441312 REVERSE   Aliases: MCO15.24, MCO15_24	10.2	10.0	0.2	0.7	100.0%	-4.9
9666	AT5G53050.3   similar to epoxide hydrolase, putative [Arabidopsis thaliana] (TAIR:At4g02340.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475819.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379); contains InterPro domain Epoxide hydrolase (InterPro:IPR000639); contains InterPro domain Alpha/beta hydrolase (InterPro:IPR003089); contains InterPro domain Alpha/beta hydrolase fold (InterPro:IPR000073)	6.0	5.7	0.3	0.7	100.0%	-4.4
9667	AT3G20770.1   Symbol: EIN3   ethylene-insensitive 3 (EIN3), identical to ethylene-insensitive3 GI:2224933 from (Arabidopsis thaliana)	7.3	6.9	0.4	0.7	100.0%	-4.5
9668	AT3G24080.1   KRR1 family protein, contains Pfam PF05178: Krr1 family   chr3:8694969-8697131 REVERSE   Aliases: F14O13.28	9.1	9.5	-0.4	-0.7	100.0%	-4.9
9669	AT3G11050.1   Symbol: ATFER2	6.6	6.2	0.4	0.7	100.0%	-4.0
9670	AT3G12780.1   Symbol: PGK1   phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase   chr3:4060978-4063230 REVERSE   Aliases: MBK21.15, PHOSPHOGLYCERATE KINASE 1	11.9	12.3	-0.4	-0.7	100.0%	-4.4
9671	AT2G14830.1   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292	2.3	2.3	-0.1	-0.7	100.0%	-5.6
9672	AT1G04840.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:1362866-1364961 REVERSE   Aliases: F13M7.17, F13M7_17	3.1	3.2	-0.1	-0.7	100.0%	-5.2
9673	AT1G45180.1   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:17101775-17104336 FORWARD   Aliases: F27F5.26, F27F5_26	3.8	3.9	-0.2	-0.7	100.0%	-4.7
9674	AT1G72460.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profiles: PF00560 leucine rich repeat (5 copies), PF00069 eukaryotic protein kinase domain   chr1:27283172-27285195 FORWARD   Aliases: T10D10.7, T10D10_7	3.3	3.1	0.1	0.7	100.0%	-5.1
9675	AT2G46370.2   Symbol: JAR1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr2:19040863-19043732 FORWARD   Aliases: F11C10.6, FAR RED INSENSITIVE 219, FIN219, JAR, JASMONATE RESISTANT 1	7.0	7.2	-0.2	-0.7	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9676	AT1G69120.1   Symbol: AP1   floral homeotic protein APETALA1 (AP1) / agamous-like MADS box protein (AGL7), identical to SP:P35631 Floral homeotic protein APETALA1 (AGL7 protein) {Arabidopsis thaliana}   chr1:25985999-25989919 REVERSE   Aliases: AGL7, APETALA1, F4N2.9, F4N2_9, FLORAL HOMEOTIC PROTEIN APETALA1	2.3	2.3	0.1	0.7	100.0%	-5.5
9677	AT3G62690.1   Symbol: ATL5   zinc finger (C3HC4-type RING finger) family protein (ATL5), identical to RING-H2 zinc finger protein ATL5 (Arabidopsis thaliana) gi:4928401:gb:AAD33583   chr3:23196331-23197677 REVERSE   Aliases: F26K9.120	4.5	4.2	0.3	0.7	100.0%	-4.4
9678	AT3G19310.1   expressed protein, similar to GB:CAB16796 from (Arabidopsis thaliana)   chr3:6694266-6696220 FORWARD   Aliases: MLD14.39	3.1	3.2	-0.1	-0.7	100.0%	-5.2
9679	AT2G04860.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:1706784-1708532 REVERSE   Aliases: F28I8.8, F28I8_8	4.0	3.7	0.3	0.7	100.0%	-4.7
9680	AT1G17810.2   Symbol: BETA TIP   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr1:6130600-6131961 FORWARD   Aliases: BETA TIP, BETA TONOPLAST INTRINSIC PROTEIN, F2H15.4, F2H15_4	3.4	3.2	0.2	0.7	100.0%	-4.5
9681	AT4G14300.1   heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative   chr4:8231013-8232987 FORWARD   Aliases: DL3190W, FCAALL.156	7.0	6.8	0.3	0.7	100.0%	-4.8
9682	AT3G12370.1   ribosomal protein L10 family protein, similar to 50S ribosomal protein L10 (Oryza sativa) GB:AAC64971 GI:3777602 (Oryza sativa)   chr3:3937197-3938101 REVERSE   Aliases: T2E22.37	7.8	8.1	-0.3	-0.7	100.0%	-4.3
9683	AT5G55960.1   expressed protein   chr5:22679802-22682259 FORWARD   Aliases: MYN21.7, MYN21_7	3.7	3.5	0.2	0.7	100.0%	-4.8
9684	AT5G57345.1   expressed protein   chr5:23246652-23247861 REVERSE   Aliases: None	4.7	4.6	0.2	0.7	100.0%	-4.6
9685	AT5G62720.2   integral membrane HPP family protein, contains Pfam domain, PF04982: HPP family   chr5:25209086-25212181 FORWARD   Aliases: MQB2.4, MQB2_4	7.2	7.4	-0.2	-0.7	100.0%	-4.4
9686	AT3G14370.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:4797852-4799511 REVERSE   Aliases: MLN21.22	2.8	3.0	-0.2	-0.7	100.0%	-4.6
9687	AT5G60440.1   MADS-box protein (AGL62), contains PfaI profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr5:24323555-24324746 FORWARD   Aliases: MUF9.24, MUF9_24	3.0	2.9	0.2	0.7	100.0%	-5.1
9688	AT5G43070.1   MFP1 attachment factor, putative, contains similarity to MFP1 attachment factor 1 similar to MFP1 attachment factor 1 (Glycine max) gi:7546729:gb:AAF63659   chr5:17306328-17307004 REVERSE   Aliases: MMG4.9, MMG4_9	3.0	3.1	-0.1	-0.7	100.0%	-5.2
9689	AT3G44080.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	0.1	0.7	100.0%	-5.7
9690	AT4G20100.1   PQ-loop repeat family protein / transmembrane family protein, similar to SP:Q10482 Seven transmembrane protein 1 {Schizosaccharomyces pombe}; contains Pfam profile PF04193: PQ loop repeat   chr4:10874009-10874875 REVERSE   Aliases: F1C12.1	3.9	3.7	0.2	0.7	100.0%	-5.0
9691	AT4G03156.1   small GTPase-related, contains weak similarity to Swiss-Prot:Q96283 ras-related protein Rab11A (Arabidopsis thaliana)   chr4:1396002-1396784 REVERSE   Aliases: None	2.5	2.6	-0.1	-0.7	100.0%	-5.5
9692	AT2G19560.1   proteasome protein-related, weak similarity to 26S proteasome non-ATPase regulatory subunit 3 (26S proteasome regulatory subunit S3) (p58) (Transplantation antigen P91A) (Tum-P91A antigen) (Swiss-Prot:P14685) (Mus musculus)   chr2:8472855-8476198 REVERSE   Aliases: F3P11.16, F3P11_16	5.2	5.4	-0.2	-0.7	100.0%	-4.8
9693	AT4G30825.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:15009611-15012325 FORWARD   Aliases: None	3.3	3.5	-0.1	-0.7	100.0%	-4.9
9694	AT3G24810.1   Symbol: ICK3   kip-related protein 5 (KRP5) / cyclin-dependent kinase inhibitor 5 (ICK5), identical to cyclin-dependent kinase inhibitor 5 (krp5) (Arabidopsis thaliana) GI:14422293   chr3:9060903-9062005 FORWARD   Aliases: K7P8.10, KRP5, Kip related protein 5	3.6	3.5	0.2	0.7	100.0%	-4.7
9695	AT5G15790.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:5148765-5151412 FORWARD   Aliases: F14F8.170, F14F8_170	3.0	2.9	0.1	0.7	100.0%	-5.2
9696	AT5G01410.1   stress-responsive protein, putative, similar to ethylene-inducible protein HEVER (Hevea brasiliensis) SWISS-PROT:Q39963   chr5:172317-173613 REVERSE   Aliases: T10O8.120, T10O8_120	10.3	9.8	0.5	0.7	100.0%	-4.3
9697	AT3G01360.2   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g55230.1); similar to TMV response-related protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD37906.1); contains InterPro domain Protein of unknown function DUF716 (InterPro:IPR006904)   chr3:137649-138738 REVERSE   Aliases: T13O15.14	5.0	4.8	0.2	0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9698	AT5G11310.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:3606403-3608608 FORWARD   Aliases: F2I11.200, F2I11_200	3.5	3.3	0.1	0.7	100.0%	-5.1
9699	AT1G02400.1   gibberellin 2-oxidase, putative / GA2-oxidase, putative, similar to GA2ox2 (GI:4678368); similar to dioxygenase GI:1666096 from (Marah macrocarpus); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:486802-489577 FORWARD   Aliases: T6A9.9, T6A9_9	3.4	3.0	0.4	0.7	100.0%	-4.3
9700	AT5G18500.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g17420.1); similar to putative kinase [Oryza sativa (japonica cultivar-group)] (GB:AAP54446.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:6138440-6141632 FORWARD   Aliases: T28N17.1	4.6	5.0	-0.4	-0.7	100.0%	-4.5
9701	AT5G18520.1   expressed protein   chr5:6145029-6146532 FORWARD   Aliases: T28N17.5	6.5	6.0	0.5	0.7	100.0%	-4.5
9702	AT1G33910.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}; contains Pfam profile PF04548: AIG1 family   chr1:12314884-12316238 FORWARD   Aliases: T3M13.7, T3M13_7	3.7	3.6	0.1	0.7	100.0%	-5.0
9703	AT1G72470.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr1:27287355-27289557 FORWARD   Aliases: T10D10.6, T10D10_6	4.3	4.5	-0.2	-0.7	100.0%	-4.8
9704	AT3G11510.1   40S ribosomal protein S14 (RPS14B), similar to 40S ribosomal protein S14 GB:P19950 (Zea mays)   chr3:3623463-3624945 REVERSE   Aliases: F24K9.19	9.3	9.8	-0.5	-0.7	100.0%	-4.4
9705	AT3G08570.1   phototropic-responsive protein, putative, similar to root phototropism RPT2 (Arabidopsis thaliana) gi:6959488:gb:AAF33112, a signal transducer of phototropic response PMID:10662859   chr3:2602264-2604281 REVERSE   Aliases: F17O14.4	4.7	4.5	0.2	0.7	100.0%	-4.7
9706	AT4G09080.1   similar to chloroplast outer envelope protein, putative [Arabidopsis thaliana] (TAIR:At3g46740.1); similar to chloroplast import-associated channel protein homolog [Oryza sativa (japonica cultivar-group)] (GB:NP_912397.1)   chr4:5803808-5806352 FORWARD   Aliases: F23J3.110, F23J3_110	3.8	3.6	0.1	0.7	100.0%	-4.9
9707	AT3G21970.1   receptor-like protein kinase-related, contains Pfam profile: PF01657 Domain of unknown function that is usually associated with protein kinase domain Pfam:PF00069; similar to receptor-like protein kinase 4 (GI:13506745) and receptor-like protein kinase 5 (GI:13506747) (Arabidopsis thaliana)   chr3:7742466-7743608 FORWARD   Aliases: MZN24.14	2.8	2.7	0.1	0.7	100.0%	-5.3
9708	AT1G79990.1   coatomer protein complex, subunit beta 2 (beta prime), putative, contains 7 WD-40 repeats (PF00400) (1 weak); similar to Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) (SP:P35606) (Homo sapiens); similar to Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) (SP:O55029) (Mus musculus)	5.6	5.8	-0.2	-0.7	100.0%	-4.7
9709	AT5G27970.1   expressed protein   chr5:10004724-10015672 FORWARD   Aliases: F15F15.40, F15F15_40	3.4	3.6	-0.3	-0.7	100.0%	-4.9
9710	AT3G49430.1   pre-mRNA splicing factor, putative, strong similarity to SP:O22315 Pre-mRNA splicing factor SF2 (SR1 protein) {Arabidopsis thaliana}   chr3:18342652-18345936 FORWARD   Aliases: T9C5.30	6.2	6.0	0.2	0.7	100.0%	-4.6
9711	AT1G28440.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor kinase GI:4105699 from (Arabidopsis thaliana)   chr1:9996810-10000433 FORWARD   Aliases: F3M18.12, F3M18_12	8.8	9.2	-0.4	-0.7	100.0%	-4.6
9712	AT3G21630.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:7615416-7618588 REVERSE   Aliases: MIL23.20	7.8	7.6	0.2	0.7	100.0%	-4.7
9713	AT3G32090.1   transcription factor-related, contains weak similarity to WIZZ (Nicotiana tabacum) gi:6472585:dbj:BAA87058   chr3:13082669-13083634 FORWARD   Aliases: F1M23.9	3.4	3.2	0.1	0.7	100.0%	-5.1
9714	AT4G02810.1   expressed protein   chr4:1256173-1257212 FORWARD   Aliases: T5J8.13, T5J8_13	5.1	4.7	0.3	0.7	100.0%	-4.4
9715	AT2G25230.1   Symbol: MYB100	2.7	2.6	0.1	0.7	100.0%	-5.8
9716	AT5G55010.1   hypothetical protein   chr5:22339126-22339455 FORWARD   Aliases: K13P22.1, K13P22_1	2.2	2.3	-0.1	-0.7	100.0%	-5.6
9717	AT1G60800.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr1:22387118-22391122 REVERSE   Aliases: F8A5.31, F8A5_31	4.3	4.6	-0.3	-0.7	100.0%	-4.4
9718	AT2G24460.1   expressed protein   chr2:10401409-10402470 FORWARD   Aliases: T28I24.19, T28I24_19	2.2	2.2	-0.1	-0.7	100.0%	-5.6
9719	AT1G27440.1   exostosin family protein, contains Pfam profile: PF03016	3.3	3.1	0.2	0.7	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9720	AT2G38510.1   MATE efflux protein-related, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr2:16131063-16132523 FORWARD   Aliases: T6A23.29, T6A23_29	2.6	2.5	0.1	0.7	100.0%	-5.4
9721	AT4G36560.1   hypothetical protein   chr4:17252662-17252994 FORWARD   Aliases: AP22.48, AP22_48	2.5	2.6	-0.1	-0.7	100.0%	-5.5
9722	AT3G12010.1   expressed protein, contains Prosite PS00626: Regulator of chromosome condensation (RCC1) signature 2   chr3:3821523-3825543 FORWARD   Aliases: MEC18.14	5.3	5.4	-0.2	-0.7	100.0%	-4.9
9723	AT2G31305.1   expressed protein   chr2:13357499-13358541 FORWARD   Aliases: None	4.4	4.3	0.1	0.7	100.0%	-5.0
9724	AT3G09735.1   DNA-binding S1FA family protein, contains Pfam profile: PF04689 DNA binding protein S1FA	9.6	9.8	-0.2	-0.7	100.0%	-4.9
9725	AT3G61770.1   expressed protein, contains Pfam domain, PF02681: Uncharacterized BCR, COG1963   chr3:22875518-22877380 FORWARD   Aliases: F21F14.5	5.2	4.9	0.2	0.7	100.0%	-4.4
9726	AT4G11850.1   Symbol: PLDGAMMA1   phospholipase D gamma 1 / PLD gamma 1 (PLDGAMMA1), identical to phospholipase D gamma 1 SP:Q9T053 from (Arabidopsis thaliana)   chr4:7129117-7133194 REVERSE   Aliases: T26M18.60, T26M18_60	4.5	4.6	-0.1	-0.7	100.0%	-5.0
9727	AT4G01920.1   DC1 domain-containing protein, similar to A. thaliana CHP-rich proteins   chr4:828890-831200 REVERSE   Aliases: T7B11.18, T7B11_18	2.8	3.0	-0.2	-0.7	100.0%	-4.7
9728	AT1G51830.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase GI:1321686 from (Arabidopsis thaliana)   chr1:19246694-19249679 REVERSE   Aliases: T14L22.4, T14L22_4	3.1	3.3	-0.2	-0.7	100.0%	-4.6
9729	AT4G19350.1   Symbol: EMB3006   expressed protein   chr4:10562034-10563768 REVERSE   Aliases: EMB3006, EMBRYO DEFECTIVE 3006, T5K18.130, T5K18_130	6.5	6.8	-0.3	-0.7	100.0%	-4.4
9730	AT3G12480.1   transcription factor, putative   chr3:3957844-3960479 FORWARD   Aliases: T2E22.20	8.3	8.0	0.2	0.7	100.0%	-5.0
9731	AT4G32530.1   vacuolar ATP synthase, putative / V-ATPase, putative, SP:P23968 Vacuolar ATP synthase 22 kDa proteolipid subunit (EC 3.6.3.14) {Saccharomyces cerevisiae}; contains Pfam profile PF00137: ATP synthase subunit C	8.3	7.6	0.7	0.7	100.0%	-4.2
9732	AT3G06660.1   PAPA-1-like family protein / zinc finger (HIT type) family protein, contains Pfam domains, PF04795: PAPA-1-like conserved region and PF04438: HIT zinc finger   chr3:2102477-2104912 FORWARD   Aliases: T8E24.3	5.8	6.1	-0.3	-0.7	100.0%	-4.5
9733	AT5G35770.1   Symbol: SAP   sterile apetala (SAP), identical to sterile apetala (GI:9758652) (Arabidopsis thaliana).   chr5:13953316-13958097 REVERSE   Aliases: MXH1.20, MXH1_20, STERILE APETALA	3.8	3.6	0.2	0.7	100.0%	-4.8
9734	AT3G23290.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g31160.1); similar to OSJNBb0072M01.12 [Oryza sativa (japonica cultivar-group)] (GB:XP_473175.1); contains InterPro domain Protein of unknown function DUF640 (InterPro:IPR006936)   chr3:8326986-8327355 FORWARD   Aliases: F28F4.1	3.2	3.3	-0.1	-0.7	100.0%	-4.9
9735	AT3G30190.1   hypothetical protein   chr3:11823753-11824820 FORWARD   Aliases: MIL15.1	2.3	2.2	0.1	0.7	100.0%	-5.7
9736	AT3G01100.2   Symbol: HYP1   similar to early-responsive to dehydration protein-related / ERD protein-related [Arabidopsis thaliana] (TAIR:At1g69450.1); similar to expressed protein (with alternative splicing) [Oryza sativa (japonica cultivar-group)] (GB:XP_469245.1); contains InterPro domain Protein of unknown function DUF221 (InterPro:IPR003864)	4.6	4.5	0.1	0.7	100.0%	-4.9
9737	AT3G07140.2   GPI transamidase component Gpi16 subunit family protein, similar to phosphatidyl inositol glycan class T (GI:14456615) (Homo sapiens); contains Pfam profile PF04113: Gpi16 subunit, GPI transamidase component   chr3:2261203-2263740 FORWARD   Aliases: T1B9.20	6.5	6.9	-0.4	-0.7	100.0%	-4.3
9738	AT2G44630.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF00646: F-box domain, PF01344: Kelch motif   chr2:18422771-18424059 REVERSE   Aliases: F16B22.12	3.3	3.4	-0.2	-0.7	100.0%	-4.8
9739	AT2G36430.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr2:15297283-15298842 FORWARD   Aliases: F1O11.6, F1O11_6	4.4	4.3	0.2	0.7	100.0%	-4.9
9740	AT3G14070.1   cation exchanger, putative (CAX9), similar to sodium/calcium exchanger protein (Mus musculus) gi:13925661:gb:AAK49407; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563	5.1	5.3	-0.3	-0.7	100.0%	-4.2
9741	AT2G15740.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:6863828-6864817 REVERSE   Aliases: F9O13.29	2.6	2.7	-0.2	-0.7	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9742	AT3G61900.1   auxin-responsive family protein, similar to auxin-induced protein SAUR-AC1 (GI:546362) (PIR:T06084) (Arabidopsis thaliana)   chr3:22936788-22937354 FORWARD   Aliases: F21F14.70	3.6	3.3	0.3	0.7	100.0%	-4.5
9743	AT5G42600.1   pentacyclic triterpene synthase, putative, similar to pentacyclic triterpene synthase (gi:6650207) (PMID: 11247608)   chr5:17070794-17075373 FORWARD   Aliases: MFO20.1, MFO20_1	4.3	4.0	0.3	0.7	100.0%	-4.5
9744	AT5G48750.1   auxin-responsive protein, putative, similar to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana);   chr5:19787278-19788045 REVERSE   Aliases: K24G6.8, K24G6_8	2.1	2.2	-0.1	-0.7	100.0%	-5.7
9745	AT1G51000.1   expressed protein, ; expression supported by MPSS   chr1:18913592-18913950 FORWARD   Aliases: F8A12.22, F8A12_22	2.6	2.6	0.1	0.7	100.0%	-5.9
9746	AT1G80600.1   acetylornithine aminotransferase, mitochondrial, putative / acetylornithine transaminase, putative / AOTA, putative / ACOAT, putative, similar to SP:O04866 Acetylornithine aminotransferase, mitochondrial precursor (EC 2.6.1.11) (ACOAT) (Acetylornithine transaminase) (AOTA) {Alnus glutinosa}; contains Pfam profile PF00202: aminotransferase, class III   chr1:30303410-30305445 REVERSE   Aliases: T21F11.7, T21F11_7	11.1	10.7	0.4	0.7	100.0%	-4.6
9747	AT2G32340.1   TraB family protein, contains Pfam domain PF01963: TraB family   chr2:13739324-13741611 FORWARD   Aliases: T32F6.14, T32F6_14	5.2	5.5	-0.3	-0.7	100.0%	-4.7
9748	AT3G26890.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g41110.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483533.1)   chr3:9908499-9912853 REVERSE   Aliases: MDJ14.23	8.8	8.7	0.1	0.7	100.0%	-5.2
9749	AT2G43530.1   Encodes a defensin-like (DEFL) family protein.   chr2:18077163-18077710 FORWARD   Aliases: T1O24.27	3.2	3.0	0.2	0.7	100.0%	-4.8
9750	AT3G21350.1   RNA polymerase transcriptional regulation mediator-related, contains weak similarity to RNA polymerase transcriptional regulation mediator, subunit 6 homolog (Activator-recruited cofactor 33 kDa component) (ARC33) (NY-REN-28 antigen) (Swiss-Prot:O75586) (Homo sapiens)   chr3:7517078-7518750 FORWARD   Aliases: MHC9.3	3.3	3.5	-0.2	-0.7	100.0%	-4.9
9751	AT1G51300.1   acyl-protein thioesterase-related, contains similarity to acyl-protein thioesterase-1 (Homo sapiens) gi:9965372:gb:AAG10063   chr1:19017928-19019771 REVERSE   Aliases: F11M15.15, F11M15_15	2.6	2.7	-0.2	-0.7	100.0%	-4.9
9752	AT2G01100.3   expressed protein   chr2:81455-83217 FORWARD   Aliases: F23H14.7, F23H14_7	9.0	8.6	0.5	0.7	100.0%	-4.9
9753	AT1G77280.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:29036362-29040776 REVERSE   Aliases: T14N5.13, T14N5_13	4.5	4.0	0.4	0.7	100.0%	-4.3
9754	AT5G61500.1   autophagy 3 (APG3), identical to autophagy 3 (Arabidopsis thaliana) GI:19912141; contains Pfam profiles PF03986: Autophagocytosis associated protein N-terminal domain, PF03987: Autophagocytosis associated protein C-terminal domain   chr5:24751131-24754074 REVERSE   Aliases: K11J9.1, K11J9_1	6.1	5.5	0.6	0.7	100.0%	-4.6
9755	AT2G43100.1   aconitase C-terminal domain-containing protein, contains Pfam profile PF00694: Aconitase C-terminal domain   chr2:17927737-17928766 FORWARD   Aliases: MFL8.14	4.5	4.2	0.3	0.7	100.0%	-4.6
9756	AT4G30940.1   potassium channel tetramerisation domain-containing protein, contains Pfam profile PF02214: K+ channel tetramerisation domain   chr4:15054879-15056832 FORWARD   Aliases: F6I18.150, F6I18_150	4.7	4.5	0.2	0.7	100.0%	-4.7
9757	AT2G17280.1   phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family   chr2:7520293-7522122 FORWARD   Aliases: F5J6.4, F5J6_4	9.5	9.0	0.5	0.7	100.0%	-4.0
9758	AT1G72150.1   Symbol: PATL1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to SEC14-like protein 2 (Alpha-tocopherol associated protein) (TAP) (bTAP) (Fragment) (SP:P58875) {Bos taurus}; similar to GI:807956 from (Saccharomyces cerevisiae); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus	8.9	8.1	0.8	0.7	100.0%	-4.3
9759	AT3G25510.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr3:9262075-9270034 REVERSE   Aliases: MWL2.22	2.3	2.2	0.1	0.7	100.0%	-5.6
9760	AT2G41060.1   RNA recognition motif (RRM)-containing protein, similar to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:17134067-17136636 FORWARD   Aliases: T3K9.17, T3K9_17	6.6	6.4	0.2	0.7	100.0%	-4.5
9761	AT5G01280.1   expressed protein   chr5:114010-116236 REVERSE   Aliases: T10O8.1	2.8	2.6	0.2	0.7	100.0%	-4.6
9762	AT5G30510.1   30S ribosomal protein S1, putative, similar to Swiss-Prot:P29344 30S ribosomal protein S1, chloroplast precursor (CS1) (Spinacia oleracea)   chr5:11636256-11638528 REVERSE   Aliases: None	10.2	10.4	-0.2	-0.7	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9763	AT5G38560.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:15456479-15460394 FORWARD   Aliases: MBB18.10, MBB18_10	7.5	7.7	-0.2	-0.7	100.0%	-4.7
9764	AT1G68650.1   expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	7.1	7.4	-0.3	-0.7	100.0%	-4.3
9765	AT2G38470.1   Symbol: WRKY33	5.4	4.9	0.4	0.7	100.0%	-4.4
9766	AT5G01500.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:198948-201551 FORWARD   Aliases: F7A7.20, F7A7_20	6.2	6.6	-0.4	-0.7	100.0%	-4.7
9767	AT2G04680.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.9	-0.2	-0.7	100.0%	-4.3
9768	AT3G47800.1   aldose 1-epimerase family protein, similar to ALDOSE 1-EPIMERASE PRECURSOR GB:P05149 (SP:P05149) from (Acinetobacter calcoaceticus); contains Pfam profile PF01263 Aldose 1-epimerase   chr3:17645795-17648595 FORWARD   Aliases: T23J7.130	4.9	5.2	-0.4	-0.7	100.0%	-4.0
9769	AT3G10460.1   self-incompatibility protein-related, similar to self-incompatibility (Papaver nudicaule) GI:3097262   chr3:3255805-3256444 FORWARD   Aliases: F13M14.26	3.5	3.3	0.2	0.7	100.0%	-4.9
9770	AT3G50250.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:18641014-18641460 REVERSE   Aliases: F11C1.90	8.4	8.0	0.4	0.7	100.0%	-4.3
9771	AT1G50800.1   expressed protein   chr1:18830577-18832006 REVERSE   Aliases: F8A12.5, F8A12_5	2.6	2.5	0.1	0.7	100.0%	-5.5
9772	AT4G25770.1   expressed protein   chr4:13117548-13120123 REVERSE   Aliases: F14M19.50, F14M19_50	4.1	3.9	0.2	0.7	100.0%	-4.5
9773	AT4G14910.1   Symbol: IGPD   imidazoleglycerol-phosphate dehydratase, putative, similar to SP:P34047 Imidazoleglycerol-phosphate dehydratase 1 (EC 4.2.1.19) (IGPD 1) {Arabidopsis thaliana}; contains Pfam profile PF00475: imidazoleglycerol-phosphate dehydratase   chr4:8528163-8530110 REVERSE   Aliases: DL3495C, FCAALL.36, IMIDAZOLEGLYCEROLPHOSPHATE DEHYDRATASE	5.7	5.4	0.3	0.7	100.0%	-4.4
9774	AT2G03350.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr2:1019576-1021183 REVERSE   Aliases: T4M8.22, T4M8_22	6.0	6.2	-0.2	-0.7	100.0%	-4.4
9775	AT4G14420.1   lesion inducing protein-related, similar to ORF, able to induce HR-like lesions (Nicotiana tabacum) gi:1762945:gb:AAC49975   chr4:8301951-8303911 REVERSE   Aliases: DL3250C, FCAALL.105	6.9	6.5	0.4	0.7	100.0%	-4.5
9776	AT1G73720.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to Will die slowly protein (SP:Q9V3J8)(Drosophila melanogaster)   chr1:27728663-27733592 FORWARD   Aliases: F25P22.14, F25P22_14	4.2	4.4	-0.2	-0.7	100.0%	-4.7
9777	AT5G43910.3   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr5:17684634-17687466 REVERSE   Aliases: F6B6.5, F6B6_5	4.2	4.4	-0.3	-0.7	100.0%	-4.2
9778	AT5G58470.2   zinc finger (Ran-binding) family protein, weak similarity to SP:Q01844 RNA-binding protein EWS (EWS oncogene) (Ewing sarcoma breakpoint region 1 protein) {Homo sapiens}; contains Pfam profiles PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), PF00641: Zn-finger in Ran binding protein and others   chr5:23654933-23658146 REVERSE   Aliases: MQJ2.7, MQJ2_7	4.4	4.2	0.2	0.7	100.0%	-4.6
9779	AT4G21450.2   vesicle-associated membrane family protein / VAMP family protein, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia)   chr4:11426034-11428354 FORWARD   Aliases: F18E5.70, F18E5_70	8.2	7.7	0.5	0.7	100.0%	-4.4
9780	AT3G08550.1   Symbol: KOB1   elongation defective 1 protein / ELD1 protein, annotation temporarily based on supporting cDNA gi:23452833:gb:AF543710.1:   chr3:2596434-2599825 FORWARD   Aliases: ABA INSENSITIVE 8, ABI8, ELD1, ELONGATION DEFECTIVE 1, F17O14.2, KOBITO	5.9	5.4	0.5	0.7	100.0%	-4.6
9781	AT1G30950.1   Symbol: UFO   unusual floral organ (UFO) / F-box family protein (FBX1), E3 ubiquitin ligase SCF complex F-box subunit; almost identical to unusual floral organs (UFO)GI:4376159 from (Arabidopsis thaliana) Landsberg-erecta; one amino acid difference   chr1:11036161-11037489 FORWARD   Aliases: F17F8.16, UFO, UNUSUAL FLORAL ORGANS	3.4	3.6	-0.1	-0.7	100.0%	-5.3
9782	AT3G31930.1   expressed protein   chr3:12930821-12931699 FORWARD   Aliases: T1O13.1	2.6	2.7	-0.1	-0.7	100.0%	-5.5
9783	AT3G14010.1   Symbol: CID4   hydroxyproline-rich glycoprotein family protein, similar to Mrs16p (GI:2737884) (Saccharomyces cerevisiae); weak similarity to ataxin-2 related protein (GI:1679686) (Homo sapiens). Included in a family of CTC interacting domain proteins found to interact with PAB2.   chr3:4636373-4640977 FORWARD   Aliases: CID4, MDC16.14	5.6	6.1	-0.5	-0.7	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9784	AT3G57960.1   emsy N terminus domain-containing protein / ENT domain-containing protein, contains Pfam profile PF03735: ENT domain   chr3:21474068-21475171 FORWARD   Aliases: T10K17.170	2.6	2.5	0.1	0.7	100.0%	-5.0
9785	AT4G29680.1   type I phosphodiesterase/nucleotide pyrophosphatase family protein, similar to SP:P06802 Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1) (Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) {Mus musculus}); contains Pfam profile PF01663: Type I phosphodiesterase / nucleotide pyrophosphatase   chr4:14537787-14539600 REVERSE   Aliases: T16L4.190, T16L4_190	6.2	6.7	-0.5	-0.7	100.0%	-4.6
9786	AT4G12570.1   Symbol: UPL5   ubiquitin-protein ligase, putative, similar to SP:P39940 Ubiquitin--protein ligase RSP5 (EC 6.3.2.-) {Saccharomyces cerevisiae}; contains Pfam profiles PF00240: Ubiquitin family, PF00632: HECT-domain (ubiquitin-transferase)   chr4:7445359-7449083 FORWARD   Aliases: T1P17.160, T1P17_160, UBIQUITIN PROTEIN LIGASE 5, UPL5	5.8	5.5	0.3	0.7	100.0%	-4.6
9787	AT5G63510.1   bacterial transferase hexapeptide repeat-containing protein, contains similarity to acetyltransferase; contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)   chr5:25441226-25443067 FORWARD   Aliases: MLE2.14, MLE2_14	9.4	9.8	-0.4	-0.7	100.0%	-4.7
9788	AT2G45450.1   expressed protein   chr2:18740351-18741056 REVERSE   Aliases: F4L23.4	3.4	3.6	-0.2	-0.7	100.0%	-4.8
9789	AT3G54380.2   SAC3/GANP family protein, contains Pfam profile: PF03399 SAC3/GANP family   chr3:20144872-20147769 REVERSE   Aliases: T14E10.7	5.7	5.5	0.1	0.7	100.0%	-5.2
9790	AT3G29075.1   glycine-rich protein   chr3:11052726-11053931 REVERSE   Aliases: MRI12.9	9.7	10.0	-0.4	-0.7	100.0%	-4.7
9791	AT5G49820.1   Symbol: EMB1879   expressed protein, contains Pfam domain, PF04884: Protein of unknown function, DUF647	6.2	6.4	-0.3	-0.7	100.0%	-4.5
9792	AT4G23070.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr4:12090701-12092088 REVERSE   Aliases: F7H19.260, F7H19_260	3.2	3.0	0.2	0.7	100.0%	-5.2
9793	AT2G17290.1   Symbol: CPK6   calcium-dependent protein kinase isoform 6 (CPK6), identical to calmodulin-domain protein kinase CDPK isoform 6 (Arabidopsis thaliana) gi:1399275:gb:AAB03246; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048	5.4	4.9	0.4	0.7	100.0%	-4.4
9794	AT5G10850.1   expressed protein   chr5:3428160-3428825 FORWARD   Aliases: T30N20.120, T30N20_120	8.2	7.8	0.3	0.7	100.0%	-4.1
9795	AT2G30960.1   expressed protein   chr2:13183781-13185405 REVERSE   Aliases: F7F1.17, F7F1_17	7.6	7.2	0.4	0.7	100.0%	-4.3
9796	AT2G22560.1   kinase interacting protein-related, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia); weak similarity to Myosin II heavy chain, non muscle (Swiss-Prot:P08799) (Dictyostelium discoideum   chr2:9593243-9595918 FORWARD   Aliases: F14M13.4, F14M13_4	3.3	3.4	-0.2	-0.7	100.0%	-4.8
9797	AT5G66020.1   Symbol: ATSAC1B/IBS2   Encodes a phosphoinositide phosphatase that modulates cellular phosphoinositide levels. Mutants in this gene are unable to express female sterility in response to beta-aminobutyric acid, as wild type plants do. non-consensus AT donor splice site at exon 7, TA donor splice site at exon 10, AT acceptor splice at exon 13   chr5:26418493-26421917 REVERSE   Aliases: ATSAC1B, IBS2, IMPAIRED IN BABA INDUCED STERILITY 2, K2A18.9, K2A18_9	3.4	3.3	0.2	0.7	100.0%	-4.8
9798	AT1G17530.1   Symbol: ATTIM23 1   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr1:6027624-6028450 FORWARD   Aliases: F11A6.23, TRANSLOCASE OF INNER MITOCHONDRIAL MEMBRANE 23	6.2	5.9	0.3	0.7	100.0%	-4.7
9799	AT1G22860.1   TGF beta receptor associated protein-related, contains weak similarity to TGF beta receptor associated protein-1 (Homo sapiens) gi:3150052:gb:AAC16903   chr1:8083389-8089225 FORWARD   Aliases: F19G10.18, F19G10_18	4.3	4.5	-0.2	-0.7	100.0%	-4.6
9800	AT1G47940.1   expressed protein   chr1:17671954-17673382 FORWARD   Aliases: T6B12.6, T6B12_6	2.9	2.8	0.1	0.7	100.0%	-5.1
9801	AT2G47140.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to 3-beta-hydroxysteroiddehydrogenase GI:15983819 from (Digitalis lanata)   chr2:19357810-19359158 REVERSE   Aliases: F14M4.3	3.0	3.2	-0.2	-0.7	100.0%	-4.8
9802	AT2G42380.2   bZIP transcription factor family protein	2.2	2.1	0.1	0.7	100.0%	-5.5
9803	AT3G26920.1   F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.8	0.1	0.7	100.0%	-5.1
9804	AT5G19420.1   zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein, similar to zinc finger protein (Arabidopsis thaliana) gi:15811367:gb:AAL08940   chr5:6547640-6552850 REVERSE   Aliases: F7K24.170, F7K24_170	3.3	3.2	0.1	0.7	100.0%	-5.1
9805	AT2G15080.2   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780	2.3	2.2	0.1	0.7	100.0%	-5.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9806	AT2G20180.2   Symbol: PIL5   basic helix-loop-helix (bHLH) family protein, contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	2.3	2.2	0.1	0.7	100.0%	-5.3
9807	AT3G06070.1   expressed protein   chr3:1831063-1831929 REVERSE   Aliases: F24F17.5, F24F17_5	2.4	2.3	0.1	0.7	100.0%	-5.5
9808	AT5G59170.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:23899214-23900348 FORWARD   Aliases: MNC17.8, MNC17_8	3.0	3.1	-0.1	-0.7	100.0%	-5.1
9809	AT1G10740.2   expressed protein   chr1:3568191-3570761 REVERSE   Aliases: T16B5.12, T16B5_12	5.7	6.0	-0.3	-0.7	100.0%	-4.5
9810	AT5G18180.1   Gar1 RNA-binding region family protein, contains Pfam profile PF04410: Gar1 protein RNA binding region   chr5:6008563-6009607 REVERSE   Aliases: MRG7.14, MRG7_14	3.4	3.6	-0.1	-0.7	100.0%	-4.9
9811	AT3G60550.1   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr3:22390821-22391616 FORWARD   Aliases: T8B10.210	2.8	2.6	0.2	0.7	100.0%	-5.1
9812	AT3G50130.1   expressed protein, ; expression supported by MPSS   chr3:18600094-18602205 REVERSE   Aliases: F3A4.210	2.1	2.2	-0.1	-0.7	100.0%	-5.7
9813	AT1G22660.2   tRNA-nucleotidyltransferase, putative / tRNA adenylyltransferase, putative, similar to tRNA nucleotidyltransferase (Lupinus albus) GI:1139585; contains Pfam profile PF01743: polyA polymerase family protein   chr1:8017386-8021582 FORWARD   Aliases: T22J18.17, T22J18_17	4.5	4.6	-0.2	-0.7	100.0%	-4.7
9814	AT3G49470.1   nascent polypeptide-associated complex (NAC) domain-containing protein, similar to alpha-NAC, non-muscle form (Mus musculus) GI:1666690; contains Pfam profile PF01849: NAC domain   chr3:18351974-18353459 FORWARD   Aliases: T9C5.70	9.7	10.0	-0.3	-0.7	100.0%	-4.3
9815	AT1G60440.1   eukaryotic pantothenate kinase family protein, similar to pantothenate kinase GI:4191500 from (Aspergillus nidulans); contains Pfam profile PF03630: Fumble   chr1:22270175-22272906 REVERSE   Aliases: T13D8.31, T13D8_31	8.7	8.6	0.1	0.7	100.0%	-5.2
9816	AT1G70400.2   similar to pre-mRNA processing ribonucleoprotein binding region-containing protein [Arabidopsis thaliana] (TAIR:At1g60170.1); similar to putative U4/U6 snRNP-associated 61 kDa protein [Oryza sativa (japonica cultivar-group)] (GB:NP_911137.2)   chr1:26535503-26537123 REVERSE   Aliases: F17O7.6, F17O7_6	3.2	3.0	0.1	0.7	100.0%	-5.1
9817	AT1G76490.1   Symbol: HMG1   similar to 3-hydroxy-3-methylglutaryl-CoA reductase 2 / HMG-CoA reductase 2 (HMGR2) [Arabidopsis thaliana] (TAIR:At2g17370.1); similar to 3-hydroxy-3-methylglutaryl coenzyme A reductase [Hevea brasiliensis] (GB:AAU08214.1); similar to HMG-CoA reductase [Cucumis melo] (GB:BAA36291.1); similar to 3-hydroxy-3-methylglutaryl-coenzyme A reductase [Hevea brasiliensis] (GB:AAQ63055.1); similar to hydroxymethylglutaryl-CoA reductase (NADPH) [Raphanus sativus] (GB:CAA48610.1); similar to 3-hydroxy-3-methylglutaryl coenzyme A reductase; HMG-CoA reductase; EuHMGR [Eucommia ulmoides] (GB:AAV54051.1); contains InterPro domain 3-hydroxy-3-methylglutaryl Coenzyme A reductase (InterPro:IPR004554); contains InterPro domain Hydroxymethylglutaryl-coenzyme A reductase (InterPro:IPR002202)   chr1:28700654-28703687 FORWARD   Aliases: 3 HYDROXY 3 METHYLGLUTARYL COA REDUCTASE, F15M4.1, HMG COA REDUCTASE, HMGR1	6.7	7.2	-0.5	-0.7	100.0%	-4.4
9818	AT3G10160.1   Symbol: ATDFC   similar to dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS2) [Arabidopsis thaliana] (TAIR:At5g05980.1); similar to tetrahydrofolylpolyglutamate synthase (EC 6.3.2.17) - human (GB:A46281); similar to folylpolyglutamate synthase [Homo sapiens] (GB:CAI39770.1); contains InterPro domain Folylpolyglutamate synthetase (InterPro:IPR001645)   chr3:3139388-3144511 REVERSE   Aliases: A. THALIANA DHFS FPGS HOMOLOG C, T22K18.1	4.7	4.9	-0.2	-0.7	100.0%	-4.7
9819	AT1G05430.1   expressed protein   chr1:1594056-1595817 REVERSE   Aliases: T25N20.8, T25N20_8	7.1	7.5	-0.3	-0.7	100.0%	-4.5
9820	AT3G13400.1   Symbol: SKS13   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr3:4355145-4357435 FORWARD   Aliases: MRP15.10, SKS13	2.5	2.5	0.1	0.7	100.0%	-5.3
9821	AT2G27700.1   eukaryotic translation initiation factor 2 family protein / eIF-2 family protein, similar to SP:P39730 Translation initiation factor IF-2 {Saccharomyces cerevisiae}; contains Pfam profiles PF00009: Elongation factor Tu GTP binding domain, PF03144: Elongation factor Tu domain 2   chr2:11821026-11823079 REVERSE   Aliases: F15K20.20, F15K20_20	3.0	2.9	0.1	0.7	100.0%	-5.6
9822	AT5G47710.1   C2 domain-containing protein, contains similarity to CLB1 (Lycopersicon esculentum) GI:2789434; contains Pfam profile PF00168: C2 domain	4.9	5.0	-0.2	-0.7	100.0%	-4.7
9823	AT3G06250.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr3:1888842-1892781 REVERSE   Aliases: F28L1.19, F28L1_19	3.2	3.3	-0.1	-0.7	100.0%	-5.3
9824	AT4G05460.1   F-box family protein (FBL20), contains similarity to N7 protein GI:3273101 from (Medicago truncatula)   chr4:2760691-2762413 REVERSE   Aliases: C6L9.140, C6L9_140	5.7	5.9	-0.2	-0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9825	AT4G14880.2   Symbol: OASA1   cysteine synthase / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase (OAS1), nearly identical to SP:P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.5-8) GI:6983573   chr4:8517955-8520406 REVERSE   Aliases: DL3480C, FCAALL.34	11.6	12.0	-0.4	-0.7	100.0%	-4.8
9826	AT4G29050.1   lectin protein kinase family protein, contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr4:14314824-14316885 REVERSE   Aliases: F19B15.80, F19B15_80	3.7	3.5	0.2	0.7	100.0%	-4.6
9827	AT5G67250.1   Symbol: SKIP2   SKP1 interacting partner 2 (SKIP2), identical to SKP1 interacting partner 2 GI:10716949 from (Arabidopsis thaliana)   chr5:26848599-26850559 REVERSE   Aliases: K21H1.6, K21H1_6, SKP1 INTERACTING PARTNER 2, VFB4, VIER F BOX PROTEINE 4	7.9	7.5	0.4	0.7	100.0%	-4.7
9828	AT2G42310.1   expressed protein   chr2:17632290-17632967 FORWARD   Aliases: MHK10.3, MHK10_3	8.3	8.6	-0.4	-0.7	100.0%	-4.6
9829	AT2G41300.1   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088; protein alignments support a CG non-consensus donor splice site.   chr2:17221315-17223370 REVERSE   Aliases: F13H10.15, F13H10_15	10.5	10.1	0.4	0.7	100.0%	-4.5
9830	AT2G16480.1   SWIB complex BAF60b domain-containing protein / plus-3 domain-containing protein, contains Pfam profiles PF02201: BAF60b domain of the SWIB complex, PF03126: Plus-3 domain   chr2:7147357-7148931 REVERSE   Aliases: F16F14.2, F16F14_2	3.9	4.2	-0.3	-0.7	100.0%	-4.6
9831	AT4G28410.1   aminotransferase-related, similar to nicotianamine aminotransferase (Hordeum vulgare subsp. vulgare) GI:6469090   chr4:14052252-14055018 FORWARD   Aliases: F20O9.90, F20O9_90	3.1	2.9	0.1	0.7	100.0%	-4.9
9832	AT3G57180.1   expressed protein   chr3:21174524-21177009 REVERSE   Aliases: F28O9.30	5.4	5.8	-0.4	-0.7	100.0%	-4.1
9833	AT1G66140.1   Symbol: ZFP4   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:24623500-24625667 REVERSE   Aliases: F15E12.19, F15E12_19, ZFP4, ZINC FINGER PROTEIN 4	5.4	5.2	0.2	0.7	100.0%	-4.5
9834	AT4G01800.1   preprotein translocase secA subunit, putative, similar to preprotein translocase secA subunit, chloroplast (precursor) SP:Q9SYI0 from (Arabidopsis thaliana); non-consensus GA donor splice site at exon 4   chr4:770926-776131 REVERSE   Aliases: T7B11.6, T7B11_6	5.3	5.5	-0.2	-0.7	100.0%	-4.8
9835	AT5G19010.1   Symbol: ATMPK16   mitogen-activated protein kinase, putative / MAPK, putative (MPK16), mitogen-activated protein kinase (MAPK)(AtMPK16), PMID:12119167; similar to ATMPK9, Arabidopsis thaliana, EMBL:AB038694   chr5:6344791-6348214 REVERSE   Aliases: T16G12.50, T16G12_50	6.1	6.5	-0.3	-0.7	100.0%	-4.7
9836	AT3G10660.1   Symbol: CPK2   calcium-dependent protein kinase isoform 2 (CPK2), identical to calcium-dependent protein kinase isoform 2 (Arabidopsis thaliana) gi:9837343:gb:AAG00535; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr3:3331403-3334273 REVERSE   Aliases: ATCPK2, CALMODULIN DOMAIN PROTEIN KINASE CDPK ISOFORM 2, F13M14.5	3.6	3.8	-0.2	-0.7	100.0%	-4.5
9837	AT4G09520.1   2,3-bisphosphoglycerate-independent phosphoglycerate mutase family protein / phosphoglyceromutase family protein, contains similarity to 2,3-bisphosphoglycerate-independent phosphoglycerate mutase 1 (EC 5.4.2.1) (Phosphoglyceromutase 1) (BPG-independent PGAM 1) (aPGAM 1) (aPGAM-Mj1). (Swiss-Prot:Q59007) (Methanococcus jannaschii); contains weak hit to Pfam profile PF01676: Metalloenzyme superfamily	4.6	4.9	-0.3	-0.7	100.0%	-4.6
9838	AT4G11800.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.9	6.6	0.2	0.7	100.0%	-4.8
9839	AT2G01220.2   expressed protein   chr2:123275-126426 FORWARD   Aliases: AT2G01230, F10A8.10, F10A8_10	6.6	6.7	-0.1	-0.7	100.0%	-5.1
9840	AT4G14340.1   Symbol: CKI1   casein kinase I (CKI1), identical to casein kinase I (Arabidopsis thaliana) gi:1103318:emb:CAA55395   chr4:8248282-8251964 REVERSE   Aliases: CASEIN KINASE I, DL3210C, FCAALL.68	5.3	5.6	-0.3	-0.7	100.0%	-4.3
9841	AT5G13390.1   Symbol: NEF1   expressed protein   chr5:4292804-4296575 FORWARD   Aliases: NO EXINE FORMATION 1, T22N19.40, T22N19_40	5.8	6.0	-0.3	-0.7	100.0%	-4.5
9842	AT5G20080.1   NADH-cytochrome b5 reductase, putative, similar to SP:P36060 NADH-cytochrome b5 reductase precursor (EC 1.6.2.2) {Saccharomyces cerevisiae}; contains Pfam profiles PF00175: Oxidoreductase NAD-binding domain, PF00970: oxidoreductase, FAD-binding   chr5:6782568-6786659 FORWARD   Aliases: F28I16.230, F28I16_230	8.1	8.7	-0.7	-0.7	100.0%	-4.4
9843	AT1G59535.1   hypothetical protein, identical to hypothetical protein GI:8778767 from (Arabidopsis thaliana)   chr1:21874873-21875192 REVERSE   Aliases: T30E16.8, T30E16_8	2.4	2.4	-0.1	-0.7	100.0%	-5.7
9844	AT4G15180.1   SET domain-containing protein, contains Pfam profile PF00856: SET domain	4.1	3.7	0.4	0.7	100.0%	-4.3
9845	AT2G46250.1   myosin heavy chain-related, contains weak similarity to Myosin heavy chain, muscle (Swiss-Prot:P05661) (Drosophila melanogaster)	3.3	3.4	-0.1	-0.7	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9846	AT5G47960.1   Symbol: SMG1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family   chr5:19438610-19439759 REVERSE   Aliases: K16F13.4, K16F13_4, SMALL MOLECULAR WEIGHT G PROTEIN 1	3.0	2.9	0.1	0.7	100.0%	-5.2
9847	AT3G10310.1   kinesin motor protein-related, similar to carboxy-terminal kinesin 2 GB:P79955 (Xenopus laevis)   chr3:3190213-3195010 FORWARD   Aliases: F14P13.9	2.5	2.6	-0.1	-0.7	100.0%	-5.4
9848	AT1G75890.1   family II extracellular lipase 2 (EXL2), EXL2 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 (Arabidopsis thaliana)   chr1:28496712-28498708 FORWARD   Aliases: T4O12.240, T4O12_240	2.3	2.4	-0.1	-0.7	100.0%	-5.5
9849	AT4G16270.1   peroxidase 40 (PER40) (P40), identical to SP:O23474 Peroxidase 40 precursor (EC 1.11.1.7) (Atperox P40) {Arabidopsis thaliana}   chr4:9205045-9206538 FORWARD   Aliases: DL4175W, FCAALL.329	2.9	3.0	-0.1	-0.7	100.0%	-5.1
9850	AT4G29480.1   mitochondrial ATP synthase g subunit family protein, contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit	12.0	12.3	-0.2	-0.7	100.0%	-4.9
9851	AT3G61920.1   expressed protein, hypothetical protein F1N19.27 - Arabidopsis thaliana, EMBL:AC009519   chr3:22943471-22944336 REVERSE   Aliases: F21F14.90	4.2	4.0	0.2	0.7	100.0%	-5.1
9852	AT5G54610.1   ankyrin repeat family protein, contains Pfam domain, PF00023: Ankyrin repeat   chr5:22202005-22203733 REVERSE   Aliases: MRB17.11, MRB17_11	2.4	2.5	-0.1	-0.7	100.0%	-5.5
9853	AT5G05800.1   expressed protein   chr5:1743087-1745246 REVERSE   Aliases: MJJ3.22, MJJ3_22	5.8	5.6	0.2	0.7	100.0%	-4.7
9854	ATCG00170.1   Symbol: RPOC2   RNA polymerase beta' subunit-2   chrC:15938-20068 REVERSE   Aliases: RPOC2	8.1	8.9	-0.8	-0.7	100.0%	-4.5
9855	AT1G04760.1   Symbol: ATVAMP726   synaptobrevin family protein, similar to Vesicle-associated membrane protein 722 (AtVAMP722) Synaptobrevin-related protein 1 (SP:P47192) {Arabidopsis thaliana}   chr1:1334759-1336069 FORWARD   Aliases: F13M7.25, F13M7_25, VAMP726	4.7	4.5	0.2	0.7	100.0%	-4.5
9856	AT5G46760.1   basic helix-loop-helix (bHLH) family protein   chr5:18991458-18993236 FORWARD   Aliases: MZA15.18, MZA15_18	5.2	5.5	-0.2	-0.7	100.0%	-4.8
9857	AT4G12790.3   similar to ATP-binding family protein [Arabidopsis thaliana] (TAIR:At5g22370.1); similar to unnamed protein product [Kluyveromyces lactis NRRL Y-1140] (GB:CAH00979.1); similar to hypothetical protein UM01243.1 [Ustilago maydis 521] (GB:EAK81850.1); contains InterPro domain Conserved hypothetical ATP binding protein (InterPro:IPR004130)   chr4:7517052-7519394 REVERSE   Aliases: T20K18.140, T20K18_140	7.4	7.8	-0.4	-0.7	100.0%	-4.5
9858	AT5G28780.1   hypothetical protein, various predicted proteins, Arabidopsis thaliana   chr5:10812911-10814177 REVERSE   Aliases: T32B20.70, T32B20_70	2.1	2.2	-0.1	-0.7	100.0%	-5.7
9859	AT1G18750.2   similar to MADS-box family protein [Arabidopsis thaliana] (TAIR:At1g69540.1); similar to putative MADS-domain transcription factor [Physcomitrella patens] (GB:CAD18831.1)   chr1:6467322-6469975 FORWARD   Aliases: F6A14.14, F6A14_14	3.6	3.8	-0.2	-0.7	100.0%	-4.9
9860	AT3G47730.1   Symbol: ATATH1	5.1	4.8	0.3	0.7	100.0%	-4.4
9861	AT5G49810.1   Symbol: MMT   methionine S-methyltransferase, identical to methionine S-methyltransferase (Arabidopsis thaliana) GI:5733429   chr5:20256574-20263606 FORWARD   Aliases: K21G20.2, K21G20_2, MET S METHYLTRANSFERASE	7.4	7.8	-0.4	-0.7	100.0%	-4.7
9862	AT5G32450.1   RNA recognition motif (RRM)-containing protein, various predicted proteins, Arabidopsis thaliana and others   chr5:12096848-12098803 FORWARD   Aliases: F18O9.60, F18O9_60	9.4	9.3	0.1	0.7	100.0%	-5.1
9863	AT2G26420.1   1-phosphatidylinositol-4-phosphate 5-kinase, putative / PIP kinase, putative / PtdIns(4)P-5-kinase, putative / diphosphoinositide kinase, putative, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr2:11246512-11249317 REVERSE   Aliases: T9J22.9, T9J22_9	2.8	2.7	0.1	0.7	100.0%	-4.9
9864	AT3G43630.1   nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313   chr3:15549804-15550406 FORWARD   Aliases: F22J12.3	4.8	4.6	0.3	0.7	100.0%	-4.7
9865	AT1G20160.2   similar to subtilase family protein [Arabidopsis thaliana] (TAIR:At1g20150.1); similar to putative subtilisin precursor [Glycine max] (GB:CAB87247.1); similar to subtilisin-like protein [Glycine max] (GB:AAK53589.1); similar to subtilisin-like protein [Picea abies] (GB:BAA13135.1); contains InterPro domain Protease-associated PA (InterPro:IPR003137); contains InterPro domain Subtilase serine protease (InterPro:IPR000209)	6.0	5.7	0.3	0.7	100.0%	-4.5
9866	AT5G28300.1   trihelix DNA-binding protein, putative, similar to GT-2 factor (Arabidopsis thaliana GI:416490   chr5:10292655-10295287 REVERSE   Aliases: T8M17.70, T8M17_70	2.6	2.7	-0.1	-0.7	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9867	AT3G44510.1   expressed protein   chr3:16119094-16120345 REVERSE   Aliases: F14L2.60	3.1	2.8	0.3	0.7	100.0%	-4.1
9868	AT4G34840.1   nucleosidase-related, contains weak similarity to MTA/SAH nucleosidase (Swiss-Prot:O51931) (Buchnera aphidicola)	4.4	4.6	-0.2	-0.7	100.0%	-4.7
9869	AT5G41170.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:16495714-16497810 REVERSE   Aliases: MEE6.24, MEE6_24	3.2	3.3	-0.1	-0.7	100.0%	-5.2
9870	AT4G17800.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr4:9895303-9896681 REVERSE   Aliases: DL4935C, FCAALL.129	4.5	4.3	0.2	0.7	100.0%	-4.8
9871	AT1G27050.1   similar to homeobox-leucine zipper protein 5 (HAT5) / HD-ZIP protein 5 / HD-ZIP protein (HB-1) [Arabidopsis thaliana] (TAIR:At3g01470.1); similar to homeodomain leucine zipper protein HDZ2 [Phaseolus vulgaris] (GB:AAK84886.1); similar to homeodomain leucine zipper protein 16 [Oryza sativa (japonica cultivar-group)] (GB:AAS68137.1); similar to Hox16 [Oryza sativa (japonica cultivar-group)] (GB:AAS83417.1); contains InterPro domain Leucine zipper, homeobox-associated (InterPro:IPR003106); contains InterPro domain Helix-turn-helix motif, lambda-like repressor (InterPro:IPR000047); contains InterPro domain Homeobox (InterPro:IPR001356); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)	4.3	4.5	-0.2	-0.7	100.0%	-4.6
9872	AT2G17970.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to At2g17960, At4g36090; contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr2:7826198-7828358 REVERSE   Aliases: T27K22.16, T27K22_16	3.1	3.0	0.1	0.7	100.0%	-5.1
9873	AT2G35635.1   Symbol: UBQ7   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr2:14988073-14989195 FORWARD   Aliases: None	10.8	10.3	0.4	0.7	100.0%	-4.4
9874	AT1G79830.1   expressed protein, weak similarity to TATA element modulatory factor (TMF) (Swiss-Prot:P82094) (Homo sapiens)   chr1:30032650-30038401 REVERSE   Aliases: F19K16.21, F19K16_21	6.7	6.4	0.2	0.7	100.0%	-4.8
9875	AT1G63070.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23388989-23390832 REVERSE   Aliases: F16M19.15, F16M19_15	2.3	2.3	-0.1	-0.7	100.0%	-6.1
9876	AT1G34430.1   Symbol: EMB3003   dihydrolipoamide S-acetyltransferase, putative, similar to dihydrolipoamide S-acetyltransferase (LTA2) (Arabidopsis thaliana) GI:5881963; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme, PF02817: e3 binding domain   chr1:12587730-12590120 REVERSE   Aliases: EMB3003, EMBRYO DEFECTIVE 3003, F12K21.24, F12K21_24	9.4	9.7	-0.4	-0.7	100.0%	-4.4
9877	AT4G02700.1   Symbol: AST77   sulfate transporter, identical to sulfate transporter (Arabidopsis thaliana) GI:2130944	2.5	2.6	-0.1	-0.7	100.0%	-5.4
9878	AT1G56590.1   clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	4.9	4.6	0.3	0.7	100.0%	-4.8
9879	AT1G36940.1   expressed protein   chr1:14006344-14007352 FORWARD   Aliases: T32E20.35, T32E20_35	3.0	3.1	-0.1	-0.7	100.0%	-5.3
9880	AT5G24430.1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK1 (Nicotiana tabacum) gi:16904222:gb:AAL30818   chr5:8339147-8343104 REVERSE   Aliases: K16H17.14, K16H17_14	6.4	6.3	0.2	0.7	100.0%	-4.7
9881	AT5G18220.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr5:6018916-6020455 REVERSE   Aliases: MRG7.18, MRG7_18	3.3	3.2	0.1	0.7	100.0%	-5.2
9882	AT1G70840.1   Bet v I allergen family protein, similar to Csf-2 (Cucumis sativus)(GI:5762258)(J Am Soc Hortic Sci 124, 136-139 (1999)) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:26716644-26717728 REVERSE   Aliases: F15H11.9, F15H11_9	3.6	3.4	0.2	0.7	100.0%	-4.7
9883	AT5G62750.1   expressed protein, predicted proteins, Caenorhabditis elegans   chr5:25220675-25221343 REVERSE   Aliases: MQB2.7, MQB2_7	2.6	2.7	-0.1	-0.7	100.0%	-5.8
9884	AT2G34750.1   RNA polymerase I specific transcription initiation factor RRN3 family protein, contains Pfam PF05327: RNA polymerase I specific transcription initiation factor RRN3; similar to RRN3 (GI:7670100) (Homo sapiens) similar to RNA polymerase I specific transcription initiation factor RRN3 (Swiss-Prot:P36070) (Saccharomyces cerevisiae)   chr2:14667387-14671345 REVERSE   Aliases: T29F13.4, T29F13_4	8.9	9.1	-0.2	-0.7	100.0%	-4.5
9885	AT2G19950.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g18190.1); similar to OSJNBa0014K08.8 [Oryza sativa (japonica cultivar-group)] (GB:NP_916062.1)   chr2:8623174-8628486 REVERSE   Aliases: F6F22.2, F6F22_2	5.0	5.2	-0.2	-0.7	100.0%	-4.6
9886	AT4G10845.1   expressed protein   chr4:6662524-6664138 FORWARD   Aliases: None	4.3	4.2	0.1	0.7	100.0%	-4.9
9887	AT3G47050.1   glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1   chr3:17339020-17341874 REVERSE   Aliases: F13I12.100	3.3	3.5	-0.2	-0.7	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9888	AT5G35400.1   tRNA pseudouridine synthase family protein, weak similarity to SP:P07649 tRNA pseudouridine synthase A (EC 4.2.1.70) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF01416: tRNA pseudouridine synthase	5.1	5.3	-0.2	-0.7	100.0%	-4.7
9889	AT3G17510.2   Symbol: CIPK1   CBL-interacting protein kinase 1 (CIPK1), identical to CBL-interacting protein kinase 1 (Arabidopsis thaliana) gi:11066952:gb:AAG28776; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 1 (CIPK1) GI:11066951   chr3:5988997-5991287 REVERSE   Aliases: CBL INTERACTING PROTEIN KINASE 1, MKP6.20	4.8	5.3	-0.5	-0.7	100.0%	-4.5
9890	AT2G46640.1   expressed protein, and genefinder; expression supported by MPSS	2.9	3.0	-0.1	-0.7	100.0%	-5.5
9891	AT4G15640.1   expressed protein   chr4:8918983-8921928 REVERSE   Aliases: DL3860C, FCAALL.350	6.3	6.8	-0.4	-0.7	100.0%	-4.2
9892	AT5G56950.1   nucleosome assembly protein (NAP), putative, similar to nucleosome assembly protein 1 (Glycine max) GI:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP)	6.5	6.8	-0.4	-0.7	100.0%	-4.7
9893	AT1G55290.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to GI:5924383 from (Daucus carota); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:20629788-20631064 REVERSE   Aliases: F7A10.24, F7A10_24	3.4	3.6	-0.2	-0.7	100.0%	-4.7
9894	AT1G06580.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:2014439-2016053 REVERSE   Aliases: F12K11.8, F12K11_8	5.0	4.8	0.3	0.7	100.0%	-4.6
9895	AT2G15570.1   Symbol: ATHM3   thioredoxin M-type 3, chloroplast (TRX-M3), identical to SP:Q9SEU7 Thioredoxin M-type 3, chloroplast precursor (TRX-M3) {Arabidopsis thaliana}   chr2:6798372-6799991 REVERSE   Aliases: F9O13.12	7.1	6.9	0.2	0.7	100.0%	-4.9
9896	AT4G04730.1   expressed protein   chr4:2401925-2402347 REVERSE   Aliases: T4B21.14, T4B21_14	2.0	1.9	0.1	0.7	100.0%	-5.8
9897	AT1G31370.1   expressed protein, ; expression supported by MPSS   chr1:11238279-11239344 REVERSE   Aliases: T8E3.14	2.2	2.2	-0.1	-0.7	100.0%	-5.7
9898	AT2G31060.2   similar to elongation factor family protein [Arabidopsis thaliana] (TAIR:At5g13650.2); similar to putative GTP-binding protein [Oryza sativa (japonica cultivar-group)] (GB:NP_916146.1); contains InterPro domain Small GTP-binding protein domain (InterPro:IPR005225); contains InterPro domain Elongation factor G, C-terminal (InterPro:IPR000640); contains InterPro domain Elongation factor, GTP-binding (InterPro:IPR000795); contains InterPro domain GTP-binding protein TypA (InterPro:IPR006298); contains InterPro domain Elongation factor Tu, domain 2 (InterPro:IPR004161)   chr2:13220275-13225662 REVERSE   Aliases: T16B12.13, T16B12_13	5.4	5.7	-0.3	-0.7	100.0%	-4.2
9899	AT1G55480.1   expressed protein   chr1:20717350-20719200 FORWARD   Aliases: T5A14.12, T5A14_12	8.5	8.2	0.3	0.7	100.0%	-4.1
9900	AT3G62610.1   myb family transcription factor, similar to myb-like transcription factor GI:168590 from (Zea mays)   chr3:23165734-23167561 FORWARD   Aliases: F26K9.40	3.2	3.4	-0.2	-0.7	100.0%	-4.8
9901	AT5G03350.1   legume lectin family protein, contains Pfam domain, PF00139: Legume lectins beta domain   chr5:815673-816657 REVERSE   Aliases: F12E4.80, F12E4_80	3.4	3.1	0.2	0.7	100.0%	-4.7
9902	AT5G43010.1   Symbol: RPT4A   26S proteasome AAA-ATPase subunit (RPT4a), gb:AAF22524.1   chr5:17265606-17268362 REVERSE   Aliases: MBD2.21, MBD2_21	7.8	8.2	-0.4	-0.7	100.0%	-4.7
9903	AT4G17790.1   expressed protein   chr4:9891064-9892807 FORWARD   Aliases: DL4930W, FCAALL.62	8.9	8.7	0.2	0.7	100.0%	-4.9
9904	AT2G39550.1   Symbol: ATGGT IB   geranylgeranyl transferase type I beta subunit (GGT-IB), nearly identical to GI:11878247   chr2:16508701-16511382 FORWARD   Aliases: GERANYLGERANYLTRANSFERASE I BETA SUBUNIT	6.6	6.9	-0.3	-0.7	100.0%	-4.4
9905	AT2G20410.1   activating signal cointegrator-related, similar to ASC-1 (GI:6581062) (Mus musculus); similar to Activating signal cointegrator 1 (ASC-1) (Thyroid receptor interacting protein 4) (TRIP-4) (Swiss-Prot:Q15650) (Homo sapiens)   chr2:8809425-8811451 FORWARD   Aliases: F11A3.4, F11A3_4	4.6	4.4	0.2	0.7	100.0%	-4.6
9906	AT2G10970.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.3	2.4	-0.1	-0.7	100.0%	-5.3
9907	AT4G05440.1   temperature sensing protein-related, contains weak similarity to D123 (GI:1236114) (Rattus norvegicus)   chr4:2757211-2758272 FORWARD   Aliases: C6L9.120, C6L9_120	5.2	5.3	-0.1	-0.7	100.0%	-4.8
9908	AT4G13960.1   F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.7	-0.2	-0.7	100.0%	-4.9
9909	AT4G38420.1   Symbol: SKS9   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr4:17982768-17985350 FORWARD   Aliases: F22I13.190, F22I13_190, SKS9	2.5	2.7	-0.1	-0.7	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9910	AT4G39370.2   Symbol: UBP27   ubiquitin-specific protease 27, putative (UBP27), similar to GI:11993494; ubiquitin specific protease 66 - Gallus gallus,PID:g3800764   chr4:18306232-18308836 FORWARD   Aliases: F23K16.5, F23K16_5, UBIQUITIN SPECIFIC PROTEASE 27	3.2	3.3	-0.1	-0.7	100.0%	-4.9
9911	AT3G59030.1   Symbol: TT12   transparent testa 12 protein (TT12) / multidrug transporter-like protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296, putative multidrug efflux protein NorM - Vibrio parahaemolyticus, EMBL:AB010463; contains Pfam profile PF01554: Uncharacterized membrane protein family; identical to cDNA multidrug transporter-like protein (tt12) GI:13624642, SP:Q9LYT3 TRANSPARENT TESTA 12 protein {Arabidopsis thaliana}, multidrug transporter-like protein (Arabidopsis thaliana) GI:13624643   chr3:21830048-21833015 FORWARD   Aliases: F17J16.80, TRANSPARENT TESTA 12	3.8	3.6	0.2	0.7	100.0%	-4.7
9912	AT5G25620.1   flavin-containing monooxygenase, putative / FMO, putative, similar to flavin-containing monooxygenases from Arabidopsis thaliana YUCCA2 GI:16555354, YUCCA3 GI:16555356; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr5:8935112-8938669 REVERSE   Aliases: T14C9.160, T14C9_160	3.5	3.7	-0.2	-0.7	100.0%	-4.7
9913	AT1G13710.1   Symbol: CYP78A5   cytochrome P450 family protein, similar to cytochrome P450 78A1 (SP:P48420) GI:349717 from (Zea mays)	2.7	2.8	-0.1	-0.7	100.0%	-5.1
9914	AT1G11050.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:3681888-3684169 FORWARD   Aliases: T19D16.6, T19D16_6	4.3	4.1	0.3	0.7	100.0%	-4.4
9915	AT4G15130.1   cholinephosphate cytidylyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidylyltransferase, putative, strong similarity to CTP:phosphorylcholine cytidylyltransferase (Arabidopsis thaliana) GI:21668498; contains Pfam profile PF01467: Cytidylyltransferase; identical to cDNA AtCCT2 for CTP:phosphorylcholine cytidylyltransferase GI:21668499   chr4:8637663-8639625 FORWARD   Aliases: DL3610W, FCAALL.209	7.6	7.8	-0.3	-0.7	100.0%	-4.9
9916	AT5G57780.1   expressed protein, similar to unknown protein (emb CAB79759.1)   chr5:23422550-23423535 REVERSE   Aliases: MTI20.1, MTI20_1	2.0	2.1	-0.1	-0.7	100.0%	-5.4
9917	ATCG00070.1   Symbol: PSBK   PSII K protein   chrC:7017-7202 FORWARD   Aliases: PSBK	5.4	5.1	0.3	0.7	100.0%	-4.5
9918	AT1G64360.1   expressed protein   chr1:23891533-23892167 FORWARD   Aliases: F15H21.8, F15H21_8	2.4	2.5	-0.1	-0.7	100.0%	-5.5
9919	AT1G29670.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif   chr1:10375753-10378144 FORWARD   Aliases: F15D2.22, F15D2_22	2.0	2.1	-0.1	-0.7	100.0%	-5.7
9920	AT4G24940.1   Symbol: SAE1A   SUMO activating enzyme 1a (SAE1a), identical to SUMO activating enzyme 1a (Arabidopsis thaliana) GI:22652850; contains Pfam profile PF00899: ThiF family   chr4:12823506-12826210 FORWARD   Aliases: AT SAE1 1, ATSAE1A, F13M23.80, F13M23_80, SUMO ACTIVATING ENZYME 1A	7.0	7.5	-0.5	-0.7	100.0%	-4.4
9921	AT1G30840.1   Symbol: ATPUP4	4.8	4.9	-0.2	-0.7	100.0%	-4.8
9922	AT1G71800.1   cleavage stimulation factor, putative, similar to cleavage stimulation factor 64 kilodalton subunit GB:AAD47839 GI:5713194 from (Drosophila melanogaster), SP:P33240 Cleavage stimulation factor, 64 kDa subunit {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:27003119-27006004 FORWARD   Aliases: F14O23.18, F14O23_18	5.2	5.4	-0.2	-0.7	100.0%	-4.8
9923	AT1G74810.1   anion exchange family protein, contains Pfam profile: PF00955 Anion exchanger family   chr1:28112135-28115195 FORWARD   Aliases: F9E10.34, F9E10_34	2.7	2.6	0.1	0.7	100.0%	-5.1
9924	AT1G44920.1   expressed protein   chr1:16985344-16986849 REVERSE   Aliases: T12C22.21, T12C22_21	6.8	6.5	0.3	0.7	100.0%	-4.1
9925	AT3G14030.1   expressed protein   chr3:4646279-4647131 REVERSE   Aliases: MDC16.17	2.5	2.6	-0.1	-0.7	100.0%	-5.3
9926	AT4G28430.1   reticulon family protein, contains Pfam profile PF02453: Reticulon   chr4:14057798-14059865 FORWARD   Aliases: F20O9.110, F20O9_110	4.5	4.3	0.1	0.7	100.0%	-4.8
9927	AT5G54740.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to 2S seed storage proteins from Arabidopsis thaliana: SP:P15457, SP:P15459, SP:P15458, SP:P15460 contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family   chr5:22255584-22256413 REVERSE   Aliases: K5F14.10, K5F14_10	2.5	2.4	0.1	0.7	100.0%	-5.4
9928	AT4G13510.1   Symbol: AMT1   ammonium transporter 1, member 1 (AMT1.1), identical to SP:P54144 High affinity ammonium transporter (AtAMT1;1) {Arabidopsis thaliana}   chr4:7858179-7859914 FORWARD   Aliases: AMMONIUM TRANSPORT 1, ATAMT1, T6G15.60, T6G15_60	5.6	5.1	0.5	0.7	100.0%	-4.4
9929	AT2G26820.1   Symbol: ATPP2 A3   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}; contains Pfam profile PF04548: AIG1 family   chr2:11444886-11449277 FORWARD   Aliases: ATPP2 A3, F12C20.14, F12C20_14	3.0	3.2	-0.2	-0.7	100.0%	-4.5
9930	AT3G28590.1   expressed protein   chr3:10719557-10719919 FORWARD   Aliases: MZN14.7	6.4	6.1	0.2	0.7	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9931	AT1G62720.1   pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR repeats Pfam Profile: PF01535   chr1:23231416-23233114 FORWARD   Aliases: F23N19.8, F23N19_8	5.6	5.3	0.2	0.7	100.0%	-5.1
9932	AT4G09560.1   Symbol: NHL22   protease-associated zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); similar to ReMembr-H2 protein JR702 (Arabidopsis thaliana) gi:6942149:gb:AAF32326   chr4:6041339-6043678 REVERSE   Aliases: T15G18.20, T15G18_20	2.8	2.6	0.1	0.7	100.0%	-5.3
9933	AT1G59590.1   Symbol: ZCF37   expressed protein   chr1:21891417-21892457 FORWARD   Aliases: T30E16.15, T30E16_15, ZCF37	4.2	3.8	0.3	0.7	100.0%	-4.4
9934	AT4G27420.1   ABC transporter family protein, D.melanogaster P element CaSpeR-1 gene (white protein),PID:g870996   chr4:13712205-13714803 REVERSE   Aliases: F27G19.20, F27G19_20	2.6	2.5	0.1	0.7	100.0%	-5.3
9935	AT5G35560.1   DENN (AEX-3) domain-containing protein, contains Pfam domain PF02141: DENN (AEX-3) domain; this cDNA may contain an anomalously spliced intron...will require further examination.   chr5:13759339-13765493 REVERSE   Aliases: MOK9.21, MOK9_21	5.2	5.0	0.3	0.7	100.0%	-4.4
9936	AT3G06060.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily   chr3:1827987-1830206 REVERSE   Aliases: F24F17.4, F24F17_4	6.6	6.3	0.3	0.7	100.0%	-4.6
9937	AT4G25430.1   hypothetical protein   chr4:12998600-13000221 FORWARD   Aliases: T30C3.7	2.4	2.3	0.1	0.7	100.0%	-5.4
9938	AT3G63140.1   mRNA-binding protein, putative, similar to mRNA binding protein precursor (GI:26453355) (Lycopersicon esculentum)   chr3:23337347-23339684 REVERSE   Aliases: T20O10.240	9.0	8.8	0.2	0.7	100.0%	-4.6
9939	AT1G31430.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:11253917-11255718 REVERSE   Aliases: T8E3.8, T8E3_8	2.8	2.9	-0.1	-0.7	100.0%	-5.0
9940	AT2G14660.1   expressed protein, contains Pfam PF04543: Family of unknown function (DUF589); similar to cThy28kD (GI:995778) (Gallus gallus); similar to thymocyte protein mThy28 (GI:23978374) (Mus musculus)	4.8	4.6	0.2	0.7	100.0%	-4.7
9941	AT5G38040.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:15202307-15203738 FORWARD   Aliases: F16F17.40, F16F17_40	3.9	3.7	0.2	0.7	100.0%	-5.0
9942	AT3G04050.1   pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Nicotiana tabacum) SWISS-PROT:Q42954   chr3:1049802-1051529 FORWARD   Aliases: T11I18.16, T11I18_16	4.0	3.8	0.2	0.7	100.0%	-5.0
9943	AT4G15690.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.5	2.5	-0.1	-0.7	100.0%	-5.5
9944	AT1G80760.1   Symbol: NIP6;1	3.4	3.2	0.2	0.7	100.0%	-4.7
9945	AT3G04270.1   expressed protein   chr3:1127911-1128087 REVERSE   Aliases: T6K12.11, T6K12_11	3.2	3.4	-0.1	-0.7	100.0%	-5.2
9946	AT3G57860.1   expressed protein   chr3:21437291-21439827 FORWARD   Aliases: T10K17.70	3.4	3.5	-0.1	-0.7	100.0%	-5.3
9947	AT3G15880.2   similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g15750.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g80490.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g80490.2); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g16830.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g15750.2); similar to putative beta transducin-like protein [Solanum bulbocastanum] (GB:AAP45184.1); similar to putative CTV.2 [Oryza sativa (japonica cultivar-group)] (GB:BAD81067.1); similar to WD-40 repeat protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_480212.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_912774.1); contains InterPro domain Lissencephaly type-1-like homology motif (InterPro:IPR006594); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680); contains InterPro domain CTLH, C-terminal to LisH motif (InterPro:IPR006595)   chr3:5364087-5372295 REVERSE   Aliases: MSJ11.27	7.7	7.9	-0.2	-0.7	100.0%	-5.1
9948	AT5G67330.1   Symbol: ATNRAMP4   NRAMP metal ion transporter 4 (NRAMP4), identical to metal transporter Nramp4 (Arabidopsis thaliana) gi:6468014:gb:AAF13279; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563   chr5:26878955-26881123 FORWARD   Aliases: K8K14.5, K8K14_5, METAL TRANSPORTER NRAMP4, NRAMP4	9.7	9.4	0.3	0.7	100.0%	-4.8
9949	AT5G46010.1   homeobox-leucine zipper transcription factor family protein, similar to to PRESSED FLOWER (GP:17907768) {Arabidopsis thaliana}; similar to HB2 homeodomain protein (GI:3955021) {Populus tremula x Populus tremuloides}   chr5:18677811-18678410 FORWARD   Aliases: MCL19.5, MCL19_5	2.5	2.6	-0.1	-0.7	100.0%	-5.5
9950	NA	2.3	2.3	0.1	0.7	100.0%	-6.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9951	AT5G63190.2   MA3 domain-containing protein, low similarity to programmed cell death 4 protein (Gallus gallus) GI:12958564; contains Pfam profile PF02847: MA3 domain   chr5:25362822-25366022 FORWARD   Aliases: MDC12.16, MDC12_16	6.7	6.4	0.3	0.7	100.0%	-4.5
9952	AT3G03070.1   NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 13 kDa-A subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-13KD-A) (CI-13KD-A) (Swiss-Prot:P23934) (Bos taurus)   chr3:696306-698163 REVERSE   Aliases: T17B22.24, T17B22_24	8.8	9.1	-0.3	-0.7	100.0%	-4.5
9953	AT4G15460.1   glycine-rich protein   chr4:8841418-8841864 REVERSE   Aliases: DL3770C, FCAALL.299	3.9	3.7	0.3	0.7	100.0%	-4.6
9954	AT3G05420.2   acyl-CoA binding family protein, similar to PIR:S68824:S68824 rngB protein, cytosolic (Dictyostelium discoideum); contains Pfam profiles PF00887: Acyl CoA binding protein, PF01344: Kelch motif	7.2	7.6	-0.4	-0.7	100.0%	-4.6
9955	AT5G07690.1   Symbol: MYB29   myb family transcription factor (MYB29), similar to myb transcription factor GI:3941436 from (Arabidopsis thaliana)   chr5:2446765-2448544 FORWARD   Aliases: MBK20.15, MBK20_15	2.6	2.5	0.1	0.7	100.0%	-5.4
9956	AT2G15090.1   fatty acid elongase, putative, similar to fatty acid elongase 1 (GI:881615)   chr2:6549338-6551029 FORWARD   Aliases: T15J14.13, T15J14_13	3.5	3.6	-0.1	-0.7	100.0%	-5.2
9957	AT3G45240.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g60550.1); similar to putative protein serine/threonine kinase [Dictyostelium discoideum] (GB:EAL67851.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:16581481-16584692 REVERSE   Aliases: F18N11.1	3.6	3.4	0.2	0.7	100.0%	-4.9
9958	AT2G41290.1   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088   chr2:17217533-17220037 REVERSE   Aliases: F13H10.16, F13H10_16	9.9	9.7	0.2	0.7	100.0%	-4.4
9959	AT1G61090.1   expressed protein   chr1:22503196-22506141 REVERSE   Aliases: T7P1.22	2.6	2.7	-0.1	-0.7	100.0%	-5.3
9960	AT5G51760.1   protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain; similar to protein phosphatase 2C (GI:10432446) (Nicotiana tabacum)   chr5:21044142-21046414 FORWARD   Aliases: MIO24.11, MIO24_11	4.5	4.2	0.3	0.7	100.0%	-4.7
9961	AT1G22930.1   T-complex protein 11, contains Pfam PF05794: T-complex protein 11   chr1:8117386-8122116 FORWARD   Aliases: F19G10.11, F19G10_11	8.1	7.9	0.3	0.7	100.0%	-4.4
9962	AT1G10480.1   Symbol: ZFP5   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr1:3449692-3451227 FORWARD   Aliases: T10024.9, T10024_9, ZFP5, ZINC FINGER PROTEIN 5	5.2	5.0	0.2	0.7	100.0%	-4.7
9963	AT5G03730.2   Symbol: CTR1   serine/threonine protein kinase (CTR1), identical to serine/threonine-protein kinase CTR1 (Arabidopsis thaliana) SWISS-PROT:Q05609   chr5:974507-979848 REVERSE   Aliases: CONSTITUTIVE TRIPLE RESPONSE 1, F17C15.150, F17C15_150, SERINE/THREONINE PROTEIN KINASE CTR1, SIS1	5.2	5.4	-0.2	-0.7	100.0%	-4.9
9964	AT5G44650.1   expressed protein   chr5:18030376-18032630 FORWARD   Aliases: K15C23.10, K15C23_10	7.6	7.4	0.2	0.7	100.0%	-4.5
9965	AT3G56000.1   Symbol: ATCSLA14   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	3.0	3.1	-0.1	-0.7	100.0%	-5.1
9966	AT4G29610.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase 6 (CDA6) (Arabidopsis thaliana) GI:3818575, cytidine deaminase homolog DesD (Arabidopsis thaliana) GI:4836446; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14517454-14518335 FORWARD   Aliases: T16L4.120, T16L4_120	3.1	3.0	0.1	0.7	100.0%	-5.0
9967	AT1G60810.1   Symbol: ACLA 2	9.3	9.6	-0.3	-0.7	100.0%	-4.7
9968	AT2G41890.1   curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein, contains Pfam profiles: PF01453 lectin (probable mannose binding), PF00024 PAN domain   chr2:17485136-17487430 REVERSE   Aliases: T11A7.1, T11A7_1	4.4	4.6	-0.2	-0.7	100.0%	-4.6
9969	AT5G57550.1   Symbol: XTR3   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (XTR3), identical to endoxyloglucan transferase GI:5533317 from (Arabidopsis thaliana)   chr5:23322114-23323647 REVERSE   Aliases: MUA2.12, MUA2_12, XYLOGLUCAN ENDOTRANSGLYCOSYLASE 3	3.0	2.9	0.1	0.7	100.0%	-5.2
9970	AT4G15410.1   Symbol: ATB' GAMMA   UBX domain-containing protein, low similarity to XY40 protein (Rattus norvegicus) GI:2547025; contains Pfam profile PF00789: UBX domain   chr4:8814820-8816805 FORWARD   Aliases: DL3750W, FCAALL.290	4.2	4.4	-0.2	-0.7	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9971	AT5G43940.1   alcohol dehydrogenase class III / glutathione-dependent formaldehyde dehydrogenase / GSH-FDH (ADHIII), identical to gi:1143388   chr5:17701421-17704165 FORWARD   Aliases: MRH10.4, MRH10_4	11.4	11.8	-0.4	-0.7	100.0%	-4.7
9972	AT5G10120.1   ethylene insensitive 3 family protein, contains Pfam profile: PF04873 ethylene insensitive 3   chr5:3169733-3171148 FORWARD   Aliases: T31P16.110, T31P16_110	2.8	2.7	0.1	0.7	100.0%	-5.6
9973	AT5G26200.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:9157145-9158780 FORWARD   Aliases: F9D12.12	4.9	4.6	0.3	0.7	100.0%	-4.1
9974	AT1G36180.1   acetyl-CoA carboxylase 2 (ACC2), nearly identical to acetyl-CoA carboxylase 2 (ACC2) (Arabidopsis thaliana) GI:11869928   chr1:13547727-13559608 FORWARD   Aliases: F15C21.2, F15C21_2	3.5	3.7	-0.2	-0.7	100.0%	-4.7
9975	AT2G35840.2   sucrose-phosphatase 1 (SPP1), identical to sucrose-phosphatase (SPP1) (Arabidopsis thaliana) GI:11127757	7.7	7.3	0.4	0.7	100.0%	-4.6
9976	AT5G24320.2   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP:Q9UGP9) (Homo sapiens)   chr5:8284861-8287654 REVERSE   Aliases: MOP9.16, MOP9_16	3.1	3.0	0.1	0.7	100.0%	-5.3
9977	AT5G45270.1   Symbol: RRS1   WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain   chr5:18348584-18349836 FORWARD   Aliases: ATWRKY52, K9E15.3, K9E15_3, RESISTANT TO RALSTONIA SOLANACEARUM 1, RRS1	4.6	5.1	-0.5	-0.7	100.0%	-4.3
9978	AT3G24230.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa)   chr3:8774623-8777414 FORWARD   Aliases: MUJ8.14	2.4	2.3	0.1	0.7	100.0%	-5.4
9979	AT1G49850.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:18458732-18460190 REVERSE   Aliases: F10F5.8, F10F5_8	5.5	5.3	0.2	0.7	100.0%	-4.5
9980	AT5G60750.1   CAAX amino terminal protease family protein, contains Pfam profile PF02517 CAAX amino terminal protease family protein   chr5:24448117-24450586 FORWARD   Aliases: MUP24.17, MUP24_17	6.5	6.4	0.2	0.7	100.0%	-4.8
9981	AT2G22720.3   expressed protein   chr2:9664567-9667856 FORWARD   Aliases: T9I22.16, T9I22_16	4.7	4.9	-0.1	-0.7	100.0%	-4.9
9982	AT1G80520.1   expressed protein   chr1:30281373-30281951 FORWARD   Aliases: T21F11.15, T21F11_15	3.9	4.0	-0.1	-0.7	100.0%	-4.8
9983	AT1G55520.2   Symbol: TBP2   transcription initiation factor IID-2 (TFIID-2) / TATA-box factor 2 / TATA sequence-binding protein 2 (TBP2), identical to Swiss-Prot:P28148:TF22_ARATH Transcription initiation factor TFIID-2 (TATA-box factor 2) (TATA sequence-binding protein 2) (TBP-2) (Arabidopsis thaliana)   chr1:20729392-20731756 REVERSE   Aliases: ATTBP2, T5A14.8, T5A14_8	6.6	6.3	0.3	0.7	100.0%	-4.5
9984	AT4G34770.1   auxin-responsive family protein, similar to auxin-induced protein X10A (SP:P33080) (Glycine max); small auxin up-regulated RNA, Malus domestica, gb:Z93766   chr4:16591234-16591897 FORWARD   Aliases: F11I11.10, F11I11_10	2.8	2.9	-0.1	-0.7	100.0%	-5.3
9985	AT3G60060.1   hypothetical protein, male sterility protein 2 - Brassica napus, PIR:T08096   chr3:22193268-22194055 FORWARD   Aliases: T2O9.40	2.6	2.5	0.1	0.7	100.0%	-5.4
9986	AT5G49560.1   expressed protein, similar to SP:P40389 Rapid response to glucose protein 1 {Schizosaccharomyces pombe}   chr5:20128187-20129011 REVERSE   Aliases: K6M13.11, K6M13_11	7.0	6.6	0.4	0.7	100.0%	-4.1
9987	AT5G24160.1   squalene monooxygenase 1,2 / squalene epoxidase 1,2 (SQP1,2), identical to SP:O65402   chr5:8183105-8186643 REVERSE   Aliases: K12G2.4, K12G2_4	3.1	2.9	0.1	0.7	100.0%	-5.1
9988	AT2G25060.1   plastocyanin-like domain-containing protein   chr2:10669331-10670177 FORWARD   Aliases: F13D4.2	3.7	3.9	-0.2	-0.7	100.0%	-4.4
9989	AT2G13070.1   hypothetical protein   chr2:5384509-5385228 FORWARD   Aliases: T17A11.6, T17A11_6	3.0	2.9	0.1	0.7	100.0%	-5.2
9990	AT3G58080.1   expressed protein   chr3:21521283-21521539 REVERSE   Aliases: F9D24.3	3.4	3.2	0.2	0.7	100.0%	-5.0
9991	AT4G15710.1   hypothetical protein   chr4:8940290-8940856 FORWARD   Aliases: DL3895W, FCAALL.366	2.8	2.7	0.1	0.7	100.0%	-5.2
9992	AT2G03810.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g13650.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g13650.1); similar to DNA topoisomerase IV subunit A [Mycoplasma penetrans HF-2] (GB:NP_758033.1)   chr2:1161538-1164569 FORWARD   Aliases: T18C20.1, T18C20_1	3.1	2.9	0.1	0.7	100.0%	-4.9
9993	AT5G22555.1   expressed protein   chr5:7489425-7490463 FORWARD   Aliases: None	3.0	3.1	-0.1	-0.7	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
9994	AT4G39080.1   vacuolar proton ATPase, putative, similar to Swiss-Prot:Q93050 vacuolar proton translocating ATPase 116 kDa subunit A isoform 1 (Clathrin-coated vesicle/synaptic vesicle proton pump 116 kDa subunit, Vacuolar proton pump subunit 1, Vacuolar adenosine triphosphatase subunit Ac116) (Homo sapiens)   chr4:18209423-18216343 FORWARD   Aliases: F19H22.180, F19H22_180	6.5	6.1	0.4	0.7	100.0%	-4.4
9995	AT2G29770.1   kelch repeat-containing F-box family protein, contains Pfam PF00646: F-box domain; contains Pfam PF01344 : Kelch motif; similar to SKP1 interacting partner 6 (GI:10716957) (Arabidopsis thaliana)   chr2:12722488-12723952 REVERSE   Aliases: T27A16.13, T27A16_13	2.9	2.8	0.1	0.7	100.0%	-5.5
9996	AT3G27920.1   Symbol: GL1   trichome differentiation protein / GLABROUS1 protein (GL1), identical to trichome differentiation protein GL1 SP:P27900 from (Arabidopsis thaliana); contains Pfam profile: PF00249 Myb-like DNA-binding domain   chr3:10363182-10364743 REVERSE   Aliases: GLABRA 1, K16N12.17, TRICHOME DIFFERENTIATION PROTEIN GL1	2.9	3.0	-0.1	-0.7	100.0%	-5.4
9997	AT2G33630.1   3-beta hydroxysteroid dehydrogenase/isomerase family protein, contains Pfam profile PF01073 3-beta hydroxysteroid dehydrogenase/isomerase domain; similar to NAD(P)-dependent cholesterol dehydrogenase (Nocardia sp.) (GI:216809)   chr2:14243467-14245866 REVERSE   Aliases: F4P9.40, F4P9_40	7.5	7.9	-0.5	-0.7	100.0%	-4.4
9998	AT5G45050.2   Symbol: TTR1   disease resistance protein-related, similar to NL27 (Solanum tuberosum) GI:3947735; contains Pfam profiles PF03106: WRKY DNA -binding domain, PF00931: NB-ARC domain, PF00560: Leucine Rich Repeat   chr5:18194141-18199032 REVERSE   Aliases: ATWRKY16, K21C13.24, K21C13_24, WRKY16	4.9	5.1	-0.2	-0.7	100.0%	-4.6
9999	AT3G21850.1   Symbol: ASK9   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At9), putative, E3 ubiquitin ligase; similar to Skp1 homolog SKP1a GI:3068807 from (Arabidopsis thaliana)   chr3:7697096-7697557 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 9, MSD21.22	2.1	2.1	0.0	0.7	100.0%	-6.0
10000	AT2G01570.1   Symbol: RGA1   gibberellin response modulator (RGA1) / gibberellin-responsive modulator, identical to GB:Y11336, member of SCARECROW family   chr2:255248-257549 REVERSE   Aliases: F2I9.19, F2I9_19, REPRESSOR OF GA1 3, REPRESSOR OF GA1 3 1, RGA, RGA1	3.9	4.1	-0.2	-0.7	100.0%	-4.6
10001	AT2G17180.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:7483917-7484729 REVERSE   Aliases: T23A1.4, T23A1_4	2.6	2.5	0.1	0.7	100.0%	-5.3
10002	AT5G58350.1   Symbol: WNK4   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:23602401-23605027 FORWARD   Aliases: MCK7.22, MCK7_22, ZIK2	3.5	3.7	-0.2	-0.7	100.0%	-4.7
10003	AT5G50180.1   protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi:1054633:emb:CAA63387   chr5:20448164-20450326 FORWARD   Aliases: K6A12.4, K6A12_4	6.9	7.2	-0.3	-0.7	100.0%	-4.3
10004	AT1G32270.1   Symbol: ATSYP24   syntaxin, putative, similar to syntaxin related protein AtVam3p (GP:8809669) (Arabidopsis thaliana); similar to syntaxin GB:CAB78776 GI:7268526 from (Arabidopsis thaliana); contains Pfam profile PF05739: SNARE domain   chr1:11642573-11644942 FORWARD   Aliases: F27G20.2, SYP24	2.7	2.6	0.1	0.7	100.0%	-5.2
10005	AT2G44900.1   armadillo/beta-catenin repeat family protein / F-box family protein, contains similarity to F-box protein FBL2 GI:6010699 from (Rattus norvegicus); contains Pfam profiles PF00514: Armadillo/beta-catenin-like repeat, PF00646: F-box domain   chr2:18518794-18522837 REVERSE   Aliases: T13E15.9	5.0	5.2	-0.2	-0.7	100.0%	-4.6
10006	AT1G61065.1   expressed protein   chr1:22493909-22495126 REVERSE   Aliases: None	7.5	7.3	0.2	0.7	100.0%	-4.6
10007	AT5G65590.1   Dof-type zinc finger domain-containing protein   chr5:26228972-26230362 REVERSE   Aliases: K21L13.10, K21L13_10	2.3	2.4	-0.1	-0.7	100.0%	-5.2
10008	AT1G57700.1   protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108   chr1:21374716-21377525 FORWARD   Aliases: T8L23.17, T8L23_17	3.4	3.6	-0.1	-0.7	100.0%	-5.0
10009	AT4G27880.1   seven in absentia (SINA) family protein, similar to siah-1A protein (Mus musculus) GI:297035; contains Pfam profile PF03145: Seven in absentia protein family   chr4:13883229-13885058 FORWARD   Aliases: T27E11.120, T27E11_120	5.8	5.5	0.3	0.7	100.0%	-4.7
10010	AT5G36280.1   expressed protein   chr5:14316465-14316692 REVERSE   Aliases: T30G6.15, T30G6_15	3.0	2.9	0.1	0.7	100.0%	-5.2
10011	AT5G62200.1   embryo-specific protein-related, contains weak similarity to embryo-specific protein 3 (GI:3335171) (Arabidopsis thaliana)   chr5:25001494-25002900 REVERSE   Aliases: MMI9.3, MMI9_3	9.4	9.0	0.5	0.7	100.0%	-4.4
10012	AT3G04760.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:1303581-1305884 REVERSE   Aliases: F7O18.25, F7O18_25	4.9	5.3	-0.4	-0.7	100.0%	-4.1
10013	AT4G35630.1   Symbol: PSAT   phosphoserine aminotransferase, chloroplast (PSAT), identical to Phosphoserine aminotransferase, chloroplast precursor (PSAT) (SP:Q96255)(Arabidopsis thaliana); contains TIGRFAM TIGR01364: phosphoserine aminotransferase; contains Pfam PF00266: aminotransferase, class V   chr4:16904064-16905727 FORWARD   Aliases: PHOSPHOSERINE AMINOTRANSFERASE	11.1	11.5	-0.4	-0.7	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10014	AT3G48360.1   speckle-type POZ	3.1	3.4	-0.3	-0.7	100.0%	-4.3
10015	AT3G42480.1   expressed protein   chr3:14639205-14639621 REVERSE   Aliases: T32A11.50	2.7	2.6	0.1	0.7	100.0%	-5.5
10016	AT2G39450.1   cation efflux family protein, contains cation efflux family protein domain, Pfam:PF01545	7.7	7.3	0.4	0.7	100.0%	-4.4
10017	AT5G05170.1   Symbol: CESA3   cellulose synthase, catalytic subunit (Ath-B), nearly identical to gi:2827143, cellulose synthase, catalytic subunit (Ath-B)   chr5:1530175-1535383 REVERSE   Aliases: ATCESA3, ATH B, CELLULASE SYNTHASE 3, CEV1, CONSTITUTIVE EXPRESSION OF VSP1 1, ISOXABEN RESISTANT 1, IXR1, K2A11.4, K2A11_4	8.0	7.3	0.7	0.7	100.0%	-4.2
10018	AT4G28030.2   similar to GCN5-related N-acetyltransferase (GNAT) family protein [Arabidopsis thaliana] (TAIR:At2g06025.1); contains InterPro domain GCN5-related N-acetyltransferase (InterPro:IPR000182)   chr4:13937682-13939150 REVERSE   Aliases: T13J8.140, T13J8_140	6.6	6.4	0.2	0.7	100.0%	-4.9
10019	AT1G72000.1   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr1:27106939-27109325 FORWARD   Aliases: F28P5.11, F28P5_11	3.8	3.7	0.2	0.7	100.0%	-4.9
10020	AT5G39790.1   5'-AMP-activated protein kinase beta-1 subunit-related, contains similarity to Swiss-Prot:P80387 5'-AMP-activated protein kinase, beta-1 subunit (AMPK beta-1 chain) (AMPKb) (40 kDa subunit) (Sus scrofa)   chr5:15949942-15952489 REVERSE   Aliases: MKM21.80, MKM21_80	2.8	2.9	-0.1	-0.7	100.0%	-5.3
10021	AT3G42060.1   myosin heavy chain-related   chr3:14262586-14265255 REVERSE   Aliases: F4M19.20	2.7	2.6	0.1	0.7	100.0%	-5.3
10022	AT4G17720.1   RNA recognition motif (RRM)-containing protein   chr4:9862459-9864676 REVERSE   Aliases: DL4895C, FCAALL.73	7.2	6.8	0.4	0.7	100.0%	-4.5
10023	AT2G29530.1   Symbol: TIM10   mitochondrial import inner membrane translocase (TIM10), identical to mitochondrial import inner membrane translocase subunit Tim10 (Arabidopsis thaliana) Swiss-Prot:Q9ZW33; contains Pfam domain, PF02953: Tim10/DDP family zinc finger   chr2:12647901-12649367 REVERSE   Aliases: F16P2.9, F16P2_9, TIM10	9.1	9.6	-0.5	-0.7	100.0%	-4.2
10024	AT5G42940.1   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:17233558-17237689 REVERSE   Aliases: MBD2.14, MBD2_14	6.4	6.9	-0.5	-0.7	100.0%	-4.4
10025	AT5G38750.1   asparaginyl-tRNA synthetase family, contains similarity to Swiss-Prot:Q9SW96 asparaginyl-tRNA synthetase, cytoplasmic 1 (Asparagine-- tRNA ligase 1) (AsnRS 1) (Arabidopsis thaliana)   chr5:15539880-15540410 FORWARD   Aliases: MKD10.8, MKD10_8	2.5	2.6	-0.1	-0.7	100.0%	-5.2
10026	AT1G52360.1   coatomer protein complex, subunit beta 2 (beta prime), putative, contains 7 WD-40 repeats (PF00400) (1 weak); similar to (SP:O55029) Coatomer beta' subunit (Beta'-coat protein) (Beta'-COP) (p102) (SP:O55029) (Mus musculus); similar to GI:298096 from (Homo sapiens)	6.4	7.4	-0.9	-0.7	100.0%	-4.3
10027	AT3G60280.1   Symbol: UCC3   uclacyanin 3 (UCC3), identical to uclacyanin 3 GI:3395770 from (Arabidopsis thaliana); contains Pfam profile PF02298: Plastocyanin-like domain; identical to cDNA uclacyanin 3 (UCC3)GI:3395769   chr3:22290639-22291636 REVERSE   Aliases: F27H5.70, UCLACYANIN 3	2.9	2.7	0.1	0.7	100.0%	-5.1
10028	AT1G02090.3   Symbol: FUS5   COP9 signalosome complex subunit 7ii / CSN complex subunit 7ii (CSN7) (COP15) / FUSCA protein (FUS5), FUSCA5, CSN7, COP15; identical to CSN complex subunit 7ii (Arabidopsis thaliana) GI:18056671, FUS5 protein of the COP9 complex GI:3288823;	5.3	5.6	-0.2	-0.7	100.0%	-4.6
10029	AT5G59850.1   40S ribosomal protein S15A (RPS15aF), cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412   chr5:24129426-24130836 REVERSE   Aliases: MMN10.16	9.0	9.4	-0.4	-0.7	100.0%	-4.4
10030	AT2G32670.1   Symbol: ATVAMP725   synaptobrevin family protein, similar to vesicle-associated membrane protein 7 (Rattus norvegicus) GI:9502258, SP:P51809 Synaptobrevin-like protein 1 {Homo sapiens}; contains Pfam profile PF00957: Synaptobrevin   chr2:13864954-13867410 FORWARD   Aliases: F24L7.19, F24L7_19, VAMP725	4.0	3.8	0.2	0.7	100.0%	-4.5
10031	AT1G15080.1   Symbol: ATPAP2	4.3	4.1	0.2	0.7	100.0%	-5.0
10032	AT3G42640.1   ATPase, plasma membrane-type, putative / proton pump, putative, strong similarity to P-type H+-ATPase from (Lycopersicon esculentum) GI:1621440, (Solanum tuberosum) GI:435001, SP:Q03194 {Nicotiana plumbaginifolia}; contains InterPro accession IPR001757: ATPase, E1-E2 type	3.7	4.0	-0.3	-0.7	100.0%	-4.5
10033	AT2G28010.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr2:11937656-11938846 REVERSE   Aliases: T1E2.7, T1E2_7	2.4	2.5	-0.1	-0.7	100.0%	-5.1
10034	AT2G16040.1   hAT dimerisation domain-containing protein / transposase-related, low similarity to transposase (Ipomoea purpurea) AB004906 GI:4063770   chr2:6983099-6984676 FORWARD   Aliases: F7H1.6, F7H1_6	2.6	2.7	-0.1	-0.7	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10035	AT1G53690.1   DNA-directed RNA polymerases I, II, and III 7 kDa subunit, putative, similar to SP:P53803 DNA-directed RNA polymerases I, II, and III 7.0 kDa polypeptide (EC 2.7.7.6) (ABC10-alpha) (RPB7.0) (RPB10alpha) {Homo sapiens}; contains Pfam profile PF03604: DNA directed RNA polymerase, 7 kDa subunit   chr1:20046308-20047012 REVERSE   Aliases: F22G10.4, F22G10_4	3.5	3.4	0.1	0.7	100.0%	-5.2
10036	AT5G47910.1   Symbol: RBOHD   respiratory burst oxidase protein D (RbohD) / NADPH oxidase, identical to respiratory burst oxidase protein D from Arabidopsis thaliana (gi:3242789)   chr5:19414669-19419287 FORWARD   Aliases: MCA23.25, MCA23_25, RESPIRATORY BURST OXIDASE, RESPIRATORY BURST OXIDASE PROTEIN D	8.1	7.9	0.2	0.7	100.0%	-5.3
10037	AT2G35795.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain   chr2:15049289-15050646 FORWARD   Aliases: T20F21.1, T20F21_1	9.9	9.7	0.2	0.7	100.0%	-4.8
10038	AT5G63280.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:25384292-25387011 FORWARD   Aliases: MDC12.25, MDC12_25	5.1	5.6	-0.5	-0.7	100.0%	-4.6
10039	AT1G52950.1   replication protein-related, low similarity to replication protein A1 GI:2258469 from (Oryza sativa)   chr1:19729151-19731675 FORWARD   Aliases: F14G24.22, F14G24_22	2.8	2.9	-0.1	-0.7	100.0%	-5.1
10040	AT2G31490.1   expressed protein   chr2:13419060-13420323 FORWARD   Aliases: T28P16.2, T28P16_2	11.9	12.0	-0.2	-0.7	100.0%	-5.1
10041	AT1G48430.1   dihydroxyacetone kinase family protein, similar to dihydroxyacetone kinases; contains Pfam profiles PF02733: DAK1 domain, PF02734: DAK2 domain   chr1:17906383-17910461 REVERSE   Aliases: T1N15.4, T1N15_4	5.8	6.2	-0.4	-0.7	100.0%	-4.4
10042	AT4G16442.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:9271887-9273111 REVERSE   Aliases: None	5.2	5.4	-0.2	-0.7	100.0%	-4.4
10043	AT5G19980.1   integral membrane family protein, contains Pfam profile: PF00892 Integral membrane protein; similar to LPG2 protein (GI:9998817)	4.3	4.0	0.3	0.7	100.0%	-4.7
10044	AT4G09620.1   expressed protein, hypothetical protein F6E13.15 - Arabidopsis thaliana,PIR2:T00682   chr4:6076989-6078959 REVERSE   Aliases: T25P22.60, T25P22_60	6.3	6.2	0.1	0.7	100.0%	-5.1
10045	AT4G01140.1   expressed protein   chr4:490749-492199 REVERSE   Aliases: F2N1.38, F2N1_38	2.9	2.7	0.2	0.7	100.0%	-4.8
10046	AT1G35040.1   hypothetical protein   chr1:12812135-12812547 FORWARD   Aliases: F11O6.10, F11O6_10	3.9	3.7	0.2	0.7	100.0%	-5.0
10047	AT3G26790.1   Symbol: FUS3   transcriptional regulator (FUSCA3), identical to FUSCA3 GB:AAC35247 (Arabidopsis thaliana) (Plant J. 6, 379-387 (1994))   chr3:9855065-9857226 REVERSE   Aliases: FUS3, FUSCA 3, MDJ14.4	2.8	2.7	0.1	0.7	100.0%	-5.2
10048	AT2G26910.1   ABC transporter family protein, similar to PDR5-like ABC transporter GI:1514643 from (Spirodela polyrhiza)   chr2:11488701-11495264 FORWARD   Aliases: F12C20.5, F12C20_5	3.6	3.7	-0.1	-0.7	100.0%	-5.2
10049	AT1G72090.1   radical SAM domain-containing protein / TRAM domain-containing protein, contains Pfam profiles PF00919: UPF0004 family protein, PF04055: radical SAM domain protein, PF01938: TRAM domain   chr1:27127237-27130557 FORWARD   Aliases: F28P5.4, F28P5_4	8.3	8.5	-0.2	-0.7	100.0%	-4.7
10050	AT5G17790.1   Symbol: VAR3   zinc finger (Ran-binding) family protein, contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others   chr5:5869712-5872720 REVERSE   Aliases: MVA3.15, MVA3_15, VARIEGATED 3	5.6	5.9	-0.3	-0.7	100.0%	-4.4
10051	AT2G18540.1   cupin family protein, contains Pfam profile PF00190: Cupin   chr2:8049464-8052090 REVERSE   Aliases: F24H14.11, F24H14_11	3.6	3.5	0.2	0.7	100.0%	-5.3
10052	AT5G44710.1   expressed protein, similar to unknown protein (ref:NP_011731.1)   chr5:18058153-18059787 FORWARD   Aliases: K23L20.5, K23L20_5	9.0	8.6	0.4	0.7	100.0%	-4.4
10053	AT2G23910.1   cinnamoyl-CoA reductase-related, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Saccharum officinarum (GI:3341511)   chr2:10184914-10187144 FORWARD   Aliases: T29E15.11, T29E15_11	5.2	5.6	-0.3	-0.7	100.0%	-4.7
10054	AT4G14410.2   basic helix-loop-helix (bHLH) family protein   chr4:8300072-8301663 FORWARD   Aliases: DL3245W, FCAALL.201	8.4	8.3	0.1	0.7	100.0%	-4.9
10055	AT5G63780.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:25541071-25544452 FORWARD   Aliases: MBK5.26, MBK5_26	7.2	7.4	-0.2	-0.7	100.0%	-4.8
10056	AT5G55360.1   long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis	3.3	3.2	0.1	0.7	100.0%	-5.2
10057	AT5G61840.1   exostosin family protein, contains Pfam profile: PF03016	6.4	6.7	-0.3	-0.7	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10058	AT3G51110.1   crooked neck protein, putative / cell cycle protein, putative, similar to Swiss-Prot:P17886 crooked neck protein (Drosophila melanogaster)   chr3:18994606-18996828 FORWARD   Aliases: F24M12.150	2.6	2.5	0.1	0.7	100.0%	-5.7
10059	AT3G07550.2   F-box family protein (FBL12), contains similarity to F-box protein FBL6 GI:6456737 from (Homo sapiens)   chr3:2409733-2411300 FORWARD   Aliases: F21O3.26	5.7	5.8	-0.1	-0.7	100.0%	-4.7
10060	AT2G37300.1   expressed protein, and genefinder   chr2:15669678-15670524 REVERSE   Aliases: F3G5.9, F3G5_9	2.9	3.0	-0.1	-0.7	100.0%	-5.0
10061	AT2G26200.1   expressed protein   chr2:11159804-11163544 FORWARD   Aliases: T1D16.16, T1D16_16	5.3	5.4	-0.1	-0.7	100.0%	-4.9
10062	AT2G21830.1   DC1 domain-containing protein, contains Pfam profilePF03107: DC1 domain   chr2:9310793-9312977 FORWARD   Aliases: F7D8.15, F7D8_15	6.5	6.2	0.2	0.7	100.0%	-4.6
10063	AT5G29090.1   expressed protein   chr5:11149626-11150544 FORWARD   Aliases: F23C8.60, F23C8_60	3.6	3.5	0.2	0.7	100.0%	-5.0
10064	AT3G62000.1   O-methyltransferase family 3 protein, several O-methyltransferases - different species; contains Pfam 01596 O-methyltransferase domain   chr3:22970176-22972184 REVERSE   Aliases: F21F14.170	5.5	5.6	-0.2	-0.7	100.0%	-4.5
10065	AT1G17350.1   auxin-induced-related / indole-3-acetic acid induced-related, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesnerian)	7.7	8.0	-0.3	-0.7	100.0%	-4.5
10066	AT5G54410.1   hypothetical protein   chr5:22111473-22112132 REVERSE   Aliases: F24B18.3, F24B18_3	2.6	2.5	0.1	0.7	100.0%	-5.4
10067	AT5G59180.1   DNA-directed RNA polymerase II, identical to Swiss-Prot:P38421 DNA-directed RNA polymerase II 19 kDa polypeptide (EC 2.7.7.6) (RNA polymerase II subunit 5) (Arabidopsis thaliana)   chr5:23900643-23902432 FORWARD   Aliases: MNC17.16, MNC17_16	8.0	7.6	0.5	0.7	100.0%	-4.5
10068	AT1G49190.1   Symbol: ARR19   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain ;contains similarity to two-component response regulator protein (ARR2) GI:4210451 from (Arabidopsis thaliana)	2.6	2.5	0.1	0.7	100.0%	-5.4
10069	AT1G28250.1   expressed protein   chr1:9874234-9875560 FORWARD   Aliases: F3H9.10, F3H9_10	3.5	3.3	0.2	0.7	100.0%	-5.0
10070	AT5G61810.2   similar to mitochondrial substrate carrier family protein [Arabidopsis thaliana] (TAIR:At5g07320.1); similar to putative small calcium-binding mitochondrial carrier 2 [Oryza sativa (japonica cultivar-group)] (GB:BAD35532.1); contains InterPro domain Mitochondrial substrate carrier (InterPro:IPR001993); contains InterPro domain Mitochondrial carrier protein (InterPro:IPR002067)   chr5:24848341-24851096 REVERSE   Aliases: MAC9.1, MAC9_1	6.2	6.0	0.2	0.7	100.0%	-4.5
10071	AT1G78220.1   Symbol: GRF13   14-3-3 protein GF14 pi (GRF13), similar to GF14 epsilon isoform GI:1022778 from (Arabidopsis thaliana); contains Pfam profile: PF00244 14-3-3 proteins   chr1:29430614-29432074 REVERSE   Aliases: GF14 PI, T11I11.16, T11I11_16	2.6	2.5	0.1	0.7	100.0%	-5.5
10072	AT3G21100.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g51520.2); similar to putative DAZ associated protein 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_479561.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr3:7399157-7402533 FORWARD   Aliases: MSA6.14	2.2	2.3	-0.1	-0.7	100.0%	-5.4
10073	AT5G46120.1   hypothetical protein   chr5:18719851-18720102 REVERSE   Aliases: MCL19.18, MCL19_18	2.4	2.5	-0.1	-0.7	100.0%	-5.8
10074	AT4G27500.1   Symbol: PPI1   expressed protein, non-consensus GA donor splice site at exon 6   chr4:13743178-13745906 FORWARD   Aliases: F27G19.100, F27G19_100, PROTON PUMP INTERACTOR 1	9.8	10.1	-0.2	-0.7	100.0%	-5.0
10075	AT5G40560.1   DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana)   chr5:16261771-16263747 FORWARD   Aliases: MNF13.8, MNF13_8	2.7	2.6	0.1	0.7	100.0%	-5.5
10076	AT1G65280.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain   chr1:24249164-24252370 FORWARD   Aliases: T8F5.5, T8F5_5	7.8	8.3	-0.5	-0.7	100.0%	-4.6
10077	AT1G04130.1   tetratricopeptide repeat (TPR)-containing protein, contains non-consensus donor splice site AT at exon 4 and acceptor splice site at exon5; Contains similarity to serine/threonine protein phosphatase gb:X83099 from S. cerevisiae, SP:O95801 Tetratricopeptide repeat protein 4 Homo sapiens; contains Pfam profile PF00515: TPR Domain   chr1:1073427-1075546 FORWARD   Aliases: F20D22.10, F20D22_10	4.5	4.6	-0.2	-0.7	100.0%	-4.8
10078	AT4G24410.1   expressed protein   chr4:12623540-12624049 REVERSE   Aliases: T22A6.240, T22A6_240	2.3	2.2	0.1	0.7	100.0%	-5.8
10079	AT1G54610.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:20397429-20400853 REVERSE   Aliases: T22H22.5, T22H22_5	7.7	7.9	-0.1	-0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10080	AT5G55930.1   Symbol: ATOPT1	4.0	3.8	0.2	0.7	100.0%	-4.4
10081	AT1G12230.1   transaldolase, putative, similar to Swiss-Prot:P30148 transaldolase B (EC 2.2.1.2) (Escherichia coli O157:H7)   chr1:4148032-4151023 FORWARD   Aliases: T28K15.4, T28K15_4	10.9	10.4	0.5	0.7	100.0%	-4.4
10082	AT1G67620.1   expressed protein, contains Pfam domain PF02410: Domain of unknown function DUF143   chr1:25344239-25345605 FORWARD   Aliases: F12B7.17, F12B7_17	4.7	5.0	-0.4	-0.7	100.0%	-4.2
10083	AT3G22425.2   imidazoleglycerol-phosphate dehydratase 1 (IGPD1), identical to SP:P34047 Imidazoleglycerol-phosphate dehydratase 1 (EC 4.2.1.19) (IGPD 1) {Arabidopsis thaliana}; supporting cDNA gi:437212:gb:U02689.1:ATU02689   chr3:7951062-7953230 FORWARD   Aliases: None	6.1	5.6	0.5	0.7	100.0%	-4.6
10084	AT1G25520.1   expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	7.8	8.0	-0.1	-0.7	100.0%	-5.1
10085	AT5G65530.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr5:26207823-26210192 REVERSE   Aliases: K21L13.3, K21L13_3	3.2	3.5	-0.3	-0.7	100.0%	-4.2
10086	AT1G71480.1   nuclear transport factor 2 (NTF2) family protein, contains Pfam domain, PF02136: Nuclear transport factor 2 (NTF2) domain   chr1:26935602-26936975 FORWARD   Aliases: F26A9.14	3.6	3.4	0.2	0.7	100.0%	-4.8
10087	AT5G13570.1   MutT/nudix family protein, similar to mRNA-decapping enzyme (Homo sapiens) GI:23268269; contains Pfam profile PF00293: NUDIX domain   chr5:4367304-4370262 FORWARD   Aliases: T6I14.5	3.7	3.6	0.2	0.7	100.0%	-4.8
10088	AT4G31115.1   expressed protein, supported by full length cDNA gi:21436034 from (Arabidopsis thaliana)	2.9	3.1	-0.2	-0.7	100.0%	-5.2
10089	AT3G28840.1   expressed protein   chr3:10839655-10841183 FORWARD   Aliases: T19N8.14	2.7	2.6	0.1	0.7	100.0%	-5.0
10090	AT1G14490.1   DNA-binding protein-related, contains similarity to DNA-binding proteins	4.1	4.3	-0.2	-0.7	100.0%	-4.6
10091	AT2G21160.1   translocon-associated protein alpha (TRAP alpha) family protein, contains Pfam profile: PF03896 translocon-associated protein (TRAP), alpha subunit   chr2:9075412-9077508 FORWARD   Aliases: F26H11.8, F26H11_8	9.7	10.0	-0.3	-0.7	100.0%	-4.5
10092	AT4G23190.1   Symbol: CRK11   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:12141043-12143844 REVERSE   Aliases: AT RLK3, CRK11, CYSTEINE RICH RLK11, F21P8.80, F21P8_80	3.6	3.7	-0.1	-0.7	100.0%	-5.2
10093	AT1G13960.2   Symbol: WRKY4   WRKY family transcription factor, similar to WKRY DNA-binding protein GB:AAD17441   chr1:4776460-4779347 FORWARD   Aliases: F16A14.18	5.1	4.8	0.2	0.7	100.0%	-4.6
10094	AT3G46240.1   protein kinase-related, similar to light repressible receptor protein kinase (GI:1321686) (Arabidopsis thaliana)	3.2	3.1	0.2	0.7	100.0%	-4.9
10095	AT1G64720.1   Symbol: CP5   expressed protein, weak similarity to SP:P53809 Phosphatidylcholine transfer protein (PC-TP) {Rattus norvegicus}   chr1:24050216-24052261 REVERSE   Aliases: CP5, F13O11.4, F13O11_4	10.0	9.7	0.3	0.7	100.0%	-4.7
10096	AT4G17280.1   auxin-responsive family protein, similar to auxin-induced protein AIR12 (GI:11357190) (Arabidopsis thaliana)   chr4:9678541-9680401 REVERSE   Aliases: DL4675C, FCAALL.393	3.1	3.4	-0.3	-0.7	100.0%	-4.3
10097	AT4G38980.1   expressed protein   chr4:18166703-18168170 REVERSE   Aliases: F19H22.80, F19H22_80	5.8	5.7	0.1	0.7	100.0%	-5.0
10098	AT3G09740.1   Symbol: SYP71   syntaxin 71 (SYP71), identified as syntaxin of plants 71 (SYP71) in Sanderfoot, A.A., et al, Plant Physiology 124:1558-69(2000); identical to SP:Q9SF29 Syntaxin 71 (AtSYP71) {Arabidopsis thaliana}   chr3:2989499-2991666 FORWARD   Aliases: ATSYP71, F11F8.33, SYNTAXIN OF PLANTS 71	7.8	7.4	0.4	0.7	100.0%	-4.5
10099	AT1G19050.1   Symbol: ARR7   two-component responsive regulator / response regulator 7 (ARR7), identical to response regulator 7 GI:3953603 from (Arabidopsis thaliana)   chr1:6577824-6579102 REVERSE   Aliases: ARR7, F14D16.20, F14D16_20, RESPONSE REGULATOR 7	7.7	8.0	-0.3	-0.7	100.0%	-4.3
10100	AT3G16040.1   expressed protein   chr3:5443097-5443957 FORWARD   Aliases: MSL1.7	3.0	2.9	0.1	0.7	100.0%	-5.6
10101	AT5G25120.1   Symbol: CYP71B11   cytochrome P450 family protein, CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438   chr5:8662854-8664435 FORWARD   Aliases: T11H3.130, T11H3_130	5.5	5.7	-0.2	-0.7	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10102	AT2G35390.3   similar to ribose-phosphate pyrophosphokinase 2 / phosphoribosyl diphosphate synthetase 2 (PRS2) [Arabidopsis thaliana] (TAIR:At1g32380.1); similar to phosphoribosyl pyrophosphate synthase [Spinacia oleracea] (GB:CAB43599.1); contains InterPro domain Phosphoribosyl pyrophosphate synthetase (InterPro:IPR000842); contains InterPro domain Phosphoribosyltransferase (InterPro:IPR000836); contains InterPro domain Ribose-phosphate pyrophosphokinase (InterPro:IPR005946)   chr2:14902358-14904874 REVERSE   Aliases: AT2G35400, T32F12.23, T32F12_23	1.9	1.9	0.1	0.7	100.0%	-5.6
10103	AT5G16040.1   regulator of chromosome condensation (RCC1) family protein, similar to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	8.5	8.9	-0.3	-0.7	100.0%	-4.5
10104	AT1G25540.1   Symbol: PFT1   phytochrome and flowering time regulatory protein (PFT1), PMID: 12815435	5.3	5.5	-0.2	-0.7	100.0%	-4.7
10105	AT2G44590.3   Symbol: ADL1D   dynamin-like protein D (DL1D), identical to dynamin-like protein D (Arabidopsis thaliana) GI:19569770; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain	3.1	3.0	0.1	0.7	100.0%	-5.2
10106	AT3G52300.2   similar to putative mitochondrial F0 ATP synthase D chain [Oryza sativa (japonica cultivar-group)] (GB:XP_482965.1)   chr3:19407543-19409355 FORWARD   Aliases: T25B15.70	13.0	13.3	-0.3	-0.7	100.0%	-5.3
10107	AT5G24165.1   expressed protein   chr5:8188563-8189279 FORWARD   Aliases: None	6.7	6.5	0.3	0.7	100.0%	-4.7
10108	AT4G01570.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:679472-681940 FORWARD   Aliases: T15B16.21, T15B16_21	4.6	4.7	-0.1	-0.7	100.0%	-4.8
10109	AT1G14790.1   Symbol: RDR1   RNA-dependent RNA polymerase, putative, similar to RNA-directed RNA polymerase GB:CAA09697 GI:4138282 (Nicotiana tabacum)   chr1:5093409-5098027 REVERSE   Aliases: ATRDRP1, F10B6.19, F10B6_19, RNA DEPENDENT RNA POLYMERASE 1	5.7	5.4	0.3	0.7	100.0%	-4.6
10110	AT5G67090.1   subtilase family protein, contains similarity to subtilisin-like protease ag12 GI:757522 from (Alnus glutinosa)   chr5:26791337-26793547 REVERSE   Aliases: K21H1.5, K21H1_5	2.9	3.1	-0.2	-0.7	100.0%	-4.7
10111	AT2G30370.1   allergen-related, weak similarity to pollen major allergen 2 protein (Juniperus ashei) gi:9955725:emb:CAC05582   chr2:12947654-12949244 REVERSE   Aliases: T9D9.18, T9D9_18	2.4	2.5	-0.1	-0.7	100.0%	-5.2
10112	AT5G58020.1   expressed protein, contains PF04641: Protein of unknown function, DUF602	9.7	9.4	0.3	0.7	100.0%	-4.6
10113	AT2G39780.1   Symbol: RNS2   ribonuclease 2 (RNS2), identical to ribonuclease 2 precursor SP:P42814, GI:289210; contains a ribonuclease T2 family histidine active site signature (PDOC00459)	9.7	9.4	0.3	0.7	100.0%	-4.9
10114	AT5G44410.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr5:17908449-17910080 REVERSE   Aliases: MFC16.3, MFC16_3	5.6	5.4	0.2	0.7	100.0%	-4.8
10115	AT4G00100.1   Symbol: ATRPS13A   40S ribosomal protein S13 (RPS13A), similar to ribosomal protein S13; PF00312 (View Sanger Pfam): ribosomal protein S15; identical to cDNA AtRPS13A mRNA for cytoplasmic ribosomal protein S13 GI:6521011   chr4:37096-38312 FORWARD   Aliases: F6N15.7, F6N15_7, PFL2, POINTED FIRST LEAF 2, RIBOSOMAL PROTEIN S13, RIBOSOMAL PROTEIN S13A, RPS13	11.3	11.6	-0.3	-0.7	100.0%	-4.7
10116	AT1G80040.2   expressed protein   chr1:30114040-30116163 REVERSE   Aliases: F18B13.13, F18B13_13	8.6	8.4	0.2	0.7	100.0%	-5.0
10117	AT4G18600.1   Symbol: wave5   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g29170.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470104.1)	4.4	4.6	-0.2	-0.7	100.0%	-4.7
10118	AT5G01460.1   LMBR1 integral membrane family protein, contains Pfam PF04791: LMBR1-like conserved region   chr5:186693-190456 FORWARD   Aliases: T10O8.170, T10O8_170	3.8	3.6	0.1	0.7	100.0%	-4.8
10119	AT3G13620.1   amino acid permease family protein, weak similarity to SP:Q9WTR6 Cystine/glutamate transporter (Amino acid transport system xc-) {Mus musculus}; contains Pfam profile PF00324: Amino acid permease   chr3:4450191-4452594 REVERSE   Aliases: K20M4.6	6.8	7.1	-0.3	-0.7	100.0%	-4.5
10120	AT3G56250.1   expressed protein   chr3:20877099-20878819 FORWARD   Aliases: F18O21.210	3.2	3.0	0.2	0.7	100.0%	-5.0
10121	AT3G60010.1   Symbol: ASK13   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At13), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1a GI:3068807 from (Arabidopsis thaliana)   chr3:22174071-22174535 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 13, ASK13, T2O9.1	2.7	2.6	0.1	0.7	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10122	AT3G60370.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, SP:Q9M222; similar to FKBP-type peptidyl-prolyl cis-trans isomerase fkpA precursor (PPIase) (Rotamase)(SP:Q8X880) (Escherichia coli O157:H7) ; contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr3:22325747-22327514 REVERSE   Aliases: T8B10.30	6.2	5.9	0.2	0.7	100.0%	-4.4
10123	AT3G01880.1   hypothetical protein   chr3:307789-309567 FORWARD   Aliases: F1C9.34	3.2	3.1	0.1	0.7	100.0%	-5.2
10124	AT5G47690.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g77600.1); similar to P0677H08.21 [Oryza sativa (japonica cultivar-group)] (GB:NP_915668.1)	4.6	5.1	-0.5	-0.7	100.0%	-4.4
10125	AT1G61150.3   expressed protein, similar to Protein C20orf11 (Swiss-Prot:Q9NWU2) (Homo sapiens)   chr1:22546221-22549281 FORWARD   Aliases: F11P17.12, F11P17_12	4.3	3.9	0.3	0.7	100.0%	-4.5
10126	AT5G50915.2   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.4	2.3	0.1	0.7	100.0%	-5.5
10127	AT1G44980.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr1:17006696-17008363 REVERSE   Aliases: F27F5.7, F27F5_7	2.7	2.6	0.1	0.7	100.0%	-5.2
10128	AT5G13670.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr5:4407147-4409014 REVERSE   Aliases: MSH12.14, MSH12_14	3.0	2.9	0.1	0.7	100.0%	-5.2
10129	AT1G69420.2   zinc finger (DHHC type) family protein, contains Pfam profile: PF01529: DHHC zinc finger domain   chr1:26096859-26100570 FORWARD   Aliases: F10D13.9, F10D13_9	3.1	3.3	-0.2	-0.7	100.0%	-5.0
10130	AT1G34180.1   Symbol: ANAC016   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM-like protein GI:8809651 from (Arabidopsis thaliana)   chr1:12448545-12451263 FORWARD   Aliases: ANAC016, F23M19.14, F23M19_14	3.8	3.7	0.1	0.7	100.0%	-5.3
10131	AT1G31450.1   aspartyl protease family protein, contains eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141   chr1:11259853-11261190 REVERSE   Aliases: T8E3.12, T8E3_12	2.6	2.6	0.1	0.7	100.0%	-5.5
10132	AT5G03920.1   expressed protein   chr5:1058145-1058762 FORWARD   Aliases: F8F6.130, F8F6_130	2.7	2.8	-0.1	-0.7	100.0%	-5.6
10133	AT1G27070.1   5'-AMP-activated protein kinase-related, contains weak similarity to Swiss-Prot:Q9QZH4 5'-AMP-activated protein kinase, beta-2 subunit (AMPK beta-2 chain) (Rattus norvegicus)   chr1:9396646-9399440 REVERSE   Aliases: T7N9.13, T7N9_13	5.2	5.0	0.2	0.7	100.0%	-4.6
10134	AT1G60400.1   F-box family protein, contains F-box domain Pfam:PF00646	2.9	3.1	-0.2	-0.7	100.0%	-5.0
10135	AT3G59170.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.5	-0.1	-0.7	100.0%	-5.6
10136	AT3G54540.1   Symbol: ATGCN4	8.8	8.5	0.3	0.7	100.0%	-4.8
10137	AT1G27385.1   expressed protein   chr1:9510925-9512847 REVERSE   Aliases: None	7.5	7.3	0.2	0.7	100.0%	-4.4
10138	AT4G20370.1   Symbol: TSF   twin sister of FT protein (TSF) / TFL1 like protein, identical to SP:Q9S7R5 TWIN SISTER of FT protein (TFL1 like protein) {Arabidopsis thaliana}; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein	3.7	3.9	-0.2	-0.7	100.0%	-4.9
10139	AT2G30925.1   hypothetical protein   chr2:13168892-13169020 FORWARD   Aliases: None	2.2	2.1	0.1	0.7	100.0%	-6.0
10140	AT5G44090.1   calcium-binding EF hand family protein, putative / protein phosphatase 2A 62 kDa B'' regulatory subunit, putative, contains Pfam profile: PF00036 EF hand; identical to cDNA protein phosphatase 2A 62 kDa B'' regulatory subunit GI:5533378   chr5:17760004-17765623 REVERSE   Aliases: MLN1.1, MLN1_1	3.9	3.7	0.3	0.7	100.0%	-4.6
10141	AT1G76920.1   F-box family protein (FBX3), contains similarity to stamina pistilloidia GI:4101570, the pea ortholog of Fim and UFO from (Pisum sativum)   chr1:28896956-28898570 FORWARD   Aliases: F22K20.2, F22K20_2	5.3	5.0	0.2	0.7	100.0%	-4.5
10142	AT3G19040.1   Symbol: HAF2   similar to HAC13 protein (HAC13) [Arabidopsis thaliana] (TAIR:At1g32750.1); similar to putative protein serine/threonine kinase [Dictyostelium discoideum] (GB:EAL61331.1); contains InterPro domain Bromodomain (InterPro:IPR001487); contains InterPro domain Ubiquitin domain (InterPro:IPR000626)   chr3:6567163-6575288 REVERSE   Aliases: HISTONE ACETYLTRANSFERASE OF THE TAFII250 FAMILY, K13E13.15	2.7	2.8	-0.1	-0.7	100.0%	-5.1
10143	ATCG00550.1   Symbol: PSBJ   PSII component   chrC:63538-63660 REVERSE   Aliases: PSBJ	10.8	11.0	-0.2	-0.7	100.0%	-5.1
10144	AT1G49790.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr1:18439805-18440736 REVERSE   Aliases: F10F5.4, F10F5_4	2.7	2.7	0.1	0.7	100.0%	-5.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10145	AT3G04800.1   Symbol: ATTIM23 3   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr3:1314485-1315051 REVERSE   Aliases: F7O18.29	2.3	2.2	0.1	0.7	100.0%	-5.5
10146	AT1G46912.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; similar to hypothetical protein GI:4589954 from (Arabidopsis thaliana) contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain;   chr1:17275131-17276069 FORWARD   Aliases: F2G19.20, F2G19_20	3.2	3.3	-0.1	-0.7	100.0%	-5.4
10147	AT1G14840.1   Symbol: ATMAP70 4   Encodes a microtubule associated protein (MAP70-4). Expressed in all tissues.   chr1:5112079-5115423 REVERSE   Aliases: ATMAP70 4, F10B6.24, F10B6_24	3.6	3.8	-0.2	-0.7	100.0%	-4.8
10148	AT3G01610.1   Symbol: CDC48C	6.2	6.4	-0.2	-0.7	100.0%	-4.8
10149	AT4G39540.2   shikimate kinase family protein, similar to shikimate kinase precursor from Lycopersicon esculentum (SP:Q00497); contains Pfam shikimate kinase domain PF01202   chr4:18378248-18380405 FORWARD   Aliases: F23K16.170, F23K16_170	6.3	5.9	0.4	0.7	100.0%	-4.7
10150	AT5G57260.1   Symbol: CYP71B10   cytochrome P450 71B10, identical to cytochrome P450 71B10 (SP:Q9LVD2) (Arabidopsis thaliana)	3.0	3.2	-0.1	-0.7	100.0%	-5.4
10151	AT1G07705.1   similar to transcription regulator NOT2/NOT3/NOT5 family protein [Arabidopsis thaliana] (TAIR:At5g59710.1); similar to putative CCR4-NOT transcription complex, subunit 2; NOT2 [Oryza sativa (japonica cultivar-group)] (GB:XP_468120.1); contains InterPro domain NOT2/NOT3/NOT5 (InterPro:IPR007282)   chr1:2382679-2386089 FORWARD   Aliases: None	4.0	3.7	0.3	0.7	100.0%	-4.6
10152	AT3G07810.2   heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative, contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:2492299-2495756 FORWARD   Aliases: F17A17.15	4.7	4.9	-0.2	-0.7	100.0%	-4.6
10153	AT3G44250.1   Symbol: CYP71B38   cytochrome P450 family protein, CYTOCHROME P450 71B7 - Arabidopsis thaliana, EMBL:X97864   chr3:15959492-15961211 REVERSE   Aliases: T10D17.40	3.2	3.1	0.2	0.7	100.0%	-4.8
10154	AT1G04330.1   expressed protein, EST gb:H76414 comes from this gene   chr1:1161310-1161885 REVERSE   Aliases: F19P19.24, F19P19_24	2.6	2.5	0.1	0.7	100.0%	-4.9
10155	AT5G12120.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627: UBA/TS-N domain   chr5:3916049-3918660 REVERSE   Aliases: MXC9.8, MXC9_8	5.9	5.7	0.2	0.7	100.0%	-4.6
10156	AT1G66460.1   protein kinase family protein, contains Pfam profile: PF00069: Eukaryotic protein kinase domain   chr1:24793398-24795651 REVERSE   Aliases: F28G11.10, F28G11_10	2.6	2.5	0.1	0.7	100.0%	-5.3
10157	AT5G54670.1   Symbol: ATK3   kinesin-like protein C (KATC)   chr5:22226698-22231360 FORWARD   Aliases: ARABIDOPSIS THALIANA KINESIN 3, KATC, KINESIN LIKE PROTEIN C, MRB17.18	4.2	4.5	-0.3	-0.7	100.0%	-4.6
10158	AT1G67450.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain; similar to hypothetical protein GI:7268472 from (Arabidopsis thaliana)	2.8	2.9	-0.1	-0.7	100.0%	-5.4
10159	AT3G59690.1   calmodulin-binding family protein, similar to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:22059731-22062650 FORWARD   Aliases: T16L24.240	4.9	4.6	0.2	0.7	100.0%	-4.7
10160	AT1G55030.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.8	-0.2	-0.7	100.0%	-5.2
10161	AT5G63940.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr5:25605324-25608684 FORWARD   Aliases: MBM17.4, MBM17_4	5.9	6.3	-0.4	-0.7	100.0%	-4.4
10162	AT3G24720.1   protein kinase family protein, protein kinase family; similar to tyrosine-protein kinase GB:P18160 from (Dictyostelium discoideum)   chr3:9028475-9029955 FORWARD   Aliases: K7P8.1	3.1	3.3	-0.2	-0.7	100.0%	-5.1
10163	AT5G01550.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:214516-216582 REVERSE   Aliases: F7A7.70, F7A7_70	3.4	3.2	0.2	0.7	100.0%	-4.5
10164	AT2G15550.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:6790268-6792262 REVERSE   Aliases: F9O13.10	4.3	4.1	0.2	0.7	100.0%	-4.5
10165	AT3G19820.2   Symbol: DWF1   cell elongation protein / DWARF1 / DIMINUTO (DIM), identical to GB:S71189 (SP:Q39085) from (Arabidopsis thaliana); contains Pfam FAD binding domain PF01565   chr3:6879624-6882265 REVERSE   Aliases: CABBAGE 1, CBB1, DIM, DIM1, DIMINUTIA, DIMINUTO 1, DW1, DWARF 1, EVE1, MPN9.6	9.9	9.4	0.4	0.7	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10166	AT1G29120.4   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g25770.1); similar to putative serine esterase [Oryza sativa (japonica cultivar-group)] (GB:AAT77089.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468171.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr1:10174268-10178475 FORWARD   Aliases: AT1G29130, F28N24.29, F28N24_29	5.9	5.6	0.2	0.7	100.0%	-4.7
10167	AT1G43570.1   expressed protein   chr1:16404310-16405356 REVERSE   Aliases: T10P12.5, T10P12_5	3.4	3.6	-0.2	-0.7	100.0%	-4.9
10168	AT5G55840.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr5:22615624-22619725 FORWARD   Aliases: MWJ3.2, MWJ3_2	3.7	3.9	-0.2	-0.7	100.0%	-4.9
10169	AT3G15150.1   expressed protein   chr3:5101992-5104147 REVERSE   Aliases: F4B12.6	3.1	3.0	0.1	0.7	100.0%	-5.0
10170	AT1G79910.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g52315.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD46051.1); contains InterPro domain Eukaryotic protein of unknown function DUF292 (InterPro:IPR005061)	2.7	2.6	0.1	0.7	100.0%	-5.2
10171	AT5G15270.2   KH domain-containing protein, various predicted proteins, Arabidopsis thaliana and Oryza sativa   chr5:4958340-4961066 FORWARD   Aliases: F8M21.160, F8M21_160	5.4	5.6	-0.2	-0.7	100.0%	-4.6
10172	AT1G04260.1   Symbol: MPI7   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor (Mus musculus) GI:7716652; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr1:1140527-1141364 REVERSE   Aliases: CAMV MOVEMENT PROTEIN INTERACTING PROTEIN 7, F19P19.30, F19P19_30, MPIP7	5.9	5.8	0.2	0.7	100.0%	-4.8
10173	AT2G34940.1   vacuolar sorting receptor, putative, similar to BP-80 vacuolar sorting receptor (Pisum sativum) GI:1737222   chr2:14747550-14750496 FORWARD   Aliases: F19I3.17, F19I3_17	3.2	3.6	-0.4	-0.7	100.0%	-4.0
10174	AT5G57630.1   Symbol: CIPK21	4.4	4.1	0.3	0.7	100.0%	-4.2
10175	AT2G03450.1   purple acid phosphatase (PAP9), identical to purple acid phosphatase (Arabidopsis thaliana) GI:20257481; contains Pfam profile: PF00149 calcineurin-like phosphoesterase; contains metallo-phosphoesterase motif (PS50185)   chr2:1041385-1043664 FORWARD   Aliases: T4M8.12, T4M8_12	5.5	5.7	-0.2	-0.7	100.0%	-4.9
10176	AT4G40040.2   similar to histone H3.2 [Arabidopsis thaliana] (TAIR:At4g40030.1); similar to histone H3.2 protein [Mus pahari] (GB:CAA56575.1); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124); contains InterPro domain Histone H3 (InterPro:IPR000164); contains InterPro domain Histone core (InterPro:IPR007125)	8.4	7.5	0.9	0.7	100.0%	-4.2
10177	AT1G32740.1   expressed protein   chr1:11844857-11846482 FORWARD   Aliases: F6N18.12, F6N18_12	4.7	4.3	0.4	0.7	100.0%	-4.4
10178	AT3G07565.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g10820.2); similar to OSJNBb0065J09.5 [Oryza sativa (japonica cultivar-group)] (GB:CAE05709.1)   chr3:2413648-2416232 FORWARD   Aliases: MLP3.1	4.5	4.3	0.2	0.7	100.0%	-4.4
10179	AT1G74860.1   expressed protein   chr1:28126980-28129543 FORWARD   Aliases: F25A4.17, F25A4_17	4.7	4.5	0.2	0.7	100.0%	-4.6
10180	AT1G21810.1   expressed protein   chr1:7656567-7658623 REVERSE   Aliases: T26F17.2	2.7	2.7	-0.1	-0.7	100.0%	-5.6
10181	AT1G24390.1   expressed protein, similar to EST emb:Z37190   chr1:8648190-8648984 FORWARD   Aliases: F21J9.5	2.9	3.0	-0.1	-0.7	100.0%	-5.3
10182	AT5G39500.1   pattern formation protein, putative, similar to SP:Q42510 Pattern formation protein EMB30 {Arabidopsis thaliana}; contains Pfam profile PF01369: Sec7 domain   chr5:15832502-15837273 FORWARD   Aliases: MUL8.180, MUL8_180	4.1	4.4	-0.3	-0.7	100.0%	-4.7
10183	AT2G13810.1   aminotransferase class I and II family protein, low similarity to Aromatic Aminotransferase from Pyrococcus horikoshii GP:14278621; contains Pfam profile PF00155 aminotransferase, classes I and II   chr2:5775528-5779341 FORWARD   Aliases: F17L24.14	3.1	2.9	0.1	0.7	100.0%	-4.9
10184	AT5G59220.1   protein phosphatase 2C, putative / PP2C, putative, ABA induced protein phosphatase 2C, Fagus sylvatica, EMBL:FSY277743   chr5:23911630-23913845 REVERSE   Aliases: MNC17.13, MNC17_13	4.3	4.1	0.2	0.7	100.0%	-5.1
10185	AT4G35990.1   expressed protein   chr4:17036349-17036826 FORWARD   Aliases: T19K4.120, T19K4_120	3.2	3.1	0.1	0.7	100.0%	-5.1
10186	AT1G67700.2   expressed protein   chr1:25377897-25379693 FORWARD   Aliases: F12A21.32	7.5	7.1	0.4	0.7	100.0%	-4.3
10187	AT3G59630.1   diphthamide synthesis DPH2 family protein, contains InterPro accession IPR002728: Diphthamide synthesis DPH2 protein   chr3:22036051-22038845 REVERSE   Aliases: T16L24.180	4.5	4.6	-0.1	-0.7	100.0%	-4.9
10188	AT5G57600.1   expressed protein   chr5:23338972-23339913 REVERSE   Aliases: MUA2.18, MUA2_18	3.5	3.7	-0.1	-0.7	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10189	AT3G28630.2   expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569   chr3:10730405-10732086 FORWARD   Aliases: MZN14.10	2.4	2.4	0.1	0.7	100.0%	-5.5
10190	AT1G66210.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr1:24669292-24672446 REVERSE   Aliases: T6J19.3, T6J19_3	2.2	2.3	-0.1	-0.7	100.0%	-5.6
10191	AT3G13700.1   RNA-binding protein, putative, similar to mec-8 (Caenorhabditis elegans) GI:1370048; contains Pfam profile:PF00076 rrm:RNA recognition motif   chr3:4491015-4493744 REVERSE   Aliases: MMM17.12	5.5	5.8	-0.3	-0.7	100.0%	-4.2
10192	AT3G13710.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor (Mus musculus) GI:7716652; contains Pfam profile PF03208: Prenyated rab acceptor (PRA1)   chr3:4490635-4493838 REVERSE   Aliases: MMM17.13	5.5	5.8	-0.3	-0.7	100.0%	-4.2
10193	AT3G62440.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.5	-0.1	-0.7	100.0%	-5.4
10194	AT3G27610.1   expressed protein   chr3:10226779-10229428 REVERSE   Aliases: MGF10.2	4.7	5.1	-0.3	-0.7	100.0%	-4.4
10195	AT2G40316.1   expressed protein   chr2:16843264-16846540 FORWARD   Aliases: AT2G40313, T7M7.21, T7M7_21	4.6	4.4	0.2	0.7	100.0%	-5.0
10196	AT1G52300.1   60S ribosomal protein L37 (RPL37B), similar to SP:Q43292 from (Arabidopsis thaliana)   chr1:19478716-19479887 REVERSE   Aliases: F19K6.12, F19K6_12	12.9	13.1	-0.2	-0.7	100.0%	-5.7
10197	AT1G69270.1   Symbol: RPK1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr1:26043986-26046365 REVERSE   Aliases: F4N2.27, F4N2_27, RECEPTOR LIKE PROTEIN KINASE 1	4.8	5.0	-0.3	-0.7	100.0%	-4.7
10198	AT2G15930.1   expressed protein, and grail   chr2:6948672-6949060 REVERSE   Aliases: F19G14.7, F19G14_7	4.4	4.2	0.2	0.7	100.0%	-4.6
10199	AT3G01390.2   Symbol: VMA10   vacuolar ATP synthase subunit G 1 (VATG1) / V-ATPase G subunit 1 (VAG1) / vacuolar proton pump G subunit 1 (VMA10), identical to SWISS-PROT:O82628 vacuolar ATP synthase subunit G 1 (V-ATPase G subunit 1, Vacuolar proton pump G subunit 1) (Arabidopsis thaliana)   chr3:150011-151169 REVERSE   Aliases: AVMA10, T13O15.3, T13O15_3, VACUOLAR MEMBRANE ATPASE 10, VACUOLAR MEMBRANE ATPASE SUBUNIT G	8.3	7.9	0.4	0.7	100.0%	-4.4
10200	AT2G40950.1   bZIP transcription factor family protein, similar to AtbZIP transcription factor GI:17065880 from (Arabidopsis thaliana); contains Pfam profile: bZIP transcription factor PF00170   chr2:17094698-17097502 REVERSE   Aliases: T20B5.15, T20B5_15	5.5	5.7	-0.3	-0.7	100.0%	-4.8
10201	AT5G16220.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein, hypothetical proteins - Arabidopsis thaliana contains Pfam profile PF00564: PB1 domain   chr5:5298306-5300607 REVERSE   Aliases: T21H19.140, T21H19_140	3.7	3.9	-0.2	-0.7	100.0%	-4.9
10202	AT3G53460.2   Symbol: CP29   29 kDa ribonucleoprotein, chloroplast / RNA-binding protein cp 29, nearly identical to SP:Q43349 29 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein cp29) {Arabidopsis thaliana}   chr3:19830646-19832483 REVERSE   Aliases: F4P12.160	8.1	7.7	0.4	0.7	100.0%	-4.4
10203	AT1G54923.1   expressed protein   chr1:20479424-20480235 REVERSE   Aliases: F14C21.35, F14C21_35	2.3	2.3	-0.1	-0.7	100.0%	-5.7
10204	AT2G27300.1   Symbol: ANAC040   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr2:11687495-11689033 REVERSE   Aliases: ANAC040, F12K2.12, F12K2_12	2.4	2.3	0.1	0.7	100.0%	-5.2
10205	AT1G65570.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase 5 (Lycopersicon esculentum) GI:2459817; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:24377761-24379509 REVERSE   Aliases: F5I14.10, F5I14_10	2.7	2.6	0.1	0.7	100.0%	-5.1
10206	AT5G27760.1   hypoxia-responsive family protein, contains Pfam profile: PF04588 hypoxia induced protein conserved region   chr5:9830368-9831787 FORWARD   Aliases: T1G16.90, T1G16_90	10.9	10.6	0.3	0.7	100.0%	-4.8
10207	AT5G20140.1   SOUL heme-binding family protein, contains Pfam profile PF04832: SOUL heme-binding protein   chr5:6798834-6800905 REVERSE   Aliases: F5O24.30, F5O24_30	5.2	5.0	0.2	0.7	100.0%	-4.7
10208	AT1G03080.1   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia)   chr1:731704-737332 REVERSE   Aliases: F10O3.10, F10O3_10	7.3	6.9	0.4	0.7	100.0%	-4.6
10209	AT4G08390.2   L-ascorbate peroxidase, stromal (sAPX), identical to stromal ascorbate peroxidase (Arabidopsis thaliana) gi:1419388:emb:CAA67425	8.9	9.2	-0.3	-0.7	100.0%	-4.4
10210	AT1G11910.1   aspartyl protease family protein, contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1   chr1:4016789-4020916 REVERSE   Aliases: F12F1.24, F12F1_24	9.7	9.1	0.6	0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10211	AT4G31150.2   endonuclease V family protein, contains Pfam PF04493: Endonuclease V   chr4:15143548-15145605 REVERSE   Aliases: F6E21.70, F6E21_70	4.3	4.1	0.2	0.7	100.0%	-4.8
10212	AT2G18480.1   mannitol transporter, putative, similar to mannitol transporter (Apium graveolens var. dulce) GI:12004316; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:8016664-8018325 REVERSE   Aliases: F24H14.17, F24H14_17	4.1	3.9	0.2	0.7	100.0%	-5.1
10213	AT1G09520.1   expressed protein   chr1:3070907-3072052 REVERSE   Aliases: F14J9.18, F14J9_18	5.7	5.4	0.3	0.7	100.0%	-4.4
10214	AT1G05810.1   Symbol: ARA   Ras-related protein (ARA-1) (ARA) / small GTP-binding protein, putative, nearly identical to SP:P19892 Ras-related protein ARA-1 (Arabidopsis thaliana) (Gene 76:313-319(1989))   chr1:1748313-1749459 FORWARD   Aliases: ARA, ARA 1, T20M3.8, T20M3_8	4.3	4.5	-0.2	-0.7	100.0%	-4.6
10215	AT1G80950.1   phospholipid/glycerol acyltransferase family protein, low similarity to SP:Q59601 1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) {Neisseria gonorrhoeae}; contains Pfam profile PF01553: Acyltransferase   chr1:30417436-30420005 REVERSE   Aliases: F23A5.31, F23A5_31	6.9	7.3	-0.4	-0.7	100.0%	-4.5
10216	AT1G65110.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr1:24187622-24191993 REVERSE   Aliases: T23K8.2, T23K8_2	3.0	3.1	-0.1	-0.7	100.0%	-5.4
10217	AT3G06620.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr3:2062212-2067422 REVERSE   Aliases: F5E6.5, F5E6_5	2.7	2.6	0.1	0.7	100.0%	-5.3
10218	AT2G19540.1   transducin family protein / WD-40 repeat family protein, contains WD-40 repeats (PF00400); similar to Glutamate-rich WD repeat protein (GRWD) (SP:Q9BQ67)(Homo sapiens)   chr2:8468844-8471596 FORWARD   Aliases: F3P11.14, F3P11_14	8.2	7.9	0.4	0.7	100.0%	-4.5
10219	AT5G14220.1   protoporphyrinogen oxidase, putative, similar to protoporphyrinogen IX oxidase, mitochondrial (PPO II) from Nicotiana tabacum (SP:O24164), Glycine max, AB025102, Spinacia oleracea (GI:14349153); contains Pfam amine oxidase, flavin-containing domain (PF015930)   chr5:4583271-4587404 REVERSE   Aliases: F18O22.10, F18O22_10	6.9	7.1	-0.2	-0.7	100.0%	-4.6
10220	AT2G15480.1   similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At4g34131.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At4g34135.1); similar to immediate-early salicylate-induced glucosyltransferase (GB:AAB36653.1); similar to betanidin-5-O-glucosyltransferase [Dorotheanthus bellidiformis] (GB:CAB56231.1); similar to phenylpropanoid:glucosyltransferase 1 [Nicotiana tabacum] (GB:AAK28303.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyl transferase (InterPro:IPR002213)   chr2:6765763-6767715 FORWARD   Aliases: F9O13.3	5.3	5.0	0.3	0.7	100.0%	-4.5
10221	AT3G22920.1   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to peptidyl-prolyl cis-trans isomerase PPlase (cyclophilin, cyclosporin A-binding protein) (Tomato) SWISS-PROT:P21568   chr3:8122720-8123418 REVERSE   Aliases: F5N5.9	3.8	3.6	0.1	0.7	100.0%	-5.1
10222	AT1G02940.1   Symbol: ATGSTF5   glutathione S-transferase, putative, similar to glutathione S-transferase GI:860955 from (Hyoscyamus muticus)	2.3	2.3	-0.1	-0.7	100.0%	-5.8
10223	AT5G42380.1   calmodulin-related protein, putative, similar to regulator of gene silencing calmodulin-related protein GI:12963415 from (Nicotiana tabacum)   chr5:16959804-16960594 REVERSE   Aliases: MDH9.7, MDH9_7	3.0	2.9	0.2	0.7	100.0%	-4.9
10224	AT1G80640.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:30316559-30319267 FORWARD   Aliases: T21F11.3, T21F11_3	4.2	4.4	-0.2	-0.7	100.0%	-4.6
10225	AT1G59530.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr1:21871927-21872373 FORWARD   Aliases: T30E16.6, T30E16_6	2.5	2.4	0.1	0.7	100.0%	-5.7
10226	AT4G18400.1   expressed protein   chr4:10169877-10171268 REVERSE   Aliases: F28J12.60, F28J12_60	7.9	7.7	0.2	0.7	100.0%	-4.8
10227	AT1G17220.1   translation initiation factor IF-2, chloroplast, putative, similar to SP:P57997:IF2C_PHAVU Translation initiation factor IF-2, chloroplast precursor (PvIF2cp) {Phaseolus vulgaris}   chr1:5885076-5890410 FORWARD   Aliases: F20D23.8, F20D23_8	8.2	8.5	-0.3	-0.7	100.0%	-4.8
10228	AT5G65110.2   Symbol: ACX2   similar to acyl-CoA oxidase, putative [Arabidopsis thaliana] (TAIR:At1g06310.1); similar to acyl-CoA oxidase homolog [Phalaenopsis sp. 'True Lady'] (GB:AAB67883.1); similar to acyl-CoA oxidase [Phalaenopsis cv. 'True Lady'] (GB:AAR00586.1); similar to acyl CoA oxidase homolog [Cucurbita sp. cv. Kurokawa Amakuri] (GB:AAC15870.1); contains InterPro domain Acyl-CoA dehydrogenase, C-terminal (InterPro:IPR006090)   chr5:26026861-26029745 REVERSE   Aliases: ACYL COA OXIDASE 2, ATACX2, MQN23.4, MQN23_4	9.1	9.3	-0.2	-0.7	100.0%	-4.7
10229	AT4G26160.1   thioredoxin family protein, low similarity to thioredoxin (Ictalurus punctatus) GI:9837585; contains Pfam profile: PF00085 Thioredoxin   chr4:13255283-13256768 FORWARD   Aliases: F20B18.270, F20B18_270	5.0	4.7	0.3	0.7	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10230	AT2G27440.1   rac GTPase activating protein, putative, similar to rac GTPase activating protein 3 (Lotus japonicus) GI:3695063; contains Pfam profiles PF00620: RhoGAP domain, PF00786: P21-Rho-binding domain	2.6	2.8	-0.1	-0.7	100.0%	-5.0
10231	AT1G56570.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:21199469-21201386 FORWARD   Aliases: F25P12.98, F25P12_98	3.6	3.4	0.2	0.7	100.0%	-4.9
10232	AT2G23170.1   Symbol: GH3.3   encodes an IAA-amido synthase that conjugates Asp and other amino acids to auxin in vitro.   chr2:9870935-9873642 REVERSE   Aliases: GH3.3, T20D16.20, T20D16_20	3.2	3.3	-0.1	-0.7	100.0%	-4.9
10233	AT3G48830.1   polynucleotide adenylyltransferase family protein / RNA recognition motif (RRM)-containing protein, similar to SP:P13685 Poly(A) polymerase (EC 2.7.7.19) {Escherichia coli O157:H7}; contains Pfam profiles PF01743: polyA polymerase family protein, PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:18114257-18121201 FORWARD   Aliases: T21J18.100	3.3	3.2	0.1	0.7	100.0%	-4.9
10234	ATMG00110.1   Symbol: CCB206	3.2	3.6	-0.4	-0.7	100.0%	-4.5
10235	AT4G34100.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:16330595-16334869 FORWARD   Aliases: F28A23.140, F28A23_140	7.5	7.2	0.2	0.7	100.0%	-4.8
10236	AT1G08600.1   SNF2 domain-containing protein / helicase domain-containing protein, similar to SP:P46100 Transcriptional regulator ATRX {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain; non-consensus GC donor splice site at exon boundary 28614	7.6	8.1	-0.5	-0.7	100.0%	-4.5
10237	AT4G28395.1   Symbol: ATA7   lipid transfer protein, putative, identical to anther-specific gene ATA7 (gi:2746339); contains Pfam protease inhibitor/seed storage/LTP family domain   chr4:14043946-14044898 FORWARD   Aliases: None	3.3	3.0	0.2	0.7	100.0%	-4.9
10238	AT5G57460.1   expressed protein   chr5:23292395-23294707 FORWARD   Aliases: MUA2.4, MUA2_4	4.1	4.3	-0.2	-0.7	100.0%	-4.8
10239	AT3G60270.1   uclacyanin, putative, similar to uclacyanin 3 GI:3395770 from (Arabidopsis thaliana); contains Pfam profile PF02298: Plastocyanin-like domain   chr3:22289004-22289737 REVERSE   Aliases: F27H5.60	3.3	3.4	-0.1	-0.7	100.0%	-5.4
10240	AT2G37220.1   29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative, similar to SP:Q43349 29 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein cp29) {Arabidopsis thaliana}   chr2:15641605-15643470 REVERSE   Aliases: F3G5.1, F3G5_1	7.8	7.3	0.5	0.7	100.0%	-4.3
10241	AT1G74870.1   expressed protein, contains similarity to hypothetical proteins   chr1:28130754-28131936 FORWARD   Aliases: F25A4.16, F25A4_16	4.8	4.6	0.2	0.7	100.0%	-4.6
10242	AT1G44222.1   expressed protein   chr1:16823799-16824056 FORWARD   Aliases: T18F15.14, T18F15_14	3.2	3.0	0.2	0.7	100.0%	-4.9
10243	AT2G26990.1   Symbol: FUS12   COP9 signalosome complex subunit 2 / CSN complex subunit 2 (CSN2), proteasome, COP9-complex and eIF3-domain protein; identical to CSN complex subunit 2 (Arabidopsis thaliana) GI:18056655; identical to cDNA CSN complex subunit 2 (CSN2) GI:18056654   chr2:11526585-11529665 REVERSE   Aliases: ATCSN2, CONSTITUTIVE PHOTOMORPHOGENIC 12, COP12, CSN2, FUSCA 12, T20P8.4, T20P8_4	9.7	10.0	-0.3	-0.7	100.0%	-4.7
10244	AT1G28640.1   GDSL-motif lipase, putative, strong similarity to lipase GB:AAA93262 GI:1145627 (Arabidopsis thaliana)   chr1:10067549-10069163 REVERSE   Aliases: F1K23.25, F1K23_25	2.2	2.3	-0.1	-0.7	100.0%	-5.7
10245	AT3G24350.1   Symbol: SYP32   syntaxin, putative (SYP32), similar to SP:Q9FFK1 Syntaxin 31 (AtSYP31) (AtSED5) {Arabidopsis thaliana}, syntaxin 5A GB:NP_003155 from (Homo sapiens) (J. Mol. Neurosci. (1997) 8 (2), 159-161)   chr3:8837653-8839589 FORWARD   Aliases: ATSYP32, K7M2.13	6.4	6.2	0.3	0.7	100.0%	-4.7
10246	AT3G17609.3   similar to bZIP protein HY5 (HY5) [Arabidopsis thaliana] (TAIR:At5g11260.1); similar to putative bZIP protein HY5 [Oryza sativa (japonica cultivar-group)] (GB:BAD32844.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr3:6023957-6024699 FORWARD   Aliases: None	4.3	4.0	0.3	0.7	100.0%	-4.5
10247	AT4G35200.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr4:16749147-16749908 REVERSE   Aliases: T12J5.70, T12J5_70	2.8	2.7	0.2	0.7	100.0%	-4.9
10248	AT5G22400.1   rac GTPase activating protein, putative, similar to rac GTPase activating protein 1 (Lotus japonicus) GI:3695059; contains Pfam profile PF00620: RhoGAP domain   chr5:7422719-7425468 REVERSE   Aliases: MWD9.20, MWD9_20	3.8	3.9	-0.1	-0.7	100.0%	-5.2
10249	AT5G11770.1   NADH-ubiquinone oxidoreductase 20 kDa subunit, mitochondrial, identical to NADH-ubiquinone oxidoreductase 20 kDa subunit mitochondrial (precursor) SP:Q42577 from (Arabidopsis thaliana); contains Pfam profile: PF01058 NADH ubiquinone oxidoreductase, 20 Kd subunit   chr5:3790807-3793001 REVERSE   Aliases: T22P22.160, T22P22_160	11.0	10.4	0.6	0.7	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10250	AT1G48910.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin monooxygenase-like protein floozy (Petunia x hybrida) GI:15010541   chr1:18095349-18097442 FORWARD   Aliases: F27K7.7, F27K7_7	3.0	2.7	0.2	0.7	100.0%	-4.7
10251	AT1G05600.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr1:1672098-1673747 FORWARD   Aliases: F3F20.5, F3F20_5	6.3	6.6	-0.3	-0.7	100.0%	-4.5
10252	AT4G29070.2   expressed protein   chr4:14321895-14323313 FORWARD   Aliases: F19B15.100, F19B15_100	6.1	6.3	-0.2	-0.7	100.0%	-4.3
10253	AT1G56310.1   3'-5' exonuclease domain-containing protein, contains Pfam profile PF01612: 3'-5' exonuclease   chr1:21086528-21088965 FORWARD   Aliases: F14G9.8, F14G9_8	4.2	4.4	-0.2	-0.7	100.0%	-4.7
10254	AT4G31590.1   Symbol: ATCSLC05   glycosyl transferase family 2 protein, similar to cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	4.1	4.3	-0.2	-0.7	100.0%	-4.9
10255	AT2G34980.1   Symbol: SETH1   phosphatidylinositolglycan synthase family protein, similar to SP:Q92535 Phosphatidylinositol-glycan biosynthesis, class C protein (PIG-C) {Homo sapiens}   chr2:14756046-14756957 FORWARD   Aliases: F19I3.21, F19I3_21	3.1	2.9	0.1	0.7	100.0%	-5.0
10256	AT3G44430.1   expressed protein   chr3:16079244-16080737 FORWARD   Aliases: T22K7.110	3.4	3.2	0.2	0.7	100.0%	-4.9
10257	AT1G18410.1   kinesin motor protein-related, similar to kinesin-related protein GB:AAF24855 GI:6692749 from (Arabidopsis thaliana)   chr1:6336521-6342453 REVERSE   Aliases: F15H18.10, F15H18_10	2.2	2.3	-0.1	-0.7	100.0%	-5.7
10258	AT1G62760.1   invertase/pectin methylesterase inhibitor family protein, low similarity to extensin (Volvox carteri) GI:21992   chr1:23241239-23242177 REVERSE   Aliases: F23N19.27, F23N19_27	3.6	3.5	0.1	0.7	100.0%	-5.3
10259	AT5G20500.1   glutaredoxin, putative, similar to glutaredoxin (Populus tremula x Populus tremuloides) gi:19548658:gb:AAL90750   chr5:6938600-6940269 FORWARD   Aliases: F7C8.90, F7C8_90	9.7	10.0	-0.3	-0.7	100.0%	-4.5
10260	AT2G40130.2   heat shock protein-related, contains similarity to 101 kDa heat shock protein; HSP101 (Triticum aestivum) gi:11561808:gb:AAC83689   chr2:16772998-16776346 FORWARD   Aliases: T7M7.2, T7M7_2	2.6	2.5	0.1	0.7	100.0%	-5.4
10261	AT1G64105.1   Symbol: ANAC027   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain   chr1:23798713-23799305 FORWARD   Aliases: ANAC027	8.6	8.3	0.3	0.7	100.0%	-4.4
10262	AT5G64110.1   peroxidase, putative, similar to peroxidase ATP3a (Arabidopsis thaliana) gi:1546698:emb:CAA67340	2.2	2.3	-0.1	-0.7	100.0%	-5.4
10263	AT1G18880.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:6520744-6523359 FORWARD   Aliases: F6A14.2, F6A14_2	10.9	10.5	0.4	0.7	100.0%	-4.7
10264	AT1G51745.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g03140.1); similar to OSJNBa0083N12.2 [Oryza sativa (japonica cultivar-group)] (GB:CAE03465.2)   chr1:19195191-19198456 FORWARD   Aliases: None	3.6	3.8	-0.2	-0.7	100.0%	-4.7
10265	ATCG00270.1   Symbol: PSBD   PSII D2 protein   chrC:32711-33772 FORWARD   Aliases: PSBD	4.7	4.4	0.4	0.7	100.0%	-4.6
10266	AT3G55180.1   esterase/lipase/thioesterase family protein, low similarity to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379   chr3:20465880-20467659 FORWARD   Aliases: T26I12.60	3.0	3.1	-0.1	-0.7	100.0%	-5.2
10267	AT3G28960.1   amino acid transporter family protein, low similarity to vesicular inhibitory amino acid transporter (Mus musculus) GI:2826776; contains INTERPRO:IPR002422 amino acid/polyamine transporter, family II   chr3:10985482-10987004 REVERSE   Aliases: K5K13.9	2.1	2.2	-0.1	-0.7	100.0%	-5.3
10268	AT1G80500.1   expressed protein, similar to Sedlin (Swiss-Prot:O14582) (Homo sapiens); similar to MBP-1 interacting protein-2A; MIP-2A (GI:9937493) (Homo sapiens)   chr1:30275429-30276934 FORWARD   Aliases: T21F11.17, T21F11_17	7.8	8.3	-0.4	-0.7	100.0%	-4.6
10269	AT5G64920.1   Symbol: CIP8   COP1-interacting protein (CIP8) / zinc finger (C3HC4-type RING finger) family protein, identical to COP1-interacting protein CIP8 (Arabidopsis thaliana) gi:5929906:gb:AAD56636; contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr5:25961114-25962668 REVERSE   Aliases: COP1 INTERACTING PROTEIN 8, COP1 INTERACTING PROTEIN CIP8, MXK3.15, MXK3_15	8.3	8.0	0.3	0.7	100.0%	-4.9
10270	AT1G44790.1   ChaC-like family protein, contains Pfam profile: PF04752 ChaC-like protein   chr1:16914594-16916104 REVERSE   Aliases: T12C22.6, T12C22_6	6.5	6.9	-0.4	-0.7	100.0%	-4.4
10271	AT1G44990.1   expressed protein   chr1:17009982-17010248 REVERSE   Aliases: F27F5.38, F27F5_38	6.3	6.0	0.3	0.7	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10272	AT4G29810.2   Symbol: ATMKK2	7.4	7.7	-0.3	-0.7	100.0%	-4.8
10273	AT2G42100.1   actin, putative, very strong similarity to SP:P53496 Actin 11 {Arabidopsis thaliana}, SP:P53493 Actin 3 {Arabidopsis thaliana}; contains Pfam profile PF00022: Actin   chr2:17567289-17569023 FORWARD   Aliases: T6D20.1, T6D20_1	3.8	3.6	0.1	0.7	100.0%	-5.1
10274	AT1G69970.1   Symbol: CLE26   CLE26, putative, CLAVATA3/ESR-Related 26 (CLE26);   chr1:26357563-26357919 REVERSE   Aliases: CLAVATA3/ESR RELATED 26, F20P5.29, F20P5_29	2.6	2.5	0.1	0.7	100.0%	-5.4
10275	AT3G12020.1   kinesin motor protein-related, similar to putative kinesin heavy chain GB:AAD23684 GI:4567271 from (Arabidopsis thaliana)   chr3:3827022-3834152 FORWARD   Aliases: MEC18.17	5.5	5.0	0.5	0.7	100.0%	-4.3
10276	AT3G19360.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr3:6707270-6709034 FORWARD   Aliases: MLD14.9	5.7	5.9	-0.2	-0.7	100.0%	-4.6
10277	AT2G31035.1   expressed protein   chr2:13215744-13215995 FORWARD   Aliases: F7F1.25, F7F1_25	2.6	2.6	-0.1	-0.7	100.0%	-5.7
10278	AT4G15880.1   Symbol: ESD4   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; low similarity to sentrin/SUMO-specific protease (Homo sapiens) GI:6906859; identical to cDNA hypothetical protein, partial (1189 bp) GI:2326349   chr4:9012660-9016128 FORWARD   Aliases: DL3980W, EARLY IN SHORT DAYS 4, FCAALL.406	5.7	5.4	0.3	0.7	100.0%	-4.5
10279	AT4G39610.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr4:18393564-18394739 REVERSE   Aliases: F23K16.240, F23K16_240	2.4	2.3	0.1	0.7	100.0%	-5.6
10280	AT2G34500.1   Symbol: CYP710A1   cytochrome P450 family protein, similar to Cytochrome P450 61 (C-22 sterol desaturase) (SP:P54781) {Saccharomyces cerevisiae}   chr2:14546558-14548485 REVERSE   Aliases: F13P17.35	3.0	2.7	0.3	0.7	100.0%	-4.2
10281	AT3G44740.1   tRNA synthetase class II (G, H, P and S) family protein, similar to SP:O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}; contains Pfam profile PF00587: tRNA synthetase class II core domain (G, H, P, S and T)	4.6	4.4	0.2	0.7	100.0%	-4.4
10282	AT1G08880.1   histone H2A, putative, Strong similarity to histone H2A Cicer arietinum SP:O65759, Picea abies SP:P35063; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4; ESTs gb:ATTS3874,gb:T46627,gb:T14194 come from this gene   chr1:2846956-2847784 REVERSE   Aliases: F7G19.24, F7G19_24	8.3	8.9	-0.5	-0.7	100.0%	-4.3
10283	AT3G50685.1   expressed protein   chr3:18845200-18845815 REVERSE   Aliases: None	9.8	9.6	0.2	0.7	100.0%	-4.8
10284	AT5G41890.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:16781520-16784128 REVERSE   Aliases: K16L22.18, K16L22_18	2.2	2.3	-0.1	-0.7	100.0%	-5.6
10285	AT3G02200.2   proteasome family protein, contains Pfam domain, PF01399: PCI domain   chr3:406609-409169 FORWARD   Aliases: F1C9.1	6.3	6.8	-0.5	-0.7	100.0%	-4.3
10286	AT4G07940.1   hypothetical protein   chr4:4792670-4794106 FORWARD   Aliases: F1K3.1, F1K3_1	4.8	4.6	0.2	0.7	100.0%	-4.9
10287	AT4G04850.1   Symbol: KEA3   K+ efflux antiporter, putative (KEA3), similar to A. thaliana K+ antiporter KEA1, GenBank accession number AF003382; Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563   chr4:2453794-2457765 FORWARD   Aliases: ATKEA3, KEA3, T4B21.3, T4B21_3	3.7	3.5	0.2	0.7	100.0%	-4.8
10288	AT4G35090.2   Symbol: CAT2   similar to catalase 3 (SEN2) [Arabidopsis thaliana] (TAIR:At1g20620.2); similar to catalase 1 [Arabidopsis thaliana] (TAIR:At1g20630.1); similar to catalase 3 (SEN2) [Arabidopsis thaliana] (TAIR:At1g20620.1); similar to catalase [Raphanus sativus] (GB:AAF71742.1); similar to catalase [Raphanus sativus] (GB:AAB86582.2); similar to catalase [Brassica juncea] (GB:AAD17935.1); similar to catalase [Brassica juncea] (GB:AAD17936.1); similar to catalase [Brassica juncea] (GB:AAD17934.1); contains InterPro domain Catalase (InterPro:IPR002226)   chr4:16700347-16703291 REVERSE   Aliases: CATALASE, CATALASE 2, T12J5.2	8.0	8.6	-0.6	-0.7	100.0%	-4.4
10289	AT5G06580.1   FAD linked oxidase family protein, similar to SP:Q12627 from Kluyveromyces lactis and SP:P32891 from Saccharomyces cerevisiae; contains Pfam FAD linked oxidases, C-terminal domain PF02913, Pfam FAD binding domain PF01565   chr5:2011289-2016540 REVERSE   Aliases: F15M7.11, F15M7_11	6.2	5.9	0.3	0.7	100.0%	-4.7
10290	AT5G65170.1   VQ motif-containing protein, contains PF05678: VQ motif   chr5:26058400-26059532 FORWARD   Aliases: MQN23.11, MQN23_11	2.9	3.0	-0.1	-0.7	100.0%	-5.3
10291	AT1G45145.1   Symbol: ATTRX5	12.0	12.2	-0.2	-0.7	100.0%	-5.3
10292	AT1G31860.1   Symbol: AT IE   histidine biosynthesis bifunctional protein (HISIE), identical to histidine biosynthesis bifunctional protein hisIE, chloroplast (precursor) SP: O82768 from (Arabidopsis thaliana); identical to cDNA phosphoribosyl-ATP pyrophosphohydrolase GI:3461883   chr1:11434089-11436587 REVERSE   Aliases: F5M6.13, F5M6_13, PHOSPHORIBOSYL ATP PYROPHOSPHOHYDROLASE	7.1	6.9	0.2	0.7	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10293	AT1G53500.1   Symbol: MUM4   NAD-dependent epimerase/dehydratase family protein, low similarity to dTDP-D-glucose-4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, Sphingomonas sp. GI:1314581; contains Pfam profile PF01370: NAD dependent epimerase/dehydratase family; putative NDP-rhamnose synthase (rh2 gene) GI:31559258   chr1:19970612-19973425 REVERSE   Aliases: F22G10.13, MUCILAGE MODIFIED 4, RHAMNOSE BIOSYNTHESIS 2, RHM2	5.9	6.2	-0.3	-0.7	100.0%	-4.5
10294	AT3G58000.1   VQ motif-containing protein, contains PF05678: VQ motif   chr3:21485927-21486454 FORWARD   Aliases: T10K17.210	2.8	2.7	0.1	0.7	100.0%	-5.1
10295	AT3G06930.2   protein arginine N-methyltransferase family protein, similar to protein arginine methyltransferase (Mus musculus) GI:5257221   chr3:2185149-2189390 REVERSE   Aliases: F17A9.8	3.7	3.9	-0.2	-0.7	100.0%	-4.7
10296	AT2G18270.1   expressed protein   chr2:7953240-7953488 REVERSE   Aliases: T30D6.22, T30D6_22	3.2	3.1	0.1	0.7	100.0%	-5.3
10297	AT1G55570.1   Symbol: SKS12   multi-copper oxidase type I family protein, nearly identical to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Multicopper oxidase domain PF00394   chr1:20761438-20763742 FORWARD   Aliases: SKS12, T5A14.1, T5A14_1	2.6	2.5	0.1	0.7	100.0%	-5.3
10298	AT2G07760.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr2:3584417-3586275 REVERSE   Aliases: T12J2.8, T12J2_8	2.7	2.6	0.1	0.7	100.0%	-5.2
10299	AT3G14280.1   expressed protein   chr3:4760984-4762402 REVERSE   Aliases: MLN21.7	4.5	4.1	0.4	0.7	100.0%	-4.1
10300	AT3G20870.1   metal transporter family protein, contains ZIP Zinc transporter domain, Pfam:PF02535   chr3:7309359-7312708 REVERSE   Aliases: MOE17.18	8.6	9.0	-0.4	-0.7	100.0%	-4.6
10301	AT5G59900.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:24141209-24143932 REVERSE   Aliases: MMN10.14, MMN10_14	3.3	3.4	-0.1	-0.7	100.0%	-5.3
10302	AT3G25190.1   nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313   chr3:9175694-9177013 FORWARD   Aliases: MJL12.26	5.0	4.6	0.3	0.7	100.0%	-4.2
10303	AT3G27570.1   expressed protein   chr3:10215233-10217973 REVERSE   Aliases: MMJ24.12	8.3	8.7	-0.4	-0.7	100.0%	-4.8
10304	AT4G09820.1   Symbol: TT8   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g63650.2); similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g63650.1); similar to anthocyanin 1 [Petunia x hybrida] (GB:AAG25928.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)	2.4	2.3	0.1	0.7	100.0%	-5.2
10305	AT3G20480.1   tetraacyldisaccharide 4'-kinase family protein, contains Pfam PF02606: tetraacyldisaccharide-1-P 4'-kinase   chr3:7151433-7153398 REVERSE   Aliases: K10D20.2	3.7	3.6	0.1	0.7	100.0%	-5.1
10306	AT1G42560.1   similar to seven transmembrane MLO family protein / MLO-like protein 5 (MLO5) [Arabidopsis thaliana] (TAIR:At2g33670.1); similar to seven transmembrane protein Mlo2 [Zea mays] (GB:AAK38338.1); contains InterPro domain Mlo-related protein (InterPro:IPR004326)   chr1:15982575-15984835 REVERSE   Aliases: T8D8.5, T8D8_5	2.6	2.8	-0.2	-0.7	100.0%	-5.4
10307	AT3G05370.1   disease resistance family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2 disease resistance protein GB:AAC15780 from (Lycopersicon pimpinellifolium)   chr3:1536020-1538725 REVERSE   Aliases: F22F7.24	3.9	4.0	-0.2	-0.7	100.0%	-5.4
10308	AT4G29940.1   Symbol: PRHA   pathogenesis-related homeodomain protein (PRHA), identical to Pathogenesis-related homeodomain protein (PRHA) (SP:P48785) (Arabidopsis thaliana)	5.3	5.7	-0.4	-0.7	100.0%	-4.9
10309	AT1G73680.1   pathogen-responsive alpha-dioxygenase, putative, similar to pathogen-inducible alpha-dioxygenase (Nicotiana attenuata) GI:12539609; contains Pfam profile PF03098: Animal haem peroxidase   chr1:27707605-27711175 REVERSE   Aliases: F25P22.10, F25P22_10	4.6	4.4	0.2	0.7	100.0%	-4.8
10310	AT4G27660.1   expressed protein, ; expression supported by MPSS   chr4:13816890-13818033 REVERSE   Aliases: T29A15.150, T29A15_150	6.6	6.3	0.3	0.7	100.0%	-4.1
10311	AT5G16810.1   expressed protein   chr5:5526767-5529921 REVERSE   Aliases: F5E19.150, F5E19_150	5.4	5.1	0.3	0.7	100.0%	-4.2
10312	AT1G48500.1   expressed protein, ; expression supported by MPSS   chr1:17936665-17938101 FORWARD   Aliases: T1N15.11, T1N15_11	3.3	3.0	0.3	0.7	100.0%	-4.4
10313	AT5G23550.1   expressed protein   chr5:7939614-7941631 REVERSE   Aliases: MQM1.18, MQM1_18	5.0	4.7	0.3	0.7	100.0%	-4.8
10314	AT5G26790.1   expressed protein   chr5:9423095-9423614 FORWARD   Aliases: F2P16.50, F2P16_50	5.1	4.8	0.3	0.7	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10315	AT5G52250.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to photomorphogenesis repressor PnCOP1 (GI:11127996) (Ipomoea nil)   chr5:21234081-21235444 FORWARD   Aliases: F17P19.15, F17P19_15	4.7	4.4	0.2	0.7	100.0%	-4.6
10316	AT1G49870.1   expressed protein, ; expression supported by MPSS   chr1:18464013-18467225 FORWARD   Aliases: F10F5.13, F10F5_13	4.0	3.7	0.3	0.7	100.0%	-4.8
10317	AT5G14700.1   cinnamoyl-CoA reductase-related, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Saccharum officinarum (GI:3341511)   chr5:4740255-4743449 REVERSE   Aliases: T9L3.2	3.8	4.1	-0.3	-0.7	100.0%	-4.7
10318	AT3G49840.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr3:18495527-18499283 FORWARD   Aliases: T16K5.190	3.1	3.2	-0.1	-0.7	100.0%	-5.2
10319	AT2G45760.1   Symbol: BAP2   BON1-associated protein (BAP1)-related, similar to BON1-associated protein 1 BAP1 (Arabidopsis thaliana) GI:15487384; contains Pfam profile PF00168: C2 domain   chr2:18854081-18854895 REVERSE   Aliases: BAL, BON ASSOCIATION PROTEIN 1 LIKE, BON ASSOCIATION PROTEIN 2, F4I18.26	4.5	4.3	0.2	0.7	100.0%	-4.7
10320	AT2G18080.1   serine carboxypeptidase S28 family protein, similar to SP:Q9NQE7 Thymus-specific serine protease precursor (EC 3.4.-.-) {Homo sapiens}; contains Pfam profile PF05577: Serine carboxypeptidase S28   chr2:7864598-7866800 FORWARD   Aliases: T27K22.5, T27K22_5	3.8	3.7	0.1	0.7	100.0%	-5.2
10321	AT5G17460.1   expressed protein   chr5:5757100-5759721 REVERSE   Aliases: K3M16.30, K3M16_30	3.0	3.2	-0.1	-0.7	100.0%	-5.1
10322	AT5G65790.1   Symbol: MYB68   myb family transcription factor (MYB68), identical to putative transcription factor (MYB68) GI:3941493 from (Arabidopsis thaliana); contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:26340174-26341804 FORWARD   Aliases: MPA24.14, MPA24_14	3.7	4.1	-0.4	-0.7	100.0%	-4.4
10323	AT5G67280.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:26859496-26862416 REVERSE   Aliases: K3G17.4, K3G17_4	5.6	5.8	-0.2	-0.7	100.0%	-5.0
10324	AT1G75510.1   transcription initiation factor IIF beta subunit (TFIIF-beta) family protein, contains Pfam profile: PF02270 transcription initiation factor IIF, beta subunit   chr1:28350716-28352379 REVERSE   Aliases: F1B16.18	7.7	8.0	-0.2	-0.7	100.0%	-4.5
10325	AT5G57610.1   protein kinase family protein, similar to protein kinase (Glycine max) GI:170047, MAP3K delta-1 protein kinase (Arabidopsis thaliana) GI:2253010; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr5:23342533-23346573 FORWARD   Aliases: MUA2.19, MUA2_19	7.4	7.1	0.3	0.7	100.0%	-4.6
10326	AT3G43100.1   hypothetical protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250   chr3:15100879-15102158 FORWARD   Aliases: F7M19.110	2.7	2.7	0.1	0.7	100.0%	-5.5
10327	AT3G04400.1   Symbol: EMB2171   60S ribosomal protein L23 (RPL23C), similar to ribosomal protein L17 GB:AAA34113.1 from (Nicotiana tabacum)   chr3:1167282-1168663 FORWARD   Aliases: EMB2171, EMBRYO DEFECTIVE 2171, T27C4.4, T27C4_4	10.8	11.0	-0.2	-0.7	100.0%	-4.7
10328	AT4G39710.1   immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative, similar to FK506 binding protein 1 (GP:21535744) (Arabidopsis thaliana)   chr4:18427033-18428353 REVERSE   Aliases: T19P19.100, T19P19_100	4.1	3.9	0.2	0.7	100.0%	-4.4
10329	AT3G19260.1   Symbol: LAG1 HOMOLOG 2	7.0	6.5	0.5	0.7	100.0%	-4.4
10330	AT1G77740.1   1-phosphatidylinositol-4-phosphate 5-kinase, putative / PIP kinase, putative / PtdIns(4)P-5-kinase, putative / diphosphoinositide kinase, putative, strong similarity to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr1:29225432-29228755 FORWARD   Aliases: T32E8.7, T32E8_7	4.4	4.6	-0.2	-0.7	100.0%	-4.6
10331	AT1G28030.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to GS-AOP loci (GI:16118889, GI:16118887, GI:16118891, GI:16118893); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:9771780-9773332 FORWARD   Aliases: F13K9.13, F13K9_13	2.8	3.0	-0.1	-0.7	100.0%	-5.0
10332	AT4G24550.2   clathrin adaptor complexes medium subunit family protein, contains Pfam profile: PF00928 adaptor complexes medium subunit family	9.3	9.5	-0.2	-0.7	100.0%	-5.1
10333	AT5G64830.2   similar to zinc finger (MYND type) family protein / programmed cell death 2 C-terminal domain-containing protein [Arabidopsis thaliana] (TAIR:At4g02220.1); similar to SPBC25H2.15 [Schizosaccharomyces pombe] (GB:CAB08774.1); similar to GA17017-PA [Drosophila pseudoobscura] (GB:EAL25480.1); contains InterPro domain Programmed cell death protein 2, C-terminal (InterPro:IPR007320)   chr5:25931864-25933830 REVERSE   Aliases: MXK3.5, MXK3_5	7.1	7.4	-0.3	-0.7	100.0%	-4.6
10334	AT1G51720.1   glutamate dehydrogenase, putative, similar to NADP-specific glutamate dehydrogenase (NADP-GDH) SP:P28724 (Giardia lamblia (Giardia intestinalis))   chr1:19184440-19190200 FORWARD   Aliases: F19C24.7, F19C24_7	8.0	8.2	-0.1	-0.7	100.0%	-4.9
10335	AT5G04830.2   expressed protein   chr5:1402087-1403962 REVERSE   Aliases: MUK11.15, MUK11_15	7.7	7.4	0.3	0.7	100.0%	-4.6
10336	AT2G22410.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:9516097-9518311 FORWARD   Aliases: F14M13.19, F14M13_19	4.3	4.5	-0.2	-0.7	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10337	AT3G19020.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein ( <i>Lycopersicon esculentum</i> ) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	2.2	2.1	0.1	0.7	100.0%	-5.8
10338	AT3G53470.2   expressed protein, ribosomal protein S25, cytosolic, <i>Arabidopsis thaliana</i> , PIR:T08568   chr3:19833728-19834384 FORWARD   Aliases: F4P12.170	5.9	5.7	0.3	0.7	100.0%	-4.2
10339	AT4G04020.1   plastid-lipid associated protein PAP, putative / fibrillin, putative, strong similarity to plastid-lipid associated proteins PAP1 GI:14248554, PAP2 GI:14248556 from ( <i>Brassica rapa</i> ), fibrillin ( <i>Brassica napus</i> ) GI:4139097; contains Pfam profile PF04755: PAP_fibrillin   chr4:1932149-1933948 FORWARD   Aliases: T24H24.16, T24H24_16	8.4	7.6	0.8	0.7	100.0%	-5.4
10340	AT4G22240.1   plastid-lipid associated protein PAP, putative, similar to plastid-lipid associated proteins PAP2 ( <i>Brassica rapa</i> ) GI:14248550 GI:14248556; contains Pfam profile PF04755: PAP_fibrillin   chr4:11765815-11767316 REVERSE   Aliases: T10I14.70, T10I14_70	8.4	7.6	0.8	0.7	100.0%	-5.4
10341	NA	8.3	8.1	0.2	0.7	100.0%	-5.6
10342	AT5G28470.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:10429817-10432361 FORWARD   Aliases: F24J2.10, F24J2_10	2.7	2.6	0.1	0.7	100.0%	-5.2
10343	AT1G35880.1   expressed protein   chr1:13341063-13342440 REVERSE   Aliases: F10O5.5, F10O5_5	2.2	2.3	-0.1	-0.7	100.0%	-5.7
10344	AT5G47100.1   Symbol: CBL9   calcineurin B-like protein 9 (CBL9), identical to calcineurin B-like protein 9 (GI:5866279) and calcium-binding protein AtCBL9 (GI:16151825) ( <i>Arabidopsis thaliana</i> ); similar to calcineurin B-like protein 1 (GI:3309082) ( <i>Arabidopsis thaliana</i> )	6.9	7.1	-0.2	-0.7	100.0%	-4.9
10345	AT3G26010.1   F-box family protein, contains Pfam:PF00646 F-box domain	3.5	3.3	0.1	0.7	100.0%	-5.1
10346	AT3G26800.1   expressed protein   chr3:9863410-9864015 FORWARD   Aliases: MDJ14.10	4.9	4.6	0.3	0.7	100.0%	-4.3
10347	AT2G17020.1   F-box family protein (FBL10), contains similarity to F-box protein Partner of Paired GI:10441427 from ( <i>Drosophila melanogaster</i> )   chr2:7403419-7405920 REVERSE   Aliases: F6P23.18, F6P23_18	3.2	3.3	-0.2	-0.7	100.0%	-4.7
10348	AT5G35390.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase PRK1, <i>Lycopersicon esculentum</i> , PIR:T07865   chr5:13614148-13616206 FORWARD   Aliases: T26D22.9, T26D22_9	2.9	2.7	0.1	0.7	100.0%	-5.1
10349	AT2G30695.2   expressed protein   chr2:13086184-13088427 REVERSE   Aliases: None	4.3	4.5	-0.2	-0.7	100.0%	-4.3
10350	AT2G38530.1   Symbol: LTP2   nonspecific lipid transfer protein 2 (LTP2), identical to nonspecific lipid-transfer protein 2 from <i>Arabidopsis thaliana</i> (SP:Q9S7I3); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:16135456-16136232 FORWARD   Aliases: LIPID TRANSFER PROTEIN, LIPID TRANSFER PROTEIN 2, LP2, T6A23.27, T6A23_27	2.6	2.8	-0.2	-0.7	100.0%	-5.2
10351	AT1G18690.1   galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, <i>Schizosaccharomyces pombe</i> (SP:Q09174)	4.5	4.8	-0.2	-0.7	100.0%	-4.5
10352	AT1G76970.1   VHS domain-containing protein / GAT domain-containing protein, weak similarity to HGF-regulated tyrosine kinase substrate ( <i>Mus musculus</i> ) GI:1089781; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain   chr1:28927560-28930298 REVERSE   Aliases: F22K20.7, F22K20_7	3.4	3.1	0.3	0.7	100.0%	-4.6
10353	AT3G17180.1   Symbol: SCPL33	3.3	3.5	-0.2	-0.7	100.0%	-4.8
10354	AT2G34410.3   similar to O-acetyltransferase-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g46340.1); similar to acetyltransferase-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g29890.1); similar to OSJNBb0035114.15 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:NP_917822.1); similar to unknown protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_475947.1)   chr2:14525485-14530648 FORWARD   Aliases: F13P17.23	3.7	3.5	0.2	0.7	100.0%	-4.8
10355	AT5G60470.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:24338196-24340016 FORWARD   Aliases: MUF9.10, MUF9_10	2.2	2.2	-0.1	-0.7	100.0%	-5.7
10356	AT1G07850.1   fringe-related protein, + weak similarity to Fringe ( <i>Schistocerca gregaria</i> )(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	2.5	2.6	-0.1	-0.7	100.0%	-5.4
10357	AT1G34320.1   expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668)   chr1:12520691-12524341 FORWARD   Aliases: F23M19.3, F23M19_3	4.4	4.1	0.2	0.7	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10358	AT1G35260.1   Bet v I allergen family protein, similar to Csf-2 (Cucumis sativus)(GI:5762258)(J Am Soc Hortic Sci 124, 136-139 (1999)) contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:12936827-12937765 REVERSE   Aliases: T9I1.17, T9I1_17	3.4	3.7	-0.3	-0.7	100.0%	-4.5
10359	AT3G03890.2   expressed protein   chr3:999474-1002040 REVERSE   Aliases: F20H23.6, F20H23_6	8.5	8.1	0.4	0.7	100.0%	-4.6
10360	AT1G47710.1   serpin, putative / serine protease inhibitor, putative, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr1:17560649-17562709 FORWARD   Aliases: T2E6.22	8.2	8.6	-0.4	-0.7	100.0%	-4.6
10361	AT1G50370.1   serine/threonine protein phosphatase, putative, nearly identical to serine/threonine protein phosphatase (Arabidopsis thaliana) GI:14582206   chr1:18662384-18665642 FORWARD   Aliases: F14I3.5, F14I3_5	6.8	7.3	-0.5	-0.7	100.0%	-4.5
10362	AT3G25670.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; +   chr3:9345769-9347538 REVERSE   Aliases: T5M7.12	3.6	3.4	0.2	0.7	100.0%	-5.1
10363	AT3G61100.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr3:22621427-22622296 REVERSE   Aliases: T27I15.190	7.4	7.7	-0.4	-0.7	100.0%	-4.0
10364	AT3G30380.1   expressed protein, ; expression supported by MPSS   chr3:11976903-11979050 FORWARD   Aliases: T6J22.18	4.1	4.4	-0.4	-0.7	100.0%	-4.9
10365	AT3G44910.1   Symbol: ATCHX12   cation/hydrogen exchanger, putative (CHX12), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr3:16403049-16405240 REVERSE   Aliases: CHX12, F28D10.100	2.5	2.4	0.1	0.7	100.0%	-5.3
10366	AT1G09270.3   similar to importin alpha-1 subunit, putative (IMPA1) [Arabidopsis thaliana] (TAIR:At3g06720.2); similar to importin alpha-1 subunit, putative (IMPA1) [Arabidopsis thaliana] (TAIR:At3g06720.1); similar to importin alpha-2 subunit [Arabidopsis thaliana] (TAIR:At4g02150.1); similar to importin alpha-2 subunit, putative [Arabidopsis thaliana] (TAIR:At1g02690.1); similar to importin alpha 1b [Oryza sativa (japonica cultivar-group)] (GB:BAA88950.1); similar to importin alpha [Lycopersicon esculentum] (GB:AAC23722.1); similar to importin alpha 2 [Capsicum annuum] (GB:AAK38727.1); similar to putative importin alpha 1b [Oryza sativa] (GB:NP_910164.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_912763.1); contains InterPro domain Armadillo repeat (InterPro:IPR000225)   chr1:2994416-2998605 FORWARD   Aliases: T12M4.2, T12M4_2	5.1	4.9	0.3	0.7	100.0%	-4.6
10367	AT4G39500.1   Symbol: CYP96A11   cytochrome P450, putative, simialrity to cytochrome P450 CYP86A1, Arabidopsis thaliana, EMBL:X90458   chr4:18366944-18368353 REVERSE   Aliases: F23K16.130, F23K16_130	3.6	3.5	0.1	0.7	100.0%	-5.2
10368	AT1G68450.1   VQ motif-containing protein, contains PF05678: VQ motif   chr1:25665164-25665902 REVERSE   Aliases: T2E12.4	3.8	4.3	-0.5	-0.7	100.0%	-4.0
10369	AT2G13610.1   ABC transporter family protein   chr2:5680770-5682913 REVERSE   Aliases: T10F5.15, T10F5_15	3.4	3.3	0.1	0.7	100.0%	-5.1
10370	AT3G18850.3   Symbol: LPAT5   similar to phospholipid/glycerol acyltransferase family protein [Arabidopsis thaliana] (TAIR:At1g75020.2); similar to phospholipid/glycerol acyltransferase family protein [Arabidopsis thaliana] (TAIR:At1g75020.1); similar to putative acyl-CoA:1-acylglycerol-3-phosphate acyltransferase [Oryza sativa (japonica cultivar-group)] (GB:BAD53283.1); contains InterPro domain Phospholipid/glycerol acyltransferase (InterPro:IPR002123)   chr3:6499421-6501345 REVERSE   Aliases: LPAT5, MCB22.2	5.1	4.8	0.2	0.7	100.0%	-4.5
10371	AT2G30300.1   nodulin-related, weak similarity to nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr2:12926478-12928299 FORWARD   Aliases: T9D9.11, T9D9_11	2.5	2.6	-0.1	-0.7	100.0%	-5.0
10372	AT2G20300.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:8763006-8767303 REVERSE   Aliases: F11A3.15, F11A3_15	4.3	4.2	0.1	0.7	100.0%	-4.8
10373	AT5G23720.3   Symbol: PHS1   similar to dual specificity protein phosphatase (DsPTP1) [Arabidopsis thaliana] (TAIR:At3g23610.1); similar to B1146B04.18 [Oryza sativa (japonica cultivar-group)] (GB:NP_908883.1); similar to P0551A11.24 [Oryza sativa (japonica cultivar-group)] (GB:NP_908585.1); similar to putative PROPYZAMIDE-HTPERSENSITIVE 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD52745.1); contains InterPro domain Tyrosine specific protein phosphatase and dual specificity protein phosphatase (InterPro:IPR000387); contains InterPro domain Dual specificity protein phosphatase (InterPro:IPR000340)   chr5:7998477-8002808 FORWARD   Aliases: MQM1.1, MQM1_1, PROPYZAMIDE HYPERSENSITIVE 1	6.6	6.8	-0.2	-0.7	100.0%	-4.6
10374	AT1G77260.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr1:29028666-29031851 REVERSE   Aliases: T14N5.19, T14N5_19	8.2	8.5	-0.4	-0.7	100.0%	-4.9
10375	AT1G16560.4   similar to Per1-like protein-related [Arabidopsis thaliana] (TAIR:At5g62130.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54701.1); contains InterPro domain Per1-like (InterPro:IPR007217)   chr1:5668406-5670701 FORWARD   Aliases: F19K19.12, F19K19_12	4.3	4.6	-0.3	-0.7	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10376	AT5G41820.1   geranylgeranyl transferase alpha subunit-related / RAB geranylgeranyltransferase alpha subunit-related, low similarity to SP:Q08602 (Rattus norvegicus)   chr5:16758032-16760661 FORWARD   Aliases: K16L22.10, K16L22_10	3.1	3.2	-0.1	-0.7	100.0%	-4.8
10377	AT3G46800.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.4	0.1	0.7	100.0%	-5.3
10378	AT5G12180.1   Symbol: CPK17   calcium-dependent protein kinase, putative / CDPK, putative   chr5:3937025-3939597 FORWARD   Aliases: MXC9.14, MXC9_14	3.0	2.9	0.1	0.7	100.0%	-5.2
10379	AT3G17080.1   self-incompatibility protein-related, similar to S1 self-incompatibility protein GB:CAA52380 (Papaver rhoeas) (Proc. Natl. Acad. Sci. U.S.A. 91 (6), 2265-2269 (1994))   chr3:5825295-5825873 FORWARD   Aliases: K14A17.15	3.3	3.1	0.2	0.7	100.0%	-4.9
10380	AT1G77080.6   Symbol: MAF1   MADS-box protein AGL27-II (AGL27) / MADS affecting flowering 1 (MAF1), contains similarity to MADS box transcription factor GI:3688591 from (Triticum aestivum); contains Pfam domain PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain); contains Pfam domain PF01486: K-box region   chr1:28963205-28963948 FORWARD   Aliases: AGL27, FLM, FLOWERING LOCUS M, MADS AFFECTING FLOWERING 1	3.2	3.3	-0.1	-0.7	100.0%	-5.3
10381	AT1G26520.1   similar to PRLI-interacting factor L, putative [Arabidopsis thaliana] (TAIR:At1g15730.1); similar to hypothetical protein [Gallus gallus] (GB:CAG31889.1); similar to PREDICTED: similar to COBW domain containing protein [Gallus gallus] (GB:XP_424924.1); contains InterPro domain Cobalamin synthesis protein/P47K (InterPro:IPR003495)   chr1:9163233-9165601 REVERSE   Aliases: T1K7.11, T1K7_11	3.4	3.3	0.1	0.7	100.0%	-4.9
10382	AT5G19030.3   RNA recognition motif (RRM)-containing protein, low similarity to Cold-inducible RNA-binding protein (Glycine-rich RNA-binding protein CIRP) from {Homo sapiens} SP:Q14011, {Rattus norvegicus} SP:Q61413, {Xenopus laevis} SP:O93235; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:6357436-6359078 REVERSE   Aliases: T16G12.70, T16G12_70	4.9	5.1	-0.2	-0.7	100.0%	-4.8
10383	AT1G08220.1   expressed protein, similar to hypothetical protein [Dictyostelium discoideum] (GB:AAO52382.1); contains InterPro domain ATP10 (InterPro:IPR007849)   chr1:2581019-2583319 REVERSE   Aliases: T23G18.8, T23G18_8	5.5	5.8	-0.3	-0.7	100.0%	-4.3
10384	AT3G46650.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:17197346-17198797 REVERSE   Aliases: F12A12.170	3.6	3.8	-0.2	-0.7	100.0%	-4.8
10385	AT2G18720.1   eukaryotic translation initiation factor 2 subunit 3, putative / eIF2S3, putative / eIF-2-gamma, putative   chr2:8122002-8123893 REVERSE   Aliases: MSF3.10, MSF3_10	4.5	4.8	-0.3	-0.7	100.0%	-4.3
10386	AT3G10230.1   Symbol: LYC   lycopene beta cyclase (LYC), identical to lycopene beta cyclase GI:1399183:GB:AAB53337 (Arabidopsis thaliana)   chr3:3164080-3166043 REVERSE   Aliases: F14P13.17, LYCOPENE BETA CYCLASE, LYCOPENE CYCLASE	7.8	7.4	0.4	0.7	100.0%	-4.7
10387	AT2G28430.1   expressed protein   chr2:12166639-12167528 REVERSE   Aliases: T1B3.5, T1B3_5	8.3	8.7	-0.3	-0.7	100.0%	-4.4
10388	AT3G19100.1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK3 (Nicotiana tabacum) gi:16904226:gb:AAL30820; contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.4	4.6	-0.3	-0.7	100.0%	-4.4
10389	AT5G50565.1   expressed protein   chr5:20598068-20599052 FORWARD   Aliases: MFB16.4	5.9	5.5	0.3	0.7	100.0%	-4.2
10390	AT5G50665.1   expressed protein   chr5:20631410-20632394 FORWARD   Aliases: None	5.9	5.5	0.3	0.7	100.0%	-4.2
10391	AT5G66370.1   expressed protein, similar to unknown protein (emb CAB62624.1)   chr5:26529426-26530050 REVERSE   Aliases: K1F13.2, K1F13_2	2.2	2.1	0.1	0.7	100.0%	-5.8
10392	AT2G11360.1   hypothetical protein   chr2:4537975-4538585 REVERSE   Aliases: F3K12.12, F3K12_12	2.4	2.5	-0.1	-0.7	100.0%	-5.4
10393	AT5G64480.1   expressed protein   chr5:25795412-25796145 FORWARD   Aliases: T12B11.7, T12B11_7	5.4	5.2	0.1	0.7	100.0%	-5.2
10394	AT2G34870.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr2:14717856-14718532 FORWARD   Aliases: F19I3.10, F19I3_10	2.2	2.3	-0.1	-0.7	100.0%	-5.5
10395	AT3G01130.1   expressed protein   chr3:44491-45597 REVERSE   Aliases: T4P13.18, T4P13_18	12.2	12.4	-0.2	-0.7	100.0%	-5.9
10396	AT1G73160.1   glycosyl transferase family 1 protein, contains Pfam profile: PF00534 Glycosyl transferases group 1   chr1:27510195-27511655 FORWARD   Aliases: T18K17.18, T18K17_18	3.5	3.7	-0.2	-0.7	100.0%	-4.9
10397	AT1G42250.1   replication protein-related, weak similarity to Replication Protein A 70	2.6	2.8	-0.2	-0.7	100.0%	-5.3
10398	AT2G40200.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.1	3.0	0.1	0.7	100.0%	-5.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10399	AT2G02390.3   Symbol: ATGSTZ1   glutathione S-transferase zeta 1 (GSTZ1) (GST18), identical to SP:Q9ZVQ3:GTZ1_ARATH Glutathione S-transferase zeta-class 1 (EC 2.5.1.18) (AtGSTZ1) (Maleylacetone isomerase) (EC 5.2.1.-) (MAI) {Arabidopsis thaliana}; contains Pfam profiles PF02798: Glutathione S-transferase, N-terminal domain and PF00043:Glutathione S-transferase, C-terminal domain	8.2	7.9	0.3	0.7	100.0%	-4.6
10400	AT4G38460.1   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative, 65% similar to geranylgeranyl pyrophosphate synthase (GI:413730);   chr4:17994779-17996198 FORWARD   Aliases: F20M13.20, F20M13_20	5.0	4.8	0.2	0.7	100.0%	-4.8
10401	AT3G05270.1   expressed protein, similar to endosome-associated protein (EEA1) (GI:1016368) (Homo sapiens); similar to smooth muscle myosin heavy chain (GI:4417214) (Homo sapiens; contains Pfam profile PF05911: Plant protein of unknown function (DUF869)   chr3:1500809-1503326 REVERSE   Aliases: T12H1.24, T12H1_24	5.6	5.8	-0.2	-0.7	100.0%	-4.7
10402	AT5G39710.1   Symbol: EMB2745   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:15912957-15915200 FORWARD   Aliases: EMB2745, EMBRYO DEFECTIVE 2745, MIJ24.190, MIJ24_190	3.4	3.6	-0.1	-0.7	100.0%	-4.9
10403	AT5G61040.1   expressed protein   chr5:24579559-24582185 REVERSE   Aliases: MAF19.5, MAF19_5	4.7	4.9	-0.1	-0.7	100.0%	-5.1
10404	AT1G21860.1   Symbol: SKS7   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr1:7671017-7674204 REVERSE   Aliases: SKS7, T26F17.7, T26F17_7	2.0	2.1	-0.0	-0.7	100.0%	-5.9
10405	AT3G63510.1   nitrogen regulation family protein, contains Pfam domain PF01207: Dihydrouridine synthase (Dus); similar to (SP:P45672) NIFR3-like protein (SP:P45672) (Azospirillum brasilense)	3.5	3.6	-0.1	-0.7	100.0%	-5.0
10406	AT4G25660.1   expressed protein   chr4:13083416-13085194 FORWARD   Aliases: L73G19.40, L73G19_40	7.9	7.6	0.3	0.7	100.0%	-5.0
10407	AT5G25550.1   leucine-rich repeat family protein / extensin family protein, similar to leucine-rich repeat/extensin 1 (GI:13809918) (Arabidopsis thaliana); contains Pfam PF00560: Leucine Rich Repeat domains	2.9	2.8	0.1	0.7	100.0%	-5.2
10408	AT4G30070.1   Symbol: LCR59   Encodes a member of a family of small,secreted, cysteine rich protein with sequence similarity to the PCP (pollen coat protein) gene family.   chr4:14697495-14698436 FORWARD   Aliases: F6G3.100, F6G3_100, LCR59, Low molecular weight cysteine rich 59	2.9	2.9	0.1	0.7	100.0%	-5.5
10409	AT5G42250.1   alcohol dehydrogenase, putative, similar to alcohol dehydrogenase ADH GI:7705214 from (Lycopersicon esculentum); contains Pfam zinc-binding dehydrogenase domain PF00107	3.9	4.2	-0.4	-0.7	100.0%	-4.1
10410	AT4G25540.1   Symbol: MSH3   DNA mismatch repair protein MSH3 (MSH3), identical to SP:O65607 DNA mismatch repair protein MSH3 (AtMsh3) {Arabidopsis thaliana}	4.5	4.7	-0.2	-0.7	100.0%	-4.8
10411	AT3G52880.1   monodehydroascorbate reductase, putative, monodehydroascorbate reductase (NADH), Lycopersicon esculentum, PIR:T06407   chr3:19612190-19615431 REVERSE   Aliases: F8J2.50	10.4	10.9	-0.4	-0.7	100.0%	-4.6
10412	AT5G62680.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:25182656-25185169 REVERSE   Aliases: MRG21.10, MRG21_10	3.3	2.9	0.4	0.7	100.0%	-4.2
10413	AT1G16980.1   Symbol: ATTPS2	2.5	2.6	-0.1	-0.7	100.0%	-5.4
10414	AT1G08410.1   GTP-binding family protein, contains Pfam domain, PF01926: GTPase of unknown function   chr1:2646186-2649376 FORWARD   Aliases: T27G7.9, T27G7_9	3.3	3.6	-0.3	-0.7	100.0%	-4.9
10415	AT4G18420.1   hypothetical protein   chr4:10174422-10174971 REVERSE   Aliases: F28J12.80, F28J12_80	4.1	3.8	0.3	0.7	100.0%	-4.4
10416	AT4G11840.1   Symbol: PLDGAMMA3   phospholipase D gamma 3 / PLD gamma 3 (PLDGAMMA3), identical to phospholipase D gamma 3 sp:Q9T052 from (Arabidopsis thaliana)   chr4:7121959-7125876 REVERSE   Aliases: T26M18.50, T26M18_50	5.4	5.0	0.3	0.7	100.0%	-4.6
10417	AT5G08300.1   succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial, putative / succinyl-CoA synthetase, alpha chain, putative / SCS-alpha, putative, identical to SP:P53586 Succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, alpha chain) (SCS-alpha) {Arabidopsis thaliana}; strong similarity to SP:P13086 Succinyl-CoA ligase (GDP-forming) alpha-chain, mitochondrial precursor {Rattus norvegicus}; contains Pfam profiles PF00549: CoA-ligase, PF02629: CoA binding domain   chr5:2667471-2669918 FORWARD   Aliases: F8L15.30, F8L15_30	12.0	12.3	-0.4	-0.7	100.0%	-4.6
10418	AT1G65660.1   Symbol: SMP1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr1:24421811-24424955 REVERSE   Aliases: F1E22.4, F1E22_4	7.7	8.1	-0.4	-0.7	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10419	AT1G01470.1   Symbol: LEA14   late embryogenesis abundant protein, putative / LEA protein, putative, similar to SP:P46518 Late embryogenesis abundant protein Lea14-A {Gossypium hirsutum}; contains Pfam profile PF03168: Late embryogenesis abundant protein   chr1:172146-172923 REVERSE   Aliases: F22L4.3, F22L4_3, LATE EMBRYOGENESIS ABUNDANT 14, LIGHT STRESS REGULATED 3, LSR3	12.5	12.1	0.4	0.7	100.0%	-4.7
10420	AT4G11400.1   ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein / Myb-like DNA-binding domain-containing protein, similar to BRG1-binding protein ELD/OSA1 (Homo sapiens) GI:18568414; contains Pfam profiles PF01388: ARID/BRIGHT DNA binding domain, PF01448: ELM2 domain, PF00249: Myb-like DNA-binding domain   chr4:6938712-6940534 FORWARD   Aliases: F25E4.20, F25E4_20	4.2	4.4	-0.1	-0.7	100.0%	-5.0
10421	AT2G23150.1   Symbol: NRAMP3	7.1	6.7	0.4	0.7	100.0%	-4.1
10422	AT2G16890.2   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:7323971-7326263 FORWARD   Aliases: F12A24.7, F12A24_7	10.0	9.6	0.4	0.7	100.0%	-4.4
10423	AT5G38440.1   self-incompatibility protein-related, low similarity to self-incompatibility (Papaver nudicaule) GI:3097262, S3 self-incompatibility protein (Papaver rhoeas) GI:1107841	4.1	4.2	-0.1	-0.7	100.0%	-5.3
10424	AT4G02260.3   Symbol: RSH1   RelA/SpoT protein, putative (RSH1), identical to RSH1 (RelA/SpoT homolog) (Arabidopsis thaliana) GI:7141304; contains Pfam profiles PF02824: TGS domain, PF01966: HD domain, PF04607: Region found in RelA / SpoT proteins   chr4:985233-991494 FORWARD   Aliases: AT RSH1, RELA SPOT HOMOLOG, T2H3.10, T2H3_10	4.6	4.4	0.2	0.7	100.0%	-4.6
10425	AT1G64130.1   expressed protein, similar to hypothetical protein GB:AAF24579 GI:6692114 from (Arabidopsis thaliana)   chr1:23806222-23807196 FORWARD   Aliases: F22C12.11, F22C12_11	2.8	2.9	-0.1	-0.7	100.0%	-5.7
10426	AT3G32130.1   hypothetical protein   chr3:13131192-13131878 FORWARD   Aliases: F1M23.22	2.3	2.4	-0.1	-0.7	100.0%	-5.8
10427	AT4G09840.1   expressed protein   chr4:6190250-6191661 REVERSE   Aliases: F17A8.190, F17A8_190	6.3	5.9	0.3	0.7	100.0%	-4.7
10428	AT2G43850.2   ankyrin protein kinase, putative (APK1), similar to ankyrin-kinase (Medicago truncatula) gi:18700701:gb:AAL78674;contains Pfam profile PF00069: Protein kinase domain; contains Pfam profile PF00023: Ankyrin repeat   chr2:18166259-18169121 REVERSE   Aliases: F18O19.4	4.3	4.2	0.2	0.7	100.0%	-4.5
10429	AT2G33470.2   glycolipid transfer protein-related, similar to phosphoinositol 4-phosphate adaptor protein-2 (GI:14165198) (Homo sapiens); similar to Glycolipid transfer protein (GLTP) (Swiss-Prot:Q9JL62) (Mus musculus); similar to Glycolipid transfer protein (GLTP) (Swiss-Prot:Q9NZD2) (Homo sapiens)   chr2:14183492-14185543 REVERSE   Aliases: F4P9.24, F4P9_24	11.2	10.9	0.3	0.7	100.0%	-4.6
10430	AT1G08170.1   histone H2B family protein, similar to histone H2B from Chlamydomonas reinhardtii (SP:P54347, SP:P54346, SP:P50565), Volvox carteri (SP:P16867, SP:P16868); contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:2562938-2563669 REVERSE   Aliases: T6D22.26	3.0	3.1	-0.1	-0.7	100.0%	-5.3
10431	AT5G43830.1   expressed protein, similar to auxin down-regulated protein ARG10 (Vigna radiata) GI:2970051, wali7 (aluminum-induced protein) (Triticum aestivum) GI:451193   chr5:17639563-17641545 REVERSE   Aliases: MQD19.19, MQD19_19	9.5	9.9	-0.4	-0.7	100.0%	-4.8
10432	AT3G17630.1   Symbol: ATCHX19   cation/hydrogen exchanger, putative (CHX19), similar to putative Na <sup>+</sup> /H <sup>+</sup> -exchanging protein GB:CAA23036 from (Arabidopsis thaliana); monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563	3.9	3.7	0.2	0.7	100.0%	-4.9
10433	AT2G37480.2   expressed protein   chr2:15744961-15746926 FORWARD   Aliases: F3G5.27, F3G5_27	4.9	4.8	0.2	0.7	100.0%	-4.9
10434	AT5G23890.1   expressed protein, weak similarity to SP:P12957 Caldesmon (CDM) {Gallus gallus}   chr5:8058694-8063204 FORWARD   Aliases: MRO11.7, MRO11_7	6.5	6.7	-0.3	-0.7	100.0%	-4.9
10435	AT4G35540.1   expressed protein, transcription factor IIIB chain BRF1, Saccharomyces cerevisiae, PIR2:A44072   chr4:16873840-16875603 FORWARD   Aliases: F8D20.50, F8D20_50	5.6	5.8	-0.3	-0.7	100.0%	-4.5
10436	AT3G19320.1   leucine-rich repeat family protein, contains leucine-rich repeats, Pfam:PF00560;	2.2	2.3	-0.1	-0.7	100.0%	-5.7
10437	AT1G62320.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr1:23045333-23048520 REVERSE   Aliases: F24O1.4, F24O1_4	2.5	2.4	0.1	0.7	100.0%	-5.1
10438	AT5G59490.1   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:P53078 SSM1 protein {Saccharomyces cerevisiae}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:23999977-24001645 REVERSE   Aliases: F2O15.11, F2O15_11	3.7	3.4	0.3	0.7	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10439	AT3G01530.1   myb family transcription factor (MYB57), contains PFAM profile: myb DNA binding domain PF00249   chr3:210126-211811 REVERSE   Aliases: F4P13.8, F4P13_8	2.8	2.6	0.1	0.7	100.0%	-5.2
10440	AT5G20380.1   transporter-related, low similarity to vesicular glutamate transporter 3 (Rattus norvegicus) GI:21685382	4.9	4.7	0.2	0.7	100.0%	-4.7
10441	AT1G20800.1   F-box family protein, contains Pfam:PF00646 F-box domain	3.2	3.0	0.2	0.7	100.0%	-5.0
10442	AT5G38580.1   hypothetical protein   chr5:15468394-15469072 REVERSE   Aliases: MBB18.13, MBB18_13	2.6	2.5	0.1	0.7	100.0%	-5.4
10443	AT5G27750.1   F-box family protein, contains F-box domain Pfam:PF00646	5.7	5.9	-0.2	-0.7	100.0%	-4.4
10444	AT5G08530.1   NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial, putative, similar to NADH-ubiquinone oxidoreductase 51 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) from {Homo sapiens} SP:P49821, {Bos taurus} SP:P25708, {Aspergillus niger} SP:Q92406; contains Pfam profile PF01512: Respiratory-chain NADH dehydrogenase 51 Kd subunit   chr5:2759320-2761860 REVERSE   Aliases: MAH20.9, MAH20_9	9.7	9.4	0.3	0.7	100.0%	-5.1
10445	AT1G30780.1   F-box family protein   chr1:10923901-10926543 REVERSE   Aliases: T17H7.3, T17H7_3	3.4	3.3	0.1	0.7	100.0%	-5.4
10446	AT5G36290.2   expressed protein, contains Pfam profile PF01169: Uncharacterized protein family UPF0016	8.3	7.9	0.4	0.7	100.0%	-4.7
10447	AT2G34580.1   expressed protein   chr2:14572932-14574719 REVERSE   Aliases: T31E10.8, T31E10_8	3.1	3.2	-0.1	-0.7	100.0%	-5.3
10448	AT3G29760.1   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr3:11591984-11594312 REVERSE   Aliases: MOD1.21	4.4	4.6	-0.2	-0.7	100.0%	-4.7
10449	AT1G54710.1   expressed protein, contains 3 WD-40 repeats (PF00400) (1 weak) submitForm();   chr1:20420437-20424702 REVERSE   Aliases: T22H22.14, T22H22_14	6.3	6.2	0.2	0.7	100.0%	-4.6
10450	AT4G14810.1   expressed protein   chr4:8504140-8504504 FORWARD   Aliases: DL3445W, FCAALL.327	3.8	4.0	-0.2	-0.7	100.0%	-5.0
10451	AT1G80780.2   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, (CAF1) (Mus musculus)   chr1:30363007-30364265 FORWARD   Aliases: F23A5.13, F23A5_13	10.0	9.8	0.2	0.7	100.0%	-4.9
10452	AT1G55270.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 4 (Arabidopsis thaliana) GI:10716953; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:20620733-20623803 REVERSE   Aliases: F7A10.28	4.9	5.0	-0.2	-0.7	100.0%	-5.0
10453	AT5G63840.1   Symbol: RSW3   alpha-glucosidase, putative, similar to alpha-glucosidase GI:2648032 from (Solanum tuberosum)   chr5:25562282-25566425 FORWARD   Aliases: MGI19.5, MGI19_5, RADIAL SWELLING 3	9.6	9.9	-0.3	-0.7	100.0%	-4.7
10454	AT5G37850.1   Symbol: SOS4   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr5:15082638-15086191 FORWARD   Aliases: K18L3.1, K18L3_1, SALT OVERLY SENSITIVE 4	6.8	7.0	-0.3	-0.7	100.0%	-4.6
10455	AT1G77200.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr1:29009251-29009985 REVERSE   Aliases: T14N5.6, T14N5_6	3.1	3.0	0.2	0.7	100.0%	-4.7
10456	AT4G36105.1   expressed protein   chr4:17083888-17085122 FORWARD   Aliases: None	2.8	2.7	0.1	0.7	100.0%	-5.0
10457	AT1G01980.1   Symbol: ATSEC1A   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:340374-341999 REVERSE   Aliases: F22M8.11, F22M8_11, SEC1A	2.4	2.5	-0.1	-0.7	100.0%	-5.1
10458	AT3G18290.1   Symbol: EMB2454   zinc finger protein-related, weak alignment to Pfam profiles: PF00097 Zinc finger, C3HC4 type (RING finger) (2 copies)   chr3:6274001-6280331 FORWARD   Aliases: EMB2454, EMBRYO DEFECTIVE 2454, MIE15.8	4.0	4.2	-0.2	-0.7	100.0%	-5.1
10459	AT3G51290.1   proline-rich family protein   chr3:19050959-19053548 FORWARD   Aliases: F24M12.330	3.6	3.7	-0.1	-0.7	100.0%	-4.8
10460	AT1G06990.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	2.5	2.4	0.1	0.7	100.0%	-5.6
10461	AT4G03550.1   Symbol: ATGSL05   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr4:1573346-1579694 FORWARD   Aliases: ATGSL5, GLUCAN SYNTHASE LIKE 5, GSL05, GSL5, PMR4, POWDERY MILDEW RESISTANT 4, T5L23.4	5.3	5.0	0.2	0.7	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10462	AT1G05610.1   Symbol: APS2   Encodes the small subunit of ADP-glucose pyrophosphorylase. The small subunit is the catalytic isoform responsible for ADP-glucose pyrophosphorylase activity. The presence of the small subunit is required for large subunit stability. Two isoforms of the small subunit (ApS1 and ApS2) have been described. ApS2 is a minor small subunit isoform present in all plant tissues tested.   chr1:1673860-1675933 REVERSE   Aliases: APS2, F3F20.6, F3F20_6	3.2	3.1	0.1	0.7	100.0%	-5.2
10463	AT2G02990.1   Symbol: RNS1   ribonuclease 1 (RNS1), identical to ribonuclease SP:P42813 Ribonuclease 1 precursor (EC 3.1.27.1) {Arabidopsis thaliana}, GI:561998 from (Arabidopsis thaliana)   chr2:873505-874810 FORWARD   Aliases: RIBONUCLEASE 1, S LIKE RIBONUCLEASE 1, S LIKE RNASE 1, T17M13.16, T17M13_16	3.2	3.1	0.1	0.7	100.0%	-5.2
10464	AT2G38150.1   alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein, low similarity to alpha-1,4-N-acetylglucosaminyltransferase, Homo sapiens (gi:5726306), Gb3 synthase, Rattus norvegicus (gi:9082162) ; contains Pfam profiles PF04572: Alpha 1,4-glycosyltransferase conserved region, PF04488: Glycosyltransferase sugar-binding region containing DXD motif   chr2:15988778-15992356 REVERSE   Aliases: F16M14.8, F16M14_8	2.5	2.6	-0.0	-0.7	100.0%	-5.9
10465	AT3G21600.2   senescence/dehydration-associated protein-related, similar to senescence-associated protein 12 (Hemerocallis hybrid cultivar) gi:3551958:gb:AAC34857; similar to early-responsive to dehydration stress ERD7 protein (Arabidopsis thaliana) gi:15320412:dbj:BAB63916   chr3:7606552-7608371 REVERSE   Aliases: MIL23.17	3.2	3.0	0.2	0.7	100.0%	-4.8
10466	AT3G21055.1   photosystem II 5 kD protein, putative, identical to Swiss-Prot:Q39195 photosystem II 5 kDa protein, chloroplast precursor (PSII-T) (Arabidopsis thaliana)   chr3:7376643-7377192 REVERSE   Aliases: None	7.8	7.3	0.5	0.7	100.0%	-4.1
10467	AT5G52530.2   dentin sialophosphoprotein-related, contains weak similarity to dentin sialophosphoprotein precursor (Dentin matrix protein-3) (DMP-3) (Swiss-Prot:P97399) (Mus musculus)   chr5:21334388-21338462 FORWARD   Aliases: T4M5.4, T4M5_4	4.8	5.0	-0.2	-0.7	100.0%	-4.8
10468	AT1G15780.1   expressed protein   chr1:5430178-5435916 REVERSE   Aliases: F7H2.12, F7H2_12	7.6	7.8	-0.3	-0.7	100.0%	-4.8
10469	AT4G34650.1   Symbol: SQS2   farnesyl-diphosphate farnesyltransferase 2 / squalene synthase 2 (SQS2), nearly identical to GI:2228795; synonymous with farnesyl-diphosphate farnesyltransferase, FPP:FPP farnesyltransferase, and squalene synthetase   chr4:16542382-16544552 FORWARD   Aliases: SQUALENE SYNTHASE 2, T4L20.230, T4L20_230	3.1	3.3	-0.1	-0.7	100.0%	-5.1
10470	AT2G26330.1   Symbol: ER   leucine-rich repeat protein kinase, putative (ERECTA), identical to uncharacterized receptor protein kinase ERECTA (Arabidopsis thaliana) gi:1389566:dbj:BAA11869; contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr2:11215261-11221049 REVERSE   Aliases: ER, ERECTA, T1D16.3, T1D16_3	2.7	2.6	0.1	0.7	100.0%	-5.5
10471	AT4G24770.1   Symbol: RBP31   31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative, similar to SP:Q04836 31 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein RNP-T) (RNA-binding protein 1/2/3) (AtRBP33) (RNA-binding protein cp31) {Arabidopsis thaliana}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr4:12766040-12768033 REVERSE   Aliases: 31 KDA RNA BINDING PROTEIN, ATRBP31, ATRBP33, CP31, F6I7.11, STEP1	8.1	7.7	0.4	0.7	100.0%	-4.1
10472	AT1G63280.1   serpin-related / serine protease inhibitor-related, similar to protein zx (Hordeum vulgare subsp. vulgare) GI:19071, serpin (Triticum aestivum) GI:1885346   chr1:23475008-23475370 FORWARD   Aliases: F9N12.10, F9N12_10	2.5	2.5	0.1	0.7	100.0%	-5.7
10473	AT4G40030.1   histone H3.2, identical to Histone H3.2, minor Lolium temulentum SP:P11105, nearly identical to histone H3.2 Mus pahari GI:515005; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr4:18555571-18556964 REVERSE   Aliases: T5J17.200, T5J17_200	10.8	10.5	0.3	0.7	100.0%	-4.8
10474	AT1G30640.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr1:10861279-10864682 FORWARD   Aliases: T5I8.9, T5I8_9	5.3	5.0	0.3	0.7	100.0%	-4.5
10475	AT5G09350.1   phosphatidylinositol 4-kinase, putative, strong similarity to gi:4467359	4.8	5.4	-0.6	-0.7	100.0%	-4.4
10476	AT5G64070.1   phosphatidylinositol 4-kinase (PI4K), nearly identical to gi:4467359   chr5:25654202-25661672 REVERSE   Aliases: MHJ24.5, MHJ24_5	4.8	5.4	-0.6	-0.7	100.0%	-4.4
10477	AT5G38720.1   expressed protein, predicted protein, Drosophila melanogaster   chr5:15525477-15527789 REVERSE   Aliases: MKD10.4, MKD10_4	7.1	7.4	-0.3	-0.7	100.0%	-4.4
10478	AT3G11450.1   DNAJ heat shock N-terminal domain-containing protein / cell division protein-related, similar to GlsA (Volvox carteri f. nagariensis) GI:4633129; contains Pfam profiles PF00226 DnaJ domain, PF00249 Myb-like DNA-binding domain   chr3:3605226-3607483 REVERSE   Aliases: F24K9.12	5.1	5.3	-0.2	-0.7	100.0%	-4.8
10479	ATCG00430.1   Symbol: PSBG   photosystem II G protein	3.7	3.4	0.3	0.7	100.0%	-4.7
10480	AT1G01460.1   Type I phosphatidylinositol-4-phosphate 5-kinase, subfamily A.   chr1:168723-171165 FORWARD   Aliases: F22L4.2, F22L4_2	2.5	2.6	-0.1	-0.7	100.0%	-5.4
10481	AT2G05500.1   expressed protein, ; expression supported by MPSS   chr2:2014365-2015403 REVERSE   Aliases: T20G20.15, T20G20_15	2.3	2.4	-0.1	-0.7	100.0%	-6.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10482	AT4G37800.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to N-terminal partial sequence of endo-xyloglucan transferase GI:2244732 from ( <i>Gossypium hirsutum</i> )   chr4:17775468-17777391 REVERSE   Aliases: T28I19.80, T28I19_80	2.4	2.5	-0.1	-0.7	100.0%	-5.3
10483	AT2G11890.2   expressed protein, contains InterPro domain Adenylate cyclase (InterPro:IPR008172)   chr2:4809865-4811457 FORWARD   Aliases: None	6.9	6.7	0.2	0.7	100.0%	-4.5
10484	AT4G35360.1   pantothenate kinase family protein, contains Pfam domain, PF01937: Protein of unknown function; similar to SP:Q9NVE7 Pantothenate kinase 4 (EC 2.7.1.33) (Pantothenic acid kinase 4) (hPanK4) { <i>Homo sapiens</i> }   chr4:16812122-16814750 REVERSE   Aliases: F23E12.80, F23E12_80	8.3	7.9	0.4	0.7	100.0%	-4.8
10485	AT4G33550.1   similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g30880.1); similar to seed specific protein Bn15D18B [ <i>Brassica napus</i> ] (GB:AAP37971.1); contains InterPro domain Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612)   chr4:16134443-16135059 FORWARD   Aliases: T16L1.40, T16L1_40	4.6	4.9	-0.3	-0.7	100.0%	-4.4
10486	AT1G71350.1   eukaryotic translation initiation factor SUI1 family protein, weak similarity to SP:P41214 Ligatin (Hepatocellular carcinoma-associated antigen 56) { <i>Homo sapiens</i> }; contains Pfam profile PF01253: Translation initiation factor SUI1   chr1:26892070-26894893 REVERSE   Aliases: F3I17.23, F3I17_23	8.6	8.3	0.3	0.7	100.0%	-4.5
10487	AT2G23260.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:9907009-9908519 REVERSE   Aliases: T20D16.11, T20D16_11	3.0	2.9	0.1	0.7	100.0%	-5.2
10488	AT3G07090.1   expressed protein   chr3:2243060-2244826 REVERSE   Aliases: T1B9.26	8.2	8.8	-0.6	-0.7	100.0%	-4.5
10489	AT1G03560.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:890164-892410 REVERSE   Aliases: F21B7.18	4.3	4.5	-0.3	-0.7	100.0%	-4.9
10490	AT5G23870.3   pectinacylesterase family protein, contains Pfam profile: PF03283 pectinacylesterase	3.4	3.3	0.1	0.7	100.0%	-5.0
10491	AT3G44440.1   expressed protein   chr3:16081969-16082243 FORWARD   Aliases: F14L2.2	4.9	4.5	0.4	0.7	100.0%	-4.8
10492	AT3G22290.1   expressed protein   chr3:7881672-7885549 FORWARD   Aliases: AT3G22280, MCB17.1	7.9	7.8	0.1	0.7	100.0%	-4.9
10493	AT5G21150.1   PAZ domain-containing protein / piwi domain-containing protein, similar to SP:O04379 Argonaute protein (AGO1) { <i>Arabidopsis thaliana</i> }; contains Pfam profile: PF02170 PAZ (Piwi Argonaut and Zwill), PF02171 Piwi domain   chr5:7192242-7198327 FORWARD   Aliases: T10F18.180, T10F18_180	2.6	2.5	0.1	0.6	100.0%	-5.3
10494	AT5G52040.2   Symbol: ATRSP41   arginine/serine-rich splicing factor RSP41 (RSP41), nearly identical to SP:P92966 Arginine/serine-rich splicing factor RSP41 { <i>Arabidopsis thaliana</i> }   chr5:21147562-21150777 FORWARD   Aliases: ARGININE/SERINE RICH SPLICING FACTOR, MSG15.12, MSG15_12	6.9	6.7	0.2	0.6	100.0%	-4.8
10495	AT1G12530.1   expressed protein, similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g56420.1)   chr1:4268990-4270772 REVERSE   Aliases: F5O11.27, F5O11_27	6.6	6.9	-0.3	-0.6	100.0%	-4.5
10496	AT2G41700.2   similar to ABC transporter family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g61730.1); similar to ATP-binding cassette, sub-family A member 3 [ <i>Homo sapiens</i> ] (GB:NP_001080.1); similar to ABCA3_MOUSE ATP-binding cassette, sub-family A, member 3 (GB:Q8R420); similar to ATP-binding cassette, sub-family A (ABC1), member 3 [ <i>Mus musculus</i> ] (GB:NP_038883.1); similar to Abca3 protein [ <i>Mus musculus</i> ] (GB:AAH42663.1); similar to PREDICTED: similar to ATP-binding cassette, sub-family A member 3; ATP-binding cassette 3; ABC transporter 3, partial [ <i>Gallus gallus</i> ] (GB:XP_414701.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain ABC transporter (InterPro:IPR003439); contains InterPro domain ATP/GTP-binding site motif A (P-loop) (InterPro:IPR001687)   chr2:17389968-17403020 REVERSE   Aliases: T32G6.22	7.6	7.4	0.3	0.6	100.0%	-4.7
10497	AT2G42870.1   expressed protein   chr2:17843493-17844327 REVERSE   Aliases: F7D19.13, F7D19_13	2.9	2.7	0.1	0.6	100.0%	-5.2
10498	AT1G60770.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein ( <i>Triticum aestivum</i> ) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr1:22370366-22372379 REVERSE   Aliases: F8A5.28, F8A5_28	3.9	4.1	-0.2	-0.6	100.0%	-4.8
10499	AT1G49430.1   Symbol: LACS2   long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase, nearly identical to acyl CoA synthetase (MF45P) GI:1617268 from ( <i>Brassica napus</i> )   chr1:18294712-18299493 FORWARD   Aliases: F13F21.14, F13F21_14, LONG CHAIN ACYL COA SYNTHETASE 2	2.9	3.1	-0.2	-0.6	100.0%	-4.5
10500	AT4G33610.1   glycine-rich protein   chr4:16146264-16146996 FORWARD   Aliases: T16L1.100, T16L1_100	3.8	3.6	0.2	0.6	100.0%	-4.7
10501	AT1G23530.1   expressed protein   chr1:8345824-8346637 FORWARD   Aliases: F28C11.16	3.1	2.9	0.1	0.6	100.0%	-4.8
10502	NA	12.1	11.9	0.2	0.6	100.0%	-5.5
10503	AT5G35550.1   Symbol: TT2   myb family transcription factor (MYB123), contains PFAM profile: myb DNA-binding domain PF00249   chr5:13743973-13745090 FORWARD   Aliases: MOK9.18, MOK9_18, MYB123, TRANSPARENT TESTA 2	2.9	2.9	0.1	0.6	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10504	AT5G39160.2   similar to germin-like protein (GER2) [Arabidopsis thaliana] (TAIR:At5g39190.1); similar to putative germin E protein precursor [Gossypium hirsutum] (GB:AAM76228.1); contains InterPro domain Cupin (InterPro:IPR006045); contains InterPro domain Cupin domain (InterPro:IPR007113); contains InterPro domain Germin (InterPro:IPR001929)   chr5:15696242-15697230 REVERSE   Aliases: K3K3.1, K3K3_1	3.8	4.2	-0.4	-0.6	100.0%	-4.7
10505	AT5G64100.1   peroxidase, putative, identical to peroxidase ATP3a (Arabidopsis thaliana) gi:1546698:emb:CAA67340   chr5:25667867-25669349 REVERSE   Aliases: MHJ24.8, MHJ24_8	3.0	3.3	-0.2	-0.6	100.0%	-4.3
10506	AT2G28840.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:12385436-12387819 FORWARD   Aliases: F8N16.13, F8N16_13	9.3	9.5	-0.2	-0.6	100.0%	-4.8
10507	AT5G55240.1   caleosin-related family protein / embryo-specific protein, putative, strong similarity to embryo-specific protein 1 (Arabidopsis thaliana) GI:3335169; contains Pfam profilePF05042: Caleosin related protein   chr5:22423152-22424577 FORWARD   Aliases: MCO15.19, MCO15_19	3.3	3.2	0.1	0.6	100.0%	-5.0
10508	AT3G59950.2   similar to autophagy 4a (APG4a) [Arabidopsis thaliana] (TAIR:At2g44140.1); similar to putative autophagy protein (with alternative splicing) [Oryza sativa (japonica cultivar-group)] (GB:XP_470812.1); similar to putative autophagy protein (with alternative splicing) [Oryza sativa (japonica cultivar-group)] (GB:XP_470811.1); contains InterPro domain Peptidase family C54 (InterPro:IPR005078)   chr3:22155328-22158609 REVERSE   Aliases: F24G16.220	6.2	6.0	0.2	0.6	100.0%	-4.6
10509	AT2G38110.1   Symbol: ATGPAT6/GPAT6   Encodes a protein with glycerol-3-phosphate acyltransferase activity.   chr2:15959685-15962572 REVERSE   Aliases: ATGPAT6, F16M14.4, F16M14_4, GPAT6	2.9	2.8	0.1	0.6	100.0%	-4.9
10510	AT5G53490.2   thylakoid lumenal 17.4 kDa protein, chloroplast, identical to SP:P81760 Thylakoid lumenal 17.4 kDa protein, chloroplast precursor (P17.4) {Arabidopsis thaliana}	4.4	4.2	0.2	0.6	100.0%	-4.6
10511	AT5G35410.1   Symbol: SOS2   CBL-interacting protein kinase 24 (CIPK24) / serine/threonine protein kinase (SOS2), identical to CBL-interacting protein kinase 24 (Arabidopsis thaliana) GP:14701910:gb:AAK72257, serine/threonine protein kinase SOS2 (Arabidopsis thaliana) GI:7453645   chr5:13651769-13655421 FORWARD   Aliases: CBL INTERACTING PROTEIN KINASE 24, CIPK24, K21B8.3, K21B8_3, SALT OVERLY SENSITIVE 2	5.9	5.6	0.3	0.6	100.0%	-4.7
10512	AT2G17390.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:7562732-7565120 FORWARD   Aliases: F5J6.15, F5J6_15	11.2	11.0	0.2	0.6	100.0%	-5.2
10513	AT3G52770.1   expressed protein, emm32, Streptococcus pyogenes, EMBL:SPEMM32G   chr3:19568699-19569985 REVERSE   Aliases: F3C22.170	2.6	2.7	-0.1	-0.6	100.0%	-5.9
10514	AT1G66610.1   seven in absentia (SINA) protein, putative, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr1:24853379-24855113 REVERSE   Aliases: T12I7.6, T12I7_6	2.4	2.5	-0.1	-0.6	100.0%	-5.4
10515	AT1G67540.1   expressed protein, ; expression supported by MPSS   chr1:25315159-25315857 REVERSE   Aliases: F12B7.9, F12B7_9	3.2	3.3	-0.1	-0.6	100.0%	-5.2
10516	AT3G13170.1   DNA topoisomerase VIA (SPO11-1), identical to AtSPO11-1 (Arabidopsis thaliana) GI:13383478; contains Pfam profile PF04406: Type IIB DNA topoisomerase; identical to cDNA putative topoisomerase VIA (SPO11 gene 1) GI:7270974   chr3:4231567-4234199 REVERSE   Aliases: MJG19.19	2.2	2.3	-0.1	-0.6	100.0%	-5.3
10517	AT4G04260.1   bromo-adjacent homology (BAH) domain-containing protein, similar to ES43 (Hordeum vulgare) GI:1345528; contains Pfam profile PF01426: BAH domain	2.5	2.4	0.1	0.6	100.0%	-5.6
10518	AT4G04770.1   Symbol: ATABC1	9.5	9.3	0.2	0.6	100.0%	-4.9
10519	AT5G39400.1   pollen specific phosphatase, putative / phosphatase and tensin, putative (PTEN1), identical to phosphatase and tensin homolog (Arabidopsis thaliana) GI:21535746	2.5	2.4	0.1	0.6	100.0%	-5.6
10520	AT5G27220.1   protein transport protein-related, low similarity to SP:P25386 Intracellular protein transport protein USO1 {Saccharomyces cerevisiae}   chr5:9578760-9582755 FORWARD   Aliases: T21B4.130, T21B4_130	3.4	3.6	-0.2	-0.6	100.0%	-4.7
10521	AT2G37340.3   Symbol: RSZ33   splicing factor RSZ33 (RSZ33), nearly identical to splicing factor RSZ33 (Arabidopsis thaliana) GI:9843663; contains Pfam profiles PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), PF00098: Zinc knuckle   chr2:15677226-15679750 REVERSE   Aliases: F3G5.13, F3G5_13	9.9	9.7	0.1	0.6	100.0%	-5.0
10522	AT5G42800.1   Symbol: DFR   dihydroflavonol 4-reductase (dihydrokaempferol 4-reductase) (DFR), nearly identical to GI:166686   chr5:17181369-17183092 REVERSE   Aliases: DIHYDROFLAVONOL 4 REDUCTASE, DIHYDROKAEMPFEROL 4 REDUCTASE, M318, MJB21.18, MJB21_18, TRANSPARENT TESTA 3, TT3	2.9	3.0	-0.1	-0.6	100.0%	-5.2
10523	AT1G77750.1   30S ribosomal protein S13, chloroplast, putative, similar to putative 30S ribosomal protein S13, chloroplast precursor GB:P42732 (Arabidopsis thaliana)   chr1:29235118-29236418 REVERSE   Aliases: RPS13, T32E8.8, T32E8_8	7.1	7.6	-0.5	-0.6	100.0%	-4.2
10524	AT5G28610.1   expressed protein   chr5:10610963-10611351 FORWARD   Aliases: T10I18.2, T10I18_2	2.9	2.5	0.4	0.6	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10525	AT3G55160.1   expressed protein   chr3:20456389-20463377 REVERSE   Aliases: T26I12.40	3.3	3.5	-0.1	-0.6	100.0%	-5.0
10526	AT1G68330.1   expressed protein   chr1:25614586-25615865 FORWARD   Aliases: T22E19.4, T22E19_4	2.4	2.5	-0.1	-0.6	100.0%	-5.3
10527	AT4G39940.1   Symbol: AKN2   adenylylsulfate kinase 2 (AKN2), identical to adenylylsulfate kinase 2, chloroplast precursor (APS kinase, Adenosine-5'phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) (Arabidopsis thaliana) SWISS-PROT:O49196   chr4:18519711-18521562 FORWARD   Aliases: ADENOSINE 5' PHOSPHOSULFATE KINASE, T5J17.110, T5J17_110	2.8	3.1	-0.3	-0.6	100.0%	-4.2
10528	AT2G16810.1   F-box family protein (FBX8), contains F-box domain PF:00646   chr2:7294494-7296027 REVERSE   Aliases: T24I21.22, T24I21_22	2.2	2.1	0.1	0.6	100.0%	-5.7
10529	AT5G58980.1   ceramidase family protein, contains Pfam domain, PF04734: Neutral/alkaline nonlysosomal ceramidase   chr5:23828675-23831621 REVERSE   Aliases: K19M22.22, K19M22_22	6.8	7.2	-0.4	-0.6	100.0%	-4.5
10530	AT3G20060.1   Symbol: UBC19   ubiquitin-conjugating enzyme 19 (UBC19), nearly identical to ubiquitin-conjugating enzyme UBC19 (Arabidopsis thaliana) GI:22530865; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	7.2	7.4	-0.2	-0.6	100.0%	-4.7
10531	AT2G44195.1   hypothetical protein   chr2:18281882-18282713 FORWARD   Aliases: F4I1.13	2.8	2.8	0.1	0.6	100.0%	-5.5
10532	AT3G09360.1   transcription factor IIB (TFIIB) family protein, contains Pfam domain, PF00382: Transcription factor TFIIB repeat   chr3:2873802-2878438 FORWARD   Aliases: F3L24.23	6.2	7.0	-0.8	-0.6	100.0%	-4.6
10533	AT5G28490.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr5:10454545-10455117 REVERSE   Aliases: F24J2.30, F24J2_30	3.6	3.5	0.1	0.6	100.0%	-4.7
10534	AT3G25545.1   expressed protein   chr3:9278130-9279866 FORWARD   Aliases: None	4.3	4.5	-0.2	-0.6	100.0%	-4.9
10535	AT5G53520.1   Symbol: ATOPT8	2.6	2.7	-0.1	-0.6	100.0%	-5.5
10536	AT5G02940.1   expressed protein   chr5:684536-689696 REVERSE   Aliases: F9G14.250, F9G14_250	2.9	2.8	0.1	0.6	100.0%	-5.3
10537	AT5G51050.1   mitochondrial substrate carrier family protein, similar to peroxisomal Ca-dependent solute carrier (Oryctolagus cuniculus) GI:2352427; contains INTERPRO:IPR001993 Mitochondrial substrate carrier family, INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:20770607-20772940 FORWARD   Aliases: K3K7.23, K3K7_23	6.9	7.1	-0.2	-0.6	100.0%	-4.6
10538	AT3G58140.1   phenylalanyl-tRNA synthetase class IIc family protein, similar to phenylalanine-tRNA synthetase (Homo sapiens) GI:3983103; contains Pfam profile PF01409: tRNA synthetases class II core domain (F)   chr3:21540708-21543549 REVERSE   Aliases: F9D24.50	7.4	7.2	0.2	0.6	100.0%	-4.8
10539	AT1G30600.1   subtilase family protein, Strong similarity to gb:U80583 proteinase TMP from Lycopersicon esculentum and is a member of the PF:00082 subtilase family   chr1:10841124-10845032 REVERSE   Aliases: T5I8.5, T5I8_5	3.4	3.6	-0.1	-0.6	100.0%	-5.1
10540	AT5G57850.1   aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV   chr5:23452528-23454552 REVERSE   Aliases: MTI20.10, MTI20_10	5.7	5.9	-0.2	-0.6	100.0%	-4.6
10541	AT2G46340.1   Symbol: SPA1   phytochrome A supressor spa1 (SPA1), identical to phytochrome A supressor spa1 (GI:4809171) (Arabidopsis thaliana); contains 8 WD-40 repeats (Pfam PF00400) (1 weak)   chr2:19029417-19034440 REVERSE   Aliases: AT2G46350, F11C10.3, PHYTOCHROME A SUPRESSOR 1, PHYTOCHROME A SUPRESSOR SPA1, SUPPRESSOR OF PHYA 105 1	4.3	4.1	0.1	0.6	100.0%	-4.9
10542	AT1G62490.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr1:23134070-23135198 REVERSE   Aliases: T3P18.5, T3P18_5	2.4	2.5	-0.1	-0.6	100.0%	-5.5
10543	AT2G40310.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to SP:P35339 Exopolygalacturonase precursor (EC 3.2.1.67) (Pectinase) {Zea mays}; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)(Galacturan 1,4-alpha-galacturonidase)   chr2:16841143-16842789 FORWARD   Aliases: T7M7.10	2.9	2.8	0.1	0.6	100.0%	-5.5
10544	AT4G15820.1   wound-responsive protein-related, contains weak similarity to KED (Nicotiana tabacum) gi:8096269:dbj:BAA95789   chr4:8992983-8995493 FORWARD   Aliases: DL3950W, FCAALL.395	5.4	5.1	0.3	0.6	100.0%	-4.6
10545	AT5G14210.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:4578380-4581376 REVERSE   Aliases: MUA22.21, MUA22_21	4.1	4.3	-0.2	-0.6	100.0%	-4.5
10546	AT3G04150.1   germin-like protein, putative, contains Pfam profile: PF01072 germin family; similar to germin type2 GB:CAA63023 (SP:P92996), GLP2A (SP:P92999) (Arabidopsis thaliana)   chr3:1089458-1090433 REVERSE   Aliases: T6K12.23, T6K12_23	2.9	3.1	-0.1	-0.6	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10547	AT3G27100.1   expressed protein   chr3:9995832-9997249 REVERSE   Aliases: MOJ10.18	8.0	7.8	0.3	0.6	100.0%	-4.6
10548	AT1G02110.1   proline-rich family protein, contains proline-rich domain, INTERPRO:IPR000694   chr1:392939-395554 FORWARD   Aliases: T7I23.5, T7I23_5	5.7	5.5	0.2	0.6	100.0%	-4.5
10549	AT1G12500.1   phosphate translocator-related, low similarity to glucose-6-phosphate/phosphate-translocator precursor (Zea mays) GI:2997589, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SP:P21727:CPTR_PEA Triose phosphate/phosphate translocator, chloroplast precursor (CTPT) {Pisum sativum}   chr1:4263148-4265028 REVERSE   Aliases: F5O11.25, F5O11_25	5.2	5.4	-0.2	-0.6	100.0%	-4.6
10550	AT5G18990.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:6340078-6341616 FORWARD   Aliases: T16G12.30, T16G12_30	2.4	2.3	0.1	0.6	100.0%	-5.4
10551	AT2G16730.1   Symbol: BGAL13	2.1	2.0	0.1	0.6	100.0%	-5.9
10552	AT5G36840.1   expressed protein, similar to At3g24380, At5g35010, At3g42740, At4g05290, At2g14770, At3g43390, At2g05560, At4g08880, At1g34730, At1g27790   chr5:14525317-14527433 REVERSE   Aliases: F5H8.10, F5H8_10	2.4	2.6	-0.1	-0.6	100.0%	-5.0
10553	AT1G54580.1   Symbol: ACP2   acyl carrier protein, chloroplast, putative / ACP, putative, strong similarity to SP:P25701 Acyl carrier protein 2, chloroplast precursor (ACP) {Arabidopsis thaliana}; contains InterPro accession IPR003881: Isochorismatase   chr1:20393100-20394682 FORWARD   Aliases: ACYL CARRIER PROTEIN 2, T22H22.3, T22H22_3	12.2	12.4	-0.2	-0.6	100.0%	-4.9
10554	AT1G54630.2   Symbol: ACP3   similar to acyl carrier protein, chloroplast, putative / ACP, putative [Arabidopsis thaliana] (TAIR:At1g54580.1); similar to acyl carrier protein [Brassica napus] (GB:CAA34248.1); contains InterPro domain Phosphopantetheine-binding domain (InterPro:IPR006163); contains InterPro domain Acyl carrier protein (ACP) (InterPro:IPR003231)   chr1:20405044-20406671 REVERSE   Aliases: ACYL CARRIER PROTEIN 3, T22H22.7, T22H22_7	12.2	12.4	-0.2	-0.6	100.0%	-4.9
10555	AT1G75400.1   expressed protein   chr1:28300580-28303347 FORWARD   Aliases: F1B16.7, F1B16_7	3.7	3.5	0.2	0.6	100.0%	-4.4
10556	AT3G06280.1   expressed protein   chr3:1898161-1898757 REVERSE   Aliases: F28L1.22, F28L1_22	2.2	2.3	-0.1	-0.6	100.0%	-5.7
10557	AT3G23700.1   S1 RNA-binding domain-containing protein, contains Pfam domain, PF00575: S1 RNA binding domain   chr3:8531436-8533774 REVERSE   Aliases: MYM9.4	7.3	7.7	-0.3	-0.6	100.0%	-4.4
10558	AT5G51430.1   conserved oligomeric Golgi complex component-related / COG complex component-related, contains weak similarity to Conserved oligomeric Golgi complex component 7 (Swiss-Prot:P83436) (Homo sapiens)   chr5:20904064-20908133 REVERSE   Aliases: MFG13.14, MFG13_14	6.7	6.9	-0.2	-0.6	100.0%	-4.8
10559	AT1G06850.2   similar to bZIP transcription factor family protein [Arabidopsis thaliana] (TAIR:At2g40620.1); similar to bZIP transcription factor RF2b [Oryza sativa (japonica cultivar-group)] (GB:AAR28765.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr1:2105054-2106732 FORWARD   Aliases: F4H5.7, F4H5_7	2.7	2.8	-0.1	-0.6	100.0%	-5.2
10560	AT2G40670.1   Symbol: ARR16   two-component responsive regulator / response regulator 16 (ARR16), identical to response regulator 16 GI:11870067 from (Arabidopsis thaliana)   chr2:16977336-16978198 FORWARD   Aliases: RESPONSE REGULATOR 16, RR16, T7D17.15, T7D17_15	3.6	3.7	-0.1	-0.6	100.0%	-5.2
10561	AT4G20210.1   terpene synthase/cyclase family protein, (+)-delta-cadinene synthase isozyme XC14, Gossypiumarboreum, PIR2:S68366   chr4:10913623-10918292 REVERSE   Aliases: F1C12.130, F1C12_130	3.6	3.4	0.2	0.6	100.0%	-4.7
10562	ATCG00050.1   Symbol: RPS16   Homologous to the bacterial ribosomal protein S16   chrC:5084-6188 REVERSE   Aliases: RPS16	5.4	6.1	-0.7	-0.6	100.0%	-4.4
10563	AT1G76320.2   similar to far-red impaired response protein (FAR1) / far-red impaired responsive protein (FAR1) [Arabidopsis thaliana] (TAIR:At4g15090.1); similar to putative FAR1 protein [Oryza sativa (japonica cultivar-group)] (GB:AAT78829.1); contains InterPro domain SWIM Zn-finger (InterPro:IPR007527); contains InterPro domain Zn-finger, PMZ type (InterPro:IPR006564); contains InterPro domain FAR1 (InterPro:IPR004330)   chr1:28636134-28638972 FORWARD   Aliases: F15M4.18	4.2	4.4	-0.1	-0.6	100.0%	-5.0
10564	AT2G29550.1   Symbol: TUB7   tubulin beta-7 chain (TUB7), identical to GB:M84704 SP:P29515 Tubulin beta-7 chain {Arabidopsis thaliana}   chr2:12651124-12653114 REVERSE   Aliases: F16P2.7, F16P2_7	7.5	7.9	-0.5	-0.6	100.0%	-4.3
10565	AT5G11390.1   expressed protein   chr5:3633668-3636562 FORWARD   Aliases: F2I11.280, F2I11_280	7.5	7.8	-0.3	-0.6	100.0%	-4.3
10566	AT3G07410.1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family   chr3:2372323-2373562 REVERSE   Aliases: F21O3.12	9.1	9.4	-0.4	-0.6	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10567	AT3G49750.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to resistance gene Hcr2-5B, Lycopersicon esculentum, EMBL:AF053997   chr3:18461418-18462479 REVERSE   Aliases: T16K5.100	4.0	3.9	0.1	0.6	100.0%	-5.1
10568	AT2G41560.1   Symbol: ACA4   calcium-transporting ATPase 4, plasma membrane-type / Ca <sup>2+</sup> -ATPase, isoform 4 (ACA4), identical to SP:O22218 Calcium-transporting ATPase 4, plasma membrane-type (EC 3.6.3.8) (Ca <sup>2+</sup> )-ATPase isoform 4) {Arabidopsis thaliana} Belongs to plant 2B ATPase??s with an N-terminal autoinhibitor.   chr2:17339162-17344276 REVERSE   Aliases: AUTO INHIBITED CA(2+) ATPASE, ISOFORM 4, T32G6.8, T32G6_8	5.3	5.1	0.2	0.6	100.0%	-4.9
10569	AT3G21080.1   ABC transporter-related, contains 4 transmembrane domains; supported by tandem duplication of ABC transporter family protein (GI:20260310) (TIGR_Ath1:At3g21090) (Arabidopsis thaliana)	2.8	3.0	-0.1	-0.6	100.0%	-5.0
10570	AT4G19450.1   nodulin-related, weak similarity to nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr4:10606464-10609346 FORWARD   Aliases: T5K18.230, T5K18_230	5.8	5.6	0.2	0.6	100.0%	-4.9
10571	AT2G06040.1   expressed protein   chr2:2354031-2355495 REVERSE   Aliases: F5K7.20, F5K7_20	2.9	2.8	0.1	0.6	100.0%	-5.1
10572	AT1G18890.1   Symbol: ATCDPK1   calcium-dependent protein kinase 1 (CDPK1), identical to calcium-dependent protein kinase (Arabidopsis thaliana) gi:604880:dbj:BAA04829; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr1:6522755-6525727 REVERSE   Aliases: CALCIUM DEPENDENT PROTEIN KINASE 1, CPK10, F6A14.1, F6A14_1	5.9	5.8	0.2	0.6	100.0%	-5.0
10573	AT1G72380.1   expressed protein   chr1:27248832-27250525 FORWARD   Aliases: T10D10.15, T10D10_15	3.6	3.7	-0.2	-0.6	100.0%	-5.0
10574	AT1G71940.1   expressed protein   chr1:27082242-27083892 FORWARD   Aliases: F17M19.9, F17M19_9	5.8	6.1	-0.3	-0.6	100.0%	-4.7
10575	AT5G42750.1   expressed protein   chr5:17160048-17161388 REVERSE   Aliases: MJB21.13, MJB21_13	3.4	3.1	0.3	0.6	100.0%	-4.4
10576	AT5G59200.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:23906019-23907791 REVERSE   Aliases: MNC17.11, MNC17_11	3.0	2.9	0.1	0.6	100.0%	-5.4
10577	AT1G80100.1   phosphotransfer family protein, similar to histidine-containing phosphotransfer protein (Catharanthus roseus) GI:13774348, ATHP3 (Arabidopsis thaliana) GI:4156245   chr1:30138711-30139545 FORWARD   Aliases: F18B13.18, F18B13_18	2.2	2.1	0.1	0.6	100.0%	-5.7
10578	AT5G01390.1   DNAJ heat shock protein, putative, similar to SP:Q9QYJ3 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr5:160263-162270 REVERSE   Aliases: T10O8.100, T10O8_100	5.2	5.4	-0.2	-0.6	100.0%	-4.6
10579	AT1G51590.2   similar to mannosyl-oligosaccharide 1,2-alpha-mannosidase, putative [Arabidopsis thaliana] (TAIR:At3g21160.1); similar to OSJNBa0035M09.7 [Oryza sativa (japonica cultivar-group)] (GB:XP_473805.1); contains InterPro domain Glycoside hydrolase, family 47 (InterPro:IPR001382)   chr1:19131812-19135986 REVERSE   Aliases: F5D21.1, F5D21_1	5.0	5.2	-0.2	-0.6	100.0%	-4.7
10580	AT5G34900.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g32840, At4g04010, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At3g29210, At2g02210, At3g32900   chr5:13231926-13236592 REVERSE   Aliases: T2L5.5, T2L5_5	2.7	2.9	-0.2	-0.6	100.0%	-5.1
10581	AT5G57490.1   porin, putative, similar to 36kDa porin II (Solanum tuberosum) GI:515360; contains Pfam profile PF01459: Eukaryotic porin   chr5:23300906-23303160 REVERSE   Aliases: MUA2.6, MUA2_6	6.8	7.1	-0.3	-0.6	100.0%	-4.4
10582	AT2G27470.1   CCAAT-box binding transcription factor subunit HAP3-related, contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to polymerase epsilon p17 subunit (DNA polymerase epsilon subunit 3) (YB-like protein 1) (YBL1) (NF-YB-like protein) (SP:Q9JKP7)	7.2	7.8	-0.7	-0.6	100.0%	-4.4
10583	AT3G60520.1   expressed protein   chr3:22372505-22373554 REVERSE   Aliases: T8B10.180	3.3	3.1	0.2	0.6	100.0%	-4.7
10584	AT5G59890.2   Symbol: ADF4   actin-depolymerizing factor 4 (ADF4), identical to SP:Q9ZSK3 Actin-depolymerizing factor 4 (ADF-4) (AtADF4) {Arabidopsis thaliana}   chr5:24139827-24141138 FORWARD   Aliases: ACTIN DEPOLYMERIZING FACTOR 4, MMN10.8, MMN10_8	12.5	12.0	0.5	0.6	100.0%	-4.5
10585	AT1G53060.1   legume lectin family protein   chr1:19779720-19780448 FORWARD   Aliases: F8L10.8, F8L10_8	3.0	3.1	-0.1	-0.6	100.0%	-5.1
10586	AT3G24570.1   peroxisomal membrane 22 kDa family protein, contains Mpv17 / PMP22 family domain, Pfam:PF04117   chr3:8966451-8968662 REVERSE   Aliases: MOB24.15	7.3	7.6	-0.2	-0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10587	AT1G65520.1   enoyl-CoA hydratase/isomerase family protein, low similarity to enoyl-CoA hydratase (Escherichia coli) GI:2764828, carnitine racemase SP:P31551 (Escherichia coli); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr1:24364705-24365556 REVERSE   Aliases: F5I14.5, F5I14_5	5.0	4.9	0.2	0.6	100.0%	-4.7
10588	AT1G33920.1   Symbol: ATPP2 A4   lectin-related, low similarity to PP2 lectin polypeptide (Cucurbita maxima) GI:410437   chr1:12319885-12320850 FORWARD   Aliases: ATPP2 A4, T3M13.6, T3M13_6	3.7	3.8	-0.2	-0.6	100.0%	-4.7
10589	AT5G62960.1   expressed protein   chr5:25286508-25288867 FORWARD   Aliases: MJH22.1, MJH22_1	3.6	3.9	-0.2	-0.6	100.0%	-4.6
10590	AT5G40670.1   PQ-loop repeat family protein / transmembrane family protein, similar to SP:O60931 Cystinosin {Homo sapiens}; contains Pfam profile PF04193: PQ loop repeat   chr5:16302939-16305013 FORWARD   Aliases: MNF13.23, MNF13_23	9.3	9.6	-0.3	-0.6	100.0%	-4.8
10591	AT2G27840.2   Symbol: HDT4   histone deacetylase-related / HD-related, similar to nucleolar histone deacetylase HD2-p39 (Zea mays) GI:2257756; contains non-consensus donor splice site AT at exon2 and acceptor splice site AC at exon3.   chr2:11869605-11870963 FORWARD   Aliases: F15K20.6, F15K20_6, HDA13, HDT04, HISTONE DEACETYLASE	6.1	6.5	-0.4	-0.6	100.0%	-4.3
10592	AT5G38280.1   Symbol: PR5K   serine/threonine protein kinase (PR5K), identical to receptor serine/threonine kinase PR5K gi:1235680:gb:AAC49208   chr5:15310351-15314553 REVERSE   Aliases: MXA21.170, MXA21_170	6.0	5.9	0.1	0.6	100.0%	-5.0
10593	AT3G58620.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr3:21691303-21694112 FORWARD   Aliases: F14P22.210	5.3	5.6	-0.3	-0.6	100.0%	-4.6
10594	AT3G46020.1   RNA-binding protein, putative, similar to Cold-inducible RNA-binding protein (Glycine-rich RNA-binding protein CIRP) from {Homo sapiens} SP:Q14011, {Rattus norvegicus} SP:Q61413, {Xenopus laevis}; SP:O93235; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	3.4	3.5	-0.1	-0.6	100.0%	-4.8
10595	AT4G22190.1   expressed protein   chr4:11741867-11743330 REVERSE   Aliases: T10I14.20, T10I14_20	5.4	5.6	-0.2	-0.6	100.0%	-4.9
10596	AT1G11090.1   hydrolase, alpha/beta fold family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:3702608-3703779 FORWARD   Aliases: T19D16.3, T19D16_3	6.4	6.1	0.3	0.6	100.0%	-4.6
10597	AT3G13820.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:4549623-4550870 FORWARD   Aliases: MCP4.3	2.7	2.8	-0.1	-0.6	100.0%	-5.2
10598	AT1G77060.1   mutase family protein, similar to carboxyvinyl-carboxyphosphonate phosphorylmutase GB:O49290 from (Arabidopsis thaliana); similar to carboxyphosphoenolpyruvate mutase (GI:47149) (Streptomyces hygroscopicus); contains Prosite PS00161: Isocitrate lyase signature   chr1:28956579-28958374 REVERSE   Aliases: F22K20.14, F22K20_14	5.0	4.7	0.3	0.6	100.0%	-4.3
10599	AT5G42120.1   lectin protein kinase family protein, contains Pfam domains PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr5:16850301-16852376 REVERSE   Aliases: MJC20.23, MJC20_23	3.2	3.0	0.1	0.6	100.0%	-5.0
10600	AT2G23230.1   terpene synthase/cyclase family protein   chr2:9899796-9902480 FORWARD   Aliases: T20D16.14, T20D16_14	3.0	2.9	0.2	0.6	100.0%	-4.9
10601	AT1G50150.1   hypothetical protein, similar to hypothetical protein GB:AAD50048 GI:5734783 from (Arabidopsis thaliana)	2.9	3.2	-0.3	-0.6	100.0%	-4.8
10602	AT4G35690.1   hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr4:16921891-16922745 FORWARD   Aliases: F8D20.200, F8D20_200	3.8	3.7	0.1	0.6	100.0%	-5.1
10603	AT4G22320.1   expressed protein   chr4:11792970-11794738 REVERSE   Aliases: T10I14.150, T10I14_150	4.1	4.3	-0.2	-0.6	100.0%	-4.7
10604	AT5G22310.1   expressed protein   chr5:7383632-7385737 REVERSE   Aliases: MWD9.9, MWD9_9	4.1	4.3	-0.2	-0.6	100.0%	-4.7
10605	AT1G61290.1   Symbol: SYP124	3.6	3.7	-0.1	-0.6	100.0%	-5.3
10606	AT2G05890.1   expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	2.0	2.2	-0.2	-0.6	100.0%	-5.2
10607	AT5G18200.1   expressed protein   chr5:6015229-6016782 FORWARD   Aliases: MRG7.16, MRG7_16	5.9	6.2	-0.4	-0.6	100.0%	-4.5
10608	AT1G03550.1   secretory carrier membrane protein (SCAMP) family protein, contains Pfam domain, PF04144: SCAMP family   chr1:885623-887956 REVERSE   Aliases: F21B7.17, F21B7_17	4.5	4.2	0.3	0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10609	AT3G18220.1   phosphatidic acid phosphatase family protein / PAP2 family protein, similar to phosphatidic acid phosphatase (Mus musculus) GI:1487873; contains Pfam profile: PF01569 phosphatase PAP2 superfamily   chr3:6247920-6249966 FORWARD   Aliases: MIE15.1	2.4	2.5	-0.1	-0.6	100.0%	-5.3
10610	AT4G12230.1   esterase/lipase/thioesterase family protein, low similarity to 2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase; OhpC (Rhodococcus sp.) GI:8926386; contains Interpro entry IPR000379   chr4:7284513-7287536 FORWARD   Aliases: T4C9.70, T4C9_70	4.7	4.4	0.3	0.6	100.0%	-4.8
10611	AT2G30010.1   expressed protein   chr2:12812801-12816462 FORWARD   Aliases: F23F1.7, F23F1_7	3.6	3.5	0.2	0.6	100.0%	-4.6
10612	AT1G55250.1   expressed protein, weak similarity to PUMA1 (Parascaris univalens) GI:3068590   chr1:20610881-20613370 FORWARD   Aliases: F7A10.17, F7A10_17	3.0	3.1	-0.1	-0.6	100.0%	-5.4
10613	NA	11.4	11.2	0.2	0.6	100.0%	-5.9
10614	AT3G15690.2   biotin carboxyl carrier protein of acetyl-CoA carboxylase-related, contains weak similarity to Biotin carboxyl carrier protein of acetyl-CoA carboxylase, chloroplast precursor (BCCP) (Swiss-Prot:Q42533) (Arabidopsis thaliana)   chr3:5316948-5319615 FORWARD   Aliases: MSJ11.9	7.4	7.1	0.4	0.6	100.0%	-4.4
10615	AT5G43880.1   expressed protein   chr5:17657202-17660817 REVERSE   Aliases: F6B6.2, F6B6_2	2.9	2.8	0.1	0.6	100.0%	-5.1
10616	AT3G55320.1   ABC transporter family protein, similar to multidrug resistant P-glycoprotein pmdr1 GI:4204793 from (Solanum tuberosum)   chr3:20518368-20524370 REVERSE   Aliases: T26I12.200	4.1	4.3	-0.3	-0.6	100.0%	-4.7
10617	AT5G02810.1   Symbol: APRR7   pseudo-response regulator 7 (APRR7), identical to pseudo-response regulator 7 GI:10281004 from (Arabidopsis thaliana)   chr5:637895-641975 REVERSE   Aliases: F9G14.120, F9G14_120, PRR7, PSEUDO RESPONSE REGULATOR 7	4.9	4.8	0.2	0.6	100.0%	-4.8
10618	AT5G54370.1   late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (GI:1350543)(Picea glauca)   chr5:22092536-22093990 FORWARD   Aliases: MDK4.20, MDK4_20	2.5	2.4	0.1	0.6	100.0%	-5.3
10619	AT3G43670.1   copper amine oxidase, putative, similar to copper amine oxidase (Cicer arietinum) gi:3819099:emb:CAA08855   chr3:15578087-15580889 FORWARD   Aliases: F23N14.50	6.6	6.9	-0.3	-0.6	100.0%	-4.6
10620	AT3G03880.1   expressed protein   chr3:997806-999268 FORWARD   Aliases: F20H23.7, F20H23_7	5.4	5.3	0.1	0.6	100.0%	-5.1
10621	AT1G54560.1   Symbol: XIE   myosin, putative, similar to myosin GI:433663 from (Arabidopsis thaliana)	3.4	3.6	-0.2	-0.6	100.0%	-4.7
10622	AT1G08890.1   sugar transporter family protein, similar to sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:2848351-2852273 FORWARD   Aliases: F7G19.23, F7G19_23	5.5	5.0	0.5	0.6	100.0%	-4.3
10623	AT1G08900.1   sugar transporter-related, contains similarity to sugar-porter family protein 2 GI:14585701 from (Arabidopsis thaliana)   chr1:2852457-2855777 FORWARD   Aliases: F7G19.22, F7G19_22	5.5	5.0	0.5	0.6	100.0%	-4.3
10624	AT5G42300.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr5:16929561-16931158 REVERSE   Aliases: K5J14.10, K5J14_10	13.2	13.3	-0.1	-0.6	100.0%	-5.5
10625	AT3G13062.3   expressed protein, weak similarity to SP:Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) {Homo sapiens}   chr3:4184576-4187091 FORWARD   Aliases: None	4.8	4.7	0.1	0.6	100.0%	-5.1
10626	AT3G01560.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr3:219589-221886 FORWARD   Aliases: F4P13.11, F4P13_11	5.3	5.1	0.2	0.6	100.0%	-4.5
10627	AT1G68640.1   Symbol: PAN   bZIP family transcription factor (PERIANTHIA), identical to transcription factor PERIANTHIA GB:AAD19660 GI:4378757 from (Arabidopsis thaliana)   chr1:25773239-25776206 REVERSE   Aliases: F24J5.12, F24J5_12, PERIANTHIA	2.4	2.5	-0.1	-0.6	100.0%	-5.6
10628	AT5G26120.1   glycosyl hydrolase family protein 51, similar to arabinoxylan arabinofuranohydrolase isoenzyme AXAH-II from GI:13398414 (Hordeum vulgare)   chr5:9121730-9125970 REVERSE   Aliases: T1N24.13, T1N24_13	3.1	3.3	-0.1	-0.6	100.0%	-5.2
10629	AT2G23770.1   protein kinase family protein / peptidoglycan-binding LysM domain-containing protein, contains Pfam domains, PF00069: Protein kinase domain and PF01476: LysM domain   chr2:10127322-10129160 REVERSE   Aliases: F27L4.5, F27L4_5	2.3	2.5	-0.1	-0.6	100.0%	-4.9
10630	AT5G01850.1   protein kinase, putative, similar to protein kinase (Arabidopsis thaliana) gi:1054633:emb:CAA63387; contains protein kinase domain, Pfam:PF00069	3.9	4.1	-0.2	-0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10631	AT4G01650.2   expressed protein   chr4:704407-706965 REVERSE   Aliases: T15B16.3, T15B16_3	3.6	3.4	0.2	0.6	100.0%	-4.7
10632	AT2G34520.1   Symbol: RPS14   ribosomal protein S14 mitochondrial family protein, identical to ribosomal protein S14 {Arabidopsis thaliana} NCBI_gi:4583554   chr2:14554863-14555837 REVERSE   Aliases: T31E10.14, T31E10_14	8.1	8.4	-0.3	-0.6	100.0%	-4.6
10633	AT3G16650.1   PP1/PP2A phosphatases pleiotropic regulator 2 (PRL2), identical to SP:Q39190 PP1/PP2A phosphatases pleiotropic regulator PRL2 {Arabidopsis thaliana}, GB:Q39190 from (Arabidopsis thaliana); contains Pfam PF00400: WD domain, G-beta repeat (7 copies, 1 weak)   chr3:5671087-5675330 FORWARD   Aliases: MGL6.10	7.1	7.4	-0.3	-0.6	100.0%	-4.1
10634	AT4G28610.1   Symbol: PHR1   myb family transcription factor, putative / phosphate starvation response regulator, putative (PHR1), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA phosphate starvation response regulator 1 (phr1 gene) GI:15384675   chr4:14132862-14135265 REVERSE   Aliases: ATPHR1, PHOSPHATE STARVATION RESPONSE 1, T5F17.60, T5F17_60	4.5	4.8	-0.3	-0.6	100.0%	-4.4
10635	AT1G67420.1   24 kDa vacuolar protein, putative, similar to 24 kDa vacuolar protein VP24 (Ipomoea batatas) gi:5821406:dbj:BAA83809   chr1:25259074-25264092 FORWARD   Aliases: T1F15.12, T1F15_12	7.2	7.5	-0.3	-0.6	100.0%	-4.7
10636	AT4G14365.1   zinc finger (C3HC4-type RING finger) family protein / ankyrin repeat family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger) and Pfam profile: PF00023 ankyrin repeat   chr4:8271460-8273733 REVERSE   Aliases: None	3.2	3.4	-0.2	-0.6	100.0%	-4.5
10637	AT4G26170.1   expressed protein   chr4:13258130-13259391 FORWARD   Aliases: T25K17.5	3.0	3.1	-0.1	-0.6	100.0%	-5.4
10638	AT3G55740.2   Symbol: ProT2   proline transporter 2 (ProT2), identical to proline transporter 2 GI:1769903 from (Arabidopsis thaliana)   chr3:20706506-20709250 FORWARD   Aliases: ATPROT2, F1I16.150, PROLINE TRANSPORTER 2	4.5	4.7	-0.2	-0.6	100.0%	-4.8
10639	AT1G04510.2   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At2g33340.1); similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At2g33340.2); similar to ENSANGP00000016070 [Anopheles gambiae str. PEST] (GB:XP_308568.2); contains InterPro domain Zn-finger, modified RING (InterPro:IPR003613); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr1:1226574-1230826 FORWARD   Aliases: F19P19.2, F19P19_2	5.9	6.5	-0.5	-0.6	100.0%	-4.6
10640	AT3G08840.3   D-alanine--D-alanine ligase family, similar to D-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase) (D-Ala-D-Ala ligase) (Swiss-Prot:O51218) (Borrelia burgdorferi); similar to D-alanine--D-alanine ligase (EC 6.3.2.4) (D-alanylalanine synthetase) (D-Ala-D-Ala ligase). (Swiss-Prot:P95803) (Streptococcus mutans)   chr3:2679898-2686193 REVERSE   Aliases: T16O11.23	2.8	2.7	0.1	0.6	100.0%	-5.1
10641	AT3G28940.1   avirulence-responsive protein, putative / avirulence induced gene (AIG) protein, putative, strong similarity to SP:P54121 AIG2 protein (avrRpt2-induced gene) {Arabidopsis thaliana}   chr3:10969337-10970585 REVERSE   Aliases: K5K13.7	7.5	8.0	-0.5	-0.6	100.0%	-4.3
10642	AT4G36400.2   FAD linked oxidase family protein, low similarity to SP:Q12627 from Kluyveromyces lactis and SP:P32891 from Saccharomyces cerevisiae; contains Pfam FAD linked oxidases, C-terminal domain PF02913, Pfam FAD binding domain PF01565   chr4:17197252-17200924 FORWARD   Aliases: AP22.14, AP22_14	3.9	4.0	-0.2	-0.6	100.0%	-4.6
10643	AT1G02830.1   60S ribosomal protein L22 (RPL22A), similar to ribosomal protein L22 GI:710294 from (Rattus norvegicus)   chr1:625145-625608 REVERSE   Aliases: F22D16.17, F22D16_17	3.7	3.8	-0.1	-0.6	100.0%	-5.0
10644	AT1G27820.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)   chr1:9691615-9692547 FORWARD   Aliases: T22C5.28, T22C5_28	3.5	3.4	0.1	0.6	100.0%	-4.9
10645	AT5G51010.1   rubredoxin family protein, similar to SP:P04170 Rubredoxin (Rd) {Desulfovibrio desulfuricans}; contains Pfam profile PF00301: Rubredoxin	7.0	6.7	0.3	0.6	100.0%	-4.3
10646	AT4G34960.1   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to cyclophilin (Arabidopsis thaliana) gi:2443755:gb:AAB71401	5.1	5.3	-0.2	-0.6	100.0%	-4.6
10647	AT3G28490.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Caenorhabditis elegans (GI:607947), Mus musculus (SP:Q60715), Homo sapiens (GI:18073925); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr3:10680286-10681891 REVERSE   Aliases: MFJ20.17	2.5	2.6	-0.1	-0.6	100.0%	-5.4
10648	AT5G43270.3   Symbol: SPL2   squamosa promoter-binding protein-like 2 (SPL2), identical to squamosa promoter binding protein-like 2 (Arabidopsis thaliana) GI:5931645; contains Pfam profile PF03110: SBP domain   chr5:17377560-17380162 REVERSE   Aliases: MNL12.9, MNL12_9, SQUAMOSA PROMOTER BINDING PROTEIN LIKE 2	3.5	3.3	0.2	0.6	100.0%	-5.0
10649	AT1G68875.1   expressed protein   chr1:25895749-25896461 FORWARD   Aliases: None	2.8	2.7	0.1	0.6	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10650	AT2G38840.1   guanylate-binding family protein, similar to SP:Q01514 Interferon-induced guanylate-binding protein 1 (Guanine nucleotide-binding protein 1) (Interferon-gamma inducible protein MAG-1) {Mus musculus}; contains Pfam profile PF02263: Guanylate-binding protein, N-terminal domain   chr2:16234407-16239434 FORWARD   Aliases: F13I13.7, F13I13_7	5.0	5.1	-0.2	-0.6	100.0%	-5.2
10651	AT5G49570.1   transglutaminase-like family protein, low similarity to peptide:N-glycanase PNGase (Mus musculus) GI:8347622; contains Pfam profile PF01841: Transglutaminase-like superfamily   chr5:20129085-20133411 REVERSE   Aliases: K6M13.12, K6M13_12	5.4	5.1	0.3	0.6	100.0%	-4.6
10652	AT5G40770.1   Symbol: ATPHB3	9.0	9.3	-0.3	-0.6	100.0%	-4.4
10653	AT5G42570.1   expressed protein, low similarity to SP:P51572 B-cell receptor-associated protein 31 (6C6-AG tumor-associated antigen) (DXS1357E) {Homo sapiens}	5.8	5.6	0.3	0.6	100.0%	-4.6
10654	AT2G23460.1   Symbol: XLG   extra-large guanine nucleotide binding protein / G-protein (XLG), identical to extra-large G-protein (XLG) (Arabidopsis thaliana) GI:3201680   chr2:10002558-10006202 FORWARD   Aliases: ATXLG1, EXTRA LARGE G PROTEIN, F26B6.11, F26B6_11, XLG	5.2	5.0	0.2	0.6	100.0%	-4.6
10655	AT2G35430.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:14907957-14909464 REVERSE   Aliases: T32F12.19, T32F12_19	3.2	3.1	0.1	0.6	100.0%	-5.0
10656	AT3G14510.1   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltransferase, putative, similar to gi:9294375; similar to geranylgeranyl pyrophosphate synthetase GB:P34802 (Arabidopsis thaliana)   chr3:4867385-4868421 REVERSE   Aliases: MOA2.15	3.7	3.5	0.1	0.6	100.0%	-5.0
10657	AT1G44760.1   universal stress protein (USP) family protein, contains Pfam profile PF00582: universal stress protein family   chr1:16899126-16901052 REVERSE   Aliases: T12C22.3, T12C22_3	3.9	4.1	-0.2	-0.6	100.0%	-4.8
10658	AT5G42090.1   expressed protein   chr5:16843926-16845682 FORWARD   Aliases: MJC20.20, MJC20_20	6.9	6.6	0.3	0.6	100.0%	-4.6
10659	AT3G21000.1   expressed protein, ; expression supported by MPSS   chr3:7363927-7365144 FORWARD   Aliases: MSA6.5	3.4	3.2	0.1	0.6	100.0%	-5.4
10660	AT1G55255.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:20613786-20616314 FORWARD   Aliases: None	6.8	6.4	0.3	0.6	100.0%	-4.9
10661	AT1G67100.1   LOB domain protein 40 / lateral organ boundaries domain protein 40 (LBD40), identical to SP:Q9ZW96 LOB domain protein 40 {Arabidopsis thaliana}   chr1:25057422-25058507 FORWARD   Aliases: F1O19.17	3.4	3.2	0.1	0.6	100.0%	-5.1
10662	AT3G22770.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:8047691-8048674 REVERSE   Aliases: MWI23.14	3.7	3.9	-0.2	-0.6	100.0%	-5.2
10663	AT5G17380.1   pyruvate decarboxylase family protein, similar to 2-hydroxyphytanoyl-CoA lyase (Homo sapiens) GI:6273457; contains InterPro entry IPR000399: Pyruvate decarboxylase   chr5:5724770-5726748 REVERSE   Aliases: T10B6.40, T10B6_40	9.5	9.8	-0.3	-0.6	100.0%	-4.7
10664	AT1G75190.1   expressed protein   chr1:28223043-28223888 FORWARD   Aliases: F22H5.8, F22H5_8	3.5	3.1	0.4	0.6	100.0%	-4.3
10665	AT2G47330.1   DEAD/DEAH box helicase, putative, similar to RNA helicase (Rattus norvegicus) GI:897915; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr2:19436034-19438762 REVERSE   Aliases: T8I13.17	7.0	7.1	-0.2	-0.6	100.0%	-4.8
10666	AT4G33890.2   expressed protein   chr4:16249727-16251384 FORWARD   Aliases: F17I5.80, F17I5_80	5.3	5.1	0.2	0.6	100.0%	-4.7
10667	AT1G79630.3   similar to protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] (TAIR:At1g16220.1); similar to putative protein phosphatase 2C [Oryza sativa (japonica cultivar-group)] (GB:XP_465582.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr1:29967538-29970688 REVERSE   Aliases: F20B17.6, F20B17_6	4.3	4.5	-0.2	-0.6	100.0%	-5.1
10668	AT5G46330.1   Symbol: FLS2   leucine-rich repeat transmembrane protein kinase, putative   chr5:18808963-18812773 FORWARD   Aliases: FLAGELLIN SENSITIVE 2, MPL12.13, MPL12.8, MPL12_13	2.5	2.6	-0.1	-0.6	100.0%	-5.2
10669	AT1G18990.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr1:6558669-6560480 REVERSE   Aliases: F14D16.14, F14D16_14	2.6	2.7	-0.1	-0.6	100.0%	-5.3
10670	AT5G20130.1   expressed protein   chr5:6797445-6798901 FORWARD   Aliases: F5O24.20, F5O24_20	6.5	6.4	0.2	0.6	100.0%	-4.6
10671	AT4G35250.1   vestitone reductase-related, low similarity to vestitone reductase (Medicago sativa subsp. sativa) GI:973249   chr4:16771180-16773369 REVERSE   Aliases: F23E12.190, F23E12_190	8.5	8.1	0.4	0.6	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10672	AT1G75130.1   Symbol: CYP721A1   cytochrome P450 family protein, similar to Cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus)   chr1:28203636-28205611 REVERSE   Aliases: F22H5.19	5.4	5.2	0.1	0.6	100.0%	-4.8
10673	AT4G34630.1   expressed protein   chr4:16536870-16537751 REVERSE   Aliases: T4L20.210, T4L20_210	6.2	6.1	0.2	0.6	100.0%	-4.8
10674	AT1G19140.2   expressed protein   chr1:6610774-6612458 REVERSE   Aliases: F14D16.30, F14D16_30	8.0	8.3	-0.3	-0.6	100.0%	-4.5
10675	AT5G24140.1   Symbol: SQP2   squalene monooxygenase 2 / squalene epoxidase 2 (SQP2), identical to SP:O65403   chr5:8164359-8167676 REVERSE   Aliases: MLE8.6, MLE8_6	2.2	2.3	-0.1	-0.6	100.0%	-5.7
10676	AT2G13560.1   malate oxidoreductase, putative, similar to NAD-dependent malic enzyme 62 kDa isoform, mitochondrial precursor (EC 1.1.1.39) (NAD-ME) (SP:P37221) {Solanum tuberosum}   chr2:5657046-5662301 FORWARD   Aliases: T10F5.10, T10F5_10	10.8	10.7	0.2	0.6	100.0%	-4.9
10677	AT4G30993.2   expressed protein   chr4:15098073-15100564 FORWARD   Aliases: None	4.4	4.2	0.2	0.6	100.0%	-4.9
10678	AT2G03560.1   F-box family protein (FBX7), identical to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana); contains F-box domain PF:00646   chr2:1079636-1082080 FORWARD   Aliases: F19B11.1, F19B11_1	2.4	2.5	-0.1	-0.6	100.0%	-5.4
10679	AT4G09390.1   hypothetical protein, various predicted proteins -Arabidopsis thaliana   chr4:5951913-5952885 FORWARD   Aliases: T15G18.190, T15G18_190	2.6	2.5	0.1	0.6	100.0%	-5.2
10680	AT2G42280.2   basic helix-loop-helix (bHLH) family protein   chr2:17618361-17620565 REVERSE   Aliases: T24P15.19, T24P15_19	2.9	3.1	-0.2	-0.6	100.0%	-4.4
10681	AT3G01270.1   pectate lyase family protein, similar to pectate lyase P59 SP:P15722 from (Lycopersicon esculentum)   chr3:82695-84904 REVERSE   Aliases: T22N4.10, T22N4_10, T4P13.4, T4P13_4	2.9	2.8	0.1	0.6	100.0%	-5.1
10682	AT4G05280.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At3g24380, At5g36840, At5g35010, At3g42740, At4g05290, At2g14770, At3g43390, At2g05560, At4g08880, At1g34730, At1g27790, At1g34740, At1g27780, At5g36850, At3g42730, At1g52020, At3g24390, At1g25886, At4g03300   chr4:2697579-2703503 FORWARD   Aliases: C17L7.200, C17L7_200	2.5	2.5	-0.1	-0.6	100.0%	-5.7
10683	AT2G37380.1   expressed protein   chr2:15693852-15694919 FORWARD   Aliases: F3G5.17, F3G5_17	5.3	5.5	-0.2	-0.6	100.0%	-4.7
10684	AT3G07640.1   expressed protein   chr3:2438144-2439847 FORWARD   Aliases: MLP3.9	6.1	6.4	-0.3	-0.6	100.0%	-4.5
10685	AT5G56220.1   expressed protein   chr5:22772097-22775146 FORWARD   Aliases: K24C1.3, K24C1_3	4.9	5.1	-0.1	-0.6	100.0%	-5.0
10686	AT5G37890.1   seven in absentia (SINA) protein, putative, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr5:15107516-15109124 REVERSE   Aliases: K18L3.9, K18L3_9	3.6	3.4	0.2	0.6	100.0%	-4.8
10687	AT3G01920.1   yrdC family protein, contains Pfam PF01300: yrdC domain; similar to Protein yciO. (Swiss-Prot:P45847) (Shigella flexneri); similar to Chain A, Crystal Structure Of E. Coli Ycio Length (GI:27573707) (Escherichia coli)	5.8	5.6	0.2	0.6	100.0%	-4.4
10688	AT2G17770.1   ABA-responsive element binding protein, putative, similar to ABA response element binding factor (Triticum aestivum) gi:21693583:gb:AAM75354   chr2:7730185-7730655 FORWARD   Aliases: T17A5.15, T17A5_15	3.0	3.1	-0.1	-0.6	100.0%	-5.0
10689	AT3G19350.1   polyadenylate-binding protein-related / PABP-related, similar to poly(A)-binding protein (Cucumis sativus) GI:7528270; contains Pfam profile PF00658: Poly-adenylate binding protein, unique domain   chr3:6705499-6706133 FORWARD   Aliases: MLD14.19	2.5	2.6	-0.1	-0.6	100.0%	-5.2
10690	AT5G26250.1   sugar transporter, putative, similar to hexose transporter (Lycopersicon esculentum) GI:5734440, sugar carrier protein {Ricinus communis} SP:Q41144, monosaccharide transporter (Nicotiana tabacum) GI:19885; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:9196761-9198684 FORWARD   Aliases: T19G15.100, T19G15_100	4.0	3.9	0.1	0.6	100.0%	-5.4
10691	AT1G53680.1   Symbol: ATGSTU28   glutathione S-transferase, putative, similar to GI:2853219 from (Carica papaya)   chr1:20042026-20042785 FORWARD   Aliases: F22G10.22, F22G10_22	3.7	3.5	0.2	0.6	100.0%	-4.7
10692	AT3G46520.1   Symbol: ACT12   actin 12 (ACT12), identical to SP:P53497 Actin 12 {Arabidopsis thaliana}   chr3:17139248-17141195 FORWARD   Aliases: ACTIN, ACTIN 12, F12A12.40	2.4	2.3	0.1	0.6	100.0%	-5.5
10693	AT3G61160.2   shaggy-related protein kinase beta / ASK-beta (ASK2), identical to shaggy-related protein kinase beta SP:O23145 GI:2569931 from (Arabidopsis thaliana)   chr3:22646989-22649792 FORWARD   Aliases: T20K12.60	4.6	4.5	0.1	0.6	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10694	AT5G03020.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr5:707255-708394 FORWARD   Aliases: F15A17.50, F15A17_50	2.8	2.7	0.1	0.6	100.0%	-5.4
10695	AT5G05430.1   expressed protein   chr5:1605276-1606704 REVERSE   Aliases: K18I23.24, K18I23_24	2.8	2.7	0.1	0.6	100.0%	-5.3
10696	AT4G38350.1   patched family protein, similar to SP:O15118 Niemann-Pick C1 protein precursor from Homo sapiens (PID:g2276463); contains Pfam profile PF02460 Patched family   chr4:17958318-17966411 REVERSE   Aliases: F22I13.120, F22I13_120	6.4	6.7	-0.2	-0.6	100.0%	-4.7
10697	AT4G14220.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:8195876-8198537 FORWARD   Aliases: DL3150W, FCAALL.146	3.5	3.7	-0.1	-0.6	100.0%	-5.1
10698	AT5G38180.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family   chr5:15247042-15247383 FORWARD   Aliases: MXA21.16, MXA21_16	2.5	2.6	-0.1	-0.6	100.0%	-5.6
10699	AT5G49400.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr5:20047956-20049392 FORWARD   Aliases: K7J8.7, K7J8_7	6.1	6.5	-0.3	-0.6	100.0%	-4.8
10700	AT1G66820.1   glycine-rich protein   chr1:24933703-24934214 FORWARD   Aliases: F4N21.5, F4N21_5	6.9	7.2	-0.2	-0.6	100.0%	-4.4
10701	AT2G43610.1   glycoside hydrolase family 19 protein, similar to chitinase GI:17799 from (Brassica napus); contains Pfam profiles PF00182: Chitinase class I, PF00187: Chitin recognition protein   chr2:18094917-18096301 REVERSE   Aliases: F18O19.28	3.5	4.1	-0.5	-0.6	100.0%	-4.4
10702	AT1G27700.1   expressed protein   chr1:9640185-9641853 REVERSE   Aliases: T22C5.15, T22C5_15	4.0	3.9	0.1	0.6	100.0%	-5.0
10703	AT2G45460.1   forkhead-associated domain-containing protein / FHA domain-containing protein   chr2:18743913-18748764 REVERSE   Aliases: F4L23.3	5.0	4.8	0.2	0.6	100.0%	-4.5
10704	AT2G31340.1   Symbol: EMB1381   expressed protein   chr2:13368583-13372277 FORWARD   Aliases: EMB1381, EMBRYO DEFECTIVE 1381, T28P16.17, T28P16_17	3.8	3.9	-0.1	-0.6	100.0%	-5.1
10705	AT5G05760.1   Symbol: SYP31   syntaxin 31 (SYP31) / SED5, identical to SP:Q9FFK1 Syntaxin 31 (AtSYP31) (AtSED5) {Arabidopsis thaliana}   chr5:1727473-1731022 REVERSE   Aliases: ATSED5, ATSY31, MJJ3.17, MJJ3_17, T SNARE SED 5	4.4	4.2	0.2	0.6	100.0%	-4.6
10706	AT5G11120.1   hypothetical protein   chr5:3542321-3542991 FORWARD   Aliases: T5K6.11	2.2	2.3	-0.1	-0.6	100.0%	-5.5
10707	AT5G12080.2   mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, contains Pfam profile PF00924: Mechanosensitive ion channel   chr5:3898048-3901521 REVERSE   Aliases: F14F18.230, F14F18_230	8.5	8.9	-0.4	-0.6	100.0%	-4.4
10708	AT5G11270.1   Symbol: OCP3   expressed protein   chr5:3595286-3597084 REVERSE   Aliases: F2I11.160, F2I11_160, OVEREXPRESSOR OF CATIONIC PEROXIDASE 3	4.5	4.3	0.2	0.6	100.0%	-4.9
10709	AT4G11790.1   Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein, contains Pfam profile PF00638: RanBP1 domain	4.2	4.4	-0.2	-0.6	100.0%	-4.9
10710	AT4G03620.1   myosin heavy chain-related, contains weak similarity to Swiss-Prot:P24733 myosin heavy chain, striated muscle (Aequipecten irradians)   chr4:1607038-1608663 REVERSE   Aliases: T5L23.11, T5L23_11	3.1	3.2	-0.1	-0.6	100.0%	-5.2
10711	AT4G25320.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr4:12954087-12956553 FORWARD   Aliases: T30C3.1	5.4	5.6	-0.2	-0.6	100.0%	-4.7
10712	AT2G30690.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593; expression supported by MPSS   chr2:13083306-13085672 FORWARD   Aliases: T11J7.8, T11J7_8	2.5	2.4	0.1	0.6	100.0%	-5.5
10713	AT1G78010.1   tRNA modification GTPase, putative, similar to tRNA modification GTPase trmE (strain PCC 7120, Anabaena sp.) SWISS-PROT:Q8YN91   chr1:29338394-29341345 FORWARD   Aliases: F28K19.23, F28K19_23	6.3	6.6	-0.3	-0.6	100.0%	-4.4
10714	AT3G08510.2   Symbol: ATPLC2	5.0	5.3	-0.3	-0.6	100.0%	-4.7
10715	AT2G19600.1   Symbol: ATKEA4	4.4	4.6	-0.2	-0.6	100.0%	-5.0
10716	AT3G61670.1   expressed protein, weak similarity to extra-large G-protein (Arabidopsis thaliana) GI:3201682   chr3:22829564-22832985 FORWARD   Aliases: F15G16.60	6.0	5.8	0.2	0.6	100.0%	-4.7
10717	AT4G02820.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr4:1258568-1260665 FORWARD   Aliases: T5J8.14, T5J8_14	3.7	3.9	-0.1	-0.6	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10718	AT1G51710.1   Symbol: UBP6   ubiquitin-specific protease 6, putative (UBP6), similar to GI:11993465   chr1:19179313-19183631 REVERSE   Aliases: F19C24.8, F19C24_8, UBIQUITIN SPECIFIC PROTEASE 6	8.8	9.2	-0.4	-0.6	100.0%	-4.4
10719	AT5G28620.1   protein kinase C-related, contains weak similarity to protein kinase C beta (Homo sapiens) gi:633224:emb:CAA44393   chr5:10612533-10613008 REVERSE   Aliases: T10I18.80, T10I18_80	2.7	2.8	-0.1	-0.6	100.0%	-5.3
10720	AT3G08020.1   PHD finger protein-related, contains low similarity to PHD-finger domain proteins   chr3:2557759-2561540 REVERSE   Aliases: F17A17.36	3.5	3.3	0.1	0.6	100.0%	-4.9
10721	AT5G51290.1   ceramide kinase-related, contains weak similarity to ceramide kinases (GI:21624342) (Mus musculus)   chr5:20861226-20865559 REVERSE   Aliases: MWD22.24, MWD22_24	3.0	2.9	0.1	0.6	100.0%	-5.2
10722	AT2G22770.1   Symbol: NAI1   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At2g22760.1); similar to putative transcription factor [Oryza sativa (japonica cultivar-group)] (GB:AAT77090.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr2:9691805-9693675 FORWARD   Aliases: T30L20.3, T30L20_3	3.2	3.3	-0.1	-0.6	100.0%	-5.2
10723	AT5G06680.1   Symbol: SPC98   tubulin family protein, similar to SP:Q96CW5 Gamma-tubulin complex component 3 {Homo sapiens}   chr5:2056588-2059748 FORWARD   Aliases: ATSPC98, MPH15.2, MPH15_2, SPINDLE POLE BODY COMPONENT 98	2.6	2.7	-0.1	-0.6	100.0%	-5.2
10724	AT3G19630.1   radical SAM domain-containing protein, similar to florfenicol resistance protein (Staphylococcus sciuri) GI:9909980; contains Pfam profile PF04055: radical SAM domain protein   chr3:6818393-6820731 REVERSE   Aliases: MMB12.10	5.4	5.7	-0.3	-0.6	100.0%	-4.7
10725	AT2G32990.1   glycosyl hydrolase family 9 protein, similar to endo-beta-1,4-glucanase GI:4972236 from (Fragaria x ananassa)   chr2:14010327-14013094 FORWARD   Aliases: T21L14.7, T21L14_7	7.5	7.7	-0.2	-0.6	100.0%	-4.4
10726	AT1G28570.2   GDSL-motif lipase, putative, similar to lipase (Arabidopsis thaliana) GI:1145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr1:10041627-10044136 REVERSE   Aliases: F1K23.19, F1K23_19	7.9	8.3	-0.3	-0.6	100.0%	-4.3
10727	AT4G37630.2   Symbol: CYCD5;1   similar to cyclin delta-1 (CYCD1) [Arabidopsis thaliana] (TAIR:At1g70210.1); similar to cyclin D1 [Helianthus tuberosus] (GB:AAL47479.1); contains InterPro domain Cyclin (InterPro:IPR006670); contains InterPro domain Cyclin, N-terminal domain (InterPro:IPR006671)   chr4:17679347-17680884 FORWARD   Aliases: CYCLIN D5;1, F19F18.120, F19F18_120	3.4	3.5	-0.1	-0.6	100.0%	-5.0
10728	AT5G06300.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At3g53450.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54293.1); contains InterPro domain Conserved hypothetical protein 730 (InterPro:IPR005269)   chr5:1921745-1925349 REVERSE   Aliases: MHF15.18, MHF15_18	3.9	3.7	0.3	0.6	100.0%	-4.2
10729	AT2G34730.1   myosin heavy chain-related, low similarity to SP:P14105 Myosin heavy chain, nonmuscle (Cellular myosin heavy chain) {Gallus gallus}   chr2:14661690-14664700 FORWARD   Aliases: T29F13.6, T29F13_6	6.2	6.7	-0.4	-0.6	100.0%	-4.3
10730	AT5G41780.1   myosin heavy chain-related, weak similarity to M protein, serotype 5 precursor (SP:P02977) {Streptococcus pyogenes} and to Myosin heavy chain, non-muscle (SP:Q99323) (Zipper protein) (Myosin II) {Drosophila melanogaster}   chr5:16740303-16742061 FORWARD   Aliases: K16L22.6, K16L22_6	2.6	2.5	0.1	0.6	100.0%	-5.6
10731	AT3G27440.1   uracil phosphoribosyltransferase, putative / UMP pyrophosphorylase, putative / UPRTase, putative, similar to SP:O65583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Arabidopsis thaliana}; contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family   chr3:10156792-10159168 FORWARD   Aliases: K1G2.27	3.0	2.9	0.1	0.6	100.0%	-5.1
10732	AT1G50760.1   expressed protein   chr1:18818615-18818928 REVERSE   Aliases: F8A12.1, F8A12_1	4.3	4.5	-0.2	-0.6	100.0%	-5.1
10733	AT2G34080.1   cysteine proteinase, putative, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas)	3.5	3.4	0.2	0.6	100.0%	-4.8
10734	AT3G59390.2   expressed protein, protein CG15643 - Drosophila melanogaster, EMBL:AE003499   chr3:21957095-21959273 FORWARD   Aliases: F25L23.250	5.5	5.3	0.2	0.6	100.0%	-4.7
10735	AT4G15740.1   C2 domain-containing protein, similar to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain   chr4:8964743-8966316 REVERSE   Aliases: DL3910C, FCAALL.373	3.4	3.7	-0.3	-0.6	100.0%	-4.2
10736	AT2G40050.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.6	0.1	0.6	100.0%	-5.4
10737	AT5G25410.1   expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr5:8831673-8833512 FORWARD   Aliases: F18G18.150, F18G18_150	3.4	3.5	-0.1	-0.6	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10738	AT1G66900.1   expressed protein   chr1:24962997-24965279 FORWARD   Aliases: T4O24.3, T4O24_3	4.7	4.5	0.2	0.6	100.0%	-4.7
10739	AT4G25340.1   immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related, immunophilin FKBP46 - Spodoptera frugiperda (fall armyworm),PIR2:A55320   chr4:12959452-12962709 REVERSE   Aliases: T30C3.20, T30C3_20	6.3	6.4	-0.1	-0.6	100.0%	-5.0
10740	AT3G14680.1   Symbol: CYP72A14   cytochrome P450, putative, similar to GB:Q05047 from (Catharanthus roseus)   chr3:4934428-4936570 FORWARD   Aliases: MIE1.1	3.6	3.3	0.3	0.6	100.0%	-4.2
10741	AT5G39930.1   expressed protein, ; expression supported by MPSS   chr5:16002477-16004468 REVERSE   Aliases: MYH19.90, MYH19_90	2.7	2.6	0.1	0.6	100.0%	-5.4
10742	AT2G07000.1   expressed protein   chr2:2901867-2902287 REVERSE   Aliases: T4E14.11, T4E14_11	5.0	4.7	0.3	0.6	100.0%	-4.5
10743	AT5G58710.1   Symbol: ROC7   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative (ROC7), similar to cyclophilin (Arabidopsis thaliana) gi:2443755:gb:AAB71401   chr5:23735018-23736975 FORWARD   Aliases: CYCLOPHILIN, MZN1.23, MZN1_23	10.5	10.8	-0.3	-0.6	100.0%	-4.9
10744	AT4G20840.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr4:11157927-11159546 FORWARD   Aliases: F21C20.190, F21C20_190	5.7	5.9	-0.2	-0.6	100.0%	-4.9
10745	AT1G31870.2   similar to splicing factor PWI domain-containing protein [Arabidopsis thaliana] (TAIR:At2g29210.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_480359.1); contains InterPro domain Bipartite nuclear localization signal (InterPro:IPR001472)   chr1:11436703-11440089 FORWARD   Aliases: F5M6.12, F5M6_12	8.6	8.9	-0.3	-0.6	100.0%	-4.4
10746	AT1G17540.1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g72760.1); similar to serine threonine kinase 1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD53152.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Usp domain (InterPro:IPR006016)	3.2	3.1	0.1	0.6	100.0%	-5.3
10747	AT5G60600.2   Symbol: CLB4   1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase, putative / GcpE family protein, similar to GcpE (Plasmodium falciparum) GI:13094969; contains Pfam profile PF04551: GcpE protein; supporting cDNA gi:27462471:gb:AF434673.1   chr5:24376207-24380677 FORWARD   Aliases: CHLOROPLAST BIOGENESIS 4, ISPG, MUP24.15, MUP24_15	7.3	6.9	0.3	0.6	100.0%	-4.5
10748	AT3G43940.1   expressed protein   chr3:15775252-15776358 REVERSE   Aliases: T15B3.80	3.3	3.1	0.1	0.6	100.0%	-5.0
10749	AT1G10170.1   NF-X1 type zinc finger family protein, contains Pfam PF01422: NF-X1 type zinc finger; similar to transcriptional repressor NF-X1 (SP:Q12986) (Homo sapiens); similar to EST gb:T21002   chr1:3333597-3337493 REVERSE   Aliases: F14N23.5, F14N23_5	4.1	4.0	0.2	0.6	100.0%	-4.7
10750	AT1G12780.1   Encodes a UDP-glucose epimerase that catalyzes the interconversion of the sugar nucleotides UDP-glucose UDP-galactose via a UDP-4-keto-hexose intermediate.   chr1:4355924-4358326 REVERSE   Aliases: F13K23.3, F13K23_3	8.5	8.1	0.4	0.6	100.0%	-4.6
10751	AT1G55820.1   hydroxyproline-rich glycoprotein family protein   chr1:20868063-20871084 FORWARD   Aliases: F20N2.19	2.8	2.8	-0.1	-0.6	100.0%	-5.8
10752	AT4G09600.1   Symbol: GASA3   gibberellin-regulated protein 3 (GASA3) / gibberellin-responsive protein 3, identical to SP:P46687 Gibberellin-regulated protein 3 precursor {Arabidopsis thaliana}   chr4:6072802-6073609 REVERSE   Aliases: T25P22.40, T25P22_40	2.8	2.9	-0.1	-0.6	100.0%	-5.4
10753	AT2G48150.1   Symbol: ATGPX4	2.4	2.3	0.1	0.6	100.0%	-5.4
10754	AT5G66640.1   LIM domain-containing protein-related, contains low similarity to Pfam profile PF00412: LIM domain   chr5:26616855-26619175 FORWARD   Aliases: MSN2.2, MSN2_2	2.5	2.4	0.1	0.6	100.0%	-5.2
10755	AT4G19410.1   pectinacylesterase, putative, similar to pectinacylesterase precursor GI:1431629 from (Vigna radiata)   chr4:10582032-10585769 REVERSE   Aliases: T5K18.190, T5K18_190	11.3	11.6	-0.3	-0.6	100.0%	-4.9
10756	AT3G22540.1   expressed protein   chr3:7984097-7984634 REVERSE   Aliases: F16J14.10	4.5	4.8	-0.4	-0.6	100.0%	-4.2
10757	AT1G25230.1   purple acid phosphatase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase; similar to purple acid phosphatase (GI:20257479) (Arabidopsis thaliana)	3.0	3.4	-0.3	-0.6	100.0%	-4.1
10758	AT4G09970.2   expressed protein   chr4:6245958-6248159 FORWARD   Aliases: T5L19.100, T5L19_100	4.9	4.7	0.2	0.6	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10759	AT1G49730.4   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g19300.1); similar to hypothetical protein kinase [Musa acuminata] (GB:AAR95997.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:18406035-18409231 REVERSE   Aliases: F14J22.6, F14J22_6	2.5	2.4	0.1	0.6	100.0%	-5.6
10760	AT5G02190.1   Symbol: PCS1   encodes an aspartic protease, has an important role in determining cell fate during embryonic development and in reproduction processes. The loss-of-function mutation of PCS1 causes degeneration of both male and female gametophytes and excessive cell death of developing embryos during torpedo stage.   chr5:435231-436895 FORWARD   Aliases: PCS1, PROMOTION OF CELL SURVIVAL1, T7H20.240, T7H20_240	2.6	2.7	-0.1	-0.6	100.0%	-5.3
10761	AT3G11200.2   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr3:3508048-3510558 REVERSE   Aliases: F11B9.12	7.1	6.8	0.3	0.6	100.0%	-4.6
10762	AT5G18460.1   expressed protein, predicted proteins, Arabidopsis thaliana Pfam profile PF03080: Arabidopsis proteins of unknown function   chr5:6123048-6126723 FORWARD   Aliases: F20L16.180, F20L16_180	2.6	2.8	-0.2	-0.6	100.0%	-4.4
10763	AT4G00950.1   expressed protein   chr4:405673-407142 REVERSE   Aliases: A_TM018A10.2, A_TM018A10_2, T18A10.4, T18A10_4	3.3	3.4	-0.1	-0.6	100.0%	-5.2
10764	AT1G32650.1   hypothetical protein   chr1:11810537-11810611 REVERSE   Aliases: F6N18.22, F6N18_22	2.4	2.5	-0.1	-0.6	100.0%	-5.7
10765	AT1G11000.1   Symbol: MLO4   seven transmembrane MLO family protein / MLO-like protein 4 (MLO4), identical to membrane protein Mlo4 (Arabidopsis thaliana) gi:14091578:gb:AAK53797; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr1:3671756-3675979 REVERSE   Aliases: T19D16.26, T19D16_26	3.0	2.9	0.1	0.6	100.0%	-5.1
10766	AT2G34700.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr2:14641218-14642706 REVERSE   Aliases: T29F13.9, T29F13_9	2.1	2.0	0.1	0.6	100.0%	-5.8
10767	AT1G33000.1   hypothetical protein   chr1:11957948-11958142 FORWARD   Aliases: F9L11.26, F9L11_26	2.5	2.6	-0.1	-0.6	100.0%	-5.3
10768	AT5G54120.1   expressed protein   chr5:21980126-21980954 FORWARD   Aliases: MJP23.10, MJP23_10	3.1	3.3	-0.2	-0.6	100.0%	-4.8
10769	AT5G12880.1   proline-rich family protein, similar to hydroxyproline-rich glycoprotein gi:169345:gb:AAA33763   chr5:4068522-4068965 REVERSE   Aliases: T24H18.50, T24H18_50	2.9	3.5	-0.7	-0.6	100.0%	-4.6
10770	AT2G01260.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g15030.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477257.1); contains InterPro domain Protein of unknown function DUF789 (InterPro:IPR008507)   chr2:135243-137802 REVERSE   Aliases: F10A8.14, F10A8_14	4.1	3.8	0.3	0.6	100.0%	-4.8
10771	AT1G11590.1   pectin methylesterase, putative, similar to fruit-specific pectin methylesterase GI:1617583 from (Lycopersicon esculentum)   chr1:3892580-3894677 FORWARD   Aliases: T23J18.25, T23J18_25	2.9	2.9	0.1	0.6	100.0%	-5.3
10772	AT1G76050.2   pseudouridine synthase family protein, contains Pfam profiles: PF00849 RNA pseudouridylate synthase, PF01479: S4 domain   chr1:28545717-28548744 FORWARD   Aliases: T4O12.210, T4O12_210	5.6	5.8	-0.2	-0.6	100.0%	-4.6
10773	AT4G34310.2   expressed protein   chr4:16414117-16419732 FORWARD   Aliases: F10M10.80, F10M10_80	3.4	3.5	-0.2	-0.6	100.0%	-4.6
10774	AT1G29760.1   expressed protein   chr1:10422316-10424312 FORWARD   Aliases: F1N18.18, F1N18_18	6.4	6.6	-0.3	-0.6	100.0%	-4.5
10775	AT2G42900.1   expressed protein   chr2:17861676-17862506 FORWARD   Aliases: F23E6.13	3.0	2.9	0.1	0.6	100.0%	-5.4
10776	AT5G20280.1   sucrose-phosphate synthase, putative, similar to sucrose-phosphate synthase (EC 2.4.1.14) isoform 1 - Citrus unshiu, EMBL:AB005023   chr5:6844716-6850065 REVERSE   Aliases: F5O24.170, F5O24_170	9.4	8.8	0.6	0.6	100.0%	-4.3
10777	AT5G24310.2   expressed protein, strong similarity to unknown protein (emb:CAB66408.1)	8.5	8.2	0.2	0.6	100.0%	-4.7
10778	AT3G27000.1   Symbol: ARP2   actin-related protein 2 (ARP2), nearly identical to actin-related protein 2 (ARP2) (Arabidopsis thaliana) GI:3818624; contains Pfam profile PF00022: Actin   chr3:9953800-9957178 REVERSE   Aliases: ACTIN RELATED PROTEIN 2, ATARP2, MOJ10.14, WRM, WURM	4.7	4.9	-0.2	-0.6	100.0%	-4.6
10779	AT1G65850.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:24498397-24502148 FORWARD   Aliases: F12P19.1, F12P19_1	2.4	2.5	-0.1	-0.6	100.0%	-5.2
10780	AT2G22570.2   isochorismatase hydrolase family protein, contains Pfam profile PF00857: isochorismatase family protein   chr2:9596629-9597937 REVERSE   Aliases: F14M13.1	5.4	5.3	0.2	0.6	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10781	AT3G07900.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr3:2520780-2523114 FORWARD   Aliases: F17A17.24	3.7	3.5	0.3	0.6	100.0%	-4.1
10782	AT2G03890.2   phosphatidylinositol 3- and 4-kinase family protein, low similarity to phosphatidylinositol 4-kinase type-II beta (Homo sapiens) GI:20159767; contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase   chr2:1185522-1188542 FORWARD   Aliases: T18C20.9, T18C20_9	6.9	6.3	0.6	0.6	100.0%	-4.3
10783	AT4G00850.1   Symbol: GIF3   SSXT family protein, low similarity to synovial sarcoma associated SS18-delta (Mus musculus) GI:17978535; contains Pfam profile PF05030: SSXT protein (N-terminal region)   chr4:357568-359194 FORWARD   Aliases: A_TM018A10.22, A_TM018A10_22, GRF1 INTERACTING FACTOR 3, T18A10.15, T18A10_15	3.4	3.5	-0.1	-0.6	100.0%	-4.8
10784	AT1G20970.1   adhesin-related, contains TIGRFAM TIGR01612: reticulocyte binding protein; contains TIGRFAM TIGR00864: polycystin cation channel protein; similar to fimbriae-associated protein Fap1 (Streptococcus parasanguinis) (GI:3929312)	4.0	4.2	-0.2	-0.6	100.0%	-5.0
10785	AT1G12660.1   expressed protein   chr1:4308941-4311499 FORWARD   Aliases: T12C24.19, T12C24_19	2.8	2.7	0.1	0.6	100.0%	-5.4
10786	AT3G57460.1   expressed protein, weak similarity to SP:O43847 Nardilysin precursor (EC 3.4.24.61) (N-arginine dibasic convertase) {Homo sapiens}   chr3:21274063-21276774 REVERSE   Aliases: T8H10.60	3.9	4.0	-0.1	-0.6	100.0%	-5.1
10787	AT5G56800.1   expressed protein   chr5:22990215-22991434 FORWARD   Aliases: MIK19.27, MIK19_27	2.5	2.6	-0.1	-0.6	100.0%	-5.3
10788	AT2G30910.2   Symbol: ARPC1A	6.6	6.8	-0.2	-0.6	100.0%	-4.4
10789	AT2G31300.1   Symbol: ARPC1b	6.6	6.8	-0.2	-0.6	100.0%	-4.4
10790	AT4G36860.2   LIM domain-containing protein, low similarity to LIM-domain protein (Branchiostoma floridae) GI:3360516, DRAL/Slim3/FHL2 (Homo sapiens) GI:7209525; contains Pfam profile PF00412: LIM domain   chr4:17358376-17361872 REVERSE   Aliases: AP22.33, AP22_33	5.8	6.0	-0.2	-0.6	100.0%	-4.5
10791	AT1G64620.1   Dof-type zinc finger domain-containing protein, similar to Dof zinc finger protein GB:CAA08755 GI:3341468 from (Nicotiana tabacum)   chr1:24010655-24012357 FORWARD   Aliases: F1N19.19, F1N19_19	5.3	5.1	0.1	0.6	100.0%	-4.8
10792	AT3G18790.1   expressed protein   chr3:6477705-6479554 FORWARD   Aliases: MVE11.17	5.9	6.2	-0.3	-0.6	100.0%	-4.7
10793	AT1G35250.1   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein   chr1:12932923-12934457 REVERSE   Aliases: T9I1.4, T9I1_4	3.4	3.6	-0.2	-0.6	100.0%	-4.8
10794	AT3G28750.1   expressed protein   chr3:10792828-10794081 REVERSE   Aliases: T19N8.4	2.6	2.7	-0.1	-0.6	100.0%	-5.1
10795	AT2G27610.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:11791004-11793610 REVERSE   Aliases: F15K20.29, F15K20_29	2.8	2.9	-0.1	-0.6	100.0%	-5.3
10796	AT3G25200.1   hypothetical protein   chr3:9178169-9179505 FORWARD   Aliases: MJL12.15	2.2	2.2	0.1	0.6	100.0%	-5.6
10797	AT1G63320.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23492549-23493195 REVERSE   Aliases: F9N12.6, F9N12_6	2.5	2.4	0.1	0.6	100.0%	-5.6
10798	AT2G40940.1   Symbol: ERS1   ethylene response sensor / ethylene-responsive sensor (ERS), identical to ethylene response sensor (ERS) (Arabidopsis thaliana) GI:1046225   chr2:17091434-17094367 REVERSE   Aliases: ERS, ETHYLENE RESPONSE SENSOR 1, T20B5.14, T20B5_14	6.2	6.5	-0.3	-0.6	100.0%	-4.3
10799	AT5G49540.1   expressed protein, contains Pfam profile PF05646: Protein of unknown function (DUF786)   chr5:20121810-20123334 REVERSE   Aliases: K6M13.9, K6M13_9	9.8	10.0	-0.1	-0.6	100.0%	-4.8
10800	AT4G12970.1   expressed protein   chr4:7586140-7586827 REVERSE   Aliases: F25G13.60, F25G13_60	3.1	3.2	-0.1	-0.6	100.0%	-5.9
10801	AT1G74520.1   Symbol: ATHVA22A   ABA-responsive protein (HVA22a), identical to AthVA22a (Arabidopsis thaliana) GI:4884932   chr1:28011635-28012870 REVERSE   Aliases: ATHVA22A, F1M20.20, F1M20_20	6.6	6.2	0.4	0.6	100.0%	-4.6
10802	AT4G36440.1   expressed protein   chr4:17206861-17210010 REVERSE   Aliases: AP22.38, AP22_38	6.5	6.3	0.2	0.6	100.0%	-4.9
10803	AT3G54190.1   expressed protein, GTP-binding regulatory protein beta chain, Dictyostelium discoideum, PIR:A47370   chr3:20072506-20075132 REVERSE   Aliases: F24B22.150	4.4	4.7	-0.3	-0.6	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10804	AT5G63020.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.7	2.9	-0.2	-0.6	100.0%	-5.1
10805	AT3G47836.1   expressed protein   chr3:17661246-17662750 REVERSE   Aliases: None	11.5	11.4	0.2	0.6	100.0%	-4.9
10806	AT5G13970.1   expressed protein   chr5:4506234-4507807 REVERSE   Aliases: MAC12.6, MAC12_6	7.5	7.7	-0.2	-0.6	100.0%	-4.9
10807	AT5G45560.1   pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein, weak similarity to SP:P79245 Steroidogenic acute regulatory protein, mitochondrial precursor (StAR) {Ovis aries}; contains Pfam profiles PF01852: START domain, PF00169: PH domain   chr5:18482582-18488153 FORWARD   Aliases: MFC19.23, MFC19_23	4.7	4.9	-0.1	-0.6	100.0%	-4.9
10808	AT3G45990.1   actin-depolymerizing factor, putative, similar to SP:Q9ZSK3 Actin-depolymerizing factor 4 (ADF-4) (AtADF4) {Arabidopsis thaliana}; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein	3.0	2.9	0.1	0.6	100.0%	-5.0
10809	AT1G23360.3   UbiE/COQ5 methyltransferase family protein, similar to 2-hexaprenyl-1,4-naphthoquinone methyltransferase GB:BAA25267 GI:2982680 from (Micrococcus luteus); contains Pfam profile PF01209: methyltransferase, UbiE/COQ5 family   chr1:8295174-8296912 REVERSE   Aliases: F26F24.24, F26F24_24	7.7	7.4	0.3	0.6	100.0%	-4.4
10810	AT2G36740.1   similar to stress responsive gene 6, Srg6 [Hordeum vulgare subsp. vulgare] (GB:CAC20595.1); similar to putative stress responsive gene 6 protein, Srg6 [Oryza sativa (japonica cultivar-group)] (GB:XP_480488.1); contains InterPro domain YL1 nuclear (InterPro:IPR008895); contains InterPro domain Bipartite nuclear localization signal (InterPro:IPR001472)	5.3	5.5	-0.2	-0.6	100.0%	-4.7
10811	AT1G07730.2   disease resistance-responsive family protein, contains Pfam PF03018: Plant disease resistance response protein   chr1:2397524-2398693 REVERSE   Aliases: None	4.5	4.9	-0.4	-0.6	100.0%	-4.0
10812	AT1G53030.1   cytochrome c oxidase copper chaperone family protein, contains Pfam domain, PF05051: Cytochrome C oxidase copper chaperone (COX17)   chr1:19763721-19765110 REVERSE   Aliases: F8L10.24, F8L10_24	6.4	6.1	0.3	0.6	100.0%	-4.5
10813	AT2G28310.2   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr2:12092516-12095126 FORWARD   Aliases: T1B3.17	5.9	6.2	-0.3	-0.6	100.0%	-4.8
10814	AT1G04990.2   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:1419140-1421638 REVERSE   Aliases: F13M7.1, F13M7_1	3.3	3.4	-0.1	-0.6	100.0%	-5.2
10815	AT1G64880.1   ribosomal protein S5 family protein, contains similarity to 30S ribosomal protein S5 GI:6969105 from (Campylobacter jejuni)   chr1:24109305-24112809 FORWARD   Aliases: F13O11.18, F13O11_18	9.0	9.3	-0.3	-0.6	100.0%	-4.5
10816	AT1G54080.2   oligouridylate-binding protein, putative, similar to oligouridylate binding protein GI:6996560 from (Nicotiana plumbaginifolia)   chr1:20187249-20190577 REVERSE   Aliases: F15I1.16, F15I1_16	7.9	7.3	0.6	0.6	100.0%	-4.5
10817	AT3G48350.1   cysteine proteinase, putative, similar to cysteine endopeptidase precursor (Ricin communis) GI:2944446; contains Pfam profile PF00112: Papain family cysteine protease	3.0	3.1	-0.2	-0.6	100.0%	-4.9
10818	AT1G69610.1   expressed protein   chr1:26190617-26193152 FORWARD   Aliases: F24J1.24	3.2	3.3	-0.1	-0.6	100.0%	-5.1
10819	AT1G69630.1   F-box family protein, contains F-box domain Pfam:PF00646	3.0	2.9	0.1	0.6	100.0%	-5.3
10820	AT2G29470.1   Symbol: ATGSTU3   glutathione S-transferase, putative, similar to glutathione S-transferase (Euphorbia esula) gb:AAF64450.1 GI:7595790   chr2:12635618-12636620 REVERSE   Aliases: F16P2.15, F16P2_15, GLUTATHIONE S TRANSFERASE 21, GST21	3.0	2.9	0.1	0.6	100.0%	-5.2
10821	AT2G13690.1   PRLI-interacting factor, putative, similar to PRLI-interacting factor G (Arabidopsis thaliana) GI:11139264 (PMID:9765207); supporting cDNA gi:26450291:dbj:AK117606.1:   chr2:5713589-5716039 REVERSE   Aliases: T10F5.21	7.0	7.3	-0.3	-0.6	100.0%	-4.8
10822	AT3G26050.1   expressed protein   chr3:9523019-9525789 FORWARD   Aliases: MPE11.22	3.1	3.2	-0.2	-0.6	100.0%	-5.0
10823	AT1G66520.1   Symbol: PDE194	3.3	3.5	-0.2	-0.6	100.0%	-4.7
10824	AT1G64450.1   proline-rich family protein, contains proline rich extensins, INTERPRO:IPR0002965   chr1:23945261-23946509 REVERSE   Aliases: F15H21.17	4.5	4.7	-0.2	-0.6	100.0%	-4.7
10825	AT5G06360.1   ribosomal protein S8e family protein, contains Pfam profile PF01201: Ribosomal protein S8e   chr5:1944772-1946725 FORWARD   Aliases: MHF15.12, MHF15_12	9.0	9.4	-0.4	-0.6	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10826	AT4G20960.1   cytidine/deoxycytidylate deaminase family protein, similar to SP:P25539 Riboflavin biosynthesis protein ribD (Includes: Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) (Riboflavin-specific deaminase); 5-amino-6-(5- phosphoribosylamino)uracil reductase (EC 1.1.1.193) (HTP reductase)) {Escherichia coli}; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region   chr4:11211957-11213651 FORWARD   Aliases: T13K14.120, T13K14_120	4.5	4.7	-0.1	-0.6	100.0%	-4.8
10827	AT1G08200.1   Symbol: AXS2   expressed protein   chr1:2573857-2576709 REVERSE   Aliases: T23G18.6, T23G18_6, UDP D APIOSE/UDP D XYLOSE SYNTHASE 2	10.2	10.5	-0.3	-0.6	100.0%	-4.9
10828	AT2G27860.1   Symbol: AXS1   expressed protein   chr2:11871470-11873975 REVERSE   Aliases: F15K20.4, F15K20_4, UDP D APIOSE/UDP D XYLOSE SYNTHASE 1	10.2	10.5	-0.3	-0.6	100.0%	-4.9
10829	AT2G39500.1   expressed protein   chr2:16496151-16496666 FORWARD   Aliases: F12L6.16, F12L6_16	6.7	6.9	-0.2	-0.6	100.0%	-4.4
10830	AT1G08570.1   thioredoxin family protein, contains Pfam profile: PF00085 Thioredoxin; similar to ESTs gb:T46281, gb:R83933, gb:N65879, emb:F14466, gb:N96726, gb:AA042340, and emb:Z18150   chr1:2712930-2714737 FORWARD   Aliases: F22O13.5, F22O13_5	4.6	4.3	0.3	0.6	100.0%	-4.8
10831	AT5G48175.1   expressed protein, contains weak similarity to thioglucoside glucohydrolase (GI:5524767) (Arabidopsis thaliana)   chr5:19556422-19557007 FORWARD   Aliases: None	2.9	3.1	-0.2	-0.6	100.0%	-4.9
10832	AT1G17360.1   COP1-interacting protein-related, similar to COP1-Interacting Protein 7 (CIP7) (GI:3327870) (Arabidopsis thaliana)   chr1:5947434-5951210 FORWARD   Aliases: F28G4.18, F28G4_18	6.5	6.7	-0.2	-0.6	100.0%	-4.7
10833	AT2G40840.1   glycoside hydrolase family 77 protein, contains Pfam profiles PF02446: 4-alpha-glucanotransferase, PF00686: Starch binding domain; contains a non-consensus AT-AC intron between at intron 5   chr2:17052041-17058025 FORWARD   Aliases: T20B5.4, T20B5_4	8.3	8.6	-0.2	-0.6	100.0%	-4.7
10834	AT3G19370.1   expressed protein   chr3:6710797-6713656 FORWARD   Aliases: MLD14.10	6.2	6.5	-0.4	-0.6	100.0%	-4.5
10835	AT5G15210.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, various predicted proteins, Arabidopsis thaliana   chr5:4937582-4939010 REVERSE   Aliases: F8M21.100, F8M21_100	4.6	4.4	0.2	0.6	100.0%	-4.5
10836	AT5G57670.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:23377626-23379690 REVERSE   Aliases: MRI1.2, MRI1_2	2.1	2.1	0.1	0.6	100.0%	-5.6
10837	AT5G50200.3   Symbol: WR3   expressed protein, similar to unknown protein (pir::T05562) isoform contains a non-consensus AT acceptor splice site at intron 1   chr5:20453406-20454952 FORWARD   Aliases: K6A12.6, K6A12_6	8.0	8.3	-0.3	-0.6	100.0%	-4.8
10838	AT3G52120.1   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / D111/G-patch domain-containing protein, contains Pfam profiles PF01585: G-patch domain, PF01805: Surp module	4.0	3.8	0.1	0.6	100.0%	-4.8
10839	AT3G47080.1   expressed protein   chr3:17349091-17351363 REVERSE   Aliases: F13I12.130	4.7	4.5	0.2	0.6	100.0%	-4.8
10840	AT2G24930.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr2:10611053-10615109 REVERSE   Aliases: F27C12.15, F27C12_15	2.7	2.6	0.1	0.6	100.0%	-5.6
10841	AT3G30720.1   expressed protein   chr3:12351626-12352205 FORWARD   Aliases: F21A17.18	3.5	3.2	0.3	0.6	100.0%	-4.4
10842	AT3G56070.1   Symbol: ROC2   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to peptidyl-prolyl cis-trans isomerase, PPIase (cyclophilin, cyclosporin A-binding protein) (Catharanthus roseus) SWISS-PROT:Q39613   chr3:20817728-20819071 REVERSE   Aliases: F18O21.30, ROTAMASE CYCLOPHILIN 2, ROTAMASE CYP 2	7.3	7.6	-0.3	-0.6	100.0%	-4.4
10843	AT5G61910.3   expressed protein   chr5:24877104-24881330 REVERSE   Aliases: K22G18.3, K22G18_3	2.4	2.3	0.1	0.6	100.0%	-5.5
10844	AT1G18130.1   tRNA synthetase-related / tRNA ligase-related, similar to SP:O04630 Threonyl-tRNA synthetase, mitochondrial precursor (EC 6.1.1.3) (Threonine--tRNA ligase) (ThrRS) {Arabidopsis thaliana}; contains Pfam profile PF03129: Anticodon binding domain   chr1:6235888-6238792 FORWARD   Aliases: T10F20.13	2.7	2.8	-0.1	-0.6	100.0%	-5.4
10845	AT5G37840.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr5:15079238-15080557 REVERSE   Aliases: K22F20.80, K22F20_80	2.8	2.9	-0.1	-0.6	100.0%	-5.2
10846	AT4G04490.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:2231955-2234636 REVERSE   Aliases: T26N6.10, T26N6_10	2.6	2.5	0.1	0.6	100.0%	-5.6
10847	AT1G72640.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g31530.1); similar to putative nucleotide-diphosphate-sugar epimerase [Streptomyces antibioticus] (GB:CAG14959.1)   chr1:27349923-27351821 REVERSE   Aliases: F28P22.17, F28P22_17	3.6	3.5	0.2	0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10848	AT5G05850.1   leucine-rich repeat family protein, contains Pfam PF00560: Leucine Rich Repeat domains; similar to (SP:Q9UQ13) Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8) (SP:Q9UQ13) {Homo sapiens}   chr5:1762415-1764679 REVERSE   Aliases: MJJ3.27, MJJ3_27	3.5	3.6	-0.1	-0.6	100.0%	-4.9
10849	AT2G05290.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:1924847-1926678 REVERSE   Aliases: F5G3.19, F5G3_19	2.5	2.6	-0.1	-0.6	100.0%	-5.3
10850	AT1G63820.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g41380.1); similar to 'unknown protein, contains CCT motif, PF06203' [Oryza sativa (japonica cultivar-group)] (GB:XP_475389.1)   chr1:23686085-23688030 REVERSE   Aliases: T12P18.16, T12P18_16	3.4	3.3	0.2	0.6	100.0%	-4.8
10851	AT2G39300.1   expressed protein, ; expression supported by MPSS   chr2:16417187-16419947 REVERSE   Aliases: T16B24.6, T16B24_6	4.5	4.4	0.1	0.6	100.0%	-5.0
10852	AT1G62960.1   Symbol: ACS10   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to GI:1173638 (GB:U35779) from (Triticum aestivum) (Plant Mol. Biol. 31 (5), 1009-1020 (1996)), GI:1813331 from Vigna radiata   chr1:23321852-23323981 REVERSE   Aliases: ACC SYNTHASE 10, F16P17.11, F16P17_11	6.7	6.5	0.1	0.6	100.0%	-4.8
10853	AT4G10000.2   expressed protein   chr4:6260320-6263178 REVERSE   Aliases: T5L19.130, T5L19_130	3.6	3.4	0.1	0.6	100.0%	-5.0
10854	AT5G22470.1   similar to poly (ADP-ribose) polymerase, putative / NAD(+) ADP-ribosyltransferase, putative / poly(ADP-ribose) synthetase, putative [Arabidopsis thaliana] (TAIR:At2g31320.1); similar to putative seed maturation protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466090.1); contains InterPro domain WGR (InterPro:IPR008893); contains InterPro domain Poly(ADP-ribose) polymerase, catalytic region (InterPro:IPR001290); contains InterPro domain BRCT (InterPro:IPR001357)	3.8	3.7	0.1	0.6	100.0%	-4.9
10855	AT1G28580.2   GDSL-motif lipase, putative, similar to lipase (Arabidopsis thaliana) GI:1145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr1:10044323-10046413 REVERSE   Aliases: F1K23.18, F1K23_18	8.8	9.0	-0.2	-0.6	100.0%	-5.0
10856	AT3G24850.1   hypothetical protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)	3.5	3.3	0.2	0.6	100.0%	-5.0
10857	AT2G31120.1   expressed protein   chr2:13268210-13269148 REVERSE   Aliases: T16B12.7, T16B12_7	3.3	3.1	0.2	0.6	100.0%	-4.7
10858	AT2G37940.1   expressed protein   chr2:15883878-15886733 FORWARD   Aliases: T8P21.15, T8P21_15	5.7	5.6	0.2	0.6	100.0%	-4.9
10859	AT2G41790.1   peptidase M16 family protein / insulinase family protein, contains Pfam domain, PF05193: Peptidase M16 inactive domain; similar to insulin-degrading enzyme (Insulysin, Insulinase, Insulin protease) (Mouse) SWISS-PROT:Q9JHR7   chr2:17436372-17443188 REVERSE   Aliases: T11A7.11, T11A7_11	6.4	6.6	-0.2	-0.6	100.0%	-4.5
10860	AT3G30820.1   hypothetical protein   chr3:12532322-12533714 FORWARD   Aliases: K11J14.16	2.2	2.1	0.1	0.6	100.0%	-5.3
10861	AT5G23300.1   Symbol: PYRD   dihydroorotate dehydrogenase, mitochondrial / dihydroorotate oxidase / DHodehase (PYRD), nearly identical to SP:P32746 Dihydroorotate dehydrogenase, mitochondrial precursor (EC 1.3.3.1) (Dihydroorotate oxidase) (DHodehase) {Arabidopsis thaliana}; identical to cDNA pyrD mRNA for dihydroorotate dehydrogenase GI:16448   chr5:7847593-7850407 REVERSE   Aliases: DIHYDROOROTATE DEHYDROGENASE, MKD15.16, MKD15_16	6.3	6.6	-0.3	-0.6	100.0%	-4.3
10862	AT5G35460.1   expressed protein   chr5:13689769-13691969 FORWARD   Aliases: MOK9.4, MOK9_4	7.4	7.0	0.4	0.6	100.0%	-4.6
10863	AT5G61930.1   Symbol: APO3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g64810.1); similar to OSJNBa0008M17.9 [Oryza sativa (japonica cultivar-group)] (GB:XP_473885.1); contains InterPro domain Arabidopsis thaliana protein of unknown function DUF794 (InterPro:IPR008512)   chr5:24883301-24885047 REVERSE   Aliases: ACCUMULATION OF PHOTOSYSTEM ONE 3, K22G18.5, K22G18_5	7.1	6.9	0.2	0.6	100.0%	-4.4
10864	AT5G08500.1   transmembrane CLPTM1 family protein, contains Pfam profile PF05602: Cleft lip and palate transmembrane protein 1 (CLPTM1)   chr5:2748218-2751772 FORWARD   Aliases: F8L15.19	7.0	6.9	0.1	0.6	100.0%	-4.9
10865	AT5G35570.1   expressed protein, similar to axi 1 (Nicotiana tabacum) GI:559921; contains Pfam profile PF03138: Plant protein family   chr5:13766941-13770688 REVERSE   Aliases: K2K18.1, K2K18_1	3.0	3.2	-0.2	-0.6	100.0%	-4.9
10866	AT1G07460.1   legume lectin family protein, contains Legume lectins beta-chain signature, PROSITE:PS00307   chr1:2290198-2290974 FORWARD   Aliases: F22G5.19, F22G5_19	2.3	2.3	-0.1	-0.6	100.0%	-5.7
10867	AT2G18970.1   expressed protein   chr2:8236198-8236837 FORWARD   Aliases: F19F24.17, F19F24_17	3.3	3.5	-0.2	-0.6	100.0%	-4.9
10868	AT4G18260.1   cytochrome B561-related, related to cytochrome b-561 (GI:20345443) (Mus musculus); multidrug resistance protein, Homo sapiens, PIR2:S71841   chr4:10093535-10097514 REVERSE   Aliases: T9A21.110, T9A21_110	5.1	5.0	0.2	0.6	100.0%	-4.6
10869	AT3G23650.1   protein kinase-related, contains similarity to protein kinases   chr3:8510696-8511203 REVERSE   Aliases: MDB19.15	3.2	3.1	0.1	0.6	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10870	AT2G46780.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:19236398-19238574 FORWARD   Aliases: F19D11.6	2.9	2.9	-0.1	-0.6	100.0%	-5.3
10871	AT3G60640.1   autophagy 8g (APG8g), identical to autophagy 8g (Arabidopsis thaliana) GI:19912163; contains Pfam profile PF02991: Microtubule associated protein 1A/1B, light chain 3; supporting cDNA gi:19912162:dbj:AB073181.1:   chr3:22426816-22428133 FORWARD   Aliases: T4C21.50	8.3	8.1	0.2	0.6	100.0%	-4.4
10872	AT4G03600.1   expressed protein   chr4:1603700-1604506 REVERSE   Aliases: T5L23.9, T5L23_9	4.6	4.5	0.1	0.6	100.0%	-5.2
10873	AT3G04090.1   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr3:1072099-1074102 REVERSE   Aliases: T6K12.29, T6K12_29	8.5	8.2	0.3	0.6	100.0%	-5.0
10874	AT1G53620.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g53610.1); similar to hypothetical protein [Neurospora crassa] (GB:XP_330065.1); similar to Hypothetical protein E02A10.2 [Caenorhabditis elegans] (GB:CAB02877.1); similar to ORF; able to induce HR-like lesions [Nicotiana tabacum] (GB:AAC49971.1); contains domain GLY_RICH (PS50315)   chr1:20015097-20015593 REVERSE   Aliases: F22G10.5	4.4	4.6	-0.2	-0.6	100.0%	-4.5
10875	AT5G59450.1   scarecrow-like transcription factor 11 (SCL11), scarecrow-like 11, Arabidopsis thaliana, EMBL:AF036307   chr5:23991894-23994017 FORWARD   Aliases: F2O15.5, F2O15_5	4.1	4.0	0.1	0.6	100.0%	-4.8
10876	AT1G72110.1   expressed protein   chr1:27132726-27135060 REVERSE   Aliases: F28P5.3, F28P5_3	2.7	2.8	-0.1	-0.6	100.0%	-5.2
10877	AT3G55780.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097948 from (Oryza sativa)   chr3:20716606-20718000 FORWARD   Aliases: F1I16.190	3.4	3.6	-0.1	-0.6	100.0%	-5.0
10878	AT1G67210.2   proline-rich spliceosome-associated (PSP) family protein / zinc knuckle (CCHC-type) family protein, contains Pfam domains PF00098: Zinc knuckle, PF04046: PSP   chr1:25144563-25147673 FORWARD   Aliases: F5A8.15	3.0	3.2	-0.2	-0.6	100.0%	-5.0
10879	AT5G22450.1   expressed protein   chr5:7437148-7442937 REVERSE   Aliases: MWD9.25, MWD9_25	7.3	7.8	-0.5	-0.6	100.0%	-4.6
10880	AT3G32910.1   expressed protein, similar to At2g15200, At2g04970, At1g32830, At2g14140, At4g03990   chr3:13467801-13469328 FORWARD   Aliases: T7B9.16	2.0	2.1	-0.0	-0.6	100.0%	-6.1
10881	AT3G51470.1   protein phosphatase 2C, putative / PP2C, putative, protein phosphatase-2C, Mesembryanthemum crystallinum, EMBL:AF075580   chr3:19108766-19110254 REVERSE   Aliases: F26O13.110	3.2	3.3	-0.1	-0.6	100.0%	-5.0
10882	AT1G04030.1   expressed protein   chr1:1040517-1042891 FORWARD   Aliases: F21M11.3, F21M11_3	3.2	3.1	0.1	0.6	100.0%	-5.0
10883	AT5G18820.1   Symbol: EMB3007   chaperonin, putative, similar to SWISS-PROT:P08926- RuBisCO subunit binding-protein alpha subunit, chloroplast precursor (60 kDa chaperonin alpha subunit, CPN-60 alpha)(Pisum sativum); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr5:6271551-6274155 FORWARD   Aliases: EMB3007, EMBRYO DEFECTIVE 3007, F17K4.70, F17K4_70	3.3	3.4	-0.1	-0.6	100.0%	-4.9
10884	AT5G56230.1   prenylated rab acceptor (PRA1) family protein, contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr5:22775994-22776597 REVERSE   Aliases: K24C1.4, K24C1_4	4.3	4.1	0.2	0.6	100.0%	-4.6
10885	AT1G80130.1   expressed protein   chr1:30145855-30147538 REVERSE   Aliases: F18B13.21, F18B13_21	3.9	3.8	0.1	0.6	100.0%	-5.2
10886	AT4G40060.1   Symbol: ATHB16	5.0	4.8	0.2	0.6	100.0%	-4.4
10887	AT5G53170.1   Symbol: FTSH11	6.7	7.1	-0.4	-0.6	100.0%	-4.3
10888	AT3G51130.1   expressed protein, contains Pfam PF03676: Uncharacterised protein family (UPF0183)   chr3:19005120-19008568 FORWARD   Aliases: F24M12.170	7.3	7.0	0.3	0.6	100.0%	-5.0
10889	AT1G13270.2   Symbol: MAP1C   metalloproteinase M24 family protein, similar to SP:Q01662 Methionine aminopeptidase 1 precursor (EC 3.4.11.18) {Saccharomyces cerevisiae}; contains Pfam profile PF00557: metalloproteinase family M24   chr1:4544953-4547295 FORWARD   Aliases: MAP1B, METHIONINE AMINOPEPTIDASE 1B	8.2	8.5	-0.3	-0.6	100.0%	-4.2
10890	AT1G17145.1   expressed protein   chr1:5860112-5862672 REVERSE   Aliases: None	6.7	6.5	0.2	0.6	100.0%	-4.8
10891	AT4G19940.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain; similar to F-box protein Fbx8 (GI:6164735) (Homo sapiens):8737673:gb:AV566223.1:AV566223	3.3	3.5	-0.1	-0.6	100.0%	-5.3
10892	AT3G30845.1   hypothetical protein   chr3:12626916-12627233 REVERSE   Aliases: MJJ16.6	2.9	2.8	0.1	0.6	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10893	NA	11.3	11.7	-0.4	-0.6	100.0%	-5.0
10894	AT3G07920.1   eukaryotic translation initiation factor 2 subunit 2, putative / eIF-2-beta, putative, similar to SP:P41035 Eukaryotic translation initiation factor 2 subunit (eIF-2-beta) {Oryctolagus cuniculus}; contains Pfam profile PF01873: Domain found in IF2B/IF5   chr3:2525180-2526235 REVERSE   Aliases: F17A17.26	3.4	3.3	0.1	0.6	100.0%	-5.2
10895	AT5G14410.1   expressed protein   chr5:4646790-4647447 REVERSE   Aliases: F18O22.200, F18O22_200	2.7	2.9	-0.1	-0.6	100.0%	-5.1
10896	AT1G67660.1   expressed protein   chr1:25367198-25368892 FORWARD   Aliases: F12A21.19, F12A21_19	5.0	5.2	-0.2	-0.6	100.0%	-4.6
10897	AT3G10590.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain   chr3:3310429-3311316 REVERSE   Aliases: F13M14.12	2.6	2.5	0.1	0.6	100.0%	-5.5
10898	AT5G48280.1   hypothetical protein   chr5:19584290-19584914 REVERSE   Aliases: MIF21.17, MIF21_17	3.0	3.1	-0.1	-0.6	100.0%	-5.5
10899	AT5G67310.1   Symbol: CYP81G1   cytochrome P450 family protein   chr5:26871249-26874167 REVERSE   Aliases: K8K14.3, K8K14_3	3.6	3.8	-0.2	-0.6	100.0%	-5.0
10900	AT2G20700.1   expressed protein   chr2:8932029-8932813 REVERSE   Aliases: F5H14.33, F5H14_33	3.9	4.1	-0.2	-0.6	100.0%	-4.8
10901	AT1G66650.1   seven in absentia (SINA) protein, putative, similar to SIAH2 protein (Brassica napus var. napus) GI:7657878; contains Pfam profile PF03145: Seven in absentia protein family   chr1:24863776-24865484 REVERSE   Aliases: None	2.6	2.7	-0.1	-0.6	100.0%	-5.3
10902	AT4G09720.2   Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB7A from (Lotus japonicus)   chr4:6133293-6135180 FORWARD   Aliases: F17A8.70, F17A8_70	9.0	8.8	0.1	0.6	100.0%	-4.9
10903	AT5G51830.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr5:21086811-21088961 FORWARD   Aliases: MIO24.3, MIO24_3	5.4	5.7	-0.3	-0.6	100.0%	-4.3
10904	AT5G08335.1   isoprenylcysteine carboxyl methyltransferase family protein / ICMT family protein, similar to SP:O60725 Protein-S isoprenylcysteine O-methyltransferase (EC 2.1.1.100) (Isoprenylcysteine carboxylmethyltransferase) {Homo sapiens}; contains Pfam profile PF04140: Isoprenylcysteine carboxyl methyltransferase (ICMT) family   chr5:2682230-2683713 FORWARD   Aliases: None	5.2	5.1	0.1	0.6	100.0%	-5.0
10905	AT4G14710.2   similar to iron-deficiency-responsive protein, putative [Arabidopsis thaliana] (TAIR:At4g14716.1); similar to submergence induced protein 2A [Oryza sativa] (GB:AAC19375.1); contains InterPro domain Acireductone dioxygenase, ARD (InterPro:IPR004313); contains InterPro domain Cupin domain (InterPro:IPR007113)   chr4:8424675-8426550 REVERSE   Aliases: DL3395C, FCAALL.141	11.7	11.2	0.5	0.6	100.0%	-4.4
10906	AT4G14716.1   iron-deficiency-responsive protein, putative, strong similarity to iron-deficiency induced gene (Hordeum vulgare) GI:14522834; contains Pfam profile PF03079: ARD/ARD' family   chr4:8430202-8431940 REVERSE   Aliases: None	11.7	11.2	0.5	0.6	100.0%	-4.4
10907	AT4G18730.1   Symbol: RPL16B	10.0	10.3	-0.3	-0.6	100.0%	-4.5
10908	AT5G45775.2   60S ribosomal protein L11 (RPL11D)   chr5:18582292-18583785 REVERSE   Aliases: None	10.0	10.3	-0.3	-0.6	100.0%	-4.5
10909	AT2G29880.1   expressed protein   chr2:12749613-12750622 FORWARD   Aliases: T27A16.36	3.1	3.2	-0.1	-0.6	100.0%	-5.2
10910	AT3G07568.1   expressed protein   chr3:2416249-2417796 REVERSE   Aliases: None	10.4	10.7	-0.3	-0.6	100.0%	-4.4
10911	AT1G51810.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase GI:1321686 from (Arabidopsis thaliana); contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19230788-19236028 REVERSE   Aliases: T14L22.2, T14L22_2	2.5	2.4	0.1	0.6	100.0%	-5.7
10912	AT2G26760.1   Symbol: CYCB1;4   cyclin, putative, similar to CYCB1-1 protein (Petunia x hybrida) GI:6093215, B-type cyclin (Nicotiana tabacum) GI:849074; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr2:11408407-11410505 FORWARD   Aliases: CYC3, CYCB1;4, CYCLIN 3, CYCLIN B1;4, F18A8.13, F18A8_13	3.3	3.0	0.3	0.6	100.0%	-4.5
10913	AT2G02970.1   nucleoside phosphatase family protein / GDA1/CD39 family protein, low similarity to SP:P55772 Ectonucleoside triphosphate diphosphohydrolase 1 (EC 3.6.1.5) (Ecto-apyrase) {Mus musculus}; contains Pfam profile PF01150: GDA1/CD39 (nucleoside phosphatase) family   chr2:865069-868288 REVERSE   Aliases: T17M13.14, T17M13_14	4.1	3.8	0.3	0.6	100.0%	-4.8
10914	AT1G78060.1   glycosyl hydrolase family 3 protein, similar to xylosidase GI:2102655 from (Aspergillus niger)   chr1:29354573-29357818 REVERSE   Aliases: F28K19.27, F28K19_27	7.1	7.6	-0.5	-0.6	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10915	AT3G23000.1   Symbol: CIPK7   CBL-interacting protein kinase 7 (CIPK7), identical to CBL-interacting protein kinase 7 (Arabidopsis thaliana) gi:13249113;gb:AAK16682; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 7 (CIPK7) GI:13249112   chr3:8172604-8174138 FORWARD   Aliases: ATSR2, ATSRPK1, CBL INTERACTING PROTEIN KINASE 7, MXC7.3, PKS7	7.6	7.9	-0.4	-0.6	100.0%	-4.6
10916	AT4G00420.2   double-stranded RNA-binding domain (DsRBD)-containing protein, contains Pfam profile PF00035: Double-stranded RNA binding motif   chr4:181323-184329 REVERSE   Aliases: A_IG005I10.3, A_IG005I10_3, F5I10.3, F5I10_3	5.0	4.8	0.2	0.6	100.0%	-4.6
10917	AT1G14830.1   Symbol: ADL1C   dynamin-like protein C (DL1C), nearly identical to dynamin-like protein C (Arabidopsis thaliana) GI:19569772   chr1:5107416-5111665 REVERSE   Aliases: ADL1C, ADL5, DYNAMIN LIKE PROTEIN 5, F10B6.23, F10B6_23	8.4	8.8	-0.4	-0.6	100.0%	-4.5
10918	AT3G48760.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr3:18086817-18089276 FORWARD   Aliases: T21J18.30	6.8	6.5	0.3	0.6	100.0%	-4.6
10919	AT2G17620.1   Symbol: CYCB2;1   cyclin, putative (CYC2a), similar to cyclin 2b protein (Arabidopsis thaliana) GI:509423; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain; identical to cDNA cyc2a mRNA for cyclin 2a protein GI:728518   chr2:7671185-7673604 FORWARD   Aliases: CYCB2;1, Cyclin B2;1, T19E12.4, T19E12_4	4.0	4.2	-0.3	-0.6	100.0%	-4.6
10920	AT4G14590.1   Symbol: EMB2739   expressed protein   chr4:8374387-8375958 FORWARD   Aliases: DL3335W, EMB2739, EMBRYO DEFECTIVE 2739, FCAALL.260	4.1	4.2	-0.1	-0.6	100.0%	-5.1
10921	AT1G15580.1   Symbol: IAA5   auxin-responsive protein / indoleacetic acid-induced protein 5 (IAA5) / auxin-induced protein (AUX2-27), identical to SP:P33078 Auxin-responsive protein IAA5 (Indoleacetic acid-induced protein 5) (Auxin-induced protein AUX2-27) {Arabidopsis thaliana}   chr1:5365660-5366455 REVERSE   Aliases: ATAUX2 27, AUX2 27, T16N11.9, T16N11_9	3.0	3.1	-0.1	-0.6	100.0%	-5.0
10922	AT5G64600.1   expressed protein, similar to axi 1 (Nicotiana tabacum) GI:559921; contains Pfam profile PF03138: Plant protein family   chr5:25842393-25845580 FORWARD   Aliases: MUB3.12, MUB3_12	6.9	7.1	-0.2	-0.6	100.0%	-4.4
10923	AT1G29960.1   signal peptidase I family protein / MADS-box protein-related, similar to inner mitochondrial membrane peptidase 2 (Homo sapiens) GI:14030456; contains Pfam profiles PF00461: Signal peptidase I, contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain); MADS-box protein AGL64   chr1:10494797-10497271 FORWARD   Aliases: T1P2.16, T1P2_16	3.7	3.6	0.1	0.6	100.0%	-5.0
10924	AT1G24530.1   transducin family protein / WD-40 repeat family protein, similar to Vegetatible incompatibility protein HET-E-1 (SP:Q00808) {Podospora anserina}; contains 7 WD-40 repeats (PF00400)   chr1:8693214-8694692 FORWARD   Aliases: F21J9.19	5.5	5.3	0.2	0.6	100.0%	-4.6
10925	AT2G30130.1   Symbol: ASL5   LOB domain protein 12 / lateral organ boundaries domain protein 12 (LBD12), identical to SP:Q8LBW3 LOB domain protein 12 {Arabidopsis thaliana}   chr2:12875707-12876801 FORWARD   Aliases: LBD12, PCK1, T27E13.13, T27E13_13	2.0	2.0	0.0	0.6	100.0%	-5.9
10926	AT2G43630.1   expressed protein   chr2:18102854-18104565 FORWARD   Aliases: F18O19.26	8.5	8.8	-0.3	-0.6	100.0%	-5.0
10927	AT2G45210.1   auxin-responsive protein-related, weakly similar to small auxin up RNA (GI:546362) {Arabidopsis thaliana}   chr2:18648640-18649778 FORWARD   Aliases: F4L23.28	4.6	4.8	-0.2	-0.6	100.0%	-4.7
10928	AT1G68010.1   Symbol: HPR   glycerate dehydrogenase / NADH-dependent hydroxypyruvate reductase, identical to hydroxypyruvate reductase (HPR) GB:D85339 (Arabidopsis thaliana) (Plant Cell Physiol 1997 Apr;38(4):449-55)   chr1:25497016-25499651 FORWARD   Aliases: None	7.9	7.7	0.2	0.6	100.0%	-4.4
10929	AT3G11870.1   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:3747004-3749099 REVERSE   Aliases: F26K24.16	2.6	2.7	-0.1	-0.6	100.0%	-5.2
10930	AT2G18370.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to lipid-transfer protein (Nicotiana glauca) GI:6782436; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:7987711-7988826 FORWARD   Aliases: T30D6.12, T30D6_12	3.1	2.9	0.2	0.6	100.0%	-4.5
10931	AT1G76730.1   5-formyltetrahydrofolate cyclo-ligase family protein, contains Pfam profile PF01812 5-formyltetrahydrofolate cyclo-ligase   chr1:28807830-28809678 REVERSE   Aliases: F28O16.10, F28O16_10	7.0	6.7	0.3	0.6	100.0%	-4.2
10932	AT4G18020.3   Symbol: APRR2   pseudo-response regulator 2 (APRR2) (TOC2), identical to pseudo-response regulator 2 GI:7576356 from (Arabidopsis thaliana)   chr4:10003987-10007455 REVERSE   Aliases: PRR2, PSEUDO RESPONSE REGULATOR 2, T6K21.200, T6K21_200	3.3	3.3	0.1	0.6	100.0%	-5.4
10933	AT5G52210.2   Symbol: ATGB1   ADP-ribosylation factor, putative, similar to arf-related protein (ARP) (SP:Q63055){Rattus norvegicus}; contains Pfam domain PF00025: ADP-ribosylation factor family   chr5:21222304-21224324 FORWARD   Aliases: ATARLB1, F17P19.11, F17P19_11, GTP BINDING PROTEIN ATGB1	6.0	5.8	0.2	0.6	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10934	AT1G13640.1   phosphatidylinositol 3- and 4-kinase family protein, low similarity to phosphatidylinositol 4-kinase type-II beta (Homo sapiens) GI:20159767; contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase   chr1:4677024-4679801 REVERSE   Aliases: F21F23.8, F21F23_8	9.2	9.0	0.2	0.6	100.0%	-4.5
10935	AT1G61010.3   similar to metallo-beta-lactamase family protein [Arabidopsis thaliana] (TAIR:At2g01730.1); similar to Cleavage and Polyadenylation Specificity Factor protein [Bos taurus] (GB:CAA65151.1); similar to PREDICTED: similar to Cleavage and polyadenylation specificity factor 3 [Rattus norvegicus] (GB:XP_216667.3); similar to unknown [Homo sapiens] (GB:AAY14858.1); similar to Cleavage and polyadenylation specific factor 3, 73kDa [Homo sapiens] (GB:AAH11654.1); similar to cleavage and polyadenylation specificity factor 3 [Mus musculus] (GB:NP_061283.2); contains InterPro domain Beta-lactamase-like (InterPro:IPR001279)   chr1:22477966-22481384 REVERSE   Aliases: T7P1.15, T7P1_15	4.9	4.7	0.1	0.6	100.0%	-5.1
10936	AT2G41960.1   expressed protein   chr2:17521131-17526371 REVERSE   Aliases: T6D20.15, T6D20_15	5.1	5.2	-0.2	-0.6	100.0%	-4.7
10937	AT3G46180.1   UDP-galactose/UDP-glucose transporter-related, contains weak similarity to UDP-galactose/UDP-glucose transporter (GI:22651763) (Arabidopsis thaliana)   chr3:16965350-16967818 REVERSE   Aliases: F12M12.150	3.6	3.7	-0.1	-0.6	100.0%	-5.2
10938	AT5G65490.1   expressed protein, similar to unknown protein (dbj BAA75199.1)   chr5:26194728-26197542 REVERSE   Aliases: K19O4.5, K19O4_5	6.2	6.5	-0.2	-0.6	100.0%	-4.6
10939	AT5G44060.1   expressed protein, similar to unknown protein (gb:AAD10670.1)   chr5:17748232-17749132 FORWARD   Aliases: MRH10.17, MRH10_17	4.3	4.5	-0.3	-0.6	100.0%	-4.6
10940	AT5G05490.2   Symbol: SYN1.1	2.2	2.2	-0.0	-0.6	100.0%	-5.8
10941	AT3G30490.1   expressed protein   chr3:12117914-12118455 REVERSE   Aliases: MSJ3.13	2.2	2.3	-0.1	-0.6	100.0%	-5.2
10942	AT2G32890.1   expressed protein   chr2:13960135-13960368 REVERSE   Aliases: T21L14.17, T21L14_17	4.3	4.1	0.1	0.6	100.0%	-5.0
10943	AT3G27670.1   expressed protein   chr3:10246371-10254530 FORWARD   Aliases: MGF10.8	5.0	5.2	-0.2	-0.6	100.0%	-4.8
10944	AT3G29130.1   expressed protein, ; expression supported by MPSS   chr3:11103783-11105084 REVERSE   Aliases: MXE2.11	5.1	5.3	-0.2	-0.6	100.0%	-4.6
10945	AT1G06540.1   expressed protein   chr1:2002876-2003392 REVERSE   Aliases: F12K11.13, F12K11_13	2.4	2.6	-0.1	-0.6	100.0%	-4.9
10946	AT1G45100.1   polyadenylate-binding protein, putative / PABP, putative, similar to polyadenylate-binding protein (poly(A)-binding protein) from {Arabidopsis thaliana} SP:P42731, (Nicotiana tabacum) GI:7673355, (Cucumis sativus) GI:7528270; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:17053071-17054629 FORWARD   Aliases: F27F5.17, F27F5_17	3.7	3.6	0.1	0.6	100.0%	-5.3
10947	AT2G36760.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:15420121-15421673 REVERSE   Aliases: F13K3.16, F13K3_16	2.7	2.8	-0.1	-0.6	100.0%	-5.3
10948	AT2G47860.2   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr2:19607018-19609262 FORWARD   Aliases: F17A22.25	2.6	2.7	-0.2	-0.6	100.0%	-4.8
10949	AT4G09760.3   choline kinase, putative, similar to GmCK2p choline kinase gi:1438881:gb:AAC49375   chr4:6148755-6151380 REVERSE   Aliases: F17A8.110, F17A8_110	6.0	5.8	0.2	0.6	100.0%	-4.5
10950	AT3G18890.1   expressed protein, similar to UV-B and ozone similarly regulated protein 1 UOS1 (Pisum sativum) GI:20339364   chr3:6511031-6514975 FORWARD   Aliases: MCB22.6	2.8	2.9	-0.1	-0.6	100.0%	-5.0
10951	AT4G00310.2   expressed protein   chr4:133662-135469 FORWARD   Aliases: A_IG005I10.17, A_IG005I10_17, F5I10.17, F5I10_17	2.9	2.8	0.1	0.6	100.0%	-5.3
10952	AT4G33650.1   Symbol: ADL2   dynamin-like protein 2a (ADL2a), identical to dynamin like protein 2a (ADL2a) (Arabidopsis thaliana) GI:19032337; supported by cDNA gi:19032336   chr4:16160938-16166932 FORWARD   Aliases: ADL2A, ARABIDOPSIS DYNAMIN LIKE 2, T16L1.140, T16L1_140	6.5	6.3	0.2	0.6	100.0%	-4.7
10953	AT4G00220.1   LOB domain protein 30 / lateral organ boundaries domain protein 30 (LBD30), identical to LOB DOMAIN 30 (Arabidopsis thaliana) GI:16660632; supported by full-length cDNA gi:16660631   chr4:90036-92237 FORWARD   Aliases: F6N15.4, F6N15_4	3.0	2.9	0.1	0.6	100.0%	-5.1
10954	AT5G14430.2   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr5:4652983-4655976 FORWARD   Aliases: F18O22.220, F18O22_220	7.5	7.8	-0.3	-0.6	100.0%	-4.6
10955	AT3G62130.1   epimerase-related, contains weak similarity to isopenicillin N epimerase (Swiss-Prot:P18549) (Streptomyces clavuligerus)	5.0	5.2	-0.2	-0.6	100.0%	-4.8
10956	AT1G34070.1   expressed protein   chr1:12402261-12403187 FORWARD   Aliases: F12G12.10, F12G12_10	3.1	3.0	0.1	0.6	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10957	AT2G34560.2   katanin, putative, similar to katanin p60 subunit (Strongylocentrotus purpuratus) GI:3098603; contains Pfam profile PF00004: ATPase AAA family   chr2:14567277-14569924 FORWARD   Aliases: T31E10.10, T31E10_10	8.3	8.6	-0.3	-0.6	100.0%	-4.7
10958	AT4G03010.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0A (Lycopersicon esculentum) gi:3894385:gb:AAC78592   chr4:1329952-1331139 FORWARD   Aliases: T4I9.11, T4I9_11	2.5	2.4	0.1	0.6	100.0%	-5.3
10959	AT5G50550.1   WD-40 repeat family protein / St12p protein, putative, contains 4 WD-40 repeats (PF0400); similar to St12p protein GI:166878 (Arabidopsis thaliana)   chr5:20594096-20596137 FORWARD   Aliases: MFB16.9	3.8	4.0	-0.2	-0.6	100.0%	-4.4
10960	AT5G50650.1   WD-40 repeat family protein / St12p protein, putative, contains 4 WD-40 repeats (PF0400); similar to St12p protein GI:166878 (Arabidopsis thaliana)   chr5:20627438-20629287 FORWARD   Aliases: None	3.8	4.0	-0.2	-0.6	100.0%	-4.4
10961	AT3G04970.2   zinc finger (DHHC type) family protein, similar to Golgi-specific DHHC zinc finger protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain   chr3:1376182-1378506 FORWARD   Aliases: T9J14.8, T9J14_8	3.2	3.1	0.1	0.6	100.0%	-5.2
10962	AT4G35450.4   Symbol: AKR2   ankyrin repeat family protein / AFT protein (AFT), contains ankyrin repeats, Pfam:PF00023; identical to cDNA AFT protein (AFT) GI:3478699   chr4:16839933-16842082 FORWARD   Aliases: AFT, ANKYRIN REPEAT CONTAINING PROTEIN 2, F15J1.20, F15J1_20	11.2	10.9	0.3	0.6	100.0%	-4.7
10963	AT2G30840.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967)   chr2:13142507-13143926 REVERSE   Aliases: F7F1.5, F7F1_5	3.0	3.3	-0.3	-0.6	100.0%	-4.1
10964	AT2G35040.1   AICARFT/IMPCHase bienzyme family protein, similar to SP:P12048 Bifunctional purine biosynthesis protein purH (Includes: Phosphoribosylaminoimidazolecarboxamide formyltransferase (EC 2.1.2.3) (AICAR transformylase); IMP cyclohydrolase (EC 3.5.4.10) (Inosinicase) (IMP synthetase) (ATIC)) {Bacillus subtilis}; contains Pfam profiles PF01808: AICARFT/IMPCHase bienzyme, PF02142: MGS-like domain   chr2:14772239-14775367 REVERSE   Aliases: F19I3.27, F19I3_27	9.8	10.2	-0.4	-0.6	100.0%	-4.1
10965	AT2G03140.1   CAAX amino terminal protease family protein, very low similarity to SP:Q40863 Late embryogenesis abundant protein EMB8 from Picea glauca; contains Pfam profile PF02517 CAAX amino terminal protease family protein   chr2:941997-950031 FORWARD   Aliases: T18E12.19, T18E12_19	4.7	4.9	-0.2	-0.6	100.0%	-4.9
10966	AT5G57860.3   ubiquitin family protein, contains Pfam profile PF00240: Ubiquitin family   chr5:23454871-23456538 FORWARD   Aliases: MTI20.11, MTI20_11	5.6	5.4	0.3	0.6	100.0%	-5.0
10967	AT5G18430.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr5:6110365-6111936 REVERSE   Aliases: F20L16.150, F20L16_150	2.0	2.0	0.0	0.6	100.0%	-5.9
10968	AT3G62280.1   similar to GDSL-motif lipase/hydrolase family protein [Arabidopsis thaliana] (TAIR:At1g56670.1); similar to putative early nodule-specific protein ENOD8 [Oryza sativa (japonica cultivar-group)] (GB:BAD54714.1); contains InterPro domain Lipolytic enzyme, G-D-S-L family (InterPro:IPR001087)   chr3:23060400-23062091 REVERSE   Aliases: T17J13.240	3.3	3.2	0.1	0.6	100.0%	-4.9
10969	AT4G09860.1   expressed protein   chr4:6194706-6195298 REVERSE   Aliases: F17A8.210, F17A8_210	2.2	2.3	-0.1	-0.6	100.0%	-6.0
10970	AT3G07660.1   expressed protein   chr3:2444784-2450567 REVERSE   Aliases: MLP3.11	3.0	3.2	-0.2	-0.6	100.0%	-5.1
10971	AT4G24480.1   serine/threonine protein kinase, putative, similar to serine/threonine-protein kinase CTR1 (Arabidopsis thaliana) SWISS-PROT:Q05609   chr4:12649997-12654994 FORWARD   Aliases: T22A6.310, T22A6_310	4.5	4.7	-0.2	-0.6	100.0%	-4.7
10972	AT1G59720.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:21943533-21945449 REVERSE   Aliases: F23H11.3, F23H11_3	3.1	3.3	-0.2	-0.6	100.0%	-5.0
10973	AT3G54310.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:20122131-20123922 REVERSE   Aliases: F24B22.270	2.9	2.8	0.1	0.6	100.0%	-5.4
10974	AT1G13470.1   expressed protein   chr1:4620242-4621539 REVERSE   Aliases: T6J4.20, T6J4_20	4.3	4.0	0.2	0.6	100.0%	-4.7
10975	AT1G75350.1   Symbol: EMB2184   ribosomal protein L31 family protein, similar to SP:O46917 from (Guillardia theta)   chr1:28275742-28276481 FORWARD   Aliases: EMB2184, EMBRYO DEFECTIVE 2184, F1B16.11, F1B16_11	9.1	9.0	0.2	0.6	100.0%	-4.6
10976	AT3G22810.1   expressed protein, ; expression supported by MPSS   chr3:8068602-8071566 FORWARD   Aliases: MWI23.18	3.4	3.5	-0.1	-0.6	100.0%	-5.0
10977	AT3G03380.1   DegP protease, putative, contains similarity to degP GI:2623992 from (Bradyrhizobium japonicum)   chr3:799622-808529 FORWARD   Aliases: AT3G03390, T21P5.20, T21P5_20	4.9	5.1	-0.1	-0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
10978	AT5G52380.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr5:21278579-21280364 REVERSE   Aliases: K24M7.12, K24M7_12	5.9	6.1	-0.2	-0.6	100.0%	-4.8
10979	AT1G53760.1   expressed protein   chr1:20072827-20074586 REVERSE   Aliases: T18A20.23, T18A20_23	3.6	3.9	-0.3	-0.6	100.0%	-4.8
10980	AT5G27160.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr5:9562599-9565844 FORWARD   Aliases: T21B4.70, T21B4_70	2.6	2.6	0.1	0.6	100.0%	-5.5
10981	AT5G22760.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr5:7571638-7577869 FORWARD   Aliases: MDJ22.18, MDJ22_18	4.4	4.6	-0.2	-0.6	100.0%	-5.0
10982	AT5G38650.1   proteasome maturation factor UMP1 family protein, contains Pfam profile PF05348: Proteasome maturation factor UMP1   chr5:15488192-15490025 REVERSE   Aliases: MBB18.20, MBB18_20	10.9	10.6	0.3	0.6	100.0%	-4.8
10983	AT3G44240.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, (CAF1) (Mus musculus)   chr3:15951171-15951890 FORWARD   Aliases: T10D17.30	3.1	3.2	-0.1	-0.6	100.0%	-5.3
10984	AT5G56180.2   Symbol: ATARP8	5.0	4.9	0.1	0.6	100.0%	-5.1
10985	AT4G15000.1   60S ribosomal protein L27 (RPL27C)   chr4:8571829-8572485 FORWARD   Aliases: DL3545W, FCAALL.99	10.2	10.5	-0.3	-0.6	100.0%	-4.8
10986	AT1G53100.1   similar to glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein [Arabidopsis thaliana] (TAIR:At3g15350.1); similar to glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein [Arabidopsis thaliana] (TAIR:At3g15350.2); similar to BGGP Beta-1-3-galactosyl-O-glycosyl-glycoprotein [Triticum aestivum] (GB:CAH10194.1); similar to putative N-acetylglucosaminyltransferase [Hordeum vulgare subsp. vulgare] (GB:AAV49991.1); similar to glycosylation enzyme-like [Oryza sativa (japonica cultivar-group)] (GB:BAD73208.1); contains InterPro domain Glycosyl transferase, family 14 (InterPro:IPR003406)   chr1:19790624-19792637 REVERSE   Aliases: F8L10.4, F8L10_4	3.1	3.0	0.1	0.6	100.0%	-4.9
10987	AT3G03720.1   Symbol: CAT4   amino acid permease family protein, similar to cationic amino acid transporter-1 (Rattus norvegicus) GI:1589917; contains Pfam profile PF00324: Amino acid permease   chr3:925692-929947 REVERSE   Aliases: CATIONIC AMINO ACID TRANSPORTER 4, F20H23.25, F20H23_25	5.5	5.2	0.3	0.6	100.0%	-4.3
10988	AT1G01900.1   subtilase family protein, contains similarity to cucumisin-like serine protease GB:AAC18851 GI:3176874 from (Arabidopsis thaliana)   chr1:310318-313130 FORWARD   Aliases: F22M8.3, F22M8_3	2.8	2.7	0.1	0.6	100.0%	-5.2
10989	AT5G20290.1   40S ribosomal protein S8 (RPS8A), ribosomal protein S8 - Zea mays, PIR:T04088   chr5:6851483-6853065 REVERSE   Aliases: F5O24.180, F5O24_180	11.8	12.0	-0.2	-0.6	100.0%	-4.8
10990	AT3G25710.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.3	2.3	0.1	0.6	100.0%	-5.8
10991	AT5G02800.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:635230-637480 REVERSE   Aliases: F9G14.110, F9G14_110	3.4	3.2	0.2	0.6	100.0%	-4.9
10992	AT1G48110.1   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr1:17772787-17777120 REVERSE   Aliases: F21D18.17, F21D18_17	4.7	4.5	0.2	0.6	100.0%	-4.8
10993	AT2G40890.1   Symbol: CYP98A3   cytochrome P450 98A3, putative (CYP98A3), identical to Cytochrome P450 98A3 (SP:O22203) (Arabidopsis thaliana); similar to gi:17978651 from Pinus taeda   chr2:17065131-17067730 REVERSE   Aliases: REF8, T20B5.9, T20B5_9	10.1	10.5	-0.4	-0.6	100.0%	-4.7
10994	AT5G67270.1   Symbol: ATEB1C	4.3	4.6	-0.3	-0.6	100.0%	-4.7
10995	AT5G10840.1   endomembrane protein 70, putative, TM4 family;   chr5:3424911-3427835 REVERSE   Aliases: T30N20.110, T30N20_110	7.5	7.9	-0.4	-0.6	100.0%	-4.5
10996	AT4G39860.2   expressed protein   chr4:18499878-18501636 FORWARD   Aliases: T5J17.30, T5J17_30	7.5	7.8	-0.3	-0.6	100.0%	-4.4
10997	AT4G30630.1   expressed protein   chr4:14950644-14952382 FORWARD   Aliases: F17I23.30, F17I23_30	4.6	4.3	0.3	0.6	100.0%	-4.7
10998	AT4G38440.1   expressed protein   chr4:17989061-17994717 FORWARD   Aliases: F22I13.210, F22I13_210	3.5	3.4	0.1	0.6	100.0%	-5.1
10999	AT3G28910.1   Symbol: MYB30   myb family transcription factor (MYB30), identical to myb-like protein GB:AJ007289 (Arabidopsis thaliana) (Plant J. 20 (1), 57-66 (1999))   chr3:10912416-10914427 FORWARD   Aliases: ATMYB30, MLD15.8, MYB30	3.5	3.4	0.1	0.6	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11000	AT5G37260.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:14768574-14770202 REVERSE   Aliases: MNJ8.4, MNJ8_4	3.9	3.6	0.3	0.6	100.0%	-4.4
11001	AT3G57760.3   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g57740.1); similar to OSJNBa0083N12.1 [Oryza sativa (japonica cultivar-group)] (GB:CAE03464.2); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:21406594-21408219 FORWARD   Aliases: F15B8.50	3.0	2.9	0.1	0.6	100.0%	-5.2
11002	AT1G68620.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr1:25769610-25770903 FORWARD   Aliases: F24J5.14, F24J5_14	4.0	3.9	0.1	0.6	100.0%	-4.8
11003	AT4G19720.1   glycosyl hydrolase family 18 protein, similar to chitinase, class V GI:899342 from (Nicotiana tabacum)   chr4:10730373-10731760 REVERSE   Aliases: T16H5.80, T16H5_80	3.1	3.4	-0.2	-0.6	100.0%	-4.6
11004	AT1G09600.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:3108619-3111320 FORWARD   Aliases: F14J9.26, F14J9_26	4.6	4.7	-0.2	-0.6	100.0%	-4.8
11005	AT3G44110.2   Symbol: ATJ3   DNAJ heat shock protein, putative (J3), identical to AtJ3 (Arabidopsis thaliana) GI:2641638, strong similarity to several plant DnaJ proteins from PGR; contains Pfam profiles PF00226 DnaJ domain, PF00684 DnaJ central domain (4 repeats), PF01556 DnaJ C terminal region   chr3:15879781-15882208 REVERSE   Aliases: ATJ, F26G5.60	9.9	9.4	0.5	0.6	100.0%	-4.9
11006	AT2G04030.2   Symbol: CR88   heat shock protein, putative, strong similarity to heat shock protein (Arabidopsis thaliana) GI:1906830; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein	6.5	6.9	-0.4	-0.6	100.0%	-4.3
11007	AT3G09060.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:2766372-2768435 REVERSE   Aliases: MZB10.9	3.4	3.5	-0.1	-0.6	100.0%	-5.2
11008	AT3G45530.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	3.1	-0.2	-0.6	100.0%	-5.0
11009	AT2G33080.1   leucine-rich repeat family protein, contains leucine rich-repeat domain Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr2:14039092-14041314 FORWARD   Aliases: F25I18.18, F25I18_18	2.6	2.7	-0.1	-0.6	100.0%	-5.4
11010	AT3G50070.1   Symbol: CYCD3;3   cyclin family protein, similar to cyclin D3.1 protein (Nicotiana tabacum) GI:4160300, CycD3;2 (Lycopersicon esculentum) GI:6434199; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr3:18576117-18577763 REVERSE   Aliases: CYCLIN D3;3, F3A4.150	4.3	4.5	-0.2	-0.6	100.0%	-5.1
11011	AT1G24320.1   alpha-glucosidase, putative, similar to alpha-glucosidase I from GI:16506680 (Arabidopsis thaliana)   chr1:8626316-8630960 REVERSE   Aliases: F3I6.26, F3I6_26	3.1	3.4	-0.3	-0.6	100.0%	-4.1
11012	AT1G02550.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Lycopersicon esculentum SP:Q43143, Arabidopsis thaliana SP:Q43867; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:536483-537211 FORWARD   Aliases: T14P4.25, T14P4_25	3.1	3.0	0.1	0.6	100.0%	-5.2
11013	AT1G76950.1   zinc finger protein (PRAF1) / regulator of chromosome condensation (RCC1) family protein, identical to zinc finger protein PRAF1 (Arabidopsis thaliana) gi:15811367:gb:AAL08940.	3.5	3.6	-0.1	-0.6	100.0%	-4.9
11014	AT5G35870.1   expressed protein, similar to unknown protein (gb:AAD25831.1)   chr5:14038252-14038842 FORWARD   Aliases: MIK22.18, MIK22_18	2.7	2.8	-0.1	-0.6	100.0%	-5.5
11015	AT1G67550.1   urease, putative / urea amidohydrolase, putative, similar to SP:P07374 Urease (EC 3.5.1.5) (Urea amidohydrolase) {Canavalia ensiformis}; contains Pfam profile PF01979: Amidohydrolase family   chr1:25316403-25320828 FORWARD   Aliases: F12B7.10, F12B7_10	4.0	4.2	-0.2	-0.6	100.0%	-4.9
11016	AT2G25540.1   Symbol: CESA10	3.0	2.9	0.1	0.6	100.0%	-5.2
11017	AT5G63820.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr5:25558802-25560119 FORWARD   Aliases: MGI19.2, MGI19_2	3.3	3.2	0.1	0.6	100.0%	-5.2
11018	AT4G23840.1   leucine-rich repeat family protein   chr4:12400355-12403413 FORWARD   Aliases: AT4G23830, T32A16.10, T32A16_10	4.0	3.9	0.1	0.6	100.0%	-5.3
11019	AT2G43420.1   3-beta hydroxysteroid dehydrogenase/isomerase family protein, contains Pfam profile PF01073 3-beta hydroxysteroid dehydrogenase/isomerase domain; similar to NAD(P)-dependent steroid dehydrogenase from Homo sapiens (SP:Q15738), Mus musculus (SP:Q9R1J0)   chr2:18038345-18042129 REVERSE   Aliases: T1O24.16	8.3	8.5	-0.2	-0.6	100.0%	-4.9
11020	AT5G46030.1   expressed protein, contains Pfam profile PF05129: Putative zinc binding domain (DUF701)   chr5:18687356-18688566 FORWARD   Aliases: MCL19.8, MCL19_8	9.5	9.7	-0.2	-0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11021	AT3G05010.1   transmembrane protein, putative, similar to GB:AAB61079; contains weak similarity to the SAPB protein (TR:E236624) (Arabidopsis thaliana); similar to seven transmembrane domain orphan receptor (GI:4321619) (Mus musculus) contains 7 transmembrane domains;   chr3:1389455-1391681 FORWARD   Aliases: T9J14.4, T9J14_4	7.7	7.2	0.6	0.6	100.0%	-4.4
11022	AT4G05030.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr4:2576788-2577972 REVERSE   Aliases: C17L7.9	2.6	2.7	-0.1	-0.6	100.0%	-5.3
11023	AT4G01500.1   DNA-binding protein, putative, similar to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857, RAV2 GI:3868859; contains Pfam profile PF02362: B3 DNA binding domain   chr4:639806-640940 FORWARD   Aliases: F11O4.9, F11O4_9	3.4	3.2	0.2	0.6	100.0%	-4.9
11024	AT5G52010.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:21138718-21140211 REVERSE   Aliases: MSG15.9, MSG15_9	7.1	6.9	0.2	0.6	100.0%	-4.8
11025	AT2G33700.1   protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain; similar to protein phosphatase-2C (PP2C) (GI:3643085) (Mesembryanthemum crystallinum)   chr2:14260500-14263069 FORWARD   Aliases: T1B8.2, T1B8_2	5.5	5.6	-0.2	-0.6	100.0%	-4.8
11026	AT2G30470.1   Symbol: HSI2   HSI2 is a member of a novel family of B3 domain proteins with a sequence similar to the ERF-associated amphiphilic repression (EAR) motif. It functions as an active repressor of the Spo minimal promoter (derived from a gene for sweet potato sporamin A1) through the EAR motif. It contains a plant-specific B3 DNA-binding domain. The Arabidopsis genome contains 42 genes with B3 domains which could be classified into three families that are represented by ABI3, ARF1 and RAV1. HSI2 belongs to the ABI3 family. It is expressed at similar levels in all organs. Treatment with 6% sucrose showed a slight increase in transcript levels after 24 h. No changes were observed after treatment with 50??M ABA. It is localized in the nucleus via a nuclear localization sequence located in the fourth conserved region of the C-terminal B3 domain.   chr2:12987584-12992110 REVERSE   Aliases: HSI2, T6B20.17, T6B20_17	4.9	6.0	-1.1	-0.6	100.0%	-4.6
11027	AT5G12460.1   fringe-related protein, similarity to predicted proteins + similar to hypothetical protein GB:AAC23643 (Arabidopsis thaliana) + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr5:4043060-4044586 FORWARD   Aliases: None	2.9	3.0	-0.1	-0.6	100.0%	-5.1
11028	AT5G60400.3   expressed protein   chr5:24308366-24309158 REVERSE   Aliases: MUF9.14, MUF9_14	6.1	6.5	-0.4	-0.6	100.0%	-4.5
11029	AT3G57340.2   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9QYI4 DnaJ homolog subfamily B member 12 Mus musculus; contains Pfam profile PF00226 DnaJ domain   chr3:21229986-21231463 FORWARD   Aliases: F28O9.190	5.3	5.1	0.2	0.6	100.0%	-4.9
11030	AT4G39010.1   glycosyl hydrolase family 9 protein, endo-1,4-beta-glucanase precursor - Fragaria x ananassa, PID:g3549291   chr4:18175896-18179177 REVERSE   Aliases: F19H22.110, F19H22_110	2.7	2.8	-0.1	-0.6	100.0%	-5.2
11031	AT5G57050.1   Symbol: ABI2   protein phosphatase 2C ABI2 / PP2C ABI2 / abscisic acid-insensitive 2 (ABI2), identical to SP:O04719 Protein phosphatase 2C ABI2 (EC 3.1.3.16) (PP2C) (Abscisic acid- insensitive 2) {Arabidopsis thaliana}   chr5:23104461-23106853 FORWARD   Aliases: ABA INSENSITIVE 2, MHM17.19, MHM17_19, PROTEIN PHOSPHATASE 2C	6.0	5.5	0.5	0.6	100.0%	-4.6
11032	AT2G04300.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:1493006-1497013 FORWARD   Aliases: T23O15.8, T23O15_8	3.0	2.9	0.1	0.6	100.0%	-5.4
11033	AT3G04700.1   expressed protein   chr3:1276674-1277830 FORWARD   Aliases: F7O18.17, F7O18_17	3.0	3.1	-0.1	-0.6	100.0%	-5.6
11034	AT3G22180.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr3:7827120-7830820 FORWARD   Aliases: MKA23.9	2.5	2.4	0.1	0.6	100.0%	-5.2
11035	AT1G16470.2   Symbol: PAB1   similar to 20S proteasome alpha subunit D2 (PAD2) (PRS1) (PRC6) [Arabidopsis thaliana] (TAIR:At5g66140.1); similar to proteasome subunit alpha type 2 [Oryza sativa (japonica cultivar-group)] (GB:AAT78811.1); contains InterPro domain Proteasome subunit, A-type (InterPro:IPR000426); contains InterPro domain Multispecific proteasome protease (InterPro:IPR001353)   chr1:5622832-5625637 FORWARD   Aliases: F3O9.27, F3O9_27, PROTEASOME SUBUNIT PAB1	9.0	9.4	-0.4	-0.6	100.0%	-4.4
11036	AT5G03170.1   Symbol: FLA11   fasciclin-like arabinogalactan-protein (FLA11)   chr5:752775-753656 REVERSE   Aliases: F15A17.200, F15A17_200	3.4	3.1	0.3	0.6	100.0%	-4.4
11037	AT2G31710.1   expressed protein   chr2:13488870-13490182 REVERSE   Aliases: T9H9.23, T9H9_23	5.7	5.9	-0.2	-0.6	100.0%	-4.8
11038	AT5G47160.1   YDG/SRA domain-containing protein, low similarity to nuclear protein np95 (Mus musculus) GI:4220590; contains Pfam profile PF02182: YDG/SRA domain   chr5:19173958-19175205 FORWARD   Aliases: MQL5.1, MQL5_1	3.1	2.9	0.1	0.6	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11039	AT4G21470.1   riboflavin kinase/FAD synthetase family protein, contains Pfam profiles PF01687: Riboflavin kinase / FAD synthetase, PF00702: haloacid dehalogenase-like hydrolase   chr4:11431135-11433332 FORWARD   Aliases: F18E5.90, F18E5_90	8.7	8.9	-0.3	-0.6	100.0%	-4.7
11040	AT4G05320.5   Symbol: UBQ10   polyubiquitin (UBQ10) (SEN3), senescence-associated protein; identical to GI:870791   chr4:2718168-2720130 FORWARD   Aliases: C17L7.240, C17L7_240, POLYUBIQUITIN 10	13.2	13.1	0.1	0.6	100.0%	-5.9
11041	AT1G50270.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:18625712-18627502 FORWARD   Aliases: F14I3.12, F14I3_12	4.1	4.3	-0.2	-0.6	100.0%	-4.8
11042	AT5G45010.1   DSS1/SEM1 family protein, contains Pfam profile PF05160: DSS1/SEM1 family   chr5:18184471-18185601 REVERSE   Aliases: K21C13.20, K21C13_20	10.7	10.4	0.2	0.6	100.0%	-4.8
11043	AT1G69180.1   Symbol: CRC   transcription factor CRC (CRABS CLAW), identical to transcription factor CRC (CRABS CLAW) GI:4836698 (Arabidopsis thaliana)   chr1:26011128-26012722 REVERSE   Aliases: CRABS CLAW, F4N2.14, F4N2_14, TRANSCRIPTION FACTOR CRC	2.1	2.0	0.1	0.6	100.0%	-5.7
11044	AT1G03470.2   similar to kinase interacting family protein [Arabidopsis thaliana] (TAIR:At2g47920.1); similar to putative centromere protein [Oryza sativa (japonica cultivar-group)] (GB:AAP53815.1); contains domain GLU_RICH (PS50313)   chr1:865915-867674 REVERSE   Aliases: F21B7.9	5.0	5.3	-0.3	-0.6	100.0%	-4.3
11045	AT1G21660.1   expressed protein, low similarity to SP:O14976 Cyclin G-associated kinase (EC 2.7.1.-) {Homo sapiens}; supporting cDNA gi:20466222:gb:AY099577.1:   chr1:7605688-7609054 FORWARD   Aliases: F8K7.8, F8K7_8	7.1	7.2	-0.2	-0.6	100.0%	-4.8
11046	AT5G53440.1   expressed protein   chr5:21700905-21705196 REVERSE   Aliases: MYN8.5, MYN8_5	8.7	8.5	0.1	0.6	100.0%	-5.0
11047	AT2G30280.1   expressed protein   chr2:12916670-12919417 REVERSE   Aliases: T9D9.9, T9D9_9	5.2	5.6	-0.4	-0.6	100.0%	-4.6
11048	AT5G19210.2   DEAD/DEAH box helicase, putative, EUKARYOTIC INITIATION FACTOR 4A-II (EIF-4A-II), Homo sapiens, SWISSPROT:IF42_HUMAN   chr5:6461425-6463868 FORWARD   Aliases: T24G5.110, T24G5_110	3.1	3.2	-0.1	-0.6	100.0%	-4.9
11049	AT2G46170.1   reticulon family protein (RTNLB5), weak similarity to Nogo-C protein (Rattus norvegicus) GI:6822251; contains Pfam profile PF02453: Reticulon   chr2:18972386-18974259 FORWARD   Aliases: T3F17.18	9.4	8.8	0.6	0.6	100.0%	-4.3
11050	AT5G51490.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:20930779-20932832 REVERSE   Aliases: K17N15.4, K17N15_4	3.0	2.9	0.1	0.6	100.0%	-5.1
11051	AT5G49240.1   Symbol: APRR4   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain; contains similarity to two-component response regulator proteins   chr5:19980160-19981577 FORWARD   Aliases: K21P3.12, K21P3_12, PRR4, PSEUDO RESPONSE REGULATOR 4	3.2	3.0	0.1	0.6	100.0%	-5.1
11052	AT4G36150.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:17104779-17108714 FORWARD   Aliases: F23E13.40, F23E13_40	4.1	4.0	0.2	0.6	100.0%	-4.7
11053	AT1G53720.1   cyclophilin-RNA interacting protein, putative   chr1:20060201-20063306 FORWARD   Aliases: F22G10.24, F22G10_24	5.9	6.5	-0.6	-0.6	100.0%	-4.5
11054	AT1G12960.1   60S ribosomal protein L27A (RPL27aA), similar to GB:BAA96068 from (Panax ginseng)   chr1:4422705-4423153 REVERSE   Aliases: F13K23.22, F13K23_22	4.1	4.2	-0.1	-0.6	100.0%	-5.0
11055	AT5G07270.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:2280672-2283594 FORWARD   Aliases: T28J14.210, T28J14_210	3.5	3.3	0.2	0.6	100.0%	-4.5
11056	AT5G03290.1   isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative, strong similarity to isocitrate dehydrogenase (NAD+) (Nicotiana tabacum) GI:3021506   chr5:793984-795995 FORWARD   Aliases: F12E4.20, F12E4_20	11.0	11.3	-0.3	-0.6	100.0%	-5.0
11057	AT1G43870.1   hypothetical protein, similar to fructose binding protein FrcB (GI:11066207)(Sinorhizobium meliloti)   chr1:16629534-16630535 FORWARD   Aliases: F28H19.12, F28H19_12	2.5	2.4	0.1	0.6	100.0%	-5.5
11058	AT5G60130.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:24229097-24230184 REVERSE   Aliases: MGO3.11, MGO3_11	2.5	2.4	0.1	0.6	100.0%	-5.6
11059	AT5G65290.2   similar to LMBR1 integral membrane protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD37233.1); contains InterPro domain LMBR1-like conserved region (InterPro:IPR006876)   chr5:26106782-26111773 FORWARD   Aliases: MNA5.1, MNA5_1	4.3	4.5	-0.2	-0.6	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11060	AT2G36670.2   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr2:15371867-15375237 REVERSE   Aliases: F13K3.7, F13K3_7	4.6	4.8	-0.1	-0.6	100.0%	-5.0
11061	AT5G38400.1   expressed protein   chr5:15393076-15393531 FORWARD   Aliases: MXI10.12, MXI10_12	3.8	3.7	0.1	0.6	100.0%	-5.0
11062	AT4G09350.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q45552 Chaperone protein dnaJ {Bacillus stearothermophilus}; contains Pfam profile PF00226: DnaJ domain   chr4:5931248-5932149 REVERSE   Aliases: T30A10.110, T30A10_110	2.5	2.4	0.1	0.6	100.0%	-5.5
11063	AT5G53160.2   expressed protein, similar to unknown protein (pir::T02893)   chr5:21577944-21579486 FORWARD   Aliases: MFH8.10, MFH8_10	6.6	6.2	0.4	0.6	100.0%	-4.7
11064	AT5G02670.1   expressed protein   chr5:602720-604604 REVERSE   Aliases: T22P11.260, T22P11_260	2.6	2.5	0.1	0.6	100.0%	-5.4
11065	AT1G23450.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:8324687-8326686 FORWARD   Aliases: F28C11.30, F28C11_30	3.3	3.4	-0.1	-0.6	100.0%	-5.5
11066	AT5G24020.1   Symbol: MIND   septum site-determining protein (MIND), identical to MinD (Arabidopsis thaliana) GI:6759277; contains Pfam PF00991 : ParA family ATPase   chr5:8116683-8118033 FORWARD   Aliases: MZF18.10, MZF18_10	5.9	5.7	0.1	0.6	100.0%	-4.7
11067	AT2G27140.1   heat shock family protein, contains similarity to Swiss-Prot:P27397 18.0 kDa class I heat shock protein (Daucus carota)   chr2:11605457-11606400 REVERSE   Aliases: T20P8.19, T20P8_19	3.0	2.9	0.1	0.6	100.0%	-4.9
11068	AT5G14450.1   GDSL-motif lipase/hydrolase family protein, similar to early nodulin ENOD8 (Medicago sativa) GI:304037, elicitor-induced glycoprotein iEP4 (Daucus carota) GI:1911765, pollen-expressed coil protein (Medicago sativa) GI:1110502; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr5:4658444-4660178 FORWARD   Aliases: F18O22.240, F18O22_240	4.5	4.6	-0.1	-0.6	100.0%	-4.7
11069	AT3G27530.1   vesicle tethering family protein, contains Pfam PF04869: Uso1 / p115 like vesicle tethering protein, head region and PF04871: Uso1 / p115 like vesicle tethering protein, C terminal region   chr3:10194806-10200913 REVERSE   Aliases: MMJ24.8	5.1	5.4	-0.3	-0.6	100.0%	-4.6
11070	AT3G20660.1   similar to sugar transporter family protein [Arabidopsis thaliana] (TAIR:At1g73220.1); similar to putative organic cation transport protein [Phaseolus vulgaris] (GB:AAO83155.1); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828)	4.0	3.8	0.2	0.6	100.0%	-4.9
11071	AT2G20900.4   similar to diacylglycerol kinase accessory domain-containing protein [Arabidopsis thaliana] (TAIR:At4g28130.1); similar to putative diacylglycerol kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_480362.1); similar to calmodulin-binding diacylglycerol kinase [Lycopersicon esculentum] (GB:AAG23128.1); similar to diacylglycerol kinase variant A [Lycopersicon esculentum] (GB:AAG23130.1); similar to diacylglycerol kinase [Lycopersicon esculentum] (GB:AAG23129.1); similar to OSJNBa0043L09.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_474019.1); contains InterPro domain Diacylglycerol kinase, catalytic domain (InterPro:IPR001206); contains InterPro domain Diacylglycerol kinase accessory domain (presumed) (InterPro:IPR000756)   chr2:8996356-9000066 REVERSE   Aliases: F5H14.13, F5H14_13	4.8	4.6	0.2	0.6	100.0%	-4.4
11072	AT1G61120.1   terpene synthase/cyclase family protein, similar to S-linalool synthase GI:1491939 from (Clarkia breweri)(PMID: 8768373)	2.7	2.6	0.1	0.6	100.0%	-5.6
11073	AT2G36100.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr2:15166823-15167801 REVERSE   Aliases: F9C22.3, F9C22_3	4.5	4.3	0.2	0.6	100.0%	-4.3
11074	AT5G28590.1   DNA-binding protein-related, contains similarity to DNA-binding proteins	3.2	3.3	-0.1	-0.6	100.0%	-4.8
11075	AT5G65130.1   encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.   chr5:26034629-26035462 FORWARD   Aliases: MQN23.6, MQN23_6	2.5	2.4	0.1	0.6	100.0%	-5.2
11076	AT5G26700.1   germin-like protein, putative, similar to germin-like protein GLP8 (SP:P93000); contains Pfam profile: PF01072 germin family   chr5:9308039-9309628 REVERSE   Aliases: None	2.4	2.5	-0.1	-0.6	100.0%	-5.3
11077	AT1G79110.2   expressed protein   chr1:29764079-29765597 FORWARD   Aliases: YUP8H12R.27, YUP8H12R_27	5.0	5.3	-0.3	-0.6	100.0%	-4.7
11078	AT3G58740.1   citrate synthase, glyoxysomal, putative, strong similarity to SP:P49299 Citrate synthase, glyoxysomal precursor {Cucurbita maxima}; contains Pfam profile PF00285: Citrate synthase   chr3:21731750-21734767 REVERSE   Aliases: T20N10.90	4.1	4.0	0.1	0.6	100.0%	-4.9
11079	AT1G74320.1   choline kinase, putative, similar to GmCK2p choline kinase gi:1438881:gb:AAC49375   chr1:27944334-27946865 FORWARD   Aliases: F1O17.1, F1O17_1	3.9	4.1	-0.3	-0.6	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11080	AT3G13220.1   ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter; similar to white protein GB:Q27256 (Anopheles gambiae)   chr3:4247975-4250710 REVERSE   Aliases: MJG19.25	2.2	2.2	0.1	0.6	100.0%	-5.4
11081	AT3G52170.1   expressed protein   chr3:19357884-19360491 REVERSE   Aliases: T25B15.1	4.9	5.2	-0.3	-0.6	100.0%	-4.4
11082	AT3G61380.1   expressed protein   chr3:22719459-22722254 REVERSE   Aliases: F2A19.4	4.5	4.7	-0.2	-0.6	100.0%	-4.6
11083	AT4G04460.1   aspartyl protease family protein, contains Pfam profiles: PF00026 eukaryotic aspartyl protease, PF03489 surfactant protein B, PF05184 saposin-like type B, region 1   chr4:2224549-2227872 FORWARD   Aliases: T26N6.7, T26N6_7	2.7	2.9	-0.2	-0.6	100.0%	-4.7
11084	AT1G74820.1   cupin family protein, similar to germin-like protein SP:P92995; contains Pfam profile PF00190: Cupin   chr1:28115543-28116226 REVERSE   Aliases: F9E10.33, F9E10_33	2.9	3.0	-0.1	-0.6	100.0%	-5.3
11085	AT1G28010.1   multidrug resistance P-glycoprotein, putative, similar to mdr-like P-glycoprotein GI:3849833 from (Arabidopsis thaliana)	2.6	2.5	0.1	0.6	100.0%	-5.3
11086	AT2G30060.1   Ran-binding protein 1b (RanBP1b), nearly identical to atranbp1b (Arabidopsis thaliana) GI:2058284   chr2:12834036-12835996 FORWARD   Aliases: T27E13.20, T27E13_20	7.6	7.8	-0.2	-0.6	100.0%	-5.0
11087	AT3G12620.2   similar to serine/threonine protein phosphatase 2C (PP2C6) [Arabidopsis thaliana] (TAIR:At3g55050.1); similar to serine/threonine protein phosphatase 2C (PP2C6) [Arabidopsis thaliana] (TAIR:At3g55050.2); similar to protein phosphatase 2C (PP2C) [Fagus sylvatica] (GB:CAB90634.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr3:4009282-4011354 REVERSE   Aliases: T2E22.7	7.0	6.6	0.4	0.6	100.0%	-4.6
11088	AT1G75330.1   Symbol: OTC   ornithine carbamoyltransferase, chloroplast / ornithine transcarbamylase / OTCase (OTC), identical to SP:O50039 Ornithine carbamoyltransferase, chloroplast precursor (EC 2.1.3.3) (OTCase) (Ornithine transcarbamylase) {Arabidopsis thaliana}   chr1:28269920-28272068 REVERSE   Aliases: F1B16.13, F1B16_13, ORNITHINE CARBAMOYLTRANSFERASE	11.5	11.2	0.3	0.6	100.0%	-4.5
11089	AT5G41450.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:16605828-16606322 REVERSE   Aliases: MYC6.15, MYC6_15	2.6	2.7	-0.1	-0.6	100.0%	-5.3
11090	AT5G16450.2   dimethylmenaquinone methyltransferase family protein, similar to bacterial S-adenosylmethionine:2-demethylmenaquinone methyltransferases; contains Pfam profile PF03737: Dimethylmenaquinone methyltransferase   chr5:5374062-5375462 FORWARD   Aliases: MQK4.18, MQK4_18	11.0	10.8	0.2	0.6	100.0%	-4.4
11091	AT3G59800.1   expressed protein   chr3:22105454-22107151 REVERSE   Aliases: F24G16.70	6.4	6.9	-0.5	-0.6	100.0%	-4.5
11092	AT5G46230.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:18759667-18760272 REVERSE   Aliases: MPL12.1, MPL12_1	5.2	4.9	0.3	0.6	100.0%	-4.7
11093	AT1G56060.1   expressed protein   chr1:20970193-20970809 REVERSE   Aliases: T6H22.17, T6H22_17	5.0	4.9	0.2	0.6	100.0%	-4.9
11094	AT4G32120.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr4:15516790-15519861 REVERSE   Aliases: F10N7.70, F10N7_70	6.5	6.3	0.2	0.6	100.0%	-4.8
11095	AT1G31470.1   nodulin-related, weak similarity to nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr1:11262918-11264817 REVERSE   Aliases: T8E3.15, T8E3_15	5.9	6.0	-0.2	-0.6	100.0%	-4.8
11096	AT3G23660.1   transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens)   chr3:8513464-8517790 REVERSE   Aliases: MDB19.16	5.0	5.2	-0.2	-0.6	100.0%	-5.1
11097	AT1G69050.1   expressed protein   chr1:25965587-25966011 FORWARD   Aliases: F4N2.3	2.1	2.2	-0.1	-0.6	100.0%	-5.5
11098	AT4G13560.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, similar to LEA protein (Cicer arietinum) GI:2909420; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr4:7879557-7880379 REVERSE   Aliases: T6G15.110, T6G15_110	2.8	2.8	-0.1	-0.6	100.0%	-5.3
11099	AT2G32040.1   integral membrane transporter family protein, contains 9 transmembrane domains; contains Pfam PF03092: BT1 family; contains TIGRFAMS TIGR00788: folate/biopterin transporter; similar to high affinity folic acid/methotrexate transporter 5 (GI:21898554) (Leishmania tarentolae)   chr2:13642187-13644907 FORWARD   Aliases: F22D22.21, F22D22_21	6.0	5.8	0.2	0.6	100.0%	-4.6
11100	AT2G31910.1   Symbol: ATCHX21   cation/hydrogen exchanger, putative, similar to monovalent cation:proton antiporter family 2 (CPA2) members (see PMID:11500563 for other members)   chr2:13578794-13581096 FORWARD   Aliases: CHX21, F20M17.5, F20M17_5	2.3	2.3	-0.0	-0.6	100.0%	-6.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11101	AT1G54490.1   Symbol: XRN4   5'-3' exoribonuclease (XRN4), identical to XRN4 (Arabidopsis thaliana) GI:11875626; contains Pfam domain PF03159: Putative 5'-3' exonuclease domain   chr1:20353858-20360583 FORWARD   Aliases: 5' 3' EXORIBONUCLEASE, F20D21.30, F20D21_30	5.5	5.8	-0.2	-0.6	100.0%	-4.8
11102	AT3G55950.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; similar to cytokinin-regulated kinase 1 (Nicotiana tabacum) gi:10998537:gb:AAG25966	6.1	6.3	-0.2	-0.6	100.0%	-5.0
11103	AT2G30540.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	5.1	5.5	-0.4	-0.6	100.0%	-4.3
11104	AT1G49710.1   Symbol: FUT12   fucosyltransferase-like protein, putative / FucT2, putative / FucTB, putative (FUT12), identical to Putative fucosyltransferase-like protein (FucTB) (FucT2) (AtFUT12) (Swiss-Prot:Q9FX97) (Arabidopsis thaliana); similar to glycoprotein 3-alpha-L-fucosyltransferase A (SP:Q9LJK1) (Arabidopsis thaliana); contains Pfam profile PF00852: Fucosyl transferase   chr1:18395006-18397595 REVERSE   Aliases: ATFUT12, F14J22.8, F14J22_8, FUCT2, FUCTB	6.5	6.2	0.3	0.6	100.0%	-4.2
11105	AT2G02280.1   Symbol: ATPP2 B4   expressed protein, low similarity to SKP1 interacting partner 3 (Arabidopsis thaliana) GI:10716951   chr2:600490-601438 REVERSE   Aliases: ATPP2 B4, T16F16.7, T16F16_7	3.1	3.3	-0.1	-0.6	100.0%	-5.1
11106	AT5G25530.1   DNAJ heat shock protein, putative, similar to SP:P25685 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) {Homo sapiens}; contains Pfam profile PF00226: DnaJ domain   chr5:8889668-8890957 REVERSE   Aliases: T14C9.70, T14C9_70	2.6	2.7	-0.1	-0.6	100.0%	-5.3
11107	AT5G17840.1   chaperone protein dnaJ-related, similar to bundle sheath defective protein 2 (GI:4732091) (Zea mays)   chr5:5895678-5897152 REVERSE   Aliases: MVA3.190, MVA3_190	8.3	8.2	0.2	0.6	100.0%	-4.8
11108	AT1G16420.1   latex-abundant protein, putative (AMC8) / caspase family protein, similar to latex-abundant protein (Hevea brasiliensis) gb:AAD13216; contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain   chr1:5612298-5613849 REVERSE   Aliases: F3O9.22, F3O9_22	2.6	2.5	0.1	0.6	100.0%	-4.9
11109	AT5G58375.1   expressed protein   chr5:23613500-23614186 FORWARD   Aliases: None	9.3	9.0	0.3	0.6	100.0%	-4.6
11110	AT3G13780.1   expressed protein   chr3:4525079-4526221 FORWARD   Aliases: MMM17.21	6.8	6.2	0.6	0.6	100.0%	-4.6
11111	AT3G50970.1   Symbol: XERO2   dehydrin xero2 (XERO2) / low-temperature-induced protein LTI30 (LTI30), identical to dehydrin Xero 2 (Low-temperature-induced protein LTI30) (Arabidopsis thaliana) SWISS-PROT:P42758   chr3:18951758-18952535 FORWARD   Aliases: F24M12.10	8.8	8.4	0.4	0.6	100.0%	-4.5
11112	AT3G07450.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to cysteine-rich 5B protein - Lycopersicon esculentum, PIR2:S39552 (GI:415833); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:2383616-2383936 REVERSE   Aliases: F21O3.16	3.3	3.1	0.2	0.6	100.0%	-4.7
11113	AT4G31570.1   expressed protein   chr4:15297067-15306042 FORWARD   Aliases: F28M20.240, F28M20_240	2.8	2.9	-0.1	-0.6	100.0%	-5.3
11114	AT5G08320.1   expressed protein, predicted proteins, Homo sapiens and Caenorhabditis elegans   chr5:2677053-2678679 FORWARD   Aliases: F8L15.50, F8L15_50	6.9	6.7	0.3	0.6	100.0%	-4.6
11115	AT5G44000.1   glutathione S-transferase C-terminal domain-containing protein, contains Pfam domain PF00043: Glutathione S-transferase, C-terminal domain   chr5:17719357-17721178 REVERSE   Aliases: MRH10.11, MRH10_11	8.9	8.7	0.2	0.6	100.0%	-4.6
11116	AT5G02390.1   expressed protein, ; expression supported by MPSS   chr5:508762-511708 REVERSE   Aliases: T1E22.150, T1E22_150	2.5	2.4	0.1	0.6	100.0%	-5.3
11117	AT1G22450.1   Symbol: COX6B   cytochrome c oxidase subunit 6b, putative (COX6b), nearly identical to subunit 6b of cytochrome c oxidase (Arabidopsis thaliana) GI:6518353   chr1:7925303-7927267 FORWARD   Aliases: ATCOX6B2, CYTOCHROME C OXIDASE 6B, F12K8.20, F12K8_20, SUBUNIT 6B OF CYTOCHROME C OXIDASE	9.5	9.7	-0.2	-0.6	100.0%	-4.7
11118	AT2G36130.1   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type	8.1	8.4	-0.3	-0.6	100.0%	-4.5
11119	AT4G29530.1   2,3-diketo-5-methylthio-1-phosphopentane phosphatase family, contains TIGRfam TIGR01489: 2,3-diketo-5-methylthio-1-phosphopentane phosphatase   chr4:14496085-14497460 FORWARD   Aliases: T16L4.40, T16L4_40	5.7	5.6	0.2	0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11120	AT1G35580.3   similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At4g09510.1); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At1g22650.1); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At4g09510.2); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At1g72000.1); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At4g34860.1); similar to invertase, putative [Oryza sativa (japonica cultivar-group)] (GB:AAX95795.1); similar to putative alkaline/neutral invertase [Oryza sativa (japonica cultivar-group)] (GB:XP_466154.1); similar to OSJNBa0084A10.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_472554.1); contains InterPro domain Plant neutral invertase (InterPro:IPR006937)   chr1:13122855-13125241 REVERSE   Aliases: F15O4.33	4.5	4.9	-0.4	-0.6	100.0%	-4.4
11121	AT1G30660.1   toprim domain-containing protein, contains Pfam profile PF01751: Toprim domain   chr1:10876835-10878999 FORWARD   Aliases: T5I8.11, T5I8_11	4.7	4.4	0.3	0.6	100.0%	-4.5
11122	AT3G62590.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr3:23158896-23161328 REVERSE   Aliases: F26K9.20	5.3	5.6	-0.2	-0.6	100.0%	-4.7
11123	AT3G52500.1   aspartyl protease family protein, contains Pfam PF00026: eukaryotic aspartyl protease   chr3:19476477-19478364 REVERSE   Aliases: F22O6.120	6.7	7.1	-0.4	-0.6	100.0%	-4.6
11124	AT3G15290.1   3-hydroxybutyryl-CoA dehydrogenase, putative, similar to S(+)-beta-hydroxybutyryl CoA dehydrogenase (3-hydroxybutyryl-CoA dehydrogenase) (Paracoccus denitrificans) GI:12003356; contains Pfam profiles PF02737: 3-hydroxyacyl-CoA dehydrogenase NAD binding, PF00725: 3-hydroxyacyl-CoA dehydrogenase C-terminal   chr3:5145023-5146863 FORWARD   Aliases: K7L4.9	7.7	7.5	0.2	0.6	100.0%	-4.5
11125	AT5G27490.1   integral membrane Yip1 family protein, contains Pfam domain, PF04893: Yip1 domain   chr5:9702838-9704678 REVERSE   Aliases: F21A20.200, F21A20_200	4.9	5.1	-0.2	-0.6	100.0%	-4.5
11126	AT1G32150.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr1:11565498-11568511 FORWARD   Aliases: F3C3.7, F3C3_7	3.9	3.8	0.1	0.6	100.0%	-5.1
11127	AT1G10320.1   U2 snRNP auxiliary factor-related, similar to U2 small nuclear ribonucleoprotein auxiliary factor 35 kD subunit related protein 1 (sp:Q15695)   chr1:3384166-3388375 REVERSE   Aliases: F14N23.20, F14N23_20	5.7	6.4	-0.7	-0.6	100.0%	-4.7
11128	AT2G20500.1   expressed protein   chr2:8842201-8843125 REVERSE   Aliases: T13C7.9, T13C7_9	2.7	2.6	0.1	0.6	100.0%	-5.1
11129	AT2G17450.1   Symbol: RHA3A   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:7583556-7584382 REVERSE   Aliases: F5J6.22, RING H2 FINGER PROTEIN RHA3A	6.9	6.7	0.2	0.6	100.0%	-4.6
11130	AT1G56620.1   pectinesterase inhibitor domain-containing protein   chr1:21223483-21224022 FORWARD   Aliases: F25P12.14, F25P12_14	2.5	2.6	-0.1	-0.6	100.0%	-5.6
11131	AT4G17910.1   zinc finger (C3HC4-type RING finger) family protein / pentatricopeptide (PPR) repeat-containing protein, contains Pfam domains PF01535: PPR repeat and PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:9948866-9960416 REVERSE   Aliases: T6K21.90, T6K21_90	3.1	3.2	-0.1	-0.6	100.0%	-5.4
11132	AT2G14330.1   expressed protein, similar to At3g45350, At4g09400   chr2:6081244-6082476 FORWARD   Aliases: T1O16.8, T1O16_8	2.3	2.4	-0.1	-0.6	100.0%	-5.8
11133	AT5G52890.1   AT hook motif-containing protein, contains Pfam profile PF02178: AT hook motif   chr5:21462061-21464440 REVERSE   Aliases: MXC20.12, MXC20_12	2.3	2.4	-0.1	-0.6	100.0%	-5.4
11134	AT2G42710.1   ribosomal protein L1 family protein   chr2:17789385-17792140 FORWARD   Aliases: F14N22.3	4.7	4.6	0.1	0.6	100.0%	-4.9
11135	AT1G73870.1   zinc finger (B-box type) family protein   chr1:27782839-27784337 FORWARD   Aliases: F2P9.26, F2P9_26	4.3	4.1	0.3	0.6	100.0%	-4.7
11136	AT3G45380.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr3:16655506-16658157 REVERSE   Aliases: F18N11.140	3.1	3.2	-0.1	-0.6	100.0%	-5.8
11137	AT4G16600.1   glycogenin glucosyltransferase (glycogenin)-related, low similarity to glycogenin-1 from Rattus norvegicus (SP:O08730), Homo sapiens (GI:496895), Mus musculus (SP:Q9R062)   chr4:9350061-9352729 FORWARD   Aliases: DL4325W, FCAALL.404	4.2	4.3	-0.1	-0.6	100.0%	-5.4
11138	AT3G58160.1   Symbol: XIJ   myosin heavy chain, putative, similar to myosin heavy chain (Arabidopsis thaliana) gi:602328:emb:CAA84067.   chr3:21545774-21552854 FORWARD   Aliases: ATMYOS3, ATXIJ, F9D24.70, MYA3	2.3	2.4	-0.1	-0.6	100.0%	-5.7
11139	AT3G60530.1   zinc finger (GATA type) family protein, identical to cDNA for GATA transcription factor 4 GI:2959735   chr3:22384252-22385362 FORWARD   Aliases: T8B10.190	3.0	3.1	-0.1	-0.6	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11140	AT2G36240.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g09900.1); similar to putative pentatricopeptide repeat protein [Oryza sativa (japonica cultivar-group)] (GB:NP_909693.1); contains InterPro domain PPR repeat (InterPro:IPR002885); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr2:15202732-15204310 FORWARD   Aliases: F2H17.15, F2H17_15	8.7	8.4	0.3	0.6	100.0%	-4.7
11141	AT1G55580.1   Symbol: LAS   scarecrow transcription factor family protein, contains Pfam profile PF03514: GRAS family transcription factor   chr1:20767772-20769109 FORWARD   Aliases: F20N2.1, LATERAL SUPPRESSOR	2.7	2.5	0.1	0.6	100.0%	-5.1
11142	AT3G13120.1   30S ribosomal protein S10, chloroplast, putative, similar to 30S ribosomal protein S10 GB:P02364 (Escherichia coli) (est matches suggest the N-terminal extension)   chr3:4219790-4221637 REVERSE   Aliases: MJG19.7	5.9	6.2	-0.3	-0.6	100.0%	-4.6
11143	AT3G29660.1   hypothetical protein   chr3:11525003-11526500 FORWARD   Aliases: MOD1.2	3.0	3.1	-0.1	-0.6	100.0%	-5.4
11144	AT4G23150.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:12125742-12128343 FORWARD   Aliases: F21P8.40, F21P8_40	2.2	2.2	-0.0	-0.6	100.0%	-5.9
11145	AT4G38150.2   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At5g61990.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD62309.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr4:17900804-17902154 REVERSE   Aliases: F20D10.270, F20D10_270	3.5	3.7	-0.2	-0.6	100.0%	-4.8
11146	AT3G19460.1   reticulon family protein (RTNLB11), weak similarity to neuroendocrine-specific protein C (Homo sapiens) GI:307311; identical to cDNA RTNLB11 GI:32331878	5.5	5.7	-0.1	-0.6	100.0%	-4.8
11147	AT2G05090.1   hypothetical protein, includes At5g37080, At5g37170, At2g05090   chr2:1818139-1820698 REVERSE   Aliases: F1013.22, F1013_22	2.5	2.6	-0.1	-0.6	100.0%	-5.7
11148	AT4G30420.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575; contains Pfam profile PF00892: Integral membrane protein   chr4:14877075-14878920 FORWARD   Aliases: F17I23.240, F17I23_240	4.2	4.5	-0.3	-0.6	100.0%	-4.3
11149	AT4G31950.1   Symbol: CYP82C3   cytochrome P450 family protein, cytochrome P450 monooxygenase, Pisum sativum, PATCHX:G894153   chr4:15455169-15457127 FORWARD   Aliases: F11C18.9	2.4	2.4	-0.1	-0.6	100.0%	-5.9
11150	AT4G05640.1   hypothetical protein   chr4:3022681-3023682 FORWARD   Aliases: F21I2.30, F21I2_30	2.4	2.3	0.1	0.6	100.0%	-4.9
11151	AT1G29900.1   Symbol: CARB   carbamoyl-phosphate synthase family protein, similar to carbamoylphosphate synthetase GI:6552726 from (Medicago sativa); contains Pfam profiles PF02786: Carbamoyl-phosphate synthase L chain ATP binding domain, PF00289: Carbamoyl-phosphate synthase L chain N-terminal domain, PF02787: Carbamoyl-phosphate synthetase large chain oligomerisation domain   chr1:10468038-10472195 FORWARD   Aliases: CARBAMOYL PHOSPHATE SYNTHETASE B, CARBAMOYL PHOSPHATE SYNTHETASE LARGE SUBUNIT, F1N18.6, F1N18_6	8.8	9.2	-0.4	-0.6	100.0%	-4.5
11152	AT3G24130.1   pectinesterase family protein, contains Pfam profile: PF01095 Pectinesterase   chr3:8711670-8713368 REVERSE   Aliases: MUJ8.16	2.5	2.4	0.1	0.6	100.0%	-5.1
11153	AT1G33640.1   hypothetical protein, contains similarity to epidermal growth factor receptor-like protein GB:AAB31972 GI:9256501 from (Xiphophorus maculatus)   chr1:12195702-12195950 REVERSE   Aliases: T1E4.1	3.3	3.5	-0.1	-0.6	100.0%	-5.2
11154	AT3G02125.1   expressed protein   chr3:378212-379389 FORWARD   Aliases: None	2.4	2.3	0.1	0.6	100.0%	-5.5
11155	AT5G54470.1   zinc finger (B-box type) family protein, similar to unknown protein (pir::T05755)   chr5:22131660-22132683 REVERSE   Aliases: F24B18.9, F24B18_9	3.9	3.7	0.2	0.6	100.0%	-5.0
11156	AT1G79360.1   transporter-related, low similarity to SP:O76082 Organic cation/carnitine transporter 2 (Solute carrier family 22, member 5) (High-affinity sodium-dependent carnitine cotransporter) {Homo sapiens}; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:29858931-29860714 REVERSE   Aliases: YUP8H12R.2, YUP8H12R_2	3.3	3.4	-0.1	-0.6	100.0%	-5.0
11157	AT4G24400.1   Symbol: CIPK8   CBL-interacting protein kinase 8 (CIPK8), identical to CBL-interacting protein kinase 8 (Arabidopsis thaliana) GP:13249115:gb:AAK16683; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain   chr4:12617299-12620693 FORWARD   Aliases: CBL INTERACTING PROTEIN KINASE 8, PKS11, PROTEIN KINASE 11, T22A6.230, T22A6_230	6.6	7.0	-0.4	-0.6	100.0%	-4.7
11158	AT2G35740.1   sugar transporter family protein, similar to proton myo-inositol transporter (Homo sapiens) GI:15211933; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:15031568-15033493 REVERSE   Aliases: T20F21.7, T20F21_7	2.6	2.7	-0.1	-0.6	100.0%	-5.3
11159	AT4G32920.1   glycine-rich protein   chr4:15887578-15896009 REVERSE   Aliases: F26P21.40, F26P21_40	4.2	4.4	-0.1	-0.6	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11160	AT5G65010.2   Symbol: ASN2   asparagine synthetase 2 (ASN2), identical to asparagine synthetase (ASN2) (Arabidopsis thaliana) GI:3859536   chr5:25986416-25989801 FORWARD   Aliases: ASPARAGINE SYNTHETASE 2, MXK3.25, MXK3_25	6.3	6.6	-0.3	-0.6	100.0%	-4.2
11161	AT4G03660.1   hypothetical protein, similar to A. thaliana hypothetical protein T6P5.8, GenBank accession number AC005970   chr4:1625144-1625893 FORWARD   Aliases: T5L23.16, T5L23_16	2.8	2.8	-0.1	-0.6	100.0%	-5.8
11162	AT3G30560.1   hypothetical protein   chr3:12154428-12160021 FORWARD   Aliases: MQP15.20	2.7	2.6	0.2	0.6	100.0%	-5.1
11163	AT4G14890.1   ferredoxin family protein, similar to SP:P00252 Ferredoxin I from Nostoc muscorum, SP:P00248 Ferredoxin from Mastigocladus laminosus, SP:P00244 Ferredoxin I from Aphanizomenon flos-aquae; contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain   chr4:8520827-8521448 FORWARD   Aliases: DL3485W, FCAALL.7	8.3	8.6	-0.3	-0.6	100.0%	-4.1
11164	AT5G49450.1   bZIP family transcription factor, similar to bZIP transcription factor GI:1769891 from (Arabidopsis thaliana)   chr5:20069055-20069961 FORWARD   Aliases: K7J8.13, K7J8_13	5.9	5.6	0.3	0.6	100.0%	-4.6
11165	AT1G78080.1   Symbol: RAP2.4	3.9	3.6	0.2	0.6	100.0%	-4.4
11166	AT2G05540.1   glycine-rich protein   chr2:2033181-2034214 FORWARD   Aliases: T20G20.11, T20G20_11	4.2	4.1	0.1	0.6	100.0%	-5.0
11167	AT4G21580.2   similar to NADP-dependent oxidoreductase, putative [Arabidopsis thaliana] (TAIR:At5g61510.1); similar to Putative quinone oxidoreductase [Oryza sativa] (GB:AAK98702.1); contains InterPro domain Zinc-containing alcohol dehydrogenase superfamily (InterPro:IPR002085)	9.8	9.4	0.3	0.6	100.0%	-4.8
11168	AT3G16130.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr3:5466252-5468780 FORWARD   Aliases: KINASE PARTNER PROTEIN LIKE, KPP LIKE, MSL1.17	2.6	2.5	0.1	0.6	100.0%	-5.5
11169	AT1G48410.2   Symbol: AGO1   argonaute protein (AGO1), identical to SP:O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain   chr1:17889766-17896236 REVERSE   Aliases: ARGONAUTE 1, ARGONAUTE1, T1N15.2, T1N15_2	9.2	9.5	-0.4	-0.6	100.0%	-4.8
11170	AT1G25530.1   lysine and histidine specific transporter, putative, similar to lysine and histidine specific transporter GI:2576361 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:8964531-8967378 REVERSE   Aliases: F2J7.5, F2J7_5	9.0	8.5	0.5	0.6	100.0%	-4.4
11171	AT3G04240.1   Symbol: SEC   O-linked N-acetyl glucosamine transferase, putative, similar to O-GlcNAc transferase, Homo sapiens (SP:O15294), Rattus norvegicus (SP:P56558); contains Pfam profile PF00515: TPR Domain; identical to cDNA GI:18139886   chr3:1113941-1120879 REVERSE   Aliases: SECRET AGENT, T6K12.14, T6K12_14	7.2	7.5	-0.2	-0.6	100.0%	-4.7
11172	AT3G27390.1   expressed protein   chr3:10134450-10137730 REVERSE   Aliases: K1G2.10	3.7	3.4	0.2	0.6	100.0%	-4.4
11173	AT4G09640.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr4:6088214-6090885 REVERSE   Aliases: T25P22.80, T25P22_80	5.9	5.7	0.2	0.6	100.0%	-4.4
11174	AT1G79370.1   Symbol: CYP79C1   cytochrome P450 family protein, similar to cytochrome P450 GI:984542 (Sorghum bicolor); similar to cytochrome P450 GI:6739530 (Manihot esculenta)   chr1:29862827-29865056 FORWARD   Aliases: YUP8H12R.1, YUP8H12R_1	2.2	2.3	-0.1	-0.6	100.0%	-5.5
11175	AT2G06030.1   expressed protein   chr2:2352158-2353770 REVERSE   Aliases: F5K7.21, F5K7_21	4.0	3.9	0.1	0.6	100.0%	-4.9
11176	AT5G03530.1   Symbol: ATRAB ALPHA   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family	4.7	4.5	0.2	0.6	100.0%	-4.9
11177	AT5G53430.1   Symbol: SDG29   PHD finger family protein / SET domain-containing protein (TX5), contains Pfam domain, PF00628: PHD-finger and PF00856: SET domain; identical to cDNA trithorax 5 (TX5) partial cds GI:16118406   chr5:21694372-21700720 FORWARD   Aliases: MYN8.4, MYN8_4, SET DOMAIN GROUP 29	3.8	4.0	-0.1	-0.6	100.0%	-4.8
11178	AT3G07890.1   RabGAP/TBC domain-containing protein, similar to plant adhesion molecule 1 (Arabidopsis thaliana) GI:3511223; contains Pfam profile PF00566: TBC domain   chr3:2516310-2518917 REVERSE   Aliases: F17A17.23	3.3	3.4	-0.1	-0.6	100.0%	-5.0
11179	AT3G63070.1   PWWP domain-containing protein, putative transcription factor HUA2, Arabidopsis thaliana, EMBL:AF116556   chr3:23313340-23320633 FORWARD   Aliases: T20O10.170	4.3	4.6	-0.3	-0.6	100.0%	-4.7
11180	AT4G37790.1   Symbol: HAT22   homeobox-leucine zipper protein 22 (HAT22) / HD-ZIP protein 22, identical to homeobox-leucine zipper protein HAT22 (HD-ZIP protein 22) (SP:P46604) (Arabidopsis thaliana)   chr4:17768130-17769600 FORWARD   Aliases: HOMEBOX PROTEIN, T28I19.70, T28I19_70	4.7	4.2	0.4	0.6	100.0%	-4.3
11181	AT3G05030.1   Symbol: NHX2   sodium proton exchanger, putative (NHX2), similar to sodium proton exchanger Nhx1 GB:AAD16946 (Arabidopsis thaliana); Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563   chr3:1393304-1396790 REVERSE   Aliases: ATNHX2, T9J14.2, T9J14_2	5.4	5.6	-0.1	-0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11182	AT4G17540.1   expressed protein   chr4:9775868-9777827 FORWARD   Aliases: DL4805W, FCAALL.37	6.6	6.8	-0.2	-0.6	100.0%	-4.6
11183	AT5G47520.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB11J Gl:1370160 from (Lotus japonicus)   chr5:19294588-19295593 REVERSE   Aliases: MNJ7.11, MNJ7_11	7.3	7.1	0.2	0.6	100.0%	-4.6
11184	AT1G04310.1   Symbol: ERS2   ethylene receptor-related, similar to ethylene receptor CS-ETR2 (Cucumis sativus) Gl:6136818; contains Pfam profiles PF01590: GAF domain, PF00512: His Kinase A (phosphoacceptor) domain	4.3	4.1	0.1	0.6	100.0%	-4.9
11185	AT5G14680.1   universal stress protein (USP) family protein, similar to ER6 protein (Lycopersicon esculentum) Gl:5669654; contains Pfam profile PF00582: universal stress protein family   chr5:4730910-4733084 REVERSE   Aliases: T15N1.170, T15N1_170	7.9	7.7	0.2	0.6	100.0%	-4.8
11186	AT4G30996.1   expressed protein   chr4:15101366-15102690 FORWARD   Aliases: None	7.5	7.7	-0.2	-0.6	100.0%	-4.9
11187	AT4G14500.1   expressed protein, weak similarity to SP:Q9UKL6 Phosphatidylcholine transfer protein (PC-TP) {Homo sapiens}   chr4:8334172-8337269 FORWARD   Aliases: DL3290W, FCAALL.198	8.3	8.4	-0.1	-0.6	100.0%	-5.0
11188	AT5G57650.1   eukaryotic translation initiation factor-related, contains weak similarity to Swiss-Prot:Q38884 eukaryotic translation initiation factor 3 subunit 2 (eIF-3 beta) (eIF3 p36) (eIF3i) (TGF-beta receptor interacting protein 1) (TRIP-1) (Arabidopsis thaliana)   chr5:23363023-23363511 REVERSE   Aliases: MUA2.24, MUA2_24	2.5	2.6	-0.1	-0.6	100.0%	-5.6
11189	AT2G18290.1   anaphase-promoting complex, subunit 10 family / APC10 family, contains Pfam PF03256: Anaphase-promoting complex, subunit 10 (APC10) domain; similar to anaphase promoting complex subunit APC10 (Gl:6463666) (Homo sapiens)   chr2:7955417-7957235 REVERSE   Aliases: T30D6.20, T30D6_20	7.3	7.5	-0.2	-0.6	100.0%	-4.8
11190	AT3G04730.1   Symbol: IAA16   auxin-responsive protein / indoleacetic acid-induced protein 16 (IAA16), identical to SP:O24407 Auxin-responsive protein IAA16 (Indoleacetic acid-induced protein 16) {Arabidopsis thaliana}   chr3:1288618-1290608 REVERSE   Aliases: F7O18.22, F7O18_22	5.3	5.8	-0.5	-0.6	100.0%	-4.6
11191	AT4G16920.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:9519192-9525710 REVERSE   Aliases: DL4490C, FCAALL.311	3.6	3.9	-0.3	-0.6	100.0%	-4.3
11192	AT5G08510.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:2753100-2755102 FORWARD   Aliases: F8L15.21	4.4	4.3	0.2	0.6	100.0%	-4.8
11193	AT2G17940.1   expressed protein, contains Pfam PF05701: Plant protein of unknown function (DUF827)   chr2:7809907-7811029 FORWARD   Aliases: T27K22.19, T27K22_19	3.4	3.2	0.1	0.6	100.0%	-5.0
11194	AT2G32930.1   Symbol: ZFN2   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:13973067-13975496 REVERSE   Aliases: T21L14.13, T21L14_13, ZINC FINGER PROTEIN 2	2.7	2.8	-0.1	-0.6	100.0%	-5.3
11195	AT5G44740.2   UMUC-like DNA repair family protein, low similarity to DNA polymerase eta (Homo sapiens) Gl:11463971; contains Pfam profile PF00817: ImpB/MucB/SamB family   chr5:18065011-18069102 REVERSE   Aliases: K23L20.8, K23L20_8	3.2	3.3	-0.1	-0.6	100.0%	-5.0
11196	AT5G51840.1   expressed protein   chr5:21089195-21091664 FORWARD   Aliases: MIO24.2, MIO24_2	5.5	5.8	-0.3	-0.6	100.0%	-4.8
11197	AT5G51110.1   expressed protein   chr5:20795360-20796660 REVERSE   Aliases: MWD22.5, MWD22_5	6.0	5.8	0.2	0.6	100.0%	-4.4
11198	AT2G02880.1   mucin-related, similar to putative mucin Gl:18071389 (Oryza sativa)   chr2:841260-843359 FORWARD   Aliases: T17M13.5, T17M13_5	6.1	6.4	-0.2	-0.6	100.0%	-4.4
11199	AT4G34040.1   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:16304285-16308608 REVERSE   Aliases: F28A23.200, F28A23_200	5.2	5.3	-0.1	-0.6	100.0%	-5.2
11200	AT3G54690.1   sugar isomerase (SIS) domain-containing protein / CBS domain-containing protein, similar to SP:Q47334 Polysialic acid capsule expression protein kpsF {Escherichia coli}; contains Pfam profiles PF01380: sugar isomerase (SIS) domain, PF00571: CBS domain   chr3:20257517-20259002 FORWARD   Aliases: T5N23.50	5.4	5.6	-0.2	-0.6	100.0%	-4.5
11201	AT1G58230.1   WD-40 repeat family protein / beige-related, contains Pfam PF00400: WD domain, G-beta repeat; similar to Lipopolysaccharide-responsive and beige-like anchor protein (CDC4-like protein) (Beige-like protein) (SP:P50851) (Homo sapiens)	4.8	5.0	-0.2	-0.6	100.0%	-4.8
11202	AT2G36380.1   ABC transporter family protein, related to multi drug resistance proteins and P-glycoproteins   chr2:15264662-15270766 FORWARD   Aliases: F1O11.1, F1O11_1	6.2	6.1	0.2	0.6	100.0%	-4.6
11203	AT1G16540.1   Symbol: ABA3/LOS5/SIR3	3.4	3.2	0.2	0.6	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11204	AT1G70720.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from <i>Lycopersicon esculentum</i> SP:Q43143, <i>Arabidopsis thaliana</i> SP:Q42534, <i>Phaseolus vulgaris</i> SP:Q43111; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:26670070-26670866 FORWARD   Aliases: F5A18.10, F5A18_10	2.2	2.3	-0.1	-0.6	100.0%	-5.5
11205	AT5G52740.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:21399756-21400406 FORWARD   Aliases: F6N7.23, F6N7_23	2.9	2.8	0.1	0.6	100.0%	-5.4
11206	AT1G69340.1   appr-1-p processing enzyme family protein, contains Pfam domain PF01661: Appr-1-p processing enzyme family   chr1:26069419-26073484 FORWARD   Aliases: F10D13.28, F10D13_28	6.3	6.5	-0.2	-0.6	100.0%	-4.9
11207	AT4G01610.2   cathepsin B-like cysteine protease, putative, similar to cathepsin B-like cysteine proteinase GI:609175 from ( <i>Nicotiana rustica</i> ); contains an unusually short, 5nt exon   chr4:694695-697126 FORWARD   Aliases: T15B16.17, T15B16_17	9.1	8.6	0.5	0.6	100.0%	-4.6
11208	AT2G22800.1   Symbol: HAT9   homeobox-leucine zipper protein 9 (HAT9) / HD-ZIP protein 9, identical to GB:U09341   chr2:9711796-9713230 REVERSE   Aliases: T30L20.6, TRANSCRIPTION FACTOR HAT9	2.8	2.3	0.4	0.6	100.0%	-4.3
11209	AT1G30700.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) ( <i>Eschscholzia californica</i> ); contains PF01565 FAD binding domain   chr1:10892552-10894554 FORWARD   Aliases: T5I8.15, T5I8_15	2.7	3.0	-0.3	-0.6	100.0%	-4.6
11210	AT3G16250.1   ferredoxin-related, contains Pfam profile: PF00111 2Fe-2S iron-sulfur cluster binding domains   chr3:5506268-5508420 REVERSE   Aliases: MYA6.6	2.7	2.9	-0.1	-0.6	100.0%	-5.1
11211	AT2G36590.1   Symbol: ProT3   proline transporter, putative, strong similarity to proline transporter 1 GI:1769901 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr2:15349758-15352416 REVERSE   Aliases: ATPROT3, F1O11.22, F1O11_22, PROLINE TRANSPORTER 3	2.7	2.6	0.1	0.6	100.0%	-5.2
11212	AT1G70250.1   receptor serine/threonine kinase, putative, similar to to receptor serine/threonine kinase PR5K gi:1235680:gb:AAC49208   chr1:26456628-26459751 FORWARD   Aliases: F20P5.3, F20P5_3	3.4	3.5	-0.1	-0.6	100.0%	-5.4
11213	AT5G16960.1   NADP-dependent oxidoreductase, putative, similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), <i>Arabidopsis thaliana</i>   chr5:5574284-5575913 REVERSE   Aliases: F2K13.110, F2K13_110	4.2	4.4	-0.2	-0.6	100.0%	-4.5
11214	AT1G79790.2   haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	6.8	6.6	0.2	0.6	100.0%	-4.8
11215	AT1G60140.1   Symbol: ATTPS10   glycosyl transferase family 20 protein / trehalose-phosphatase family protein, contains Pfam profile: PF02358 trehalose-phosphatase   chr1:22180599-22184495 REVERSE   Aliases: T13D8.4, T13D8_4, TPS10	5.0	4.7	0.3	0.6	100.0%	-4.5
11216	AT3G03410.1   calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced SP:P25070 from ( <i>Arabidopsis thaliana</i> )   chr3:811331-811726 REVERSE   Aliases: T21P5.17, T21P5_17	2.9	2.8	0.1	0.6	100.0%	-5.1
11217	AT1G68570.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:25750400-25753938 FORWARD   Aliases: F24J5.19, F24J5_19	3.3	3.2	0.2	0.6	100.0%	-4.9
11218	AT3G50640.1   expressed protein   chr3:18815008-18815644 REVERSE   Aliases: T3A5.20	3.1	3.2	-0.1	-0.6	100.0%	-5.2
11219	AT3G26310.1   Symbol: CYP71B35   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr3:9642326-9644016 REVERSE   Aliases: F20C19.3	3.5	3.4	0.2	0.6	100.0%	-4.9
11220	AT4G01430.2   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from ( <i>Medicago truncatula</i> )   chr4:585609-588027 FORWARD   Aliases: F3D13.4, F3D13_4	8.5	8.0	0.5	0.6	100.0%	-4.5
11221	AT4G35420.1   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family, similar to dihydroflavonol 4-reductase ( <i>Rosa hybrid cultivar</i> , GI:1332411), CPRD14 protein ( <i>Vigna unguiculata</i> , GI:1854445)   chr4:16833950-16835624 REVERSE   Aliases: F15J1.1	3.1	3.0	0.1	0.6	100.0%	-4.9
11222	AT2G31380.1   Symbol: STH   zinc finger (B-box type) family protein / salt tolerance-like protein (STH), contains Pfam profile PF00643: B-box zinc finger; identical to cDNA B-box zinc finger protein STH GI:12698721, SP:Q9SID1 Salt tolerance-like protein ( <i>Arabidopsis thaliana</i> )   chr2:13389030-13390834 FORWARD   Aliases: STO HOMOLOG, T28P16.13, T28P16_13	4.0	3.8	0.2	0.6	100.0%	-4.6
11223	AT1G61760.1   harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, similar to hin1 ( <i>Nicotiana tabacum</i> ) GI:1619321   chr1:22811105-22811779 REVERSE   Aliases: T13M11.12, T13M11_12	2.2	2.2	-0.1	-0.6	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11224	AT5G39600.1   expressed protein   chr5:15871157-15872420 REVERSE   Aliases: MIJ24.9, MIJ24_9	6.5	6.8	-0.3	-0.6	100.0%	-4.3
11225	AT2G39330.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767, myrosinase binding protein (Brassica napus) GI:1711296; contains Pfam profile PF01419 jacalin-like lectin domain	2.9	3.0	-0.1	-0.6	100.0%	-5.2
11226	AT4G14560.1   Symbol: IAA1   auxin-responsive protein / indoleacetic acid-induced protein 1 (IAA1), identical to SP:P49677 Auxin-responsive protein IAA1 (Indoleacetic acid-induced protein 1) {Arabidopsis thaliana}	4.8	4.6	0.2	0.6	100.0%	-4.7
11227	AT1G11860.2   aminomethyltransferase, putative, similar to aminomethyltransferase, mitochondrial precursor SP:O49849 from (Flaveria anomala)   chr1:4001294-4003441 FORWARD   Aliases: F12F1.30, F12F1_30	9.5	9.7	-0.2	-0.6	100.0%	-4.9
11228	AT3G03770.1   leucine-rich repeat transmembrane protein kinase, putative, may contain C-terminal ser/thr protein kinase domain, similar to serine/threonine protein kinase Pto GB:AAB47421 (Lycopersicon esculentum)   chr3:945149-949045 REVERSE   Aliases: F20H23.20, F20H23_20	3.8	3.9	-0.1	-0.6	100.0%	-5.2
11229	AT3G46450.2   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, contains Pfam PF00650 : CRAL/TRIO domain; similar to polyphosphoinositide binding protein Ssh1p (GI::2739044) {Glycine max}   chr3:17103923-17106580 REVERSE   Aliases: F18L15.170	3.8	3.7	0.1	0.6	100.0%	-5.2
11230	AT5G15860.2   expressed protein   chr5:5178508-5181293 REVERSE   Aliases: F14F8.240, F14F8_240	7.0	6.6	0.4	0.6	100.0%	-4.4
11231	AT1G70895.1   Symbol: CLE17   CLE17, putative, CLAVATA3/ESR-Related 17 (CLE17)   chr1:26731561-26732416 FORWARD   Aliases: CLAVATA3/ESR RELATED 17	3.4	3.5	-0.1	-0.6	100.0%	-5.1
11232	AT1G01750.1   actin-depolymerizing factor, putative, strong similarity to SP:P30175 Actin-depolymerizing factor (ADF) {Lilium longiflorum}; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein   chr1:275366-276310 FORWARD   Aliases: T1N6.16, T1N6_16	3.0	3.3	-0.2	-0.6	100.0%	-4.3
11233	AT1G31500.3   endonuclease/exonuclease/phosphatase family protein, low similarity to SP:P31384 Glucose-repressible alcohol dehydrogenase transcriptional effector (Carbon catabolite repressor protein 4) {Saccharomyces cerevisiae}; contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr1:11273617-11276518 REVERSE   Aliases: F27M3.27, F27M3_27	3.0	3.2	-0.1	-0.6	100.0%	-5.0
11234	AT5G46690.1   basic helix-loop-helix (bHLH) family protein, contains similarity to bHLH DNA-binding protein   chr5:18962842-18964864 FORWARD   Aliases: MZA15.10, MZA15_10	1.9	2.0	-0.1	-0.6	100.0%	-5.8
11235	AT4G27390.1   expressed protein, hypothetical protein, Synechocystis sp., PIR2:S77328   chr4:13703145-13704699 REVERSE   Aliases: F27G19.8	4.2	4.1	0.1	0.6	100.0%	-5.0
11236	AT1G49980.1   similar to UMUC-like DNA repair family protein [Arabidopsis thaliana] (TAIR:At5g44740.2); similar to putative DNA-directed polymerase, having alternative splicing products [Oryza sativa (japonica cultivar-group)] (GB:AAT81654.1); contains InterPro domain UMUC-like DNA-repair protein (InterPro:IPR001126)	6.1	5.9	0.2	0.6	100.0%	-5.2
11237	AT3G28020.1   expressed protein   chr3:10419143-10420386 REVERSE   Aliases: MMG15.6	3.9	3.7	0.2	0.6	100.0%	-4.9
11238	AT5G64800.1   Symbol: CLE21   CLE21, putative, CLAVATA3/ESR-Related 21 (CLE21)   chr5:25923309-25923629 FORWARD   Aliases: CLAVATA3/ESR RELATED 21, MXK3.2, MXK3_2	2.8	2.7	0.1	0.6	100.0%	-5.3
11239	AT5G51550.1   phosphate-responsive 1 family protein, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr5:20956720-20958121 REVERSE   Aliases: K17N15.10, K17N15_10	7.6	7.1	0.6	0.6	100.0%	-4.2
11240	AT3G25210.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 domain of unknown function   chr3:9181625-9183076 FORWARD   Aliases: MJL12.16	4.4	4.5	-0.1	-0.6	100.0%	-5.2
11241	AT5G26840.1   expressed protein   chr5:9442291-9442608 REVERSE   Aliases: F2P16.100, F2P16_100	4.6	4.4	0.2	0.6	100.0%	-5.0
11242	AT4G14605.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr4:8378476-8380635 FORWARD   Aliases: None	3.5	3.6	-0.1	-0.6	100.0%	-5.1
11243	AT4G36890.1   glycosyl transferase family 43 protein, low similarity to Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1, Homo sapiens (SP:Q9P2W7), Rattus norvegicus (SP:O35789); contains Pfam domain Glycosyltransferase family 43 (PF03360)   chr4:17379173-17381777 REVERSE   Aliases: AP22.51, AP22_51	8.1	7.6	0.5	0.6	100.0%	-4.6
11244	AT2G40640.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g05230.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468527.1)   chr2:16968261-16970283 REVERSE   Aliases: T7D17.18, T7D17_18	2.7	2.8	-0.1	-0.6	100.0%	-5.4
11245	AT5G55570.1   expressed protein   chr5:22531756-22532486 REVERSE   Aliases: MDF20.1, MDF20_1	3.8	3.5	0.2	0.6	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11246	AT2G16070.2   expressed protein   chr2:6990974-6992544 REVERSE   Aliases: F7H1.9, F7H1_9	8.3	8.1	0.2	0.6	100.0%	-4.5
11247	AT2G26230.1   uricase / urate oxidase / nodulin 35, putative, identical to uricase SP:O04420 from (Arabidopsis thaliana)   chr2:11171668-11174268 FORWARD   Aliases: T1D16.13, T1D16_13	7.2	7.6	-0.4	-0.6	100.0%	-4.6
11248	AT1G27550.1   F-box family protein, similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)   chr1:9568800-9569317 REVERSE   Aliases: T17H3.5, T17H3_5	2.5	2.4	0.1	0.6	100.0%	-5.7
11249	AT5G62840.1   phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family   chr5:25245451-25246909 REVERSE   Aliases: MQB2.16, MQB2_16	5.6	5.3	0.3	0.6	100.0%	-4.1
11250	AT2G33150.1   Symbol: PED1   acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative, similar to 3-ketoacyl-CoA thiolase (E.C. 2.3.1.16) from (Arabidopsis thaliana) GI:2981616, (Cucumis sativus) GI:393707, (Cucurbita cv. Kurokawa Amakuri) GI:1694621; contains InterPro accession IPR002155: Thiolase	9.1	8.5	0.6	0.6	100.0%	-4.5
11251	AT1G31260.1   Symbol: ZIP10   metal transporter, putative (ZIP10), identical to putative metal transporter ZIP10 (Arabidopsis thaliana) gi:17385792:gb:AAL38436; similar to iron-regulated transporter 2 GB:AAD30549 GI:4836773 from (Lycopersicon esculentum); member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563   chr1:11175540-11177343 REVERSE   Aliases: T19E23.6, T19E23_6	3.2	3.1	0.1	0.6	100.0%	-5.2
11252	AT3G28430.1   expressed protein, non-consensus GC donor splice site at exon 16	3.3	3.4	-0.1	-0.6	100.0%	-5.1
11253	AT3G03830.1   auxin-responsive protein, putative, similar to auxin-inducible SAUR (Small Auxin Up RNAs) (GI:3043536) (Raphanus sativus)   chr3:979991-980495 REVERSE   Aliases: F20H23.15, F20H23_15	2.5	2.6	-0.1	-0.6	100.0%	-5.5
11254	AT3G49450.1   F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	-0.1	-0.6	100.0%	-5.7
11255	AT2G23550.2   similar to hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] (TAIR:At2g23580.1); similar to B Chain B, Structural And Biochemical Studies Identify Tobacco Sabp2 As A Methylsalicylate Esterase And Further Implicate It In Plant Innate Immunity, Northeast Structural Genomics Target Ar2241 (GB:1Y7I); similar to D Chain D, Crystal Structure Of Salicylic Acid-Binding Protein 2 (Sabp2) From Nicotiana Tabacum, Nesg Target Ar2241 (GB:1XKL)   chr2:10034666-10035857 REVERSE   Aliases: F26B6.20, F26B6_20	3.1	3.0	0.1	0.6	100.0%	-5.3
11256	AT5G63860.1   Symbol: UVR8   UVB-resistance protein (UVR8), identical to UVB-resistance protein UVR8 (GI:5478530, GB:AAD43920.1) (Arabidopsis thaliana); contains Pfam 00415: Regulator of chromosome condensation (RCC1)   chr5:25571734-25575978 REVERSE   Aliases: MGI19.7, MGI19_7, UV REPAIR DEFICIENT 8, UVB RESISTANCE 8	6.1	5.8	0.3	0.6	100.0%	-4.6
11257	AT3G47833.1   expressed protein   chr3:17659618-17661125 FORWARD   Aliases: None	9.6	9.7	-0.1	-0.6	100.0%	-5.0
11258	AT4G36530.2   hydrolase, alpha/beta fold family protein, low similarity to hydrolase (Sphingomonas sp.) GI:3426124; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:17239961-17241938 REVERSE   Aliases: AP22.96, AP22_96	8.2	8.0	0.1	0.6	100.0%	-4.9
11259	AT4G10260.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr4:6371482-6372766 REVERSE   Aliases: T9A4.3	3.0	3.2	-0.1	-0.6	100.0%	-5.1
11260	AT2G34370.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:14517561-14518970 FORWARD   Aliases: F13P17.21, F13P17_21	3.3	3.2	0.1	0.6	100.0%	-5.2
11261	AT2G38490.1   Symbol: CIPK22	3.2	3.1	0.1	0.6	100.0%	-4.8
11262	AT3G50010.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.6	4.6	0.1	0.6	100.0%	-5.7
11263	AT3G24640.1   expressed protein   chr3:8992296-8992768 FORWARD   Aliases: MSD24.4	2.2	2.3	-0.1	-0.6	100.0%	-5.6
11264	AT4G17245.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:9669377-9670017 FORWARD   Aliases: None	2.2	2.2	-0.1	-0.6	100.0%	-5.4
11265	AT4G38110.1   similar to PREDICTED: similar to MGC53988 protein [Gallus gallus] (GB:XP_415906.1)   chr4:17888521-17892120 REVERSE   Aliases: F20D10.230, F20D10_230	2.6	2.7	-0.1	-0.6	100.0%	-5.2
11266	AT1G65430.1   zinc finger protein-related, contains weak similarity to zinc finger proteins and a Pfam:PF01485 IBR domain   chr1:24304561-24309899 REVERSE   Aliases: T8F5.21, T8F5_21	7.0	6.7	0.2	0.6	100.0%	-4.6
11267	AT4G36350.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.4	3.5	-0.1	-0.6	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11268	AT5G65050.1   Symbol: AGL31   MADS-box protein (MAF2)	5.1	4.9	0.2	0.6	100.0%	-4.6
11269	AT5G65060.2   Symbol: MAF3   similar to MADS-box protein AGL27-II (AGL27) / MADS affecting flowering 1 (MAF1) [Arabidopsis thaliana] (TAIR:At1g77080.4); similar to flowering locus C [Brassica oleracea var. capitata] (GB:AAP31677.1); contains InterPro domain Transcription factor, MADS-box (InterPro:IPR002100); contains InterPro domain Transcription factor, K-box (InterPro:IPR002487)   chr5:26004723-26008538 FORWARD   Aliases: F15O5.2, F15O5_2, MADS AFFECTING FLOWERING 3	5.1	4.9	0.2	0.6	100.0%	-4.6
11270	AT2G36640.1   Symbol: ATECP63   late embryogenesis abundant protein (ECP63) / LEA protein, nearly identical to to LEA protein in group 3 (Arabidopsis thaliana) GI:1526424; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr2:15363933-15365691 REVERSE   Aliases: EMBRYONIC CELL PROTEIN 63, F13K3.4, F13K3_4, LEA	3.4	3.6	-0.2	-0.6	100.0%	-4.9
11271	AT5G20910.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:7092240-7094448 REVERSE   Aliases: F22D1.80, F22D1_80	5.2	5.4	-0.3	-0.6	100.0%	-4.6
11272	AT4G04690.1   F-box family protein (FBX15), contains F-box domain PF:00646   chr4:2373997-2375133 REVERSE   Aliases: T19J18.6, T19J18_6	3.3	3.2	0.1	0.6	100.0%	-5.1
11273	AT2G26460.1   RED family protein, similar to Red protein (RER protein) (Swiss-Prot:Q9Z1M8) (Mus musculus)   chr2:11262010-11266051 REVERSE   Aliases: T9J22.13, T9J22_13	6.3	6.5	-0.2	-0.6	100.0%	-5.0
11274	AT2G18350.1   zinc finger homeobox family protein / ZF-HD homeobox family protein   chr2:7978099-7979163 REVERSE   Aliases: T30D6.14, T30D6_14	3.9	3.7	0.2	0.6	100.0%	-4.6
11275	AT5G44280.1   zinc finger (C3HC4-type RING finger) family protein, contains similarity to polycomb-M33 interacting protein Ring1B (Mus musculus) GI:2239142; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:17853090-17856481 REVERSE   Aliases: K9L2.3, K9L2_3	2.8	2.9	-0.2	-0.6	100.0%	-5.1
11276	AT5G01990.1   auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547   chr5:377228-379908 REVERSE   Aliases: T7H20.40, T7H20_40	5.3	5.1	0.2	0.6	100.0%	-4.8
11277	AT5G38160.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family   chr5:15242997-15243438 FORWARD   Aliases: MXA21.18, MXA21_18	3.4	3.5	-0.2	-0.6	100.0%	-5.0
11278	AT3G29090.1   pectinesterase family protein, similar to pectinesterase precursor GB:Q43043 (Petunia integrifolia); contains Pfam profile: PF01095 pectinesterase   chr3:11074948-11076683 FORWARD   Aliases: MXE2.5	7.6	7.4	0.2	0.6	100.0%	-4.7
11279	AT4G16000.1   expressed protein   chr4:9063857-9064493 REVERSE   Aliases: DL4040C, FCAALL.25	3.2	3.3	-0.1	-0.6	100.0%	-5.1
11280	AT5G03905.1   hesB-like domain-containing protein, low similarity to HesB (Cyanothecae sp. PCC 8801) GI:2183309; contains Pfam profile PF01521: HesB-like domain   chr5:1052579-1054231 FORWARD   Aliases: None	6.1	6.2	-0.1	-0.6	100.0%	-4.9
11281	AT3G47390.1   cytidine/deoxycytidylate deaminase family protein, similar to riboflavin-specific deaminase (Actinobacillus pleuropneumoniae) GI:1173516; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding region   chr3:17473079-17475640 FORWARD   Aliases: T21L8.140	5.3	5.5	-0.2	-0.6	100.0%	-4.9
11282	AT1G43310.1   triose phosphate/phosphate translocator-related, similar to SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}   chr1:16348414-16348915 REVERSE   Aliases: F1I21.17, F1I21_17	9.4	10.1	-0.7	-0.6	100.0%	-4.7
11283	AT5G33320.1   Symbol: CUE1   triose phosphate/phosphate translocator, putative, similar to SWISS-PROT:P52178 triose phosphate/phosphate translocator (Cauliflower) {Brassica oleracea}   chr5:12606068-12608978 FORWARD   Aliases: ARAPPT, CAB UNDEREXPRESSED 1, F19N2.40, F19N2_40, PHOSPHATE/PHOSPHOENOLPYRUVATE TRANSLOCATOR, PHOSPHOENOLPYRUVATE/PHOSPHATE TRANSLOCATOR, PPT	9.4	10.1	-0.7	-0.6	100.0%	-4.7
11284	AT3G15870.1   fatty acid desaturase family protein, similar to delta 9 acyl-lipid desaturase (ADS1) GI:2970034 from (Arabidopsis thaliana)   chr3:5363124-5364431 FORWARD   Aliases: MSJ11.4	2.6	2.7	-0.1	-0.6	100.0%	-5.3
11285	AT5G06340.1   diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase, putative, similar to diadenosine 5',5'''-P1,P4-tetraphosphate hydrolase from (Lupinus angustifolius) GI:1888557, (Hordeum vulgare subsp. vulgare) GI:2564253; contains Pfam profile PF00293: NUDIX domain   chr5:1936407-1938112 FORWARD   Aliases: MHF15.14, MHF15_14	9.1	8.7	0.4	0.6	100.0%	-4.3
11286	AT5G07160.1   bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor   chr5:2220213-2220710 REVERSE   Aliases: T28J14.100, T28J14_100	2.4	2.5	-0.1	-0.6	100.0%	-5.5
11287	AT1G67970.1   Symbol: AT HSF A8   heat shock factor protein, putative (HSF5) / heat shock transcription factor, putative (HSTF5), identical to heat shock transcription factor 5 (HSF5) SP:Q9S7U5 from (Arabidopsis thaliana); contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr1:25488362-25490125 REVERSE   Aliases: HSF A8, T23K23.18, T23K23_18	5.1	4.9	0.2	0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11288	AT4G04070.1   expressed protein, low similarity to protective antigen (Streptococcus pyogenes) GI:8996050, fibrinogen-binding protein (Streptococcus equi) GI:3093478   chr4:1951540-1954606 REVERSE   Aliases: T24H24.5, T24H24_5	2.6	2.5	0.1	0.6	100.0%	-5.6
11289	AT1G35150.1   hypothetical protein   chr1:12864136-12866216 REVERSE   Aliases: T32G9.31, T32G9_31	2.6	2.5	0.1	0.6	100.0%	-5.7
11290	AT4G02450.1   glycine-rich protein, similar to several proteins containing a tandem repeat region such as Plasmodium falciparum GGM tandem repeat protein (GB:U27807)   chr4:1073774-1075878 REVERSE   Aliases: T14P8.5, T14P8_5	9.9	9.8	0.2	0.6	100.0%	-4.9
11291	AT3G10990.1   F-box family protein, contains TIGRfam:TIGR01640 F-box protein interaction domain   chr3:3446468-3447001 REVERSE   Aliases: F9F8.19	2.8	2.9	-0.1	-0.6	100.0%	-5.2
11292	AT2G21450.1   Symbol: CHR34   SNF2 domain-containing protein / helicase domain-containing protein, low similarity to SP:Q61687 Transcriptional regulator ATRX {Mus musculus}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr2:9186490-9189436 REVERSE   Aliases: CHR34, F3K23.21, F3K23_21	2.7	2.6	0.1	0.6	100.0%	-5.5
11293	AT3G24520.1   Symbol: AT HSFC1   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr3:8941073-8942881 FORWARD   Aliases: HSFC1, MOB24.9	6.2	6.0	0.3	0.6	100.0%	-4.6
11294	AT5G49190.1   Symbol: SUS2   sucrose synthase / sucrose-UDP glucosyltransferase (SUS2), nearly identical to SP:Q00917 Sucrose synthase (EC 2.4.1.13) (Sucrose-UDP glucosyltransferase) {Arabidopsis thaliana} (SUS2); contains Pfam profile: PF00862 sucrose synthase	3.0	3.0	0.1	0.6	100.0%	-5.3
11295	NA	12.1	12.0	0.1	0.6	100.0%	-6.0
11296	AT4G34860.2   similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At4g09510.1); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At1g35580.2); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At1g35580.1); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At1g22650.1); similar to beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative [Arabidopsis thaliana] (TAIR:At1g72000.1); similar to neutral invertase-like protein [Ipomoea batatas] (GB:BAD18099.1); similar to invertase, putative [Oryza sativa (japonica cultivar-group)] (GB:AAX95795.1); similar to putative alkaline/neutral invertase [Oryza sativa (japonica cultivar-group)] (GB:XP_466154.1); similar to OSJNBa0084A10.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_472554.1); similar to putative alkaline/neutral invertase [Oryza sativa (japonica cultivar-group)] (GB:XP_463958.1); contains InterPro domain Plant neutral invertase (InterPro:IPR006937)   chr4:16609344-16612625 REVERSE   Aliases: F11I11.100, F11I11_100	5.8	5.5	0.3	0.6	100.0%	-4.5
11297	AT1G07470.1   transcription factor IIA large subunit, putative / TFIIA large subunit, putative, nearly identical to transcription factor IIA large subunit GI:2826884 from (Arabidopsis thaliana); contains Pfam profile: PF03153 transcription factor IIA, alpha/beta subunit	7.3	7.7	-0.4	-0.6	100.0%	-4.2
11298	AT1G07480.2   transcription factor IIA large subunit / TFIIA large subunit (TFIIA-L), identical to transcription factor IIA large subunit GI:2826884 from (Arabidopsis thaliana)   chr1:2296471-2299467 REVERSE   Aliases: F22G5.14, F22G5_14	7.3	7.7	-0.4	-0.6	100.0%	-4.2
11299	AT1G25390.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:8906439-8908841 REVERSE   Aliases: F2J7.14, F2J7_14	5.1	5.3	-0.2	-0.6	100.0%	-4.3
11300	AT4G11930.1   hypothetical protein   chr4:7164898-7165716 FORWARD   Aliases: T26M18.140, T26M18_140	3.4	3.6	-0.1	-0.6	100.0%	-5.3
11301	AT2G05590.2   expressed protein, similar to nucleolar protein C7C (GI:13540302) (Rattus norvegicus)   chr2:2067094-2069203 FORWARD   Aliases: T20G20.6, T20G20_6	4.7	4.5	0.2	0.6	100.0%	-4.7
11302	AT2G30430.1   hypothetical protein   chr2:12975253-12975489 FORWARD   Aliases: T6B20.26, T6B20_26	2.2	2.2	-0.1	-0.6	100.0%	-5.8
11303	AT3G21580.2   expressed protein   chr3:7601975-7603727 REVERSE   Aliases: MIL23.15	5.2	5.0	0.2	0.6	100.0%	-4.6
11304	AT3G62370.1   expressed protein   chr3:23091734-23094240 FORWARD   Aliases: T12C14.70	7.4	7.1	0.3	0.6	100.0%	-4.6
11305	AT3G59300.1   expressed protein, hypothetical protein T2J13.20 - Arabidopsis thaliana, PIR:T46116   chr3:21929432-21933683 FORWARD   Aliases: F25L23.160	4.0	3.8	0.2	0.6	100.0%	-4.6
11306	AT3G14100.1   oligouridylate-binding protein, putative, similar to GB:CAB75429 (GI:6996560) from (Nicotiana glauca), contains Pfam profiles: PF00076 RNA recognition motif (3 copies)	8.2	7.8	0.4	0.6	100.0%	-4.7
11307	AT2G30100.1   ubiquitin family protein, low similarity to SP:Q9UQ13 Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8) {Homo sapiens}; contains Pfam profiles PF00240: Ubiquitin family, PF01535: PPR repeat, PF00560: Leucine Rich Repeat	6.1	6.4	-0.3	-0.6	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11308	AT5G01830.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr5:320692-323165 FORWARD   Aliases: T20L15.100, T20L15_100	5.2	4.9	0.3	0.6	100.0%	-4.5
11309	AT5G61430.1   Symbol: ANAC100   no apical meristem (NAM) family protein, PF02365 : No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (GI:1944132) (Arabidopsis thaliana)	3.2	3.3	-0.1	-0.6	100.0%	-5.1
11310	AT5G64520.3   Symbol: XRCC2   similar to LOC443613 protein [Xenopus laevis] (GB:AAH73049.1)   chr5:25805260-25807536 FORWARD   Aliases: MUB3.4, MUB3_4	4.3	4.0	0.3	0.6	100.0%	-4.2
11311	AT4G01290.1   expressed protein   chr4:538097-543869 REVERSE   Aliases: F2N1.34, F2N1_34	6.2	6.6	-0.3	-0.6	100.0%	-4.7
11312	AT5G16870.1   expressed protein   chr5:5546814-5548739 REVERSE   Aliases: F2K13.20, F2K13_20	3.9	3.8	0.1	0.6	100.0%	-5.0
11313	AT1G79650.3   Symbol: RAD23   DNA repair protein RAD23, putative, similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform II GI:1914685 from (Daucus carota); contains Pfam profiles PF00240: Ubiquitin family, PF00627: UBA/TS-N domain   chr1:29977003-29980147 REVERSE   Aliases: F20B17.8, F20B17_8	5.3	5.0	0.3	0.6	100.0%	-4.7
11314	AT1G63830.2   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; contains 1 predicted transmembrane domain   chr1:23689014-23690985 FORWARD   Aliases: T12P18.15, T12P18_15	8.0	7.6	0.4	0.6	100.0%	-4.4
11315	AT1G34590.1   expressed protein   chr1:12665145-12667796 FORWARD   Aliases: F12K21.7, F12K21_7	2.6	2.6	0.1	0.6	100.0%	-5.3
11316	ATCG00670.1   Symbol: CLPP1   Encodes the only ClpP (caseinolytic protease) encoded within the plastid genome. Contains a highly conserved catalytic triad of Ser-type proteases (Ser-His-Asp). Part of the 350 kDa chloroplast Clp complex. The name reflects nomenclature described in Adam et. al (2001).	9.7	9.3	0.4	0.6	100.0%	-4.6
11317	AT3G08950.1   electron transport SCO1/SenC family protein, similar to SP:P23833 SCO1 protein, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF02630: SCO1/SenC   chr3:2727220-2729606 FORWARD   Aliases: T16O11.9	7.2	7.0	0.2	0.6	100.0%	-4.4
11318	AT3G25580.1   thioredoxin-related, contains weak similarity to thioredoxin (Swiss-Prot:O17486) (Echinococcus granulosus)   chr3:9293725-9295584 FORWARD   Aliases: MWL2.25	5.2	5.0	0.2	0.6	100.0%	-4.4
11319	AT5G51090.1   expressed protein   chr5:20789463-20790420 REVERSE   Aliases: MWD22.3, MWD22_3	2.2	2.3	-0.1	-0.6	100.0%	-5.5
11320	AT1G63850.1   PRLI-interacting factor-related, similar to PRLI-interacting factor G (GI:11139264) (Arabidopsis thaliana); contains Prosite PS00037: Myb DNA-binding domain repeat signature 1   chr1:23700625-23702371 FORWARD   Aliases: T12P18.13, T12P18_13	4.3	4.4	-0.1	-0.6	100.0%	-5.0
11321	AT4G19000.1   IWS1 C-terminus family protein, contains Pfam profile PF05909: IWS1 C-terminus   chr4:10405514-10407350 FORWARD   Aliases: F13C5.170, F13C5_170	2.7	2.6	0.1	0.6	100.0%	-5.6
11322	AT2G47350.2   PAPA-1-like family protein / zinc finger (HIT type) family protein, contains Pfam domains, PF04795: PAPA-1-like conserved region and PF04438: HIT zinc finger   chr2:19440861-19444319 FORWARD   Aliases: T8I13.19	4.8	4.7	0.2	0.6	100.0%	-5.0
11323	AT3G42250.1   hypothetical protein   chr3:14414669-14414971 FORWARD   Aliases: F26B15.50	3.1	3.2	-0.1	-0.6	100.0%	-5.6
11324	AT5G56500.2   similar to chaperonin, putative [Arabidopsis thaliana] (TAIR:At1g26230.1); similar to RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta [Arabidopsis thaliana] (TAIR:At1g55490.2); similar to chaperonin, putative [Arabidopsis thaliana] (TAIR:At3g13470.1); similar to RuBisCO subunit binding-protein beta subunit, chloroplast / 60 kDa chaperonin beta subunit / CPN-60 beta [Arabidopsis thaliana] (TAIR:At1g55490.1); similar to putative RuBisCO subunit binding-protein beta subunit, chloroplast precursor [Oryza sativa (japonica cultivar-group)] (GB:XP_463795.1); similar to chaperonin [Secale cereale] (GB:CAA93139.1); similar to chaperonin 62.5K beta chain - rape (GB:PW0007); similar to putative chaperonin 60 beta precursor [Oryza sativa (japonica cultivar-group)] (GB:NP_910308.1); similar to chaperonin precursor [Pisum sativum] (GB:AAA66365.1); contains InterPro domain Chaperonin Cpn60 (InterPro:IPR001844); contains InterPro domain Chaperonin Cpn60/TCP-1 (InterPro:IPR002423)   chr5:22891017-22894622 FORWARD   Aliases: MCD7.27, MCD7_27	11.1	11.4	-0.3	-0.6	100.0%	-4.9
11325	AT5G60310.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:24285237-24287208 FORWARD   Aliases: F15L12.19, F15L12_19	3.2	3.1	0.1	0.6	100.0%	-5.0
11326	AT5G20200.1   nucleoporin-related, contains weak similarity to Nucleoporin NUP1 (Nuclear pore protein NUP1) (Swiss-Prot:P20676) (Saccharomyces cerevisiae)   chr5:6816709-6821812 FORWARD   Aliases: F5O24.90, F5O24_90	4.4	4.6	-0.2	-0.6	100.0%	-4.8
11327	AT4G38550.1   expressed protein   chr4:18025653-18028794 FORWARD   Aliases: F20M13.110, F20M13_110	4.3	4.0	0.4	0.6	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11328	AT1G32040.1   expressed protein   chr1:11518398-11520050 FORWARD   Aliases: T12O21.6, T12O21_6	2.6	2.6	0.1	0.6	100.0%	-5.3
11329	AT4G20290.1   expressed protein   chr4:10955169-10955594 REVERSE   Aliases: F1C12.200, F1C12_200	2.8	2.7	0.1	0.6	100.0%	-5.1
11330	AT1G32220.1   expressed protein   chr1:11607881-11609713 FORWARD   Aliases: F3C3.2, F3C3_2	8.1	8.5	-0.4	-0.6	100.0%	-4.3
11331	AT5G12220.1   las1-like family protein, similar to Las1p (Saccharomyces cerevisiae) GI:495504; contains Pfam profile PF04031: Las1-like   chr5:3950156-3953086 FORWARD   Aliases: MXC9.18, MXC9_18	3.9	4.0	-0.1	-0.6	100.0%	-4.9
11332	AT4G29710.1   phosphodiesterase/nucleotide pyrophosphatase-related, weak similarity to SP:Q13822 Ectonucleotide pyrophosphatase/phosphodiesterase 2 {Homo sapiens}   chr4:14547007-14547408 REVERSE   Aliases: T16L4.220, T16L4_220	2.9	3.0	-0.1	-0.6	100.0%	-5.3
11333	AT1G67580.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:25330802-25335042 REVERSE   Aliases: F12B7.13, F12B7_13	5.4	5.6	-0.3	-0.6	100.0%	-4.6
11334	AT3G03800.1   Symbol: SYP131	3.4	3.3	0.1	0.6	100.0%	-5.3
11335	AT1G12190.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.5	0.1	0.6	100.0%	-5.4
11336	AT5G02180.1   amino acid transporter family protein, belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II	2.9	2.8	0.1	0.6	100.0%	-5.3
11337	AT4G16700.1   phosphatidylserine decarboxylase, similar to SP:P27465 Phosphatidylserine decarboxylase proenzyme (EC 4.1.1.65 {Cricetulus griseus}); contains Pfam profile PF02666: phosphatidylserine decarboxylase   chr4:9395658-9398330 REVERSE   Aliases: DL4375C, FCAALL.4	3.0	3.1	-0.1	-0.6	100.0%	-5.2
11338	AT5G15300.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:4968166-4970037 REVERSE   Aliases: F8M21.190, F8M21_190	3.1	3.2	-0.2	-0.6	100.0%	-5.1
11339	ATMG01400.1   Symbol: ORF105B   hypothetical protein   chrM:363725-364042 FORWARD   Aliases: ORF105B	2.7	3.0	-0.2	-0.6	100.0%	-4.7
11340	AT3G07590.1   small nuclear ribonucleoprotein D1, putative / snRNP core protein D1, putative / Sm protein D1, putative, similar to SWISS-PROT:SP:P13641 small nuclear ribonucleoprotein Sm D1 (snRNP core protein D1, Sm-D1, Sm-D autoantigen)(Mouse)   chr3:2423091-2424170 FORWARD   Aliases: MLP3.4	6.5	6.2	0.3	0.6	100.0%	-4.5
11341	AT1G48160.1   signal recognition particle 19 kDa protein, putative / SRP19, putative, similar to signal recognition particle 19 kDa protein subunit SRP19 GI:624221 (Oryza sativa (japonica cultivar-group)); contains Pfam profile: PF01922 SRP19 protein   chr1:17790214-17792693 REVERSE   Aliases: F21D18.11, F21D18_11	10.3	10.5	-0.2	-0.6	100.0%	-4.7
11342	AT1G67623.1   F-box family protein, hypothetical protein ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:25345774-25346906 FORWARD   Aliases: F12A21.25, F12A21_25	3.8	3.7	0.2	0.6	100.0%	-5.1
11343	AT1G55170.1   expressed protein   chr1:20583990-20585642 FORWARD   Aliases: T7N22.12, T7N22_12	6.9	6.7	0.2	0.6	100.0%	-4.6
11344	AT5G15520.1   40S ribosomal protein S19 (RPS19B), 40S RIBOSOMAL PROTEIN S19 - Oryza sativa, SWISSPROT:RS19_ORYSA   chr5:5037024-5038170 REVERSE   Aliases: T20K14.130, T20K14_130	7.0	7.2	-0.2	-0.6	100.0%	-4.4
11345	AT5G24710.1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g38560.1); similar to OSJNBb0006H05.17 [Oryza sativa (japonica cultivar-group)] (GB:NP_917302.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr5:8459151-8468176 REVERSE   Aliases: MXC17.10, MXC17_10	3.4	3.6	-0.1	-0.6	100.0%	-5.2
11346	AT2G25080.1   Symbol: ATGPX1	7.5	7.9	-0.4	-0.6	100.0%	-4.6
11347	AT5G41920.1   scarecrow transcription factor family protein   chr5:16796977-16798427 FORWARD   Aliases: MJC20.2, MJC20_2	5.3	5.4	-0.1	-0.6	100.0%	-5.1
11348	AT4G21150.1   ribophorin II (RPN2) family protein, contains Pfam domain PF05817: Ribophorin II (RPN2)   chr4:11278439-11283858 FORWARD   Aliases: F7J7.90, F7J7_90	6.5	6.9	-0.3	-0.6	100.0%	-4.5
11349	AT4G03030.1   kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	7.4	7.2	0.2	0.6	100.0%	-4.7
11350	AT4G36610.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoate hydrolase (Pseudomonas fluorescens) GI:1871461; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:17265396-17267320 REVERSE   Aliases: AP22.94, AP22_94	3.7	4.0	-0.3	-0.6	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11351	AT3G42590.1   hypothetical protein, similar to At2g16170, At2g06640, At2g12110, At2g12100, At2g05460   chr3:14707244-14707936 FORWARD   Aliases: T12K4.40	3.1	3.2	-0.1	-0.6	100.0%	-5.6
11352	AT5G03370.1   acylphosphatase family, contains Pfam PF00708: Acylphosphatase   chr5:825572-827033 REVERSE   Aliases: F12E4.110, F12E4_110	5.3	5.4	-0.1	-0.6	100.0%	-4.7
11353	AT5G47820.2   Symbol: FRA1   kinesin-like protein (FRA1), identical to kinesin-like protein (Arabidopsis thaliana) GI:27260890; contains Pfam profile PF00225: Kinesin motor domain   chr5:19383709-19389978 FORWARD   Aliases: FRAGILE FIBER 1, MCA23.16, MCA23_16	3.5	3.3	0.2	0.6	100.0%	-5.0
11354	AT1G71050.1   heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID:9701579); similar to farnesylated protein ATPF7 (GI:4097555); contains heavy-metal-associated domain PF00403   chr1:26806817-26807954 REVERSE   Aliases: F23N20.4, F23N20_4	2.3	2.4	-0.1	-0.6	100.0%	-5.4
11355	AT1G10510.1   Symbol: EMB2004   leucine-rich repeat family protein, similar to ribonuclease inhibitor (GI:164639) (Sus scrofa (pig)); contains Pfam PF00560: Leucine Rich Repeat domains   chr1:3461640-3465787 FORWARD   Aliases: EMB2004, EMBRYO DEFECTIVE 2004, T10O24.12, T10O24_12	6.7	6.9	-0.2	-0.6	100.0%	-4.7
11356	AT2G34150.2   Symbol: WAVE1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g29170.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470104.1)	2.4	2.5	-0.1	-0.6	100.0%	-5.3
11357	AT1G54330.1   Symbol: ANAC020   similar to no apical meristem (NAM) family protein [Arabidopsis thaliana] (TAIR:At1g65910.1); similar to nam-like protein 11 [Petunia x hybrida] (GB:AAM34774.1); contains InterPro domain No apical meristem (NAM) protein (InterPro:IPR003441)   chr1:20283234-20284619 REVERSE   Aliases: ANAC020, F20D21.15, F20D21_15	2.0	2.0	-0.1	-0.6	100.0%	-5.9
11358	AT4G00040.1   chalcone and stilbene synthase family protein, similar to chalcone synthase homolog PrChS1, Pinus radiata, gb:U90341; similar to anther-specific protein (Nicotiana glauca)(GI:2326774), YY2 protein (Oryza sativa)(GI:2645170)   chr4:14627-16079 FORWARD   Aliases: F6N15.12, F6N15_12	6.3	6.1	0.3	0.6	100.0%	-4.5
11359	AT2G45070.3   Symbol: SEC61 BETA   similar to sec61beta family protein [Arabidopsis thaliana] (TAIR:At3g60540.1); similar to sec61beta family protein [Arabidopsis thaliana] (TAIR:At3g60540.2); similar to GA10096-PA [Drosophila pseudoobscura] (GB:EAL25183.1); contains InterPro domain Sec61beta (InterPro:IPR005609)   chr2:18594092-18595334 REVERSE   Aliases: SEC 61 BETA SUBUNIT, T14P1.12	12.0	12.2	-0.1	-0.6	100.0%	-5.0
11360	AT4G02890.3   Symbol: UBQ14   polyubiquitin (UBQ14), identical to GI:166795; similar to N. sylvestris hexameric polyubiquitin, GenBank accession number M74101   chr4:1278530-1280028 REVERSE   Aliases: T5J8.21, T5J8_21	10.4	10.6	-0.2	-0.6	100.0%	-4.7
11361	AT2G45100.1   transcription factor IIB (TFIIB) family protein, contains Pfam domain, PF00382: Transcription factor TFIIB repeat   chr2:18602423-18605163 REVERSE   Aliases: T14P1.9	5.6	5.9	-0.2	-0.6	100.0%	-4.6
11362	AT1G50600.1   scarecrow-like transcription factor 5 (SCL5), similar to SCARECROW GB:AAB06318 GI:1497987 from (Arabidopsis thaliana)   chr1:18740800-18743215 REVERSE   Aliases: F11F12.8, F11F12_8	5.9	5.5	0.4	0.6	100.0%	-4.6
11363	AT2G18090.1   PHD finger family protein / SWIB complex BAF60b domain-containing protein / GYF domain-containing protein, contains Pfam profiles PF02201: BAF60b domain of the SWIB complex, PF02213: GYF domain, PF00628: PHD-finger   chr2:7871396-7874848 FORWARD   Aliases: T27K22.4, T27K22_4	4.0	4.3	-0.3	-0.6	100.0%	-4.7
11364	AT5G66050.2   expressed protein   chr5:26429324-26431754 REVERSE   Aliases: K2A18.12, K2A18_12	4.7	4.4	0.3	0.6	100.0%	-4.5
11365	AT1G04540.1   C2 domain-containing protein, low similarity to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain   chr1:1237255-1239060 FORWARD   Aliases: T1G11.21, T1G11_21	2.9	2.8	0.2	0.6	100.0%	-4.9
11366	AT3G21740.1   Symbol: APO4   expressed protein, contains Pfam PF05634: Arabidopsis thaliana protein of unknown function (DUF794)   chr3:7662368-7664017 REVERSE   Aliases: ACCUMULATION OF PHOTOSYSTEM ONE 4, MSD21.5	4.0	4.2	-0.1	-0.6	100.0%	-4.8
11367	AT2G32765.1   small ubiquitin-like modifier 5 (SUMO), similar to ubiquitin-like protein SMT3 SP:P55852 (Arabidopsis thaliana); contains INTERPRO:IPR000626 ubiquitin domain; contains Pfam profile PF00240: Ubiquitin family; contains Pfam profile PF00240: Ubiquitin family;	3.8	3.9	-0.1	-0.6	100.0%	-5.0
11368	AT1G06410.1   Symbol: ATTPS7	8.5	8.3	0.2	0.6	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11369	AT5G12350.1   similar to zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] (TAIR:At5g42140.1); similar to zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] (TAIR:At1g69710.1); similar to regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] (TAIR:At3g23270.1); similar to zinc finger protein, putative / regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] (TAIR:At5g19420.1); similar to zinc finger protein (PRAF1) / regulator of chromosome condensation (RCC1) family protein [Arabidopsis thaliana] (TAIR:At1g76950.1); similar to unknown prtein [Oryza sativa (japonica cultivar-group)] (GB:AAT77332.1); similar to P0431G06.4-like [Solanum tuberosum] (GB:AAU89751.1); similar to OSJNBa0070M12.5 [Oryza sativa (japonica cultivar-group)] (GB:XP_474427.1); similar to putative zinc finger protein [Solanum demissum] (GB:AAU93591.1); similar to P0431G06.4 [Oryza sativa (japonica cultivar-group)] (GB:NP_914656.1); contains InterPro domain Regulator of chromosome condensation, RCC1 (InterPro:IPR000408); contains InterPro domain Zn-finger, FYVE type (InterPro:IPR000306)   chr5:3995808-4000802 FORWARD   Aliases: None	3.5	3.4	0.1	0.6	100.0%	-5.1
11370	AT5G25380.1   Symbol: CYCA2;1   cyclin 3a (CYC3a), nearly identical to cyclin 3a (Arabidopsis thaliana) GI:509425; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr5:8815233-8817569 FORWARD   Aliases: CYCLIN A2;1, F18G18.15, F18G18_15	2.1	2.2	-0.1	-0.6	100.0%	-5.6
11371	AT2G16020.1   hypothetical protein, and genefinder   chr2:6980438-6980668 FORWARD   Aliases: F7H1.4, F7H1_4	3.4	3.4	0.1	0.6	100.0%	-5.5
11372	AT2G26810.1   expressed protein, and genefinder   chr2:11440811-11443156 REVERSE   Aliases: F12C20.15, F12C20_15	5.6	5.4	0.2	0.6	100.0%	-4.5
11373	AT4G20390.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:11007046-11008075 FORWARD   Aliases: F9F13.40, F9F13_40	4.2	4.4	-0.2	-0.6	100.0%	-4.3
11374	AT3G47600.1   Symbol: MYB94   myb family transcription factor (MYB94), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA putative transcription factor (MYB94) GI:3941527	3.1	3.0	0.1	0.6	100.0%	-5.1
11375	AT5G54050.1   DC1 domain-containing protein   chr5:21950849-21953221 REVERSE   Aliases: K19P17.23, K19P17_23	2.8	3.0	-0.2	-0.6	100.0%	-4.7
11376	AT5G38480.2   Symbol: GRF3   similar to 14-3-3 protein GF14 nu (GRF7) [Arabidopsis thaliana] (TAIR:At3g02520.1); similar to 14-3-3 e-1 protein [Nicotiana tabacum] (GB:BAD12176.1); similar to 14-3-3 e-2 protein [Nicotiana tabacum] (GB:BAD12177.1); contains InterPro domain 14-3-3 protein (InterPro:IPR000308)   chr5:15426927-15428746 FORWARD   Aliases: GENERAL REGULATORY FACTOR 3, GF14PSI ISOFORM, MXI10.21, MXI10_21, RCI1	9.0	9.4	-0.4	-0.6	100.0%	-4.6
11377	AT5G02530.1   RNA and export factor-binding protein, putative, BcDNA.LD24793, Drosophila melanogaster, EMBL:AF172637   chr5:564084-565856 REVERSE   Aliases: T22P11.120, T22P11_120	7.6	7.3	0.3	0.6	100.0%	-4.6
11378	AT4G08620.1   Symbol: SULTR1;1   sulfate transporter, identical to sulfate transporter (Arabidopsis thaliana) GI:3777483   chr4:5500310-5506262 FORWARD   Aliases: SULTR1.2	3.2	3.4	-0.2	-0.6	100.0%	-4.4
11379	AT1G27630.1   cyclin family protein, similar to cyclin T1 (Homo sapiens) GI:2981196; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr1:9611090-9614321 FORWARD   Aliases: T22C5.8	4.0	3.7	0.3	0.6	100.0%	-4.6
11380	AT3G17840.1   Symbol: RLK902	3.3	3.4	-0.2	-0.6	100.0%	-4.7
11381	AT3G08900.1   Symbol: RGP3   reversibly glycosylated polypeptide-3 (RGP3), nearly identical to reversibly glycosylated polypeptide-3 (Arabidopsis thaliana) GI:11863238; contains non-consensus GA-donor splice site at intron 2   chr3:2708092-2709720 REVERSE   Aliases: REVERSIBLY GLYCOSYLATED POLYPEPTIDE 3, RGP, T16O11.16	3.3	3.3	-0.1	-0.6	100.0%	-5.7
11382	AT2G24210.1   Symbol: TPS10   myrcene/ocimene synthase (TPS10), nearly identical to GI:9957293; contains Pfam profile: PF01397 terpene synthase family   chr2:10301410-10304567 FORWARD   Aliases: F27D4.12, F27D4_12, TPS10	2.4	2.3	0.1	0.6	100.0%	-5.3
11383	AT1G59600.1   Symbol: ZCW7   expressed protein, similar to B-lymphocyte antigen precursor (B-lymphocyte surface antigen) (721P) (Protein XE7) (Swiss-Prot:Q02040) (Homo sapiens); supporting cDNA gi:6520226.dbj:AB028230.1.   chr1:21893422-21895627 REVERSE   Aliases: T30E16.16, T30E16_16, ZCW7	5.2	5.4	-0.2	-0.6	100.0%	-4.9
11384	AT1G20930.1   Symbol: CDKB2;2   cell division control protein, putative, cdc2MsF (Medicago sativa) gi:1806146:emb:CAA65982   chr1:7292561-7294735 REVERSE   Aliases: CDKB2;2, CYCLIN DEPENDENT KINASE B2;2, Cyclin dependent kinase B2;2, F9H16.8, F9H16_8	6.3	6.7	-0.4	-0.6	100.0%	-4.5
11385	AT1G51340.2   MATE efflux family protein, contains Pfam profile PF01554: MatE   chr1:19035665-19038647 FORWARD   Aliases: F11M15.20, F11M15_20	2.2	2.1	0.1	0.6	100.0%	-5.5
11386	AT1G54050.1   17.4 kDa class III heat shock protein (HSP17.4-CIII), contains Pfam profile: PF00011 Hsp20/alpha crystallin family; identified as class CIII in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.   chr1:20183090-20183947 REVERSE   Aliases: F15I1.13, F15I1_13	5.7	5.5	0.2	0.6	100.0%	-4.6
11387	AT3G24010.1   PHD finger family protein, contains Pfam profile: PF00628 PHD-finger   chr3:8675965-8678227 REVERSE   Aliases: F14O13.20	9.1	8.9	0.2	0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11388	AT5G23660.1   Symbol: MTN3   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr5:7971654-7973928 REVERSE   Aliases: MQM1.8, MQM1_8	3.9	3.6	0.4	0.6	100.0%	-4.2
11389	AT5G27400.1   expressed protein, hypothetical proteins - different species   chr5:9676351-9678506 FORWARD   Aliases: F21A20.110, F21A20_110	7.3	7.5	-0.2	-0.6	100.0%	-4.6
11390	AT3G09600.2   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At5g02840.2); similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At5g02840.1); similar to myb family transcription factor-like [Oryza sativa (japonica cultivar-group)] (GB:BAD29385.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005); contains InterPro domain Myb-like DNA-binding domain, SHAQKYF class (InterPro:IPR006447)   chr3:2946423-2948205 FORWARD   Aliases: AT3G09610, F11F8.19	2.5	2.5	-0.0	-0.6	100.0%	-6.1
11391	AT2G32010.1   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr2:13631869-13636223 FORWARD   Aliases: F22D22.24, F22D22_24	3.3	3.4	-0.1	-0.6	100.0%	-5.1
11392	AT5G66810.1   expressed protein, similar to unknown protein (gb:AAB71479.1:)   chr5:26690152-26693821 FORWARD   Aliases: MUD21.5, MUD21_5	4.0	4.2	-0.2	-0.6	100.0%	-4.7
11393	AT5G25570.2   expressed protein   chr5:8901758-8903219 FORWARD   Aliases: T14C9.110, T14C9_110	4.1	3.8	0.2	0.6	100.0%	-4.6
11394	AT1G14800.1   expressed protein   chr1:5099567-5102553 FORWARD   Aliases: F10B6.21, F10B6_21	3.3	3.0	0.2	0.6	100.0%	-4.7
11395	AT3G19400.2   cysteine proteinase, putative, non-consensus AT acceptor site at exon 3; contains similarity to cysteine protease CYP1 GI:2828252, TDI-65 GI:5726641 from (Lycopersicon esculentum)   chr3:6725474-6726584 FORWARD   Aliases: MLD14.12	7.6	7.8	-0.2	-0.6	100.0%	-4.7
11396	AT3G25950.1   expressed protein   chr3:9497593-9498348 FORWARD   Aliases: MPE11.12	4.7	4.6	0.1	0.6	100.0%	-5.1
11397	AT4G31230.1   protein kinase family protein, contains Pfam profiles PF00069: Protein kinase domain, PF00582: universal stress protein family   chr4:15172903-15176115 REVERSE   Aliases: F8F16.50, F8F16_50	2.6	2.6	0.1	0.6	100.0%	-5.8
11398	AT4G25050.1   Symbol: ACP4   acyl carrier family protein / ACP family protein, similar to Acyl carrier protein, chloroplast precursor from {Spinacia oleracea} SP:P23235, {Casuarina glauca} SP:P93092; contains InterPro accession IPR003881: Isochorismatase   chr4:12870077-12871228 FORWARD   Aliases: F13M23.190, F24A6.4	7.3	6.9	0.4	0.6	100.0%	-4.2
11399	AT4G00510.1   cyclic nucleotide-binding domain-containing protein, contains Pfam profile: PF00027 cyclic nucleotide-binding domain   chr4:227726-228874 FORWARD   Aliases: F6N23.2, F6N23_2	3.2	3.3	-0.1	-0.6	100.0%	-5.4
11400	AT1G06970.1   Symbol: ATCHX14   cation/hydrogen exchanger, putative (CHX14), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr1:2138108-2140817 FORWARD   Aliases: CHX14, F10K1.31, F10K1_31	2.6	2.5	0.1	0.6	100.0%	-5.3
11401	AT1G63170.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to SP:Q06003 Goliath protein (G1 protein) {Drosophila melanogaster}; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:23429017-23430974 FORWARD   Aliases: F16M19.7, F16M19_7	4.4	4.6	-0.2	-0.6	100.0%	-4.7
11402	AT1G48060.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.2	2.1	0.1	0.6	100.0%	-5.8
11403	AT5G15060.1   expressed protein   chr5:4874988-4875759 REVERSE   Aliases: F2G14.180, F2G14_180	3.3	3.4	-0.1	-0.6	100.0%	-5.2
11404	AT4G32050.1   neurochondrin family protein, contains Pfam PF05536: Neurochondrin   chr4:15496543-15500849 FORWARD   Aliases: F10N7.130, F10N7_130	2.8	2.7	0.1	0.6	100.0%	-5.5
11405	AT5G17040.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, similar to UDP glucose:flavonoid 3-o-glucosyltransferase GI:13620861 from (Vitis vinifera); contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:5605287-5606973 REVERSE   Aliases: F2K13.190, F2K13_190	3.5	3.3	0.2	0.6	100.0%	-4.7
11406	AT3G50370.1   expressed protein   chr3:18687041-18694926 REVERSE   Aliases: F11C1.210	3.2	3.7	-0.5	-0.6	100.0%	-4.5
11407	AT1G17850.1   expressed protein   chr1:6146305-6148813 REVERSE   Aliases: F2H15.8, F2H15_8	3.2	3.3	-0.1	-0.6	100.0%	-5.1
11408	AT1G28610.2   GDSL-motif lipase, putative, similar to lipase (Arabidopsis thaliana) GI:1145627; contains Pfam profile: PF00657 Lipase/Acylhydrolase with GDSL-like motif   chr1:10053603-10055717 REVERSE   Aliases: F1K23.16, F1K23_16	2.9	2.8	0.1	0.6	100.0%	-5.4
11409	AT1G33710.1   expressed protein, ; expression supported by MPSS   chr1:12219637-12220269 FORWARD   Aliases: F14M2.21, F14M2_21	2.2	2.2	-0.1	-0.6	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11410	AT3G42730.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At3g24380, At5g36840, At5g35010, At3g42740, At4g05290, At2g14770, At3g43390, At2g05560, At4g08880, At1g34730, At1g27790, At1g34740, At1g27780, At5g36850, At1g52020, At3g24390, At4g05280, At1g25886, At4g03300   chr3:14856224-14862091 FORWARD   Aliases: F7P3.20	1.9	1.8	0.0	0.6	100.0%	-6.0
11411	AT5G37880.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:15101690-15102218 REVERSE   Aliases: K18L3.7, K18L3_7	3.4	3.3	0.1	0.6	100.0%	-5.5
11412	AT2G26640.1   beta-ketoacyl-CoA synthase, putative, similar to beta-ketoacyl-CoA synthase (Simmondsia chinensis)(GI:1045614)   chr2:11336948-11339528 FORWARD   Aliases: F18A8.1, F18A8_1	3.8	3.9	-0.1	-0.6	100.0%	-4.7
11413	AT4G12240.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr4:7287889-7288983 FORWARD   Aliases: T4C9.80, T4C9_80	5.1	5.4	-0.3	-0.6	100.0%	-4.7
11414	AT3G60080.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:22198284-22199771 FORWARD   Aliases: T2O9.60	3.9	3.7	0.2	0.6	100.0%	-4.9
11415	AT3G30510.1   hypothetical protein   chr3:12123056-12123207 FORWARD   Aliases: MSJ3.14	2.9	2.9	-0.1	-0.6	100.0%	-5.5
11416	AT3G25070.1   Symbol: RIN4   RPM1-interacting protein 4 (RIN4), identical to SP:Q8GYN5 RPM1-interacting protein 4 {Arabidopsis thaliana}   chr3:9132317-9134037 FORWARD   Aliases: MJL12.1, RPM1 INTERACTING PROTEIN 4	5.5	5.4	0.1	0.6	100.0%	-5.1
11417	AT3G46700.1   similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At3g46680.1); similar to UDP-glucuronosyl/UDP-glucosyl transferase family protein [Arabidopsis thaliana] (TAIR:At3g46690.1); similar to UDP-glucose: chalcononaringenin 2'-O-glucosyltransferase [Dianthus caryophyllus] (GB:BAD52007.1); contains InterPro domain UDP-glucuronosyl/UDP-glucosyl transferase (InterPro:IPR002213)   chr3:17211304-17212874 REVERSE   Aliases: T6H20.270	3.1	3.2	-0.1	-0.6	100.0%	-4.9
11418	AT5G16140.1   peptidyl-tRNA hydrolase family protein, contains Pfam profile PF01195: peptidyl-tRNA hydrolase   chr5:5270311-5271520 REVERSE   Aliases: T21H19.60, T21H19_60	4.1	4.2	-0.2	-0.6	100.0%	-4.7
11419	AT2G30740.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 (Pti1)(Lycopersicon esculentum) gi:3668069:gb:AAC61805   chr2:13103434-13105671 FORWARD   Aliases: T11J7.13, T11J7_13	4.9	5.2	-0.3	-0.6	100.0%	-4.2
11420	AT1G26910.1   60S ribosomal protein L10 (RPL10B), Nearly identical to ribosomal protein L10.e, Wilm's tumor suppressor homologue, gi:17682 (Z15157), however differences in sequence indicate this is a different member of the L10 family   chr1:9321637-9322947 FORWARD   Aliases: T2P11.10, T2P11_10	7.4	7.6	-0.2	-0.6	100.0%	-4.5
11421	AT1G10090.1   expressed protein   chr1:3290059-3296181 REVERSE   Aliases: T27I1.11, T27I1_11	4.4	4.3	0.1	0.6	100.0%	-5.0
11422	AT5G03040.1   calmodulin-binding family protein, similar to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr5:710100-712787 REVERSE   Aliases: F15A17.70, F15A17_70	4.1	4.3	-0.2	-0.6	100.0%	-4.6
11423	AT3G15440.1   expressed protein   chr3:5211930-5212361 REVERSE   Aliases: MJK13.10	3.0	2.9	0.1	0.6	100.0%	-5.4
11424	AT2G44980.2   transcription regulatory protein SNF2, putative, similar to SNF2P (Oryza sativa (japonica cultivar-group)) GI:23193483; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain; CG donor site annotated in one isoform based on protein alignments.   chr2:18559515-18563744 REVERSE   Aliases: T14P1.22	4.0	4.2	-0.1	-0.6	100.0%	-5.0
11425	AT5G60820.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:24486813-24488121 FORWARD   Aliases: MAE1.6, MAE1_6	5.5	5.3	0.2	0.6	100.0%	-4.8
11426	AT2G28690.1   expressed protein   chr2:12313967-12315705 REVERSE   Aliases: T8O18.2, T8O18_2	3.0	2.8	0.2	0.6	100.0%	-4.9
11427	AT3G53930.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:19977330-19981791 FORWARD   Aliases: F5K20.230	4.9	4.8	0.2	0.6	100.0%	-4.6
11428	AT2G38590.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr2:16149975-16151262 FORWARD   Aliases: T6A23.21, T6A23_21	3.1	3.0	0.1	0.6	100.0%	-5.6
11429	AT2G10340.1   expressed protein   chr2:3991114-3991371 REVERSE   Aliases: F12P23.15, F12P23_15	2.2	2.3	-0.1	-0.6	100.0%	-5.3
11430	AT2G37250.1   Symbol: ADK/ATPADK1   adenylate kinase family protein, contains Pfam profile: PF00406 adenylate kinase   chr2:15649016-15650797 FORWARD   Aliases: ADK, ATPADK1, F3G5.4, F3G5_4	9.0	9.2	-0.2	-0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11431	AT3G24740.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g25910.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468005.1)   chr3:9032404-9033790 FORWARD   Aliases: K7P8.3	4.2	4.0	0.2	0.6	100.0%	-4.6
11432	AT1G24420.1   transferase family protein, similar to deacetylindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034), acetyl-CoA:benzylalcohol acetyltransferase (Clarkia concinna)(GI:6166330)(PMID:10588064)   chr1:8656676-8657986 FORWARD   Aliases: F21J9.8	2.4	2.5	-0.1	-0.6	100.0%	-5.3
11433	AT3G53030.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:19673262-19675481 FORWARD   Aliases: F8J2.200	5.4	5.6	-0.2	-0.6	100.0%	-4.9
11434	AT4G08480.1   Symbol: MAPKKK9   mitogen-activated protein kinase, putative, similar to mitogen-activated protein kinase (Arabidopsis thaliana) gi:1255448:dbj:BAA09057; contains Pfam PF00069: Protein kinase domain   chr4:5387649-5391504 REVERSE   Aliases: T15F16.3, T15F16_3	2.2	2.2	0.0	0.6	100.0%	-5.8
11435	AT2G37890.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr2:15868766-15871087 REVERSE   Aliases: T8P21.20, T8P21_20	5.3	5.1	0.2	0.6	100.0%	-4.4
11436	AT5G60950.1   phytochelatin synthetase-related, contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region   chr5:24544383-24545232 REVERSE   Aliases: MSL3.7, MSL3_7	4.0	4.3	-0.3	-0.6	100.0%	-4.3
11437	AT4G35740.2   DNA helicase (RECQ13), identical to DNA Helicase (Arabidopsis thaliana) GI:11121447; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr4:16936125-16940337 FORWARD   Aliases: F8D20.250, F8D20_250	6.0	6.3	-0.3	-0.6	100.0%	-4.5
11438	AT3G53390.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to Dystrophia myotonica-containing WD repeat motif protein DMR-N9 protein (DMWD) (DM9) (SP:Q08274) (Mus musculus); similar to DMR protein GI:18028289 (Homo sapiens);   chr3:19803509-19807731 FORWARD   Aliases: F4P12.90	5.6	5.9	-0.3	-0.6	100.0%	-4.8
11439	AT5G28720.1   hypothetical protein   chr5:10776059-10776956 FORWARD   Aliases: T32B20.10, T32B20_10	2.7	2.8	-0.1	-0.6	100.0%	-5.4
11440	AT4G32420.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, weak similarity to CARS-Cyp (Homo sapiens) GI:1117968; contains Pfam profile PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr4:15647352-15652760 REVERSE   Aliases: F8B4.120, F8B4_120	6.9	7.2	-0.3	-0.6	100.0%	-4.3
11441	AT4G32450.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:15661098-15662711 FORWARD   Aliases: F8B4.150, F8B4_150	3.1	3.6	-0.5	-0.6	100.0%	-4.7
11442	AT5G49220.1   expressed protein   chr5:19973663-19976059 FORWARD   Aliases: K21P3.10, K21P3_10	3.6	3.7	-0.1	-0.6	100.0%	-5.1
11443	AT5G07250.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr5:2273555-2275991 REVERSE   Aliases: T28J14.190, T28J14_190	5.5	5.3	0.2	0.6	100.0%	-4.7
11444	AT1G04950.3   Symbol: TAFII59   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g54360.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g54360.1); similar to SPCC16C4.18c [Schizosaccharomyces pombe] (GB:CAA20756.1); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124); contains InterPro domain TATA box binding protein associated factor (TAF) (InterPro:IPR004823)   chr1:1402555-1407495 REVERSE   Aliases: F13M7.6, F13M7_6	4.6	4.7	-0.1	-0.6	100.0%	-4.9
11445	AT3G20015.1   similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:At3g18490.1); similar to putative aspartic proteinase nepenthesin I [Oryza sativa (japonica cultivar-group)] (GB:NP_909181.1); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461)   chr3:6978483-6980374 REVERSE   Aliases: MZE19.7	3.7	3.9	-0.3	-0.6	100.0%	-4.2
11446	AT3G03430.1   polcalcin, putative / calcium-binding pollen allergen, putative, almost identical to polcalcin Bra r 2/Bra n 2 (calcium-binding pollen allergen Bra r 2/Bra n 2) SP:Q39406 from (Brassica napus)	2.6	2.5	0.1	0.6	100.0%	-5.6
11447	AT1G78700.1   brassinosteroid signalling positive regulator-related, contains similarity to BZR1 protein (Arabidopsis thaliana) gi:20270971:gb:AAM18490   chr1:29604242-29606575 FORWARD   Aliases: F9K20.26, F9K20_26	3.1	3.0	0.1	0.6	100.0%	-5.1
11448	AT1G32750.1   Symbol: HAF01   HAC13 protein (HAC13), identical to HAC13 (Arabidopsis thaliana) gi:21105767:gb:AAM34782; contains Pfam domains, PF00439: Bromodomain and PF00240: Ubiquitin family   chr1:11846227-11856241 REVERSE   Aliases: F6N18.13, F6N18_13, GTD01, GTD1, HAC13, HAF1	8.7	8.5	0.2	0.6	100.0%	-4.9
11449	AT3G57970.1   emsy N terminus domain-containing protein / ENT domain-containing protein, contains Pfam profile PF03735: ENT domain   chr3:21476203-21477654 FORWARD   Aliases: T10K17.180	2.5	2.4	0.1	0.6	100.0%	-5.3
11450	AT2G29920.1   expressed protein   chr2:12761571-12762461 FORWARD   Aliases: F6K5.5, F6K5_5	3.5	3.3	0.2	0.6	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11451	AT5G25180.1   Symbol: CYP71B14   cytochrome P450 71B14, putative (CYP71B14), Identical to cytochrome P450 71B14 (SP:P58051) (Arabidopsis thaliana); cytochrome P450 71B1, Thlaspi arvense, SWISSPROT:C7B1_THLAR; similar to cytochrome P450 CYP83D1p (Gli:2739002) (Glycine max)   chr5:8694633-8696224 REVERSE   Aliases: F21J6.102, F21J6_102	2.9	3.0	-0.1	-0.6	100.0%	-5.4
11452	AT5G55380.1   membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related,	4.6	4.4	0.2	0.6	100.0%	-4.6
11453	AT4G25140.1   glycine-rich protein / oleosin   chr4:12900440-12901587 FORWARD   Aliases: F24A6.9	2.5	2.4	0.1	0.6	100.0%	-5.6
11454	AT4G19440.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:10600801-10604531 REVERSE   Aliases: T5K18.220, T5K18_220	3.1	3.0	0.1	0.6	100.0%	-5.2
11455	AT3G12870.1   expressed protein   chr3:4094424-4095044 REVERSE   Aliases: MJM20.1	4.8	5.2	-0.4	-0.6	100.0%	-4.1
11456	AT2G32250.2   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr2:13700182-13704036 FORWARD   Aliases: T32F6.23, T32F6_23	5.8	6.3	-0.6	-0.6	100.0%	-4.7
11457	AT2G44930.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr2:18536598-18538827 REVERSE   Aliases: T13E15.6	3.4	3.3	0.1	0.6	100.0%	-5.1
11458	AT3G51770.2   similar to tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] (TAIR:At5g58550.1); similar to tetratricopeptide repeat (TPR)-containing protein [Arabidopsis thaliana] (TAIR:At4g02680.1); similar to TPR repeat [Prochlorococcus marinus str. MIT 9313] (GB:CAE20471.1); contains InterPro domain BTB/POZ domain (InterPro:IPR000210); contains InterPro domain TPR repeat (InterPro:IPR001440)   chr3:19210760-19215441 REVERSE   Aliases: ATEM1.2	3.1	3.0	0.1	0.6	100.0%	-5.2
11459	AT4G27890.1   nuclear movement family protein, contains Pfam profile: PF03593 nuclear movement protein	3.1	3.0	0.1	0.6	100.0%	-5.2
11460	AT2G39690.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g12540.1); similar to putative ternary complex factor [Oryza sativa (japonica cultivar-group)] (GB:XP_550141.1); contains InterPro domain Protein of unknown function DUF547 (InterPro:IPR006869)   chr2:16548104-16550456 FORWARD   Aliases: F17A14.6, F17A14_6	2.1	2.3	-0.1	-0.6	100.0%	-5.0
11461	AT5G03910.1   Symbol: ATATH12   ABC transporter family protein, ABC-type transport protein sll1276, Synechocystis sp., PIR:S77239   chr5:1054077-1057166 REVERSE   Aliases: F8F6.120, F8F6_120	6.1	6.3	-0.2	-0.6	100.0%	-4.8
11462	AT2G24220.1   Symbol: ATPUP5	4.1	3.9	0.2	0.6	100.0%	-4.7
11463	AT5G52900.1   expressed protein   chr5:21469668-21471034 REVERSE   Aliases: MXC20.13, MXC20_13	2.8	2.7	0.1	0.6	100.0%	-5.2
11464	AT1G76150.1   maoC-like dehydratase domain-containing protein, contains similarity to Swiss-Prot:P51659 estradiol 17 beta-dehydrogenase 4 (17-beta-HSD 4) (17-beta-hydroxysteroid dehydrogenase 4) (Homo sapiens); contains Pfam profile PF01575: MaoC like domain   chr1:28579860-28582570 REVERSE   Aliases: T23E18.9, T23E18_9	8.6	8.2	0.4	0.6	100.0%	-4.8
11465	ATCG00820.1   Symbol: RPS19   Encodes a 6.8-kDa protein of the small ribosomal subunit.   chrC:84005-84283 REVERSE   Aliases: RPS19	11.2	11.7	-0.5	-0.6	100.0%	-5.0
11466	AT5G64200.2   Symbol: ATSC35	5.7	5.4	0.3	0.6	100.0%	-4.7
11467	AT2G34480.1   60S ribosomal protein L18A (RPL18aB)   chr2:14539787-14541280 REVERSE   Aliases: F13P17.34	11.0	11.3	-0.2	-0.6	100.0%	-5.2
11468	AT1G69450.1   early-responsive to dehydration protein-related / ERD protein-related, low similarity to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr1:26110783-26113444 REVERSE   Aliases: F10D13.27, F10D13_27	5.5	5.3	0.2	0.6	100.0%	-4.3
11469	AT5G11050.1   Symbol: MYB64   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA binding domain; identical to cDNA putative transcription factor MYB64 (MYB64) GI:15375309   chr5:3502093-3503835 FORWARD   Aliases: T5K6.40, T5K6_40	3.2	3.4	-0.2	-0.6	100.0%	-5.0
11470	AT3G44880.1   Symbol: ACD1   Rieske (2Fe-2S) domain-containing protein, similar to lethal leaf-spot 1 from Zea mays (gi:1935909); contains Pfam PF00355 Rieske (2Fe-2S) domain   chr3:16394580-16397296 FORWARD   Aliases: ACCELERATED CELL DEATH 1, F28D10.70, LLS1	5.8	6.0	-0.2	-0.6	100.0%	-4.4
11471	AT1G60240.1   apical meristem formation protein-related, contains similarity to CUC1 (Arabidopsis thaliana) gi:12060422:dbj:BAB20598 and NAM (Petunia x hybrida) gi:1279640:emb:CAA63101   chr1:22218866-22219695 REVERSE   Aliases: T13D8.13, T13D8_13	2.6	2.5	0.1	0.6	100.0%	-5.5
11472	AT2G39670.2   radical SAM domain-containing protein, similar to hypothetical protein PIR:S76698:S76698 contains Pfam profile PF04055: radical SAM domain protein   chr2:16541311-16544396 FORWARD   Aliases: F17A14.4, F17A14_4	4.0	4.2	-0.2	-0.6	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11473	AT1G12020.1   expressed protein   chr1:4062460-4063335 REVERSE   Aliases: F12F1.11, F12F1_11	3.7	3.6	0.1	0.6	100.0%	-5.1
11474	AT3G12560.1   Symbol: TRFL9   telomeric DNA-binding protein, putative, similar to telomeric DNA-binding protein 1 (Arabidopsis thaliana) gi:13641340:gb:AAK31590   chr3:3981991-3985557 REVERSE   Aliases: T2E22.13, TRF LIKE 9	5.0	4.8	0.2	0.6	100.0%	-4.8
11475	AT3G47570.1   leucine-rich repeat transmembrane protein kinase, putative, protein kinase Xa21 - Oryza sativa, PIR:A57676   chr3:17538492-17541914 FORWARD   Aliases: F1P2.120	5.0	5.1	-0.1	-0.6	100.0%	-5.0
11476	AT1G63060.1   expressed protein   chr1:23387708-23388703 FORWARD   Aliases: F16M19.2, F16M19_2	3.4	3.6	-0.1	-0.6	100.0%	-5.1
11477	AT4G02320.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:1022725-1026118 REVERSE   Aliases: T14P8.1, T14P8_1	2.4	2.3	0.1	0.6	100.0%	-5.5
11478	AT3G03590.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr3:865190-867015 REVERSE   Aliases: T12J13.13, T12J13_13	4.0	3.9	0.1	0.6	100.0%	-5.0
11479	AT5G17320.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to Roc1 (GI:1907210) (Oryza sativa); contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain   chr5:5703382-5707639 REVERSE   Aliases: MKP11.28, MKP11_28	3.0	3.1	-0.1	-0.6	100.0%	-5.5
11480	AT1G80240.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr1:30176249-30177718 REVERSE   Aliases: F18B13.30, F18B13_30	2.8	2.7	0.2	0.6	100.0%	-4.6
11481	AT3G60800.1   zinc finger (DHHC type) family protein, contains DHHC zinc finger domain PF01529	6.3	6.7	-0.4	-0.6	100.0%	-4.6
11482	AT3G17440.2   Symbol: NPSN13	5.4	5.1	0.3	0.6	100.0%	-4.7
11483	AT5G35930.1   AMP-dependent synthetase and ligase family protein, similar to iturin A synthetase C (Bacillus subtilis) GI:16040972; contains Pfam profile PF00501: AMP-binding enzyme   chr5:14084222-14091981 REVERSE   Aliases: F14A1.10, F14A1_10	4.6	4.8	-0.2	-0.6	100.0%	-4.6
11484	AT4G18450.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr4:10190261-10191172 REVERSE   Aliases: F28J12.110, F28J12_110	3.3	3.4	-0.1	-0.6	100.0%	-5.4
11485	AT5G63770.1   diacylglycerol kinase, putative, similar to diacylglycerol kinase, theta (diglyceride kinase, DGK- theta, DAG kinase theta). (Homo sapiens) SWISS-PROT:P52824   chr5:25535867-25540125 FORWARD   Aliases: MBK5.25, MBK5_25	5.2	5.8	-0.5	-0.6	100.0%	-4.6
11486	AT2G07290.1   expressed protein   chr2:3029558-3030032 FORWARD   Aliases: T13E11.6, T13E11_6	3.0	2.9	0.1	0.6	100.0%	-5.2
11487	AT1G17300.1   expressed protein   chr1:5926987-5927433 FORWARD   Aliases: T13M22.4, T13M22_4	2.9	3.0	-0.1	-0.6	100.0%	-5.4
11488	AT5G53030.2   expressed protein   chr5:21522300-21523846 FORWARD   Aliases: MNB8.9, MNB8_9	3.2	3.0	0.1	0.6	100.0%	-4.9
11489	AT3G44840.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292)(Mol Plant Pathol (2001) 2(3):159-169)   chr3:16383484-16384744 REVERSE   Aliases: F28D10.30	2.6	2.7	-0.1	-0.6	100.0%	-5.5
11490	AT5G15070.1   expressed protein   chr5:4876518-4885824 FORWARD   Aliases: F2G14.190, F2G14_190	4.3	4.5	-0.2	-0.6	100.0%	-4.8
11491	ATMG01130.1   Symbol: ORF106F   hypothetical protein   chrM:289197-289517 REVERSE   Aliases: ORF106F	3.5	3.7	-0.2	-0.6	100.0%	-4.9
11492	AT1G73170.1   expressed protein   chr1:27515331-27518458 REVERSE   Aliases: T18K17.17, T18K17_17	7.0	6.9	0.2	0.6	100.0%	-4.6
11493	AT1G13590.1   Symbol: ATPSK1	4.7	5.0	-0.4	-0.6	100.0%	-4.2
11494	AT3G17090.2   similar to protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] (TAIR:At4g38520.2); similar to protein phosphatase 2C family protein / PP2C family protein [Arabidopsis thaliana] (TAIR:At4g38520.1); similar to protein phosphatase 2c-like protein [Thellungiella halophila] (GB:AAM19705.1); contains InterPro domain Protein phosphatase 2C-like (InterPro:IPR001932)   chr3:5826809-5829627 FORWARD   Aliases: K14A17.4	10.3	10.5	-0.2	-0.6	100.0%	-4.8
11495	AT1G27390.1   Symbol: TOM20 2   mitochondrial import receptor subunit TOM20-2 (TOM20-2), identical to mitochondrial import receptor subunit TOM20-2 SP:P82873 from (Arabidopsis thaliana)   chr1:9513076-9514988 REVERSE   Aliases: F17L21.18, F17L21_18, TRANSLOCASE OUTER MEMBRANE 20 2	5.7	5.9	-0.2	-0.6	100.0%	-4.7
11496	AT5G15410.2   Symbol: DND1   cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC2), identical to cyclic nucleotide-gated cation channel GI:3894399 from (Arabidopsis thaliana)   chr5:5003317-5006820 REVERSE   Aliases: ATCNGC2, CNGC2, CYCLIC NUCLEOTIDE GATED CHANNEL 2, DEFENSE NO DEATH 1	5.2	5.4	-0.2	-0.6	100.0%	-4.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11497	AT1G30473.1   similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:At3g05220.1); contains InterPro domain Heavy metal binding (InterPro:IPR006191); contains InterPro domain Heavy metal transport/detoxification protein (InterPro:IPR006121)   chr1:10787197-10788089 FORWARD   Aliases: None	2.8	2.7	0.1	0.6	100.0%	-5.2
11498	AT3G29290.1   Symbol: EMB2076   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:11239348-11241516 FORWARD   Aliases: EMB2076, EMBRYO DEFECTIVE 2076, MMF24.4	3.6	3.7	-0.1	-0.6	100.0%	-4.9
11499	AT4G18610.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr4:10250709-10251553 FORWARD   Aliases: F28A21.20, F28A21_20	5.3	5.4	-0.2	-0.6	100.0%	-4.6
11500	AT3G28920.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, contains Pfam PF04770: ZF-HD protein dimerisation region; contains Pfam TIGR01566: ZF-HD homeobox protein Cys/His-rich domain; contains TIGRFAM TIGR01565: homeobox domain, ZF-HD class; similar to ZF-HD homeobox protein (GI:13277220) (Flaveria bidentis)   chr3:10941683-10943070 REVERSE   Aliases: MYI13.1	3.3	3.2	0.1	0.6	100.0%	-5.0
11501	AT1G66310.1   F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.6	0.1	0.6	100.0%	-5.4
11502	AT3G07430.1   Symbol: EMB1990   YGGT family protein, contains Pfam profile PF02325: YGGT family (unknown function)   chr3:2379199-2380204 FORWARD   Aliases: EMB1990, EMBRYO DEFECTIVE 1990, F21O3.14	5.4	5.2	0.2	0.6	100.0%	-4.9
11503	AT5G66760.1   Symbol: SDH1 1	10.4	10.7	-0.3	-0.6	100.0%	-4.7
11504	AT3G29310.1   calmodulin-binding protein-related   chr3:11250889-11253057 FORWARD   Aliases: MUO10.1	3.9	4.6	-0.7	-0.6	100.0%	-4.4
11505	AT1G50420.1   Symbol: SCL3   scarecrow-like transcription factor 3 (SCL3), identical to GB:AAD24404 GI:4580515 from (Arabidopsis thaliana) (Plant J. 18 (1), 111-119 (1999))   chr1:18681598-18683740 REVERSE   Aliases: F11F12.22, F11F12_22	5.7	5.9	-0.2	-0.6	100.0%	-4.6
11506	AT1G73440.1   calmodulin-related, low similarity to calmodulin 8 (Arabidopsis thaliana) GI:5825600; contains Pfam profiles PF02809: Ubiquitin interaction motif, PF00036: EF hand   chr1:27615045-27616032 FORWARD   Aliases: T9L24.51, T9L24_51	4.8	4.7	0.1	0.6	100.0%	-5.0
11507	AT1G30620.2   Symbol: MUR4   similar to NAD-dependent epimerase/dehydratase family protein [Arabidopsis thaliana] (TAIR:At5g44480.1); similar to NAD-dependent epimerase/dehydratase family protein [Arabidopsis thaliana] (TAIR:At4g20460.1); similar to UDP-galactose 4-epimerase-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAC24804.1); similar to putative UDP-glucose 4-epimerase [Oryza sativa (japonica cultivar-group)] (GB:XP_479925.1); similar to putative UDP-glucose 4-epimerase [Oryza sativa (japonica cultivar-group)] (GB:XP_476598.1); similar to OSJNBa0093O08.14 [Oryza sativa (japonica cultivar-group)] (GB:XP_473906.1); similar to PREDICTED P0582D05.120 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_507116.1); contains InterPro domain NAD-dependent epimerase/dehydratase (InterPro:IPR001509); contains InterPro domain UDP-glucose 4-epimerase (InterPro:IPR005886)   chr1:10854587-10858196 FORWARD   Aliases: MURUS 4, T5I8.7, T5I8_7, UXE1	6.2	6.0	0.2	0.6	100.0%	-4.4
11508	AT3G60110.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr3:22208802-22212426 FORWARD   Aliases: T2O9.90	4.1	4.3	-0.2	-0.6	100.0%	-5.0
11509	AT1G75420.1   glycosyl transferase family 1 protein, contains Pfam glycosyl transferase, group 1 family protein domain PF00534	4.2	4.1	0.2	0.6	100.0%	-4.8
11510	AT4G12060.1   Clp amino terminal domain-containing protein, contains Pfam profile: PF02861 Clp amino terminal domain   chr4:7228001-7229935 REVERSE   Aliases: F16J13.130, F16J13_130	8.8	9.0	-0.2	-0.6	100.0%	-4.7
11511	AT3G23260.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:8313341-8314429 FORWARD   Aliases: K14B15.17	3.9	4.1	-0.3	-0.6	100.0%	-4.8
11512	AT5G26780.3   glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, strong similarity to SP:P50433 Serine hydroxymethyltransferase, mitochondrial precursor (EC 2.1.2.1) (Serine methylase) (Glycine hydroxymethyltransferase) (SHMT) {Solanum tuberosum}; contains Pfam profile PF00464: serine hydroxymethyltransferase   chr5:9418198-9422094 FORWARD   Aliases: F2P16.40, F2P16_40	7.7	8.1	-0.4	-0.6	100.0%	-4.6
11513	AT3G48940.1   remorin family protein, contains Pfam domain, PF03766: Remorin, N-terminal region and Pfam domain, PF03763: Remorin, C-terminal region   chr3:18153848-18155148 REVERSE   Aliases: T2J13.220	3.0	2.8	0.1	0.6	100.0%	-4.9
11514	AT5G47470.1   nodulin MtN21 family protein, integral membrane protein domain (PF00892); similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr5:19271825-19273605 FORWARD   Aliases: MNJ7.6, MNJ7_6	2.7	2.6	0.1	0.6	100.0%	-5.4
11515	AT1G25500.2   choline transporter-related, contains weak similarity to CD92 protein (Homo sapiens) gi:16945323:emb:CAC82175   chr1:8955295-8957936 REVERSE   Aliases: F2J7.7, F2J7_7	4.9	5.0	-0.1	-0.6	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11516	AT4G31960.1   expressed protein   chr4:15459113-15459774 REVERSE   Aliases: F11C18.11	2.3	2.2	0.1	0.6	100.0%	-5.7
11517	AT2G26190.1   calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr2:11154717-11157588 REVERSE   Aliases: T1D16.17, T1D16_17	4.9	5.5	-0.5	-0.6	100.0%	-4.3
11518	AT2G39410.2   hydrolase, alpha/beta fold family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:16462647-16465295 FORWARD   Aliases: F12L6.7, F12L6_7	2.9	3.1	-0.2	-0.6	100.0%	-4.3
11519	AT3G22630.1   Symbol: PBD1   20S proteasome beta subunit D (PBD1) (PRGB), identical to GB:CAA74026 from (Arabidopsis thaliana) ( FEBS Lett. (1997) 416 (3), 281-285); identical to cDNA proteasome subunit prgb GI:2511589   chr3:8009547-8010851 REVERSE   Aliases: F16J14.20, MULTICATALYTIC ENDOPEPTIDASE COMPLEX, PROTEASOME COMPONENT, BETA SUBUNIT, PRCGB, PROTEASOME SUBUNIT PRGB	10.2	10.5	-0.3	-0.6	100.0%	-4.7
11520	AT1G44750.3   Symbol: ATPUP11   similar to purine permease family protein [Arabidopsis thaliana] (TAIR:At4g08700.1); similar to putative purine permease [Oryza sativa (japonica cultivar-group)] (GB:XP_467223.1); contains InterPro domain Protein of unknown function DUF250 (InterPro:IPR004853)   chr1:16896163-16897905 FORWARD   Aliases: T12C22.2, T12C22_2	6.6	6.4	0.2	0.6	100.0%	-4.6
11521	AT1G23540.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:8346931-8349775 REVERSE   Aliases: F28C11.17	2.4	2.5	-0.1	-0.6	100.0%	-5.2
11522	AT1G77220.1   expressed protein, contains Pfam profile PF03619: Domain of unknown function   chr1:29017665-29020697 FORWARD   Aliases: T14N5.8, T14N5_8	4.9	5.0	-0.2	-0.6	100.0%	-4.8
11523	AT1G80480.1   PRLI-interacting factor L, putative, similar to PRLI-interacting factor L (Arabidopsis thaliana) GI:11139268; contains Pfam profile PF02492: Cobalamin synthesis protein/P47K   chr1:30262968-30265462 REVERSE   Aliases: T21F11.27, T21F11_27	7.8	7.6	0.2	0.6	100.0%	-4.7
11524	AT5G11740.1   Symbol: AGP15   arabinogalactan-protein (AGP15), identical to gi:10880507:gb:AAG24283   chr5:3784252-3784793 FORWARD   Aliases: ARABINOGALACTAN PROTEIN 15, T22P22.130, T22P22_130	8.8	8.4	0.4	0.6	100.0%	-4.4
11525	AT3G03000.1   calmodulin, putative, similar to calmodulin SP:P04352 from (Chlamydomonas reinhardtii); contains Pfam profile: PF00036 EF hand (4 copies)   chr3:677247-678091 FORWARD   Aliases: F13E7.5, F13E7_5	3.0	2.8	0.2	0.6	100.0%	-4.5
11526	AT5G59680.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:24064018-24068027 FORWARD   Aliases: MTH12.14, MTH12_14	4.0	3.7	0.2	0.6	100.0%	-4.3
11527	AT5G16730.1   expressed protein, weak similarity to microtubule binding protein D-CLIP-190 (Drosophila melanogaster) GI:2773363, SMC2-like condensin (Arabidopsis thaliana) GI:14279543   chr5:5497893-5500848 FORWARD   Aliases: F5E19.70, F5E19_70	6.4	5.8	0.5	0.6	100.0%	-4.4
11528	AT2G18740.1   small nuclear ribonucleoprotein E, putative / snRNP-E, putative / Sm protein E, putative, similar to SWISS-PROT:P08578 small nuclear ribonucleoprotein E (snRNP-E) (Sm protein E, Sm-E, SmE) (Chicken)   chr2:8130303-8132086 FORWARD   Aliases: MSF3.12, MSF3_12	5.5	6.0	-0.5	-0.6	100.0%	-4.6
11529	AT3G06180.1   expressed protein   chr3:1871694-1873751 FORWARD   Aliases: F28L1.12, F28L1_12	6.9	6.7	0.2	0.6	100.0%	-5.1
11530	AT2G33360.1   expressed protein   chr2:14147058-14150194 FORWARD   Aliases: F4P9.13, F4P9_13	4.4	4.5	-0.1	-0.6	100.0%	-5.3
11531	AT4G22460.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family   chr4:11839172-11839573 REVERSE   Aliases: F7K2.40, F7K2_40	3.0	2.9	0.2	0.6	100.0%	-4.8
11532	AT2G25560.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain   chr2:10887749-10890946 FORWARD   Aliases: F13B15.22, F13B15_22	7.1	7.3	-0.2	-0.6	100.0%	-4.8
11533	AT1G67770.1   RNA-binding protein, putative, similar to terminal ear1 gb:AAC39463.1   chr1:25411706-25413816 FORWARD   Aliases: F12A21.10, F12A21_10	3.3	3.4	-0.1	-0.6	100.0%	-5.4
11534	AT3G52740.1   expressed protein   chr3:19557352-19557942 REVERSE   Aliases: F3C22.140	7.1	6.9	0.2	0.6	100.0%	-4.7
11535	AT4G14800.1   Symbol: PBD2   20S proteasome beta subunit D2 (PBD2) (PRCGA), identical to SP:O24633 Proteasome subunit beta type 2-2 (EC 3.4.25.1) (20S proteasome alpha subunit D2) {Arabidopsis thaliana}, cDNA proteasome subunit prcga GI:2511571   chr4:8500283-8502224 FORWARD   Aliases: 20S PROTEASOME BETA SUBUNIT 2, 20S PROTEASOME BETA SUBUNIT PBD2, DL3440W, FCAALL.135	10.8	11.1	-0.3	-0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11536	AT1G56100.1   pectinesterase inhibitor domain-containing protein, contains TIGRFAM TIGR01614: pectinesterase inhibitor domain; contains weak hit to Pfam PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:20984034-20987644 REVERSE   Aliases: T6H22.11, T6H22_11	2.4	2.3	0.1	0.6	100.0%	-5.2
11537	AT5G51700.1   Symbol: PBS2   RAR1 disease resistance protein (RAR1), Contains a 3 nt micro-exon at exon 2.   chr5:21018438-21020431 REVERSE   Aliases: ATRAR1, MIO24.17, MIO24_17, PPHB SUSCEPTIBLE 2, RAR1, RPR2	5.1	4.9	0.2	0.6	100.0%	-4.7
11538	AT2G32310.1   expressed protein   chr2:13731746-13733451 FORWARD   Aliases: T32F6.17, T32F6_17	2.8	2.9	-0.1	-0.6	100.0%	-5.3
11539	AT5G27860.1   expressed protein   chr5:9874838-9876467 REVERSE   Aliases: F14I23.20, F14I23_20	2.8	2.6	0.3	0.6	100.0%	-4.5
11540	AT5G49260.1   hypothetical protein   chr5:19984025-19984753 FORWARD   Aliases: K21P3.14, K21P3_14	2.2	2.2	-0.0	-0.6	100.0%	-5.8
11541	AT2G15240.1   UNC-50 family protein, contains Pfam profile PF05216: UNC-50 family; contains 5 transmembrane domains; similar to inner nuclear membrane RNA-binding protein unc-50 related protein (GI:2735550) (Rattus norvegicus)   chr2:6622607-6626045 REVERSE   Aliases: F15A23.2, F15A23_2	6.6	6.3	0.3	0.6	100.0%	-4.5
11542	AT2G04520.1   eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative, strong similarity to translation initiation factor (eIF-1A) (Beta vulgaris) GI:17977975; contains Pfam profile PF01176: Eukaryotic initiation factor 1A   chr2:1574589-1575856 REVERSE   Aliases: T1O3.7, T1O3_7	8.8	9.0	-0.2	-0.6	100.0%	-4.8
11543	AT3G48185.1   expressed protein   chr3:17803996-17804528 REVERSE   Aliases: None	6.5	6.3	0.3	0.6	100.0%	-4.6
11544	AT3G45050.4   expressed protein   chr3:16486964-16488948 FORWARD   Aliases: F14D17.120	3.8	4.0	-0.2	-0.6	100.0%	-4.5
11545	ATCG01010.1   Symbol: NDHF   Chloroplast encoded NADH dehydrogenase unit.   chrC:110398-112638 REVERSE   Aliases: NDHF	2.8	3.2	-0.4	-0.6	100.0%	-4.6
11546	AT5G67430.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr5:26927562-26929327 FORWARD   Aliases: K8K14.17, K8K14_17	4.1	3.8	0.3	0.6	100.0%	-4.0
11547	AT1G19620.1   expressed protein   chr1:6784011-6785066 FORWARD   Aliases: F14P1.5	3.0	3.2	-0.2	-0.6	100.0%	-4.8
11548	AT1G49150.1   expressed protein   chr1:18182245-18182691 FORWARD   Aliases: F27J15.8, F27J15_8	2.7	2.8	-0.1	-0.6	100.0%	-5.3
11549	AT1G78030.1   expressed protein   chr1:29347051-29348718 FORWARD   Aliases: F28K19.25, F28K19_25	2.5	2.4	0.1	0.6	100.0%	-5.0
11550	AT5G60570.1   kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain   chr5:24365939-24367120 FORWARD   Aliases: MUF9.20, MUF9_20	5.7	5.4	0.3	0.6	100.0%	-4.6
11551	AT4G17940.1   expressed protein   chr4:9965754-9966978 FORWARD   Aliases: T6K21.120, T6K21_120	9.2	8.9	0.3	0.6	100.0%	-5.2
11552	AT3G11240.1   arginine-tRNA-protein transferase, putative / arginyltransferase, putative / arginyl-tRNA-protein transferase, putative, similar to SP:Q9ZT48 Arginine-tRNA-protein transferase 1 (EC 2.3.2.8) (R-transferase 1) (Arginyltransferase 1) (Arginyl-tRNA--protein transferase 1) {Arabidopsis thaliana}; contains Pfam profiles PF04377: Arginine-tRNA-protein transferase C terminus, PF04376: Arginine-tRNA-protein transferase N terminus   chr3:3518490-3521121 REVERSE   Aliases: F11B9.16	3.2	3.3	-0.1	-0.6	100.0%	-5.2
11553	AT1G04750.2   Symbol: VAMP7B	10.3	9.9	0.4	0.6	100.0%	-4.5
11554	AT5G16520.1   expressed protein   chr5:5394656-5397458 REVERSE   Aliases: MQK4.27, MQK4_27	4.7	4.5	0.2	0.6	100.0%	-4.5
11555	AT5G39820.1   Symbol: ANAC094   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; NAC domain protein NAM, Arabidopsis thaliana, gb:AAD17313   chr5:15956528-15957719 REVERSE   Aliases: ANAC094, MKM21.110, MKM21_110	2.6	2.7	-0.1	-0.6	100.0%	-5.5
11556	AT1G03445.1   Symbol: BSU1   similar to kelch repeat-containing serine/threonine phosphoesterase family protein [Arabidopsis thaliana] (TAIR:At4g03080.1); similar to protein serine/threonine phosphatase, putative [Plasmodium berghei] (GB:CAH95465.1); similar to protein serine/threonine phosphatase alpha [Plasmodium yoelii yoelii] (GB:EAA18849.1); contains InterPro domain Kelch repeat (InterPro:IPR006652); contains InterPro domain Metallo-phosphoesterase (InterPro:IPR004843); contains InterPro domain Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase (InterPro:IPR006186)   chr1:854409-859701 REVERSE   Aliases: F21B7.7	4.4	4.2	0.2	0.6	100.0%	-4.6
11557	AT4G39040.2   expressed protein, contains PF01985: Uncharacterised protein family   chr4:18189006-18190550 REVERSE   Aliases: F19H22.140, F19H22_140	8.5	8.3	0.2	0.6	100.0%	-4.6
11558	AT5G43820.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr5:17636175-17639095 FORWARD   Aliases: MQD19.18, MQD19_18	5.8	6.0	-0.2	-0.6	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11559	AT1G08390.1   expressed protein   chr1:2642211-2643282 FORWARD   Aliases: T27G7.27	6.1	6.3	-0.2	-0.6	100.0%	-4.3
11560	AT4G22650.1   hypothetical protein, various predicted proteins, Arabidopsis thaliana   chr4:11913568-11914038 FORWARD   Aliases: T12H17.40	2.5	2.5	-0.1	-0.6	100.0%	-5.5
11561	AT5G16250.1   expressed protein   chr5:5310100-5310954 REVERSE   Aliases: T21H19.170, T21H19_170	3.8	4.0	-0.2	-0.6	100.0%	-4.4
11562	AT3G22880.1   Symbol: ATDMC1	8.6	8.2	0.4	0.6	100.0%	-4.7
11563	AT5G56920.1   expressed protein   chr5:23042122-23043141 FORWARD   Aliases: MHM17.3, MHM17_3	3.6	3.7	-0.1	-0.6	100.0%	-5.4
11564	AT1G20080.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr1:6962227-6964903 FORWARD   Aliases: T20H2.13, T20H2_13	3.5	3.4	0.1	0.6	100.0%	-5.3
11565	AT4G23730.1   aldose 1-epimerase family protein, similar to apospory-associated protein C; APOC (Chlamydomonas reinhardtii) GI:6970044 Pfam profile PF01263: Aldose 1-epimerase   chr4:12362494-12365104 FORWARD   Aliases: F9D16.200, F9D16_200	3.5	3.4	0.2	0.6	100.0%	-5.1
11566	AT2G02440.1   expressed protein   chr2:638011-639304 FORWARD   Aliases: T16F16.23, T16F16_23	4.1	4.0	0.2	0.6	100.0%	-5.0
11567	AT1G07360.1   zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein, similar to SP:O59800 Cell cycle control protein cwf5 {Schizosaccharomyces pombe}, RNA Binding Protein 47 (Nicotiana plumbaginifolia) GI:9663769; contains Pfam profile: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain)   chr1:2260387-2262845 REVERSE   Aliases: F22G5.30, F22G5_30	6.3	6.5	-0.2	-0.6	100.0%	-4.8
11568	AT5G61720.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:24818780-24820395 FORWARD   Aliases: MAC9.3, MAC9_3	2.4	2.3	0.1	0.6	100.0%	-5.7
11569	AT1G53860.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr1:20110775-20113160 REVERSE   Aliases: T18A20.9, T18A20_9	2.8	2.7	0.1	0.6	100.0%	-5.3
11570	AT5G10870.1   Symbol: ATCM2   chorismate mutase, cytosolic (CM2), identical to gi:5732016   chr5:3430547-3432463 REVERSE   Aliases: None	4.7	4.9	-0.2	-0.6	100.0%	-4.7
11571	AT2G22120.1   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At1g11020.1); similar to zinc finger (C3HC4-type RING finger) protein -like [Oryza sativa (japonica cultivar-group)] (GB:BAD52533.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr2:9400903-9404102 FORWARD   Aliases: T16B14.3, T16B14_3	4.4	4.2	0.2	0.6	100.0%	-4.8
11572	AT4G20060.1   Symbol: EMB1895   expressed protein, ; expression supported by MPSS   chr4:10854800-10859340 REVERSE   Aliases: EMB1895, EMBRYO DEFECTIVE 1895, F18F4.160, F18F4_160	3.8	4.0	-0.1	-0.6	100.0%	-5.3
11573	AT5G06410.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P36540 Chaperone protein hscB (HSC20) {Escherichia coli O157:H7}; contains Pfam profile PF00226 DnaJ domain   chr5:1959537-1961159 REVERSE   Aliases: MHF15.7, MHF15_7	4.4	4.6	-0.2	-0.6	100.0%	-4.8
11574	AT3G58210.1   mepirin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:21573419-21575044 REVERSE   Aliases: F9D24.120	2.6	2.6	0.1	0.6	100.0%	-5.8
11575	AT2G09840.1   expressed protein   chr2:3712042-3712533 REVERSE   Aliases: T14C8.6, T14C8_6	2.3	2.3	0.1	0.6	100.0%	-5.7
11576	AT4G26970.1   aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative, strong similarity to SP:P49608 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Cucurbita maxima}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain   chr4:13542924-13549101 FORWARD   Aliases: F10M23.310, F10M23_310	11.9	12.0	-0.1	-0.6	100.0%	-5.4
11577	AT2G02810.1   UDP-galactose/UDP-glucose transporter, contains transmembrane domains; identical to UDP-galactose/UDP-glucose transporter (GI:22651763) (Arabidopsis thaliana) similar to UGTrel1 (GI:1669564) (Rattus rattus); identical to cDNA UDP-galactose/UDP-glucose transporter GI:22651762   chr2:801529-803435 FORWARD   Aliases: T20F6.5, T20F6_5	5.1	5.2	-0.1	-0.6	100.0%	-5.1
11578	AT4G03750.1   hypothetical protein   chr4:1667202-1668886 FORWARD   Aliases: T5L23.27, T5L23_27	3.6	3.4	0.2	0.6	100.0%	-4.7
11579	AT4G39235.1   expressed protein   chr4:18268043-18269320 FORWARD   Aliases: None	7.2	7.0	0.2	0.6	100.0%	-4.5
11580	AT2G27650.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr2:11799902-11804789 REVERSE   Aliases: F15K20.25, F15K20_25	3.1	3.2	-0.1	-0.6	100.0%	-5.0
11581	AT3G04290.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile: lipase/acylhydrolase with GDSL-like motif   chr3:1133331-1136297 REVERSE   Aliases: T6K12.9, T6K12_9	2.5	2.4	0.1	0.6	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11582	AT3G28130.2   similar to nodulin MtN21 family protein [Arabidopsis thaliana] (TAIR:At3g28100.1); similar to putative nodulin MtN21 protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475475.1); contains InterPro domain Protein of unknown function DUF6 (InterPro:IPR000620)   chr3:10466753-10470148 FORWARD   Aliases: MMG15.31	3.0	3.2	-0.2	-0.6	100.0%	-4.5
11583	AT1G19200.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);   chr1:6625095-6625847 REVERSE   Aliases: T29M8.7, T29M8_7	3.7	3.5	0.1	0.6	100.0%	-5.1
11584	AT1G27610.1   expressed protein, identical to hypothetical protein GB:AAF24964 GI:6693038 from (Arabidopsis thaliana)   chr1:9607098-9607564 REVERSE   Aliases: T22C5.5	2.7	2.6	0.1	0.6	100.0%	-5.2
11585	AT2G39680.1   Symbol: TAS2   Trans-acting siRNA primary transcript. RDR6-dependent trans-acting siRNA-generating locus. Regulated by miR173.   chr2:16546796-16547050 FORWARD   Aliases: F17A14.5, F17A14_5, TAS2	2.3	2.3	-0.1	-0.6	100.0%	-5.8
11586	AT3G10910.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:3412916-3414024 REVERSE   Aliases: T7M13.1	2.5	2.2	0.3	0.6	100.0%	-4.1
11587	AT4G19980.1   expressed protein, ; expression supported by MPSS   chr4:10828163-10828546 REVERSE   Aliases: F18F4.80, F18F4_80	2.2	2.3	-0.1	-0.6	100.0%	-5.3
11588	AT1G65260.1   PspA/IM30 family protein, contains Pfam PF04012: PspA/IM30 family profile; similar to Membrane-associated 30 kDa protein, chloroplast precursor (M30) (Swiss-Prot:Q03943) (Pisum sativum); similar to phage shock protein A (GI:28806161) (Vibrio parahaemolyticus); similar to Phage shock protein A. (Swiss-Prot:P23853) (Shigella flexneri)   chr1:24239923-24244322 FORWARD   Aliases: T8F5.2, T8F5_2	7.7	7.3	0.3	0.6	100.0%	-4.5
11589	AT5G25290.1   F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.6	-0.1	-0.6	100.0%	-5.5
11590	AT1G79770.1   expressed protein   chr1:30019254-30019971 FORWARD   Aliases: F20B17.20, F20B17_20	2.9	2.7	0.1	0.6	100.0%	-4.9
11591	AT4G12760.1   expressed protein, ; expression supported by MPSS   chr4:7504873-7506088 FORWARD   Aliases: T20K18.110, T20K18_110	7.3	7.1	0.2	0.6	100.0%	-4.7
11592	AT2G47340.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr2:19439238-19440086 FORWARD   Aliases: T8I13.18	2.9	2.8	0.1	0.6	100.0%	-5.1
11593	AT1G24290.1   AAA-type ATPase family protein, similar to Werner helicase interacting protein (Homo sapiens) GI:14349166; contains Pfam profiles PF00004: ATPase family associated with various cellular activities (AAA), PF00627: UBA/TS-N domain; contains ATP/GTP-binding site motif A (P-loop)   chr1:8612261-8614266 REVERSE   Aliases: F3I6.23, F3I6_23	3.2	3.1	0.1	0.6	100.0%	-5.1
11594	AT2G04845.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:1702220-1704000 REVERSE   Aliases: None	5.4	5.7	-0.2	-0.6	100.0%	-4.3
11595	AT4G24020.1   RWP-RK domain-containing protein, similar to nodule inception protein (Lotus japonicus) GI:6448579; contains Pfam profile: PF02042 RWP-RK domain	4.4	4.6	-0.2	-0.6	100.0%	-4.5
11596	AT1G02150.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat   chr1:408622-410611 FORWARD   Aliases: T6A9.13	6.5	6.6	-0.1	-0.6	100.0%	-5.1
11597	AT4G28150.2   expressed protein   chr4:13977309-13979012 REVERSE   Aliases: F26K10.30, F26K10_30	3.5	3.4	0.1	0.6	100.0%	-4.8
11598	AT5G16780.1   SART-1 family protein, contains Pfam domain, PF03343: SART-1 family   chr5:5517528-5522261 REVERSE   Aliases: F5E19.120, F5E19_120	8.4	8.0	0.4	0.6	100.0%	-4.2
11599	AT1G29750.2   Symbol: RKF1   leucine-rich repeat transmembrane protein kinase, putative / serine/threonine kinase, putative (RKF1), similar to receptor-like serine/threonine kinase GI:2465923 from (Arabidopsis thaliana); identical to cDNA receptor-like serine/threonine kinase (RKF1) GI:2465922   chr1:10413866-10420509 REVERSE   Aliases: F1N18.19, F1N18_19, RECEPTOR LIKE KINASE IN FLOWERS 1, RECEPTOR LIKE SERINE/THREONINE KINASE	4.7	4.8	-0.2	-0.6	100.0%	-4.7
11600	AT5G14800.1   Symbol: P5CR   pyrroline-5-carboxylate reductase, identical to pyrroline-5-carboxylate reductase SP:P54904 from (Arabidopsis thaliana)   chr5:4785965-4787840 REVERSE   Aliases: AT P5C1, AT P5R, PYRROLINE 5 CARBOXYLATE (P5C) REDUCTASE, T9L3.100, T9L3_100	10.8	10.5	0.2	0.6	100.0%	-4.4
11601	AT1G24706.1   expressed protein   chr1:8741926-8755544 FORWARD   Aliases: F5A9.21, F5A9_21	4.6	4.8	-0.2	-0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11602	AT5G48140.1   polygalacturonase, putative / pectinase, putative, strong similarity to polygalacturonase PGA3 (Arabidopsis thaliana) GI:3152948; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:19535996-19537752 REVERSE   Aliases: MIF21.3, MIF21_3	2.2	2.3	-0.1	-0.6	100.0%	-5.6
11603	NA	3.1	3.2	-0.1	-0.6	100.0%	-5.3
11604	AT2G32800.1   protein kinase family protein, contains dual protein kinase domains, Pfam:PF00069   chr2:13923529-13926629 FORWARD   Aliases: F24L7.6, F24L7_6	4.6	4.8	-0.2	-0.6	100.0%	-4.5
11605	AT5G43280.1   enoyl-CoA hydratase/isomerase family protein, similar to Delta 3,5-delta2,4-dienoyl-CoA isomerase, mitochondrial (ECH1) from Rattus norvegicus (SP:Q62651), from Homo sapiens (SP:Q13011); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr5:17385116-17386542 FORWARD   Aliases: MNL12.10, MNL12_10	6.7	6.5	0.2	0.6	100.0%	-4.9
11606	AT1G63350.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.6	2.7	-0.1	-0.6	100.0%	-5.3
11607	AT1G32330.1   Symbol: ATHSFA1D   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr1:11656966-11660356 REVERSE   Aliases: F27G20.6, HSFA1D	3.8	4.0	-0.2	-0.6	100.0%	-5.0
11608	AT1G33811.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	2.1	2.1	0.1	0.6	100.0%	-5.7
11609	AT4G36550.1   U-box domain-containing protein, low similarity to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain	4.6	4.9	-0.3	-0.6	100.0%	-4.6
11610	AT5G22820.1   expressed protein   chr5:7624026-7626978 REVERSE   Aliases: MRN17.5, MRN17_5	3.0	3.1	-0.1	-0.6	100.0%	-5.3
11611	AT3G02490.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:513532-515932 FORWARD   Aliases: F16B3.12, F16B3_12	6.9	7.0	-0.2	-0.6	100.0%	-4.7
11612	AT3G02880.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat (5 copies)   chr3:634660-637289 FORWARD   Aliases: F13E7.17, F13E7_17	6.5	6.2	0.3	0.6	100.0%	-4.8
11613	AT1G77990.1   Symbol: AST56   similar to sulfate transporter [Arabidopsis thaliana] (TAIR:At5g10180.1); similar to low affinity sulphate transporter [Stylosanthes hamata] (GB:CAA57831.1); similar to Putative sulfate transporter [Oryza sativa (japonica cultivar-group)] (GB:AAN59769.1); similar to Putative sulfate transporter [Oryza sativa (japonica cultivar-group)] (GB:AAN59770.1); similar to sulfate permease [Brassica juncea] (GB:CAA11413.1); contains InterPro domain Sulphate transporter (InterPro:IPR001902); contains InterPro domain Sulfate transporter/antisigma-factor antagonist STAS (InterPro:IPR002645)	3.8	3.5	0.3	0.6	100.0%	-4.4
11614	AT4G33680.1   Symbol: AGD2   aminotransferase class I and II family protein, low similarity to Aromatic Aminotransferase from Pyrococcus horikoshii GP:14278621; contains Pfam profile PF00155 aminotransferase, classes I and II   chr4:16171697-16174681 REVERSE   Aliases: ABERRANT GROWTH AND DEATH 2, T16L1.170, T16L1_170	11.5	11.9	-0.4	-0.6	100.0%	-5.0
11615	AT5G57190.1   phosphatidylserine decarboxylase, putative, similar to SP:P53037 Phosphatidylserine decarboxylase proenzyme 2 precursor (EC 4.1.1.65) {Saccharomyces cerevisiae}; contains Pfam profile PF02666: phosphatidylserine decarboxylase   chr5:23188757-23192590 REVERSE   Aliases: MUL3.14, MUL3_14	4.9	5.1	-0.2	-0.6	100.0%	-4.8
11616	AT1G78440.1   gibberellin 2-oxidase / GA2-oxidase (GA2OX1), identical to gibberellin 2- oxidase ga2ox1 (GI:4678366) from (Arabidopsis thaliana)   chr1:29516492-29517944 REVERSE   Aliases: F3F9.5, F3F9_5	3.7	3.5	0.1	0.6	100.0%	-5.0
11617	AT3G57670.1   zinc finger (C2H2 type) protein (WIP2), identical to WIP2 protein (Arabidopsis thaliana) gi:18027012:gb:AAL55722; contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:21381880-21384423 FORWARD   Aliases: F15B8.140	3.8	3.7	0.1	0.6	100.0%	-5.0
11618	AT3G44580.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:16171499-16171990 REVERSE   Aliases: F14L2.130	2.8	2.8	0.1	0.6	100.0%	-5.5
11619	AT4G31060.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr4:15116856-15117662 FORWARD   Aliases: F6I18.30, F6I18_30	3.7	3.9	-0.2	-0.6	100.0%	-4.8
11620	AT4G34440.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:16465832-16468960 FORWARD   Aliases: T4L20.20, T4L20_20	2.5	2.5	0.1	0.6	100.0%	-5.4
11621	AT2G47890.2   zinc finger (B-box type) family protein   chr2:19615066-19616702 FORWARD   Aliases: F17A22.28	6.0	6.2	-0.2	-0.6	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11622	AT2G24850.1   Symbol: TAT3   aminotransferase, putative, similar to nicotianamine aminotransferase from <i>Hordeum vulgare</i> (GI:6498122, GI:6469087); contains Pfam profile PF00155 aminotransferase, classes I and II   chr2:10589909-10592295 REVERSE   Aliases: F27C12.23, F27C12_23, TAT, TYROSINE AMINOTRANSFERASE 3	2.5	2.7	-0.1	-0.6	100.0%	-5.3
11623	AT4G23760.1   expressed protein   chr4:12379384-12383044 FORWARD   Aliases: F9D16.230, F9D16_230	3.5	3.7	-0.2	-0.6	100.0%	-4.6
11624	AT3G62230.1   F-box family protein, contains Pfam:PF00646 F-box domain	2.7	2.6	0.1	0.6	100.0%	-5.4
11625	AT3G10500.1   Symbol: ANAC053   no apical meristem (NAM) family protein, similar to to NAC2 (GI:645671) ( <i>Arabidopsis thaliana</i> ); contains Pfam PF02365: No apical meristem (NAM) protein   chr3:3271617-3274035 FORWARD   Aliases: ANAC053, F13M14.22	7.1	7.3	-0.2	-0.6	100.0%	-4.5
11626	AT5G62140.1   expressed protein   chr5:24971732-24972610 REVERSE   Aliases: MTG10.17, MTG10_17	3.5	3.4	0.1	0.6	100.0%	-5.0
11627	AT4G36520.1   trichohyalin-related, low similarity to SP:Q07283 Trichohyalin { <i>Homo sapiens</i> }   chr4:17230592-17235438 REVERSE   Aliases: AP22.19, AP22_19	4.2	3.9	0.3	0.6	100.0%	-4.2
11628	AT4G32650.3   Symbol: ATKC1   similar to inward rectifying potassium channel (KAT2) [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g18290.1); similar to potassium channel [ <i>Daucus carota</i> ] (GB:CAB62555.1); contains InterPro domain Cation channel, non-ligand gated (InterPro:IPR005820); contains InterPro domain EAG/ELK/ERG potassium channel (InterPro:IPR003938); contains InterPro domain Ion transport protein (InterPro:IPR005821); contains InterPro domain Cyclic nucleotide-binding domain (InterPro:IPR000595)	2.7	2.9	-0.2	-0.6	100.0%	-4.5
11629	ATCG00540.1   Symbol: PETA   Encodes cytochrome f apoprotein; involved in photosynthetic electron transport chain; encoded by the chloroplast genome and is transcriptionally repressed by a nuclear gene HCF2.   chrC:61657-62619 FORWARD   Aliases: PETA	10.2	10.6	-0.4	-0.6	100.0%	-4.6
11630	AT5G59300.1   Symbol: UBC7   ubiquitin-conjugating enzyme 7 (UBC7), E2; identical to gi:992703, SP:P42747   chr5:23937094-23938517 REVERSE   Aliases: ATUBC7, MNC17.22, MNC17_22	5.4	5.6	-0.2	-0.6	100.0%	-4.8
11631	AT5G59090.3   similar to subtilase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g58820.1); similar to subtilase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g59100.1); similar to subtilase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g59130.1); similar to subtilase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g58840.1); similar to subtilase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g59120.1); similar to pre-pro-cucumisin [ <i>Cucumis melo</i> ] (GB:BAA06905.1); contains InterPro domain Protease-associated PA (InterPro:IPR003137); contains InterPro domain Subtilase serine protease (InterPro:IPR000209)   chr5:23869131-23872501 REVERSE   Aliases: K18B18.5, K18B18_5	2.8	2.7	0.1	0.6	100.0%	-5.2
11632	AT3G46270.1   receptor protein kinase-related, contains weak similarity to light repressible receptor protein kinase (GI:1321686) ( <i>Arabidopsis thaliana</i> )   chr3:17011699-17015222 REVERSE   Aliases: F12M12.240	2.0	2.0	0.0	0.6	100.0%	-5.9
11633	AT4G33300.2   Symbol: ADR1 L1   similar to disease resistance protein (NBS-LRR class), putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g47280.1); similar to disease resistance protein (CC-NBS-LRR class), putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g04720.1); similar to disease resistance protein (CC-NBS-LRR class), putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g33560.1); similar to disease resistance protein-like protein MsR1 [ <i>Medicago sativa</i> ] (GB:AAN62760.1); contains InterPro domain NB-ARC domain (InterPro:IPR002182); contains InterPro domain Disease resistance protein (InterPro:IPR000767); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr4:16050233-16056530 REVERSE   Aliases: ADR1 L1, ADR1 LIKE 1, F17M5.60, F17M5_60	7.3	7.5	-0.2	-0.6	100.0%	-4.6
11634	AT4G11170.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:6811123-6817126 FORWARD   Aliases: T22B4.150, T22B4_150	2.5	2.4	0.1	0.6	100.0%	-5.4
11635	AT3G18990.1   Symbol: VRN1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr3:6548875-6551847 REVERSE   Aliases: K13E13.10, REDUCED VERNALIZATION RESPONSE 1, REM39	5.9	6.1	-0.2	-0.6	100.0%	-4.7
11636	AT2G41140.1   Symbol: CRK1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK3 ( <i>Nicotiana tabacum</i> ) gi:16904226:gb:AAL30820   chr2:17157465-17160768 FORWARD   Aliases: CDPK RELATED KINASE 1, T3K9.9, T3K9_9	5.3	5.5	-0.2	-0.6	100.0%	-4.6
11637	NA	2.3	2.2	0.0	0.6	100.0%	-5.8
11638	AT3G53100.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382) ( <i>Arabidopsis thaliana</i> ), SP:P40603 Anther-specific proline-rich protein APG { <i>Brassica napus</i> }; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr3:19695725-19697575 REVERSE   Aliases: T4D2.30	2.1	2.4	-0.3	-0.6	100.0%	-4.7
11639	AT1G18500.1   2-isopropylmalate synthase, putative, strong similarity to 2-isopropylmalate synthase (IMS1) ( <i>Arabidopsis thaliana</i> ) GI:12330687; contains Pfam profile PF00682: HMGL-like   chr1:6369340-6373018 FORWARD   Aliases: F15H18.3, F15H18_3	10.2	10.5	-0.3	-0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11640	AT2G04560.1   glycotransferase family protein 19, low similarity to lipid-A-disaccharide synthase from Haemophilus influenzae (gi:1694783) and Escherichia coli (SP:P10441); contains InterPro IPR003835: Glycosyl transferase, family 19   chr2:1591987-1592664 REVERSE   Aliases: T1O3.3, T1O3_3	3.5	3.3	0.2	0.6	100.0%	-4.9
11641	AT3G61150.1   homeobox-leucine zipper family protein / homeodomain GLABRA2 like protein 1 (HD-GL2-1), similar to Anthocyaninless2 (ANL2) (GP:5702094) Arabidopsis thaliana, EMBL:AF077335   chr3:22641585-22645950 FORWARD   Aliases: T20K12.50	4.7	4.9	-0.2	-0.6	100.0%	-4.5
11642	AT5G36080.1   hypothetical protein   chr5:14201653-14202507 FORWARD   Aliases: MAB16.2, MAB16_2	2.5	2.6	-0.1	-0.6	100.0%	-5.7
11643	AT5G52680.1   heavy-metal-associated domain-containing protein, low similarity to pneumococcal surface protein A PspA (Streptococcus pneumoniae) GI:7800654; contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:21383039-21384089 FORWARD   Aliases: F6N7.17, F6N7_17	3.4	3.6	-0.1	-0.6	100.0%	-5.0
11644	AT5G28640.1   Symbol: AN3   SSXT protein-related / glycine-rich protein, contains weak hit to Pfam profile PF05030: SSXT protein (N-terminal region)   chr5:10647575-10649896 REVERSE   Aliases: ANGUSITFOLIA3, F4I4.20, F4I4_20, GIF, GIF1, GRF1 INTERACTING FACTOR	2.8	2.9	-0.1	-0.6	100.0%	-5.3
11645	AT5G10090.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr5:3153723-3155746 REVERSE   Aliases: T31P16.80, T31P16_80	2.9	2.9	-0.1	-0.6	100.0%	-5.2
11646	AT1G17430.1   hydrolase, alpha/beta fold family protein, low similarity to SP:Q02104 Lipase 1 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Psychrobacter immobilis}, contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:5982260-5984004 FORWARD   Aliases: F28G4.9	6.7	6.9	-0.2	-0.6	100.0%	-4.6
11647	AT1G48980.2   similar to oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] (TAIR:At2g17970.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP51882.1); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)   chr1:18121700-18124270 FORWARD   Aliases: F27J15.23, F27J15_23	2.5	2.4	0.1	0.6	100.0%	-5.4
11648	AT1G24330.1   armadillo/beta-catenin repeat family protein / U-box domain-containing family protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:8631768-8634824 FORWARD   Aliases: F3I6.27, F3I6_27	3.5	3.7	-0.1	-0.6	100.0%	-4.7
11649	AT1G22030.1   expressed protein   chr1:7759153-7760545 REVERSE   Aliases: F2E2.8, F2E2_8	6.3	6.1	0.2	0.6	100.0%	-4.6
11650	AT4G18100.1   60S ribosomal protein L32 (RPL32A), ribosomal protein L32, human, PIR1:R5HU32   chr4:10035497-10036552 REVERSE   Aliases: F15J5.70, F15J5_70	9.3	9.6	-0.4	-0.6	100.0%	-4.4
11651	AT5G46430.2   60S ribosomal protein L32 (RPL32B)   chr5:18850494-18851791 FORWARD   Aliases: K11I1.2, K11I1_2	9.3	9.6	-0.4	-0.6	100.0%	-4.4
11652	AT5G52820.1   WD-40 repeat family protein / notchless protein, putative, similar to notchless (Xenopus laevis) GI:3687833; contains Pfam PF00400: WD domain, G-beta repeat (8 copies)   chr5:21418582-21421579 FORWARD   Aliases: MXC20.4, MXC20_4	9.0	8.8	0.2	0.6	100.0%	-4.5
11653	AT5G19220.1   Symbol: ADG2   Encodes the large subunit of ADP-glucose pyrophosphorylase which catalyzes the first, rate limiting step in starch biosynthesis.	2.8	2.9	-0.1	-0.6	100.0%	-5.0
11654	AT1G47750.1   peroxisomal biogenesis factor 11 family protein / PEX11 family protein, contains Pfam PF05648: Peroxisomal biogenesis factor 11 (PEX11)   chr1:17571217-17572599 REVERSE   Aliases: T2E6.18, T2E6_18	5.0	5.1	-0.1	-0.6	100.0%	-5.0
11655	AT2G17975.1   zinc finger (Ran-binding) family protein, contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others   chr2:7829320-7831052 REVERSE   Aliases: T27K22.20	4.1	3.9	0.2	0.6	100.0%	-4.9
11656	AT2G47160.1   Symbol: BOR1   anion exchange family protein, contains some similarity to SWISS-PROT:P04919 anion transport protein (anion exchange protein 1) (Mouse) {Mus musculus}   chr2:19364556-19368213 REVERSE   Aliases: REQUIRES HIGH BORON 1, T3D7.3	3.0	3.3	-0.3	-0.6	100.0%	-4.5
11657	AT5G08590.1   Symbol: ASK2   serine/threonine protein kinase (ASK2), identical to serine/threonine-protein kinase ASK2, SWISS-PROT: P43292; contains protein kinase domain, Pfam:PF00069   chr5:2783410-2786095 FORWARD   Aliases: ARABIDOPSIS SERINE/THREONINE KINASE 2, MAH20.15, MAH20_15	8.0	8.3	-0.2	-0.6	100.0%	-4.5
11658	AT2G04630.1   DNA-directed RNA polymerase II, putative, similar to SP:Q24320 DNA-directed RNA polymerase II 14.4 kDa polypeptide (EC 2.7.7.6) (RPB6) {Drosophila melanogaster}; contains Pfam profile PF01192: RNA polymerases K / 14 to 18 kDa subunit   chr2:1618933-1620308 REVERSE   Aliases: F28I8.33, F28I8_33	9.8	9.7	0.1	0.6	100.0%	-4.8
11659	AT5G46300.1   expressed protein   chr5:18800837-18802013 FORWARD   Aliases: MPL12.8, MPL12_8	2.4	2.5	-0.1	-0.6	100.0%	-5.7
11660	AT3G43110.1   expressed protein   chr3:15102698-15103396 REVERSE   Aliases: F7M19.120	3.1	3.0	0.1	0.6	100.0%	-4.9
11661	AT1G80000.2   expressed protein, identical to unknown protein GB:AAD55481 (Arabidopsis thaliana)   chr1:30097822-30102058 FORWARD   Aliases: F19K16.3, F19K16_3	3.5	3.4	0.1	0.6	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11662	AT5G54960.1   Symbol: PDC2   pyruvate decarboxylase, putative, strong similarity to pyruvate decarboxylase 1 (Vitis vinifera) GI:10732644; contains InterPro entry IPR000399: Pyruvate decarboxylase   chr5:22327913-22329987 REVERSE   Aliases: MBG8.23, MBG8_23, PYRUVATE DECARBOXYLASE, PYRUVATE DECARBOXYLASE 2	9.2	8.9	0.3	0.6	100.0%	-4.9
11663	AT2G36485.1   expressed protein   chr2:15314035-15314869 REVERSE   Aliases: None	3.8	4.0	-0.2	-0.6	100.0%	-4.8
11664	AT3G17890.1   expressed protein   chr3:6127047-6127880 FORWARD   Aliases: MEB5.11	5.3	5.6	-0.2	-0.6	100.0%	-4.3
11665	AT2G25710.2   Symbol: HCS1   holocarboxylase synthetase 1 (HCS1), identical to holocarboxylase synthetase 1 (hcs1) (Arabidopsis thaliana) GI:19698365	5.0	5.3	-0.3	-0.6	100.0%	-4.5
11666	ATMG00010.1   Symbol: ORF153A   hypothetical protein   chrM:273-734 REVERSE   Aliases: ORF153A	3.1	3.5	-0.4	-0.6	100.0%	-4.5
11667	AT5G55420.1   expressed protein   chr5:22479129-22479544 FORWARD   Aliases: MTE17.13, MTE17_13	2.7	2.7	0.1	0.6	100.0%	-5.4
11668	AT4G23620.1   50S ribosomal protein-related, contains weak similarity to 50S ribosomal protein L25 (TL5). (Swiss-Prot:P56930) (Thermus thermophilus)   chr4:12314035-12316725 REVERSE   Aliases: F9D16.90, F9D16_90	7.5	7.7	-0.2	-0.6	100.0%	-4.5
11669	AT1G60090.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max)   chr1:22159247-22161730 FORWARD   Aliases: T2K10.15, T2K10_15	3.5	3.3	0.2	0.6	100.0%	-4.8
11670	AT3G28390.1   P-glycoprotein, putative, similar to P-glycoprotein homologue GI:2292907 from (Hordeum vulgare subsp. vulgare)   chr3:10630662-10635204 REVERSE   Aliases: MFJ20.6	3.6	3.5	0.1	0.6	100.0%	-5.0
11671	AT3G48450.1   nitrate-responsive NOI protein, putative, similar to nitrate-induced NOI protein (Zea mays) GI:2642213   chr3:17955017-17955873 REVERSE   Aliases: T29H11.30	3.8	4.0	-0.2	-0.6	100.0%	-4.5
11672	AT3G12720.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain   chr3:4043317-4044616 REVERSE   Aliases: MBK21.26	2.2	2.2	-0.1	-0.6	100.0%	-5.7
11673	AT1G23190.1   phosphoglucomutase, cytoplasmic, putative / glucose phosphomutase, putative, strong similarity to SP:P93805 Phosphoglucomutase, cytoplasmic 2 (EC 5.4.2.2) (Glucose phosphomutase 2) (PGM 2) {Zea mays}; contains InterPro accession IPR006352: Phosphoglucosamine mutase   chr1:8219879-8224458 FORWARD   Aliases: T26J12.5, T26J12_5	11.7	12.2	-0.5	-0.6	100.0%	-5.0
11674	AT4G10750.1   HpCh/HpaI aldolase family protein, similar to 2,4-dihydroxydec-2-ene-1,10-dioic acid aldolase (Sphingopyxis macrogoltabida) GI:23330203; contains Pfam profile PF03328: HpCh/HpaI aldolase family   chr4:6618672-6619935 FORWARD   Aliases: T12H20.10, T12H20_10	8.6	8.8	-0.2	-0.6	100.0%	-4.8
11675	AT5G02720.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:613780-614311 REVERSE   Aliases: F9G14.30, F9G14_30	2.9	2.8	0.1	0.6	100.0%	-5.4
11676	AT5G15280.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:4962296-4966143 FORWARD   Aliases: F8M21.170, F8M21_170	3.8	4.0	-0.1	-0.6	100.0%	-4.9
11677	AT5G26340.1   Symbol: MSS1   hexose transporter, putative, strong similarity to hexose transporter, Lycopersicon esculentum, GI:5734440; contains Pfam profile PF00083: major facilitator superfamily protein	2.5	2.6	-0.1	-0.6	100.0%	-5.4
11678	AT5G28680.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:10719441-10722017 REVERSE   Aliases: F4I4.60, F4I4_60	3.4	3.3	0.1	0.6	100.0%	-5.2
11679	AT3G07770.1   heat shock protein-related, strong similarity to heat-shock protein (Secale cereale) GI:556673; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein   chr3:2479561-2484171 FORWARD   Aliases: MLP3.22	9.1	9.5	-0.4	-0.6	100.0%	-4.5
11680	AT4G14380.1   expressed protein   chr4:8285767-8286768 FORWARD   Aliases: DL3230W, FCAALL.187	4.1	3.9	0.2	0.6	100.0%	-4.8
11681	AT1G45230.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g46630.1); similar to DCL protein [Coffea arabica] (GB:CAD12248.1)   chr1:17171979-17173901 REVERSE   Aliases: None	4.0	3.7	0.3	0.6	100.0%	-4.4
11682	AT1G16300.1   glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, similar to glyceraldehyde-3-phosphate dehydrogenase (Pinus sylvestris) GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain   chr1:5574304-5577616 FORWARD   Aliases: F3O9.10, F3O9_10	8.7	7.9	0.8	0.6	100.0%	-4.3
11683	AT1G79530.1   glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, similar to glyceraldehyde-3-phosphate dehydrogenase (Pinus sylvestris) GI:1100223; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain   chr1:29920795-29924127 REVERSE   Aliases: T8K14.5, T8K14_5	8.7	7.9	0.8	0.6	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11684	AT3G03610.1   phagocytosis and cell motility protein ELMO1-related, contains weak similarity to ELMO1 (Mus musculus) gi:16118551:gb:AAL14464   chr3:868831-871818 FORWARD   Aliases: T12J13.11, T12J13_11	7.7	7.4	0.3	0.6	100.0%	-4.9
11685	AT4G37470.1   hydrolase, alpha/beta fold family protein, low similarity to SP:Q59093 3-oxoadipate enol-lactonase I (EC 3.1.1.24) (Enol-lactone hydrolase I) (Beta-ketoadipate enol-lactone hydrolase I) {Acinetobacter calcoaceticus}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:17616653-17618452 REVERSE   Aliases: F6G17.120, F6G17_120	9.1	8.9	0.1	0.6	100.0%	-4.9
11686	AT3G58680.1   ethylene-responsive transcriptional coactivator, putative, similar to ethylene-responsive transcriptional coactivator (Lycopersicon esculentum) gi:5669634:gb:AAD46402   chr3:21718253-21719881 FORWARD   Aliases: T20N10.30, T20N10_30	10.7	10.4	0.3	0.6	100.0%	-4.9
11687	AT5G08565.1   expressed protein   chr5:2775899-2777400 FORWARD   Aliases: None	6.1	6.3	-0.2	-0.6	100.0%	-4.4
11688	AT1G61580.1   Symbol: ARP2/RPL3B   60S ribosomal protein L3 (RPL3B), identical to ribosomal protein GI:806279 from (Arabidopsis thaliana)   chr1:22724366-22726815 REVERSE   Aliases: ARABIDOPSIS RIBOSOMAL PROTEIN 2, ARP2, RIBOSOMAL PROTEIN L3, RPL3B, T25B24.7, T25B24_7	5.7	5.9	-0.2	-0.6	100.0%	-4.8
11689	AT2G11270.1   citrate synthase-related, contains similarity to Swiss-Prot:P20115 citrate synthase, mitochondrial precursor (Arabidopsis thaliana)   chr2:4491802-4492390 FORWARD   Aliases: T13H18.17, T13H18_17	3.6	3.3	0.3	0.6	100.0%	-4.6
11690	AT4G17000.1   expressed protein   chr4:9567065-9569932 REVERSE   Aliases: DL4530C, FCAALL.326	3.9	4.0	-0.2	-0.6	100.0%	-4.7
11691	AT5G01980.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:375242-377205 FORWARD   Aliases: T7H20.30, T7H20_30	5.9	5.8	0.2	0.6	100.0%	-4.5
11692	AT1G73830.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.2	3.1	0.1	0.6	100.0%	-5.2
11693	AT2G48060.1   expressed protein   chr2:19665165-19669751 REVERSE   Aliases: T9J23.21	3.8	3.7	0.1	0.6	100.0%	-5.1
11694	AT1G10640.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:3515366-3516975 REVERSE   Aliases: F20B24.8, F20B24_8	2.8	2.7	0.1	0.6	100.0%	-5.2
11695	AT5G52640.1   Symbol: HSP81 1   heat shock protein 81-1 (HSP81-1) / heat shock protein 83 (HSP83), nearly identical to SP:P27323 Heat shock protein 81-1 (HSP81-1) (Heat shock protein 83) {Arabidopsis thaliana}; contains Pfam profiles PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein, PF00183: Hsp90 protein   chr5:21369660-21372587 FORWARD   Aliases: ATHS83, F6N7.13, F6N7_13, HEAT SHOCK PROTEIN 81 1, HEAT SHOCK PROTEIN 83, HSP81 1, HSP81.1, HSP83	7.0	6.8	0.2	0.6	100.0%	-4.7
11696	AT4G05230.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:2687001-2687621 FORWARD   Aliases: C17L7.150, C17L7_150	3.4	3.2	0.2	0.6	100.0%	-4.8
11697	AT3G21560.1   UDP-glucosyltransferase, putative, similar to UDP-glucose:sinapate glucosyltransferase GI:9794913 from (Brassica napus)   chr3:7595812-7597583 FORWARD   Aliases: MIL23.13	5.1	5.0	0.1	0.6	100.0%	-5.0
11698	AT4G08190.1   Ras-related GTP-binding protein, putative, similar to Ras-related protein Rab11A (Swiss-Prot:Q96283) (Arabidopsis thaliana)   chr4:5174520-5175473 REVERSE   Aliases: T12G13.30, T12G13_30	2.6	2.6	-0.1	-0.6	100.0%	-5.8
11699	AT2G24340.1   expressed protein   chr2:10362510-10366626 REVERSE   Aliases: T28I24.7, T28I24_7	2.5	2.6	-0.1	-0.6	100.0%	-5.4
11700	AT1G61720.1   Symbol: BAN   dihydroflavonol 4-reductase (dihydrokaempferol 4-reductase) family (BAN), similar to dihydroflavonol 4-reductase GI:1332411 from (Rosa hybrida)   chr1:22794846-22796465 REVERSE   Aliases: BANYULS, T13M11.8, T13M11_8	2.3	2.3	-0.1	-0.6	100.0%	-5.6
11701	AT3G16520.3   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:5619134-5620879 REVERSE   Aliases: MDC8.15	8.8	9.1	-0.4	-0.6	100.0%	-4.0
11702	AT5G27580.1   MADS-box family protein, contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain); MADS-box protein AGL89   chr5:9736654-9737325 FORWARD   Aliases: F15A18.40, F15A18_40	2.7	2.6	0.1	0.6	100.0%	-5.3
11703	AT4G08640.1   hypothetical protein, low similarity to chaperonin-containing-TCP1 theta subunit from Tetrahymena pyriformis (GI:4959731), Homo sapiens (SP:P50990)   chr4:5513310-5514171 FORWARD   Aliases: T3F12.5, T3F12_5	2.2	2.3	-0.1	-0.6	100.0%	-5.5
11704	AT5G67400.1   peroxidase 73 (PER73) (P73) (PRXR11), identical to SP:Q43873 Peroxidase 73 precursor (EC 1.11.1.7) (Atperox P73) (PRXR11) (ATP10a) {Arabidopsis thaliana}   chr5:26912082-26913714 FORWARD   Aliases: K8K14.13, K8K14_13	2.8	3.0	-0.2	-0.6	100.0%	-4.5
11705	AT4G21500.1   expressed protein, ; expression supported by MPSS   chr4:11441077-11441724 REVERSE   Aliases: F18E5.120, F18E5_120	3.0	3.1	-0.1	-0.6	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11706	AT1G53080.1   legume lectin family protein   chr1:19785036-19785887 FORWARD   Aliases: F8L10.6, F8L10_6	2.7	2.8	-0.1	-0.6	100.0%	-5.6
11707	AT5G66140.1   Symbol: PAD2   20S proteasome alpha subunit D2 (PAD2) (PRS1) (PRC6), identical to SP:O24616 Proteasome subunit alpha type 7-2 (EC 3.4.25.1) (20S proteasome alpha subunit D2) {Arabidopsis thaliana}   chr5:26454396-26455947 REVERSE   Aliases: 20S PROTEASOME SUBUNIT PAD2, K2A18.22, K2A18_22	9.4	9.0	0.4	0.6	100.0%	-4.6
11708	AT4G16130.1   Symbol: ARA1   GHMP kinase family protein, contains GHMP kinases putative ATP-binding protein domain, Pfam:PF00288   chr4:9120879-9127950 FORWARD   Aliases: ARABINOSE KINASE, ARABINOSE SENSITIVE 1, ATISA1, DL4105W, FCAALL.288, ISA1	7.2	6.9	0.3	0.6	100.0%	-4.6
11709	AT2G18960.1   Symbol: AHA1   ATPase 1, plasma membrane-type, putative / proton pump 1, putative / proton-exporting ATPase, putative, strong similarity to SP:P20649 ATPase 1, plasma membrane-type (EC 3.6.3.6) (Proton pump 1) {Arabidopsis thaliana}; contains InterPro accession IPR001757: ATPase, E1-E2 type; contains Pfam profile PF00690: Cation transporter/ATPase, N-terminus   chr2:8228713-8234701 FORWARD   Aliases: F19F24.16, F19F24_16, PLASMA MEMBRANE PROTON ATPASE, PMA	12.2	12.4	-0.2	-0.6	100.0%	-5.3
11710	AT1G66880.1   serine/threonine protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290   chr1:24950591-24959274 FORWARD   Aliases: F4N21.1, F4N21_1	4.7	4.9	-0.2	-0.6	100.0%	-4.8
11711	AT1G18450.1   Symbol: ATARP4	6.1	6.3	-0.2	-0.6	100.0%	-4.8
11712	AT5G22320.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr5:7388007-7390454 REVERSE   Aliases: MWD9.11, MWD9_11	7.5	7.9	-0.4	-0.6	100.0%	-4.7
11713	AT1G80290.1   glycosyltransferase family protein 47, similar to exostosin, Homo sapiens (SP:O43909), (SP:Q16394)   chr1:30193213-30194618 FORWARD   Aliases: F5I6.4, F5I6_4	5.1	4.9	0.2	0.6	100.0%	-4.8
11714	AT5G25100.1   endomembrane protein 70, putative, TM4 family;   chr5:8648106-8651115 REVERSE   Aliases: T11H3.110, T11H3_110	7.1	7.3	-0.2	-0.6	100.0%	-5.0
11715	AT1G78550.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to naringenin,2-oxoglutarate 3-dioxygenase (flavonone-3-hydroxylase) (SP:Q06942)(Malus domestica); contains PF03171 2OG-Fe(II) oxygenase superfamily domain	5.8	5.6	0.2	0.6	100.0%	-4.7
11716	AT1G52620.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:19607479-19609955 FORWARD   Aliases: F6D8.16, F6D8_16	3.1	3.0	0.1	0.6	100.0%	-5.1
11717	AT5G19810.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:6693054-6693803 FORWARD   Aliases: T29J13.230, T29J13_230	3.2	3.3	-0.1	-0.6	100.0%	-5.0
11718	AT3G58600.1   expressed protein, hypothetical protein F21M11.17 - Arabidopsis thaliana, EMBL:AC003027   chr3:21679173-21682140 REVERSE   Aliases: F14P22.190	8.8	8.5	0.3	0.6	100.0%	-4.9
11719	AT2G21140.1   Symbol: ATPRP2	2.9	3.1	-0.2	-0.6	100.0%	-4.9
11720	AT4G01340.1   CHP-rich zinc finger protein-related, similar to A. thaliana CHP-rich zinc finger proteins   chr4:554539-556961 FORWARD   Aliases: F2N1.28, F2N1_28	2.8	2.7	0.1	0.6	100.0%	-5.4
11721	AT5G47390.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:19244017-19246085 FORWARD   Aliases: MQL5.25, MQL5_25	5.5	5.2	0.3	0.6	100.0%	-4.6
11722	AT5G50960.1   nucleotide-binding family protein, similar to Nucleotide-binding protein 1 (NBP 1) (SP:Q9R060) (Mus musculus); contains Pfam PF00991 : ParA family ATPase   chr5:20751403-20753281 FORWARD   Aliases: K3K7.12, K3K7_12	7.3	7.5	-0.2	-0.6	100.0%	-4.7
11723	AT5G03250.1   phototropic-responsive NPH3 family protein, contains some similarity to root phototropism RPT2 (Arabidopsis thaliana) gi:6959488:gb:AAF33112, a signal transducer of phototropic response PMID:10662859   chr5:774590-776854 FORWARD   Aliases: F15A17.280, F15A17_280	3.6	3.5	0.1	0.6	100.0%	-5.2
11724	AT1G45616.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591   chr1:17185990-17188974 REVERSE   Aliases: F2G19.6, F2G19_6	2.3	2.3	-0.1	-0.6	100.0%	-5.7
11725	AT5G56540.1   Symbol: AGP14   arabinogalactan-protein (AGP14), identical to gi:10880505:gb:AAG24282   chr5:22910377-22910868 FORWARD   Aliases: ARABINO GALACTAN PROTEIN 14, MKN22.5, MKN22_5	5.3	5.7	-0.4	-0.6	100.0%	-4.3
11726	AT1G66670.1   Symbol: CLPP3   ATP-dependent Clp protease proteolytic subunit (ClpP3), identical to ATP-dependent Clp protease (nClpP3) GI:5360591 (Arabidopsis thaliana)   chr1:24867448-24869363 REVERSE   Aliases: F4N21.19, F4N21_19, NCLPP3, NCLPP4	8.7	8.9	-0.2	-0.6	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11727	AT4G29700.1   type I phosphodiesterase/nucleotide pyrophosphatase family protein, similar to SP:P22413 Ectonucleotide pyrophosphatase/phosphodiesterase 1 (Plasma-cell membrane glycoprotein PC-1) (Includes: Alkaline phosphodiesterase I (EC 3.1.4.1); Nucleotide pyrophosphatase (EC 3.6.1.9) {Homo sapiens}); contains Pfam profile PF01663: Type I phosphodiesterase / nucleotide pyrophosphatase   chr4:14543463-14545144 REVERSE   Aliases: T16L4.210, T16L4_210	2.7	2.9	-0.2	-0.6	100.0%	-4.6
11728	AT5G26620.1   expressed protein   chr5:9366700-9366966 REVERSE   Aliases: None	2.6	2.5	0.1	0.6	100.0%	-5.6
11729	AT4G23900.1   nucleoside diphosphate kinase 4 (NDK4), contains Pfam PF00334 : Nucleoside diphosphate kinase domain; identical to nucleoside diphosphate kinase 4 (GI:11990430)	5.6	5.5	0.1	0.6	100.0%	-4.6
11730	AT4G16360.2   similar to 5'-AMP-activated protein kinase beta-2 subunit, putative [Arabidopsis thaliana] (TAIR:At5g21170.1); similar to SNF1-related kinase complex anchoring protein SIP1 [Lycopersicon esculentum] (GB:AAG41995.1); contains InterPro domain 5-AMP-activated protein kinase, beta subunit, complex-interacting region (InterPro:IPR006828)   chr4:9245139-9247270 FORWARD   Aliases: DL4210W, FCAALL.163	5.6	5.2	0.3	0.6	100.0%	-4.7
11731	AT1G31200.1   Symbol: ATPP2 A9   expressed protein   chr1:11146904-11147659 REVERSE   Aliases: ATPP2 A9, F28K20.16, F28K20_16	3.4	3.2	0.2	0.6	100.0%	-4.9
11732	AT5G49640.1   expressed protein   chr5:20168389-20169068 FORWARD   Aliases: MNI5.2, MNI5_2	2.6	2.5	0.1	0.6	100.0%	-5.8
11733	AT1G29790.1   expressed protein   chr1:10429961-10432018 FORWARD   Aliases: F1N18.26, F1N18_26	7.4	7.2	0.2	0.6	100.0%	-4.9
11734	NA	12.9	12.8	0.1	0.6	100.0%	-5.8
11735	AT1G77490.1   L-ascorbate peroxidase, thylakoid-bound (tAPX), identical to thylakoid-bound ascorbate peroxidase GB:CAA67426 (Arabidopsis thaliana)   chr1:29122504-29125109 FORWARD   Aliases: T5M16.8, T5M16_8	4.9	4.7	0.2	0.6	100.0%	-4.4
11736	AT2G30630.2   expressed protein, similar to H1-1flk (Arabidopsis thaliana) GI:388260   chr2:13053755-13056296 REVERSE   Aliases: T11J7.2, T11J7_2	2.4	2.4	-0.1	-0.6	100.0%	-5.8
11737	AT5G11400.1   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:3636615-3638060 REVERSE   Aliases: F2I11.290, F2I11_290	2.3	2.3	0.1	0.6	100.0%	-5.4
11738	AT5G26920.1   similar to calmodulin-binding protein [Arabidopsis thaliana] (TAIR:At4g25800.1); similar to putative calmodulin-binding protein [Oryza sativa (japonica cultivar-group)] (GB:BAD27989.1)	2.2	2.2	0.1	0.6	100.0%	-5.8
11739	AT1G30460.1   similar to YT521-B-like family protein [Arabidopsis thaliana] (TAIR:At4g11970.2); similar to YT521-B-like family protein [Arabidopsis thaliana] (TAIR:At4g11970.1); similar to PREDICTED: similar to YTH domain containing 2, partial [Bos taurus] (GB:XP_614159.1); contains InterPro domain YT521-B-like protein (InterPro:IPR007275); contains InterPro domain Zn-finger, C-x8-C-x5-C-x3-H type (InterPro:IPR000571)   chr1:10771451-10775305 REVERSE   Aliases: F26G16.6, F26G16_6	3.2	3.4	-0.1	-0.6	100.0%	-5.0
11740	AT1G13190.1   RNA recognition motif (RRM)-containing protein   chr1:4498893-4501973 FORWARD   Aliases: F3F19.21, F3F19_21	6.5	6.3	0.2	0.6	100.0%	-4.8
11741	AT1G02780.1   Symbol: EMB2386   60S ribosomal protein L19 (RPL19A), similar to ribosomal protein L19 GI:36127 from (Homo sapiens)   chr1:607821-609435 REVERSE   Aliases: EMB2386, EMBRYO DEFECTIVE 2386, T14P4.34	11.5	11.8	-0.3	-0.6	100.0%	-4.4
11742	AT3G45810.1   ferric reductase-like transmembrane component family protein, similar to respiratory burst oxidase protein D RbohD from Arabidopsis thaliana, EMBL:AF055357 (gi:3242789), similar to respiratory burst oxidase protein D RbohD from Arabidopsis thaliana, EMBL:AF055357 (gi:3242789), respiratory burst oxidase homolog from Solanum tuberosum (GI:16549089); contains Pfam profile PF01794 Ferric reductase like transmembrane component   chr3:16843868-16848554 REVERSE   Aliases: F16L2.20	2.6	2.7	-0.1	-0.6	100.0%	-5.4
11743	AT5G18540.2   expressed protein, contains InterPro domain Bipartite nuclear localization signal (InterPro:IPR001472)   chr5:6153871-6156168 FORWARD   Aliases: T28N17.20, T28N17_20	5.4	5.1	0.3	0.6	100.0%	-4.6
11744	AT5G12040.2   carbon-nitrogen hydrolase family protein, similar to Nit protein 2 (Homo sapiens) GI:9367116; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family   chr5:3885155-3888055 FORWARD   Aliases: F14F18.210, F14F18_210	9.5	9.7	-0.2	-0.6	100.0%	-4.9
11745	AT1G57760.1   expressed protein   chr1:21393747-21398199 FORWARD   Aliases: T8L23.22, T8L23_22	4.7	4.6	0.1	0.6	100.0%	-4.9
11746	AT5G27350.1   Symbol: SFP1   sugar-porter family protein 1 (SFP1), identical to sugar-porter family protein 1 (Arabidopsis thaliana) GI:14585699   chr5:9648670-9654429 FORWARD   Aliases: F21A20.60, F21A20_60, sugar porter family protein 1	3.5	3.7	-0.2	-0.6	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11747	AT5G58640.2   similar to selenoprotein-related [Arabidopsis thaliana] (TAIR:At3g47300.1); similar to P0446G04.25 [Oryza sativa (japonica cultivar-group)] (GB:NP_915340.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr5:23715117-23716993 FORWARD   Aliases: MZN1.9, MZN1_9	8.1	8.4	-0.3	-0.6	100.0%	-4.6
11748	AT3G20020.1   protein arginine N-methyltransferase family protein, similar to SP:Q96LA8 Protein arginine N-methyltransferase 6 (EC 2.1.1.-) {Homo sapiens}   chr3:6983711-6988105 REVERSE   Aliases: MAL21.12	3.5	3.6	-0.1	-0.6	100.0%	-5.1
11749	AT4G07480.1   hypothetical protein   chr4:4268922-4270170 FORWARD   Aliases: T3E15.12, T3E15_12	2.8	2.9	-0.1	-0.6	100.0%	-5.2
11750	AT5G02900.1   Symbol: CYP96A13   cytochrome P450, putative, cytochrome P450 homolog, Arabidopsis thaliana, PIR:T09367	3.0	2.9	0.1	0.6	100.0%	-5.3
11751	AT2G30110.1   Symbol: ATUBA1	7.4	7.7	-0.3	-0.6	100.0%	-5.0
11752	AT5G08650.1   GTP-binding protein LepA, putative   chr5:2806324-2813227 REVERSE   Aliases: T2K12.1	5.6	5.4	0.2	0.6	100.0%	-4.7
11753	AT1G71696.2   Symbol: SOL1   carboxypeptidase D, putative, similar to carboxypeptidase D (Anas platyrhynchos) gi:2789654:gb:AAB96915   chr1:26970549-26974234 FORWARD   Aliases: F14O23.7, F14O23_7, SOL1 SPLICE VARIANT A1B1, SOL1 SPLICE VARIANT A1B2, SOL1 SPLICE VARIANT A2B1, SOL1 SPLICE VARIANT A3B1, SOL1.1	3.0	3.2	-0.1	-0.6	100.0%	-5.0
11754	AT2G01720.1   ribophorin I family protein, similar to SP:P04843 Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit precursor (EC 2.4.1.119) (Ribophorin I) {Homo sapiens}; contains Pfam profile PF04597: Ribophorin I   chr2:317032-320249 REVERSE   Aliases: T8O11.11, T8O11_11	10.7	10.9	-0.2	-0.6	100.0%	-5.0
11755	AT2G14260.2   Symbol: PIP   proline iminopeptidase, identical to GP:1710151:U72711   chr2:6048353-6050769 REVERSE   Aliases: None	8.1	8.2	-0.1	-0.6	100.0%	-4.9
11756	AT1G63450.1   exostosin family protein, contains Pfam profile: PF03016	2.6	2.7	-0.1	-0.6	100.0%	-5.1
11757	AT3G47060.1   Symbol: FTSH7   encodes an FtsH protease that is localized to the chloroplast   chr3:17343970-17347951 FORWARD   Aliases: F13I12.110, FTSH7	4.7	4.9	-0.2	-0.6	100.0%	-4.6
11758	AT5G57200.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, low similarity to clathrin assembly protein AP180 (Xenopus laevis) GI:6492344; contains Pfam profile PF01417: ENTH domain   chr5:23194922-23197827 FORWARD   Aliases: MJB24.1, MJB24_1	2.3	2.2	0.1	0.6	100.0%	-5.4
11759	AT4G28830.1   expressed protein   chr4:14232452-14234005 FORWARD   Aliases: F16A16.60, F16A16_60	9.0	8.7	0.2	0.6	100.0%	-4.4
11760	AT5G52460.1   F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.6	0.1	0.6	100.0%	-5.4
11761	AT4G04630.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr4:2331675-2332798 REVERSE   Aliases: F4H6.15, F4H6_15	3.1	3.0	0.1	0.6	100.0%	-5.3
11762	AT2G20860.1   Symbol: LIP1   lipoic acid synthase (LIP1), identical to gi:3928758 contains Pfam profile PF04055: radical SAM domain protein   chr2:8986660-8988286 FORWARD   Aliases: F5H14.17, F5H14_17, LIPOIC ACID SYNTHASE	10.7	10.4	0.3	0.6	100.0%	-4.8
11763	AT5G59110.1   subtilisin-like serine protease-related, similar to prepro-cucumisin GI:807698 from (Cucumis melo), subtilisin-like protease C1 (Glycine max) GI:13325079   chr5:23880756-23881274 REVERSE   Aliases: K18B18.9	2.3	2.4	-0.1	-0.6	100.0%	-5.0
11764	AT3G11400.1   Symbol: EIF3G1	9.1	8.8	0.3	0.6	100.0%	-4.6
11765	AT4G38130.1   Symbol: HD1   histone deacetylase (RPD3A), identical to SP:O22446 Histone deacetylase (HD) {Arabidopsis thaliana}   chr4:17896286-17899474 REVERSE   Aliases: ATHD1, ATRPD3A, F20D10.250, F20D10_250, HDA1, HDA19, HISTONE DEACETYLASE, RPD3A	6.7	6.9	-0.2	-0.6	100.0%	-4.7
11766	AT3G17280.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:5903459-5904619 REVERSE   Aliases: MGD8.12	3.8	3.9	-0.1	-0.6	100.0%	-5.0
11767	AT5G43330.1   malate dehydrogenase, cytosolic, putative, strong similarity to cytosolic malate dehydrogenase (EC 1.1.1.37) SP:O24047 {Mesembryanthemum crystallinum}, SP:O48905 {Medicago sativa}, (Prunus persica) GI:15982948; contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr5:17407661-17409867 FORWARD   Aliases: MWF20.2, MWF20_2	10.8	11.3	-0.5	-0.6	100.0%	-4.5
11768	AT1G48620.1   histone H1/H5 family protein, weak similarity to HMG I/Y like protein (Glycine max) GI:15706274, HMG-I/Y protein HMGa (Triticum aestivum) GI:20502966; contains Pfam profiles PF00538: linker histone H1 and H5 family, PF02178: AT hook motif   chr1:17977365-17980057 REVERSE   Aliases: T1N15.25, T1N15_25	5.9	5.7	0.2	0.6	100.0%	-4.7
11769	AT1G63520.1   expressed protein   chr1:23563550-23565806 FORWARD   Aliases: F2K11.12, F2K11_12	2.5	2.4	0.1	0.6	100.0%	-5.2
11770	AT5G18310.2   expressed protein, predicted proteins, Drosophila melanogaster   chr5:6061734-6063024 FORWARD   Aliases: F20L16.30, F20L16_30	9.3	9.5	-0.2	-0.6	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11771	AT2G44990.1   Symbol: CCD7   dioxygenase-related, low similarity to carotenoid cleavage dioxygenase 1 (Arabidopsis thaliana) GI:3096910; contains Pfam profile PF03055: Retinal pigment epithelial membrane protein   chr2:18566013-18568408 FORWARD   Aliases: MAX3, T14P1.21	3.2	3.0	0.1	0.6	100.0%	-5.2
11772	AT4G23870.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr4:12414240-12415059 FORWARD   Aliases: T32A16.40, T32A16_40	3.5	3.8	-0.2	-0.6	100.0%	-4.6
11773	AT5G42100.2   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097948 from (Oryza sativa)   chr5:16847064-16848467 REVERSE   Aliases: MJC20.21, MJC20_21	5.2	5.0	0.2	0.6	100.0%	-4.7
11774	AT4G25200.1   Symbol: ATHSP23.6 MITO	3.6	3.5	0.2	0.6	100.0%	-4.6
11775	AT2G10090.1   expressed protein   chr2:3830613-3830972 REVERSE   Aliases: F7B19.23, F7B19_23	2.7	2.6	0.1	0.6	100.0%	-5.4
11776	AT5G24560.1   Symbol: ATPP2 B12   F-box family protein / SKP1 interacting partner 3-related, contains similarity to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)   chr5:8402208-8403269 FORWARD   Aliases: ATPP2 B12, K18P6.9, K18P6_9	3.6	3.7	-0.2	-0.6	100.0%	-4.9
11777	AT4G37295.1   expressed protein   chr4:17553554-17554099 FORWARD   Aliases: None	4.9	5.1	-0.2	-0.6	100.0%	-4.8
11778	AT2G48100.4   similar to exonuclease family protein [Arabidopsis thaliana] (TAIR:At3g27970.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_908385.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087); contains InterPro domain Exonuclease (InterPro:IPR006055)   chr2:19677571-19680362 FORWARD   Aliases: None	7.6	7.4	0.2	0.6	100.0%	-4.6
11779	AT2G36960.2   Symbol: TKI1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:15530027-15534556 FORWARD   Aliases: T1J8.14, T1J8_14	5.1	5.0	0.1	0.6	100.0%	-4.8
11780	AT5G26940.4   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr5:9480597-9482772 FORWARD   Aliases: F2P16.200, F2P16_200	7.2	7.4	-0.2	-0.6	100.0%	-4.5
11781	AT2G26790.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:11432348-11434747 REVERSE   Aliases: F12C20.17, F12C20_17	2.6	2.5	0.1	0.6	100.0%	-5.7
11782	AT1G66240.1   copper homeostasis factor, putative / copper chaperone, putative (CCH), similar to gi:3168840 contains Pfam profile PF00403: Heavy-metal-associated domain   chr1:24689940-24690995 REVERSE   Aliases: T6J19.6, T6J19_6	9.7	9.8	-0.1	-0.6	100.0%	-5.1
11783	AT5G54600.2   50S ribosomal protein L24, chloroplast (CL24), identical to SP:P92959 50S ribosomal protein L24, chloroplast precursor {Arabidopsis thaliana}   chr5:22200204-22201793 FORWARD   Aliases: MRB17.10, MRB17_10	9.1	9.3	-0.2	-0.6	100.0%	-4.6
11784	AT3G29390.1   hydroxyproline-rich glycoprotein family protein, sequencing discrepancy between cDNA and genomic sequence prevents representation of entire coding sequence   chr3:11290853-11295965 FORWARD   Aliases: MUO10.13	3.8	4.2	-0.3	-0.6	100.0%	-4.6
11785	AT5G52110.2   expressed protein, similar to hypothetical protein OSJNBa0096G08.1 [Oryza sativa (japonica cultivar-group)] (GB:AAO00695.1)   chr5:21188860-21191207 REVERSE   Aliases: MSG15.21, MSG15_21	3.4	3.5	-0.1	-0.6	100.0%	-5.1
11786	AT3G51660.1   macrophage migration inhibitory factor family protein / MIF family protein, contains Pfam profile: PF01187 Macrophage migration inhibitory factor family(MIF)   chr3:19175042-19176151 REVERSE   Aliases: T18N14.40	2.8	3.1	-0.3	-0.6	100.0%	-4.9
11787	AT4G35000.1   Symbol: APX3   L-ascorbate peroxidase 3 (APX3), identical to ascorbate peroxidase 3 (Arabidopsis thaliana) GI:2444019, L-ascorbate peroxidase (Arabidopsis thaliana) gi:1523791:emb:CAA66926; similar to ascorbate peroxidase (Gossypium hirsutum) gi:1019946:gb:AAB52954   chr4:16664827-16667710 REVERSE   Aliases: ASCORBATE PEROXIDASE 3, M4E13.60, M4E13_60	9.4	9.8	-0.5	-0.6	100.0%	-4.6
11788	AT4G33050.3   similar to calmodulin-binding family protein [Arabidopsis thaliana] (TAIR:At2g26190.1); similar to putative calmodulin-binding protein [Oryza sativa (japonica cultivar-group)] (GB:BAD45140.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048)   chr4:15944325-15947029 REVERSE   Aliases: F4I10.2	3.4	3.7	-0.3	-0.6	100.0%	-4.4
11789	AT2G42570.1   expressed protein   chr2:17724453-17727158 REVERSE   Aliases: F14N22.16, F14N22_16	9.0	9.2	-0.2	-0.6	100.0%	-4.7
11790	AT4G30770.1   expressed protein   chr4:14986146-14986619 REVERSE   Aliases: T10C21.120, T10C21_120	1.9	2.0	-0.1	-0.6	100.0%	-6.0
11791	AT5G03770.1   3-deoxy-D-manno-octulosonic acid transferase-related, similar to 3-deoxy-D-manno-octulosonic acid transferase, Escherichia coli, PIR:JU0467; contains Pfam profile PF04413: 3-Deoxy-D-manno-octulosonic-acid transferase (kdottransferase)   chr5:995159-997847 FORWARD   Aliases: F17C15.190, F17C15_190	4.9	5.0	-0.2	-0.6	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11792	AT1G26590.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:9189611-9190696 FORWARD   Aliases: T1K7.4, T1K7_4	3.2	3.1	0.1	0.6	100.0%	-5.3
11793	AT2G07020.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:2908470-2911195 REVERSE   Aliases: T4E14.13, T4E14_13	4.6	4.7	-0.1	-0.6	100.0%	-5.1
11794	AT1G79500.4   Symbol: KDSA   similar to 2-dehydro-3-deoxyphosphooctonate aldolase, putative / phospho-2-dehydro-3-deoxyoctonate aldolase, putative / 3-deoxy-D-manno-octulosonic acid 8-phosphate synthetase, putative [Arabidopsis thaliana] (TAIR:At1g16340.1); similar to putative 2-dehydro-3-deoxyphosphooctonate aldolase [Oryza sativa (japonica cultivar-group)] (GB:AAO72599.1); contains InterPro domain DAHP synthetase I/KDSA superfamily (InterPro:IPR006218); contains InterPro domain 2-dehydro-3-deoxyphosphooctonate aldolase (InterPro:IPR006269)   chr1:29908408-29911452 FORWARD   Aliases: T8K14.8, T8K14_8	7.3	7.1	0.2	0.6	100.0%	-4.3
11795	AT5G45080.1   Symbol: ATPP2 A6   disease resistance protein-related, weak similarity to disease resistance protein rps4-RLD (Arabidopsis thaliana) GI:5823585; contains Pfam profile PF01582: TIR domain   chr5:18208802-18210434 REVERSE   Aliases: ATPP2 A6, K17O22.4, K17O22_4	3.5	3.8	-0.3	-0.6	100.0%	-4.2
11796	AT5G23210.2   Symbol: SCPL34	2.4	2.6	-0.1	-0.6	100.0%	-4.8
11797	AT1G49930.1   expressed protein   chr1:18488600-18489307 FORWARD   Aliases: F2J10.20, F2J10_20	4.2	3.9	0.3	0.6	100.0%	-4.6
11798	AT3G16830.1   WD-40 repeat family protein, contains 10 WD-40 repeats (PF00400) (1 weak)   chr3:5731540-5737778 FORWARD   Aliases: K20I9.6	5.3	5.5	-0.3	-0.6	100.0%	-5.1
11799	AT5G11920.1   glycosyl hydrolase family 32 protein, similar to fructan 1-exohydrolase IIa GI:13940209 from (Cichorium intybus); contains Pfam profile PF00251: Glycosyl hydrolases family 32   chr5:3839392-3842372 FORWARD   Aliases: F14F18.90, F14F18_90	3.2	3.0	0.1	0.6	100.0%	-5.0
11800	AT2G17740.1   DC1 domain-containing protein   chr2:7714164-7714910 REVERSE   Aliases: T17A5.16, T17A5_16	2.8	2.7	0.1	0.6	100.0%	-5.1
11801	AT4G22100.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max); furostanol glycoside 26-O-beta-glucosidase F26G, Costus speciosus, PATCHX:S78099   chr4:11707382-11709944 REVERSE   Aliases: F1N20.200, F1N20_200	2.7	2.8	-0.1	-0.6	100.0%	-5.3
11802	AT4G22540.3   similar to oxysterol-binding family protein [Arabidopsis thaliana] (TAIR:At4g08180.2); similar to oxysterol-binding family protein [Arabidopsis thaliana] (TAIR:At4g08180.1); similar to oxysterol-binding family protein [Arabidopsis thaliana] (TAIR:At4g08180.3); similar to oxysterol-binding family protein [Arabidopsis thaliana] (TAIR:At2g31020.1); similar to oxysterol-binding family protein [Arabidopsis thaliana] (TAIR:At4g12460.1); similar to putative oxysterol binding protein [Oryza sativa (japonica cultivar-group)] (GB:AAM97165.2); similar to putative oxysterol-binding protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54957.1); contains InterPro domain Oxysterol-binding protein (InterPro:IPR000648)   chr4:11860455-11864388 REVERSE   Aliases: F7K2.120, F7K2_120	3.7	3.9	-0.2	-0.6	100.0%	-4.8
11803	AT2G33790.1   pollen Ole e 1 allergen protein containing 14.6% proline residues, similar to arabinogalactan protein (Daucus carota) GI:11322245, SP:Q03211 Pistil-specific extensin-like protein precursor (PELP) {Nicotiana tabacum}; contains Pfam profile PF01190: Pollen proteins Ole e I family   chr2:14300637-14302347 REVERSE   Aliases: T1B8.9, T1B8_9	2.6	2.7	-0.1	-0.6	100.0%	-5.2
11804	AT1G70350.1   expressed protein   chr1:26510777-26511932 REVERSE   Aliases: F17O7.11, F17O7_11	6.1	5.8	0.3	0.6	100.0%	-4.4
11805	AT3G44350.1   Symbol: ANAC061   no apical meristem (NAM) family protein, Tobacco elicitor-responsive gene (TERN), NAC-domain protein, Nicotiana tabacum, EMBL:AB021178   chr3:16033823-16035474 REVERSE   Aliases: ANAC061, T22K7.30	2.2	2.2	0.1	0.6	100.0%	-6.0
11806	AT2G17760.1   aspartyl protease family protein, contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141   chr2:7720396-7723546 FORWARD   Aliases: T17A5.8, T17A5_8	6.3	6.0	0.2	0.6	100.0%	-4.6
11807	AT1G50590.1   pirin, putative, similar to SP:O00625 Pirin {Homo sapiens}; contains Pfam profile PF02678: Pirin	3.6	3.9	-0.2	-0.6	100.0%	-4.5
11808	AT2G20040.1   protein kinase, putative, similar to protein kinase (Homo sapiens) gi:1052737:emb:CAA59733   chr2:8656515-8658454 REVERSE   Aliases: T2G17.16, T2G17_16	5.8	6.0	-0.2	-0.6	100.0%	-4.4
11809	AT4G15780.1   Symbol: ATVAMP724   synaptobrevin-related family protein, similar to Vesicle-associated membrane protein 722 (AtVAMP722) Synaptobrevin-related protein 1 (SP:P47192) {Arabidopsis thaliana}   chr4:8979890-8981773 REVERSE   Aliases: DL3930C, FCAALL.378, VAMP724	4.3	3.8	0.5	0.6	100.0%	-4.7
11810	AT3G16940.1   calmodulin-binding protein, similar to anther ethylene-upregulated protein ER1 GI:11612392 from (Nicotiana tabacum); contains Pfam profile: PF00612 IQ calmodulin-binding motif (3 copies)   chr3:5781781-5785991 FORWARD   Aliases: K14A17.29	5.4	5.7	-0.3	-0.6	100.0%	-4.9
11811	AT5G50820.1   Symbol: ANAC097   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to unknown protein (pir::T07182)   chr5:20696459-20697351 FORWARD   Aliases: ANAC097, K7B16.4, K7B16_4	3.9	3.7	0.1	0.6	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11812	AT5G51770.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:21048256-21050220 FORWARD   Aliases: MIO24.10, MIO24_10	5.2	5.0	0.2	0.6	100.0%	-4.6
11813	AT4G25350.1   EXS family protein / ERD1/XPR1/SYG1 family protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family   chr4:12963392-12966458 REVERSE   Aliases: T30C3.10, T30C3_10	2.7	2.6	0.1	0.5	100.0%	-5.2
11814	AT5G03980.1   GDSL-motif lipase/hydrolase family protein, similar to lipase (Arabidopsis thaliana) GI:1145627; contains Pfam profile:PF00657 Lipase/Acylhydrolase with GDSL-like motif	4.0	3.9	0.1	0.5	100.0%	-5.2
11815	AT5G51210.1   glycine-rich protein / oleosin   chr5:20837327-20838117 FORWARD   Aliases: MWD22.16, MWD22_16	4.1	4.0	0.1	0.5	100.0%	-5.0
11816	AT1G30270.2   Symbol: CIPK23	5.1	5.4	-0.3	-0.5	100.0%	-4.7
11817	AT2G37910.1   cation/hydrogen exchanger, putative (CHX21), and similar to hypothetical proteins; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr2:15875477-15876175 FORWARD   Aliases: T8P21.18, T8P21_18	3.2	3.0	0.1	0.5	100.0%	-5.3
11818	AT1G52240.1   member of KPP-like gene family, homologs of KPP (kinase partner protein) gene in tomato.	2.7	2.9	-0.2	-0.5	100.0%	-4.5
11819	AT3G58690.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:21720168-21722358 FORWARD   Aliases: T20N10.40	5.4	5.6	-0.2	-0.5	100.0%	-4.7
11820	AT5G48820.1   Symbol: ICK6   kip-related protein 3 (KRP3) / cyclin-dependent kinase inhibitor 3 (ICK3), identical to cyclin-dependent kinase inhibitor 3 (krp3) (Arabidopsis thaliana) GI:14422289   chr5:19809834-19811572 REVERSE   Aliases: K24G6.15, K24G6_15, KRP3, Kip related protein 3	2.8	2.9	-0.1	-0.5	100.0%	-5.2
11821	AT2G11010.1   hypothetical protein   chr2:4368951-4373001 FORWARD   Aliases: F15K19.8, F15K19_8	2.6	2.6	0.1	0.5	100.0%	-5.4
11822	AT5G38900.1   DSBA oxidoreductase family protein, contains Pfam profile: PF01323 DSBA-like thioredoxin domain   chr5:15590735-15592848 REVERSE   Aliases: K15E6.80, K15E6_80	6.2	6.0	0.2	0.5	100.0%	-4.3
11823	AT2G31360.1   Symbol: ADS2   delta 9 desaturase (ADS2), identical to delta 9 acyl-lipid desaturase (ADS2) GI:2970036 from (Arabidopsis thaliana)   chr2:13378739-13380680 REVERSE   Aliases: DELTA 9 DESATURASE, T28P16.15, T28P16_15	7.6	7.3	0.3	0.5	100.0%	-4.8
11824	AT1G09630.1   Symbol: ATRAB11C   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:1370146 from (Lotus japonicus)   chr1:3118205-3119710 REVERSE   Aliases: F21M12.2, F21M12_2, RAS RELATED SMALL GTPASE	8.8	9.2	-0.4	-0.5	100.0%	-4.5
11825	AT3G02090.2   Symbol: MPPBETA   mitochondrial processing peptidase beta subunit, putative, similar to mitochondrial processing peptidase beta subunit, mitochondrial precursor, Beta-MPP (Human) SWISS-PROT:O75439   chr3:365556-368918 FORWARD   Aliases: F1C9.12, F1C9_12, MPPBETA	11.4	11.8	-0.4	-0.5	100.0%	-4.9
11826	AT2G37460.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr2:15733527-15736176 REVERSE   Aliases: F3G5.25, F3G5_25	4.3	4.1	0.2	0.5	100.0%	-4.2
11827	AT3G25050.1   Symbol: XTH3   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endoxyloglucan transferase EXGT-A4 GI:5533315 from (Arabidopsis thaliana)   chr3:9126879-9128417 FORWARD   Aliases: K3G3.6, XYLOGLUCAN ENDOTRANSGLYCOSYLASE/HYDROLASE 3	2.8	2.7	0.1	0.5	100.0%	-5.7
11828	AT5G07830.1   glycosyl hydrolase family 79 N-terminal domain-containing protein, similar to beta-glucuronidase GI:8918740 from (Scutellaria baicalensis)   chr5:2503325-2507213 FORWARD   Aliases: F13G24.30	8.0	8.2	-0.2	-0.5	100.0%	-4.7
11829	AT1G17090.1   expressed protein, Pfam   chr1:5842209-5842875 REVERSE   Aliases: F20D23.31, F20D23_31	3.6	3.4	0.3	0.5	100.0%	-4.3
11830	AT1G16390.1   organic cation transporter-related, low similarity to Organic cation/carnitine transporter 2 (Solute carrier family 22, member 5) (High-affinity sodium-dependent carnitine cotransporter) from {Homo sapiens} SP:O76082, {Rattus norvegicus} SP:O70594; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:5602867-5604657 FORWARD   Aliases: F3O9.19, F3O9_19	3.7	3.5	0.2	0.5	100.0%	-4.7
11831	AT3G62730.1   expressed protein, DESSICATION-RELATED PROTEIN PCC13-62 PRECURSOR - Craterostigma plantagineum, PIR:E45509   chr3:23218830-23220446 REVERSE   Aliases: F26K9.160	3.0	3.1	-0.1	-0.5	100.0%	-5.3
11832	AT1G56500.1   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:P95649 CbbY protein {Rhodobacter sphaeroides}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:21163409-21170986 FORWARD   Aliases: AT1G56505, F13N6.21, F13N6_21	6.8	6.7	0.2	0.5	100.0%	-4.7
11833	AT3G60540.2   sec61beta family protein, similar to SP:P52870 Protein transport protein SEC61 beta 1 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF03911: Sec61beta family   chr3:22385938-22386840 REVERSE   Aliases: T8B10.200	6.8	6.6	0.2	0.5	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11834	AT2G40210.1   MADS-box family protein, contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)   chr2:16800291-16801406 REVERSE   Aliases: T7M7.9, T7M7_9	3.9	4.1	-0.2	-0.5	100.0%	-4.7
11835	AT2G12520.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At4g04070.1)   chr2:5111500-5112898 REVERSE   Aliases: T27D6.9, T27D6_9	3.2	3.1	0.1	0.5	100.0%	-5.3
11836	AT5G58290.1   Symbol: RPT3   26S proteasome AAA-ATPase subunit (RPT3), identical to 26S proteasome AAA-ATPase subunit RPT3 GI:6652882 from (Arabidopsis thaliana)   chr5:23586304-23588556 FORWARD   Aliases: 26S PROTEASOME AAA ATPASE SUBUNIT RPT3, MCK7.16, MCK7_16	10.8	10.4	0.4	0.5	100.0%	-5.0
11837	AT5G07430.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:2352460-2354203 FORWARD   Aliases: T2I1.140, T2I1_140	2.0	2.1	-0.1	-0.5	100.0%	-5.7
11838	AT1G12330.1   expressed protein   chr1:4194656-4196735 FORWARD   Aliases: F5O11.6, F5O11_6	5.4	5.1	0.3	0.5	100.0%	-4.6
11839	AT1G63550.1   similar to receptor-like protein kinase-related [Arabidopsis thaliana] (TAIR:At1g63570.1); similar to receptor-like protein kinase homolog RK20-1 [Phaseolus vulgaris] (GB:AAD21872.1); contains InterPro domain Protein of unknown function DUF26 (InterPro:IPR002902)   chr1:23573201-23574770 FORWARD   Aliases: F2K11.9, F2K11_9	3.1	3.0	0.1	0.5	100.0%	-5.2
11840	AT4G13230.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, similar to late embryogenesis abundant protein (Picea glauca) GI:1161171; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr4:7675659-7676676 REVERSE   Aliases: F17N18.16	2.8	3.0	-0.1	-0.5	100.0%	-5.0
11841	AT3G61140.1   Symbol: FUS6   COP9 signalosome complex subunit 1 / CSN complex subunit 1 (CSN1) / COP11 protein (COP11) / FUSCA protein (FUS6), FUSCA6, COP11, CSN1; identical to FUS6 GI:432446, SP:P45432 from (Arabidopsis thaliana); contains Pfam profile PF01399: PCI domain; identical to cDNA CSN complex subunit 1 (CSN1) GI:18056652	7.0	7.4	-0.4	-0.5	100.0%	-4.6
11842	AT5G18280.1   Symbol: ATAPY2	5.5	5.3	0.1	0.5	100.0%	-5.0
11843	AT3G23960.1   F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.6	0.1	0.5	100.0%	-5.3
11844	AT3G17310.2   methyltransferase family protein, similar to cytosine methyltransferase (GI:7658293) (Arabidopsis thaliana)   chr3:5909007-5913248 REVERSE   Aliases: MGD8.15	4.9	5.1	-0.2	-0.5	100.0%	-4.5
11845	AT4G16860.1   Symbol: RPP4   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:9488485-9495835 REVERSE   Aliases: DL4460C, FCAALL.47, RECOGNITION OF PERONOSPORA PARASITICA 4	2.9	2.8	0.1	0.5	100.0%	-5.5
11846	AT3G46150.1   expressed protein   chr3:16960516-16961130 REVERSE   Aliases: F12M12.120	3.4	3.3	0.1	0.5	100.0%	-5.4
11847	AT1G13250.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 Glycosyl transferase family 8   chr1:4528620-4530060 REVERSE   Aliases: T6J4.1, T6J4_1	3.3	3.4	-0.1	-0.5	100.0%	-4.9
11848	AT3G51610.1   expressed protein   chr3:19150536-19153057 REVERSE   Aliases: T18N14.2	8.2	7.9	0.3	0.5	100.0%	-4.6
11849	AT2G40150.1   expressed protein   chr2:16782520-16784321 FORWARD   Aliases: T7M7.4, T7M7_4	6.5	6.7	-0.2	-0.5	100.0%	-4.8
11850	AT3G61620.1   Symbol: RRP41   exonuclease RRP41 (RRP41), identical to exonuclease RRP41 (Arabidopsis thaliana) GI:6164938   chr3:22812212-22814083 REVERSE   Aliases: EXONUCLEASE RRP41, F15G16.10	6.3	6.4	-0.2	-0.5	100.0%	-4.8
11851	AT1G52080.1   Symbol: AR791   actin binding protein family, contains Prosite PS00019: Actinin-type actin-binding domain signature 1; similar to actin binding protein (GI:28071265) (Arabidopsis thaliana); similar to A-type inclusion protein (ATI) (Swiss-Prot:P16602) (Cowpox virus)   chr1:19372800-19375734 FORWARD   Aliases: AR791, F5F19.14, F5F19_14	5.5	5.7	-0.2	-0.5	100.0%	-4.4
11852	AT1G52530.1   similar to LIG1 [Physarum polycephalum] (GB:AAF65575.1); contains InterPro domain Hus1-like protein (InterPro:IPR007150)	3.5	3.6	-0.1	-0.5	100.0%	-5.0
11853	AT1G47370.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:17368338-17371143 REVERSE   Aliases: T3F24.3, T3F24_3	2.6	2.5	0.1	0.5	100.0%	-5.4
11854	AT2G29970.1   heat shock protein-related, contains similarity to 101 kDa heat shock protein; HSP101 (Triticum aestivum) gi:11561808:gb:AAC83689   chr2:12783463-12787015 FORWARD   Aliases: F23F1.11, F23F1_11	7.7	7.5	0.3	0.5	100.0%	-4.8
11855	AT2G01330.1   transducin family protein / WD-40 repeat family protein, contains 10 WD-40 repeats (PF00400); similar to 66kDa stress protein (SWISS-PROT: P90587)(Physarum polycephalum (Slime mold))   chr2:158282-160857 REVERSE   Aliases: F10A8.21, F10A8_21	5.4	5.2	0.2	0.5	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11856	AT5G54010.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	3.7	3.6	0.1	0.5	100.0%	-5.0
11857	AT2G39870.1   expressed protein   chr2:16650621-16652455 FORWARD   Aliases: T28M21.3, T28M21_3	3.6	3.5	0.1	0.5	100.0%	-5.1
11858	AT4G02710.1   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia)   chr4:1193516-1197061 REVERSE   Aliases: T10P11.22, T10P11_22	4.8	5.0	-0.2	-0.5	100.0%	-4.9
11859	AT5G09810.1   Symbol: ACT7   actin 7 (ACT7) / actin 2, identical to SP:P53492 Actin 7 (Actin-2) {Arabidopsis thaliana}   chr5:3052167-3054615 FORWARD   Aliases: ACTIN_2, MYH9.2, MYH9_2	11.3	10.9	0.4	0.5	100.0%	-4.8
11860	AT1G07430.1   protein phosphatase 2C, putative / PP2C, putative, similar to GB:CAB90633 from (Fagus sylvatica)	9.0	8.6	0.4	0.5	100.0%	-4.5
11861	AT4G36770.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr4:17329833-17331630 REVERSE   Aliases: AP22.28, AP22_28	3.1	3.1	0.1	0.5	100.0%	-5.4
11862	AT5G59830.2   expressed protein   chr5:24122304-24124406 FORWARD   Aliases: MMN10.5, MMN10_5	8.0	7.9	0.1	0.5	100.0%	-4.8
11863	AT1G19480.1   HhH-GPD base excision DNA repair family protein, contains Pfam PF00730: HhH-GPD superfamily base excision DNA repair; similar to DNA-3-methyladenine glycosylase 1 (3-methyladenine DNA glycosidase 1) (3MEA DNA glycosylase 1) (SP:Q92383) {Schizosaccharomyces pombe}   chr1:6744344-6746399 FORWARD   Aliases: F18O14.25, F18O14_25	4.9	4.8	0.1	0.5	100.0%	-4.9
11864	AT2G21230.2   bZIP family transcription factor, contains a bZIP transcription factor basic domain signature (PDOC00036)   chr2:9101413-9103407 REVERSE   Aliases: F7O24.5, F7O24_5	5.2	5.0	0.2	0.5	100.0%	-4.6
11865	AT4G22580.1   exostosin family protein, contains Pfam profile: PF03016	2.9	2.8	0.1	0.5	100.0%	-5.4
11866	NA	10.9	10.8	0.2	0.5	100.0%	-5.7
11867	AT5G39640.1   hypothetical protein, contains Pfam profile PF04396: Protein of unknown function, DUF537	3.0	3.2	-0.2	-0.5	100.0%	-4.7
11868	AT5G12860.1   oxoglutarate/malate translocator, putative, similar to 2-oxoglutarate/malate translocator precursor, spinach, SWISSPROT:Q41364   chr5:4059689-4061953 REVERSE   Aliases: T24H18.30, T24H18_30	8.2	7.5	0.7	0.5	100.0%	-4.5
11869	AT2G37090.1   Symbol: IXR9   Encodes a protein with similarity to glycosyltransferases. Mutants have irregular xylem phenotype suggesting a role in secondary cell wall biosynthesis.	3.9	4.1	-0.3	-0.5	100.0%	-4.2
11870	AT5G44500.2   similar to small nuclear ribonucleoprotein associated protein B, putative / snRNP-B, putative / Sm protein B, putative [Arabidopsis thaliana] (TAIR:At4g20440.1); similar to small nuclear ribonucleoprotein associated protein B, putative / snRNP-B, putative / Sm protein B, putative [Arabidopsis thaliana] (TAIR:At4g20440.2); similar to snRNP-associated protein; SmB [Danio rerio] (GB:AAF72188.1); similar to GD:SNRPB [Homo sapiens] (GB:CAB46715.1); similar to small nuclear ribonucleoprotein B' [Erinaceus europaeus] (GB:AAD54481.1); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Small nuclear ribonucleoprotein (Sm protein) (InterPro:IPR001163)   chr5:17944680-17945670 FORWARD   Aliases: MFC16.18, MFC16_18	3.4	3.5	-0.1	-0.5	100.0%	-5.0
11871	AT2G33070.2   similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:At3g16400.1); similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:At3g16390.1); similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:At3g16410.1); similar to putative D-protein [Oryza sativa (japonica cultivar-group)] (GB:XP_450269.1); contains InterPro domain Jacalin-related lectin (InterPro:IPR001229); contains InterPro domain Kelch repeat (InterPro:IPR006652)   chr2:14036264-14038146 REVERSE   Aliases: F25I18.19, F25I18_19	3.8	3.7	0.1	0.5	100.0%	-5.0
11872	AT5G46290.2   Symbol: KAS I   similar to 3-ketoacyl-ACP synthase, putative [Arabidopsis thaliana] (TAIR:At1g74960.1); similar to 3-ketoacyl-ACP synthase, putative [Arabidopsis thaliana] (TAIR:At1g74960.2); similar to beta-ketoacyl-ACP synthetase I-2 [Glycine max] (GB:AAF61731.1); similar to beta-ketoacyl-ACP synthase I [Perilla frutescens] (GB:AAC04691.1); similar to beta-ketoacyl-ACP synthetase I [Glycine max] (GB:AAF61730.1); contains InterPro domain Beta-ketoacyl synthase (InterPro:IPR000794)   chr5:18791313-18793962 REVERSE   Aliases: 3 KETOACYL ACYL CARRIER PROTEIN SYNTHASE I, MPL12.7, MPL12_7	7.5	7.8	-0.3	-0.5	100.0%	-4.8
11873	AT5G53210.1   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At3g06120.1); similar to basic helix-loop-helix-like [Oryza sativa (japonica cultivar-group)] (GB:BAD27965.1); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr5:21603832-21606167 REVERSE   Aliases: MFH8.15	2.6	2.8	-0.1	-0.5	100.0%	-5.3
11874	AT1G04700.1   protein kinase family protein, low similarity to EDR1 (Arabidopsis thaliana) GI:11127925; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr1:1316918-1320918 FORWARD   Aliases: T1G11.5, T1G11_5	3.7	3.6	0.1	0.5	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11875	AT2G17860.1   pathogenesis-related thaumatin family protein, similar to receptor serine/threonine kinase PR5K (Arabidopsis thaliana) GI:1235680; contains Pfam profile PF00314: Thaumatin family   chr2:7769339-7770100 REVERSE   Aliases: T13L16.12, T13L16_12	2.4	2.3	0.1	0.5	100.0%	-5.6
11876	AT1G39430.1   expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	3.9	4.1	-0.2	-0.5	100.0%	-4.7
11877	AT1G01930.1   zinc finger protein-related, contains Pfam PF00023: Ankyrin repeat; contains Pfam PF00096: Zinc finger, C2H2 type domain and Prosite PS00028: Zinc finger, C2H2 type, domain   chr1:319836-322860 REVERSE   Aliases: F22M8.6, F22M8_6	4.9	5.2	-0.3	-0.5	100.0%	-4.5
11878	AT5G19290.1   esterase/lipase/thioesterase family protein, low similarity to monoglyceride lipase (Homo sapiens) GI:14594904; contains Interpro entry IPR000379   chr5:6494057-6495286 FORWARD   Aliases: F7K24.40, F7K24_40	6.8	6.5	0.3	0.5	100.0%	-4.6
11879	AT5G18110.1   Symbol: NCBP   novel cap-binding protein (nCBP), identical to novel cap-binding protein nCBP (Arabidopsis thaliana) GI:3108209; contains Pfam profile PF01652: Eukaryotic initiation factor 4E   chr5:5988746-5990683 REVERSE   Aliases: MRG7.7, MRG7_7, NOVEL CAP BINDING PROTEIN	6.5	6.3	0.2	0.5	100.0%	-5.0
11880	AT1G78500.1   pentacyclic triterpene synthase, putative, similar to pentacyclic triterpene synthase (04C11) (gi:6650208) (PMID:11247608); similar to beta-Amyrin Synthase GI:3688600 from (Panax ginseng)   chr1:29536539-29540070 FORWARD   Aliases: T30F21.16, T30F21_16	3.4	3.5	-0.1	-0.5	100.0%	-5.5
11881	AT4G13090.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endoxyloglucan transferase EXGT-A1 GI:5533309 from (Arabidopsis thaliana)   chr4:7631532-7632867 REVERSE   Aliases: F25G13.180, F25G13_180	2.3	2.4	-0.1	-0.5	100.0%	-5.6
11882	AT5G51270.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr5:20852363-20855488 REVERSE   Aliases: MWD22.22, MWD22_22	2.9	3.1	-0.1	-0.5	100.0%	-4.9
11883	AT5G38760.1   expressed protein, similar to ABA-inducible protein (Fagus sylvatica) GI:3901016, cold-induced protein kin1 (Brassica napus) GI:167146   chr5:15541408-15542207 FORWARD   Aliases: MKD10.60, MKD10_60	2.2	2.1	0.0	0.5	100.0%	-6.1
11884	AT4G37850.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.5	2.6	-0.1	-0.5	100.0%	-5.6
11885	AT2G41730.1   expressed protein   chr2:17416541-17417015 FORWARD   Aliases: T11A7.17, T11A7_17	3.6	3.4	0.2	0.5	100.0%	-4.7
11886	AT3G62970.1   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At5g18650.1); similar to putative PGPD14 protein (pollen germination related protein) [Oryza sativa (japonica cultivar-group)] (GB:NP_916676.1); similar to zinc finger protein ZFP-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87761.1); contains InterPro domain CHY zinc finger (InterPro:IPR008913); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr3:23281609-23283895 FORWARD   Aliases: T20O10.70	9.2	8.9	0.3	0.5	100.0%	-4.4
11887	AT3G48250.1   pentatricopeptide (PPR) repeat-containing protein, vacontains Pfam profile PF01535: PPR repeat   chr3:17881049-17882914 REVERSE   Aliases: T29H11.230	3.1	3.2	-0.1	-0.5	100.0%	-5.2
11888	AT2G23760.3   Symbol: BLH4   similar to BEL1-like homeobox 2 protein (BLH2) [Arabidopsis thaliana] (TAIR:At4g36870.1); similar to BEL1-related homeotic protein 13 [Solanum tuberosum] (GB:AAN03623.1); contains InterPro domain POX (InterPro:IPR006563); contains InterPro domain Homeobox (InterPro:IPR001356)   chr2:10114789-10120085 REVERSE   Aliases: BEL1 like homeobox 4, F27L4.6, F27L4_6	2.8	2.6	0.3	0.5	100.0%	-4.2
11889	AT2G43000.1   Symbol: ANAC042   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr2:17887694-17889661 REVERSE   Aliases: ANAC042, F23E6.1, F23E6_1	2.4	2.4	-0.1	-0.5	100.0%	-5.6
11890	AT1G23130.1   Bet v I allergen family protein, similar to Csf-2 (Cucumis sativus)(GI:5762258)(J Am Soc Hortic Sci 124, 136-139 (1999)); location of ESTs gb:T45139 and gb:T43456 ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:8200372-8201223 FORWARD   Aliases: T26j12.10, T26j12_10	2.8	2.8	0.1	0.5	100.0%	-5.5
11891	AT2G42190.1   expressed protein, ; similar to GP:9826:X07453   chr2:17589947-17591272 FORWARD   Aliases: T24P15.10, T24P15_10	8.0	7.6	0.4	0.5	100.0%	-4.6
11892	AT5G15480.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:5025955-5027163 REVERSE   Aliases: T20K14.90, T20K14_90	2.6	2.5	0.1	0.5	100.0%	-5.4
11893	AT1G72810.1   threonine synthase, putative, strong similarity to SP:Q9S7B5 Threonine synthase, chloroplast precursor (EC 4.2.3.1) (TS) {Arabidopsis thaliana}   chr1:27402253-27404079 REVERSE   Aliases: F3N23.1, F3N23_1	7.5	7.7	-0.2	-0.5	100.0%	-4.9
11894	AT3G16370.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from (Arabidopsis thaliana); contains Pfam profile: PF00657 Lipase Acylhydrolase with GDSL-like motif   chr3:5556716-5558595 FORWARD   Aliases: T2O4.2	2.4	2.5	-0.1	-0.5	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11895	AT4G30540.1   glutamine amidotransferase class-I domain-containing protein, similar to defense-related protein (Brassica carinata) GI:14009290; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr4:14923333-14925112 FORWARD   Aliases: F17I23.120, F17I23_120	2.3	2.2	0.1	0.5	100.0%	-5.8
11896	AT5G66290.1   expressed protein   chr5:26495003-26496667 REVERSE   Aliases: K1L20.7, K1L20_7	4.9	4.7	0.2	0.5	100.0%	-4.8
11897	AT5G28860.1   expressed protein   chr5:10883456-10884287 REVERSE   Aliases: F7P1.40, F7P1_40	2.3	2.2	0.1	0.5	100.0%	-5.5
11898	AT1G31040.1   zinc-binding protein-related, similar to zinc-binding protein (Pisum sativum) GI:16117799   chr1:11069774-11070085 REVERSE   Aliases: F17F8.4	3.5	3.4	0.1	0.5	100.0%	-5.1
11899	AT3G16200.1   expressed protein   chr3:5491412-5493635 REVERSE   Aliases: MYA6.1	5.5	5.7	-0.2	-0.5	100.0%	-4.4
11900	AT1G11650.2   Symbol: ATRBP45B   RNA-binding protein 45 (RBP45), putative, similar to gb:U90212 DNA binding protein ACBF from Nicotiana tabacum and contains 3 PF:00076 RNA recognition motif domains. ESTs gb:T44278, gb:R65195, gb:N65904, gb:H37499, gb:R90487, gb:N95952, gb:T44278, gb:Z20166, gb:N96891, gb:W43137, gb:F15504, gb:F1   chr1:3914774-3918163 FORWARD   Aliases: ATRBP45B, F25C20.21, F25C20_21	10.7	10.5	0.2	0.5	100.0%	-4.9
11901	AT1G02410.1   cytochrome c oxidase assembly protein CtaG / Cox11 family, similar to cytochrome c oxidase assembly protein cox11 GI:1244782 from (Saccharomyces cerevisiae); similar to Cytochrome c oxidase assembly protein COX11, mitochondrial precursor (SP:Q9Y6N1){Homo sapiens}; contains Pfam PF04442: Cytochrome c oxidase assembly protein CtaG / Cox11   chr1:490925-492862 FORWARD   Aliases: T6A9.10, T6A9_10	8.1	7.7	0.4	0.5	100.0%	-4.6
11902	AT1G80740.1   Symbol: CMT1   chromomethylase 1 (CMT1), identical to chromomethylase GB:AAC02660 GI:2865416 from (Arabidopsis thaliana)   chr1:30347286-30351940 FORWARD   Aliases: CHROMOMETHYLASE 1, F23A5.9, F23A5_9	3.2	3.3	-0.1	-0.5	100.0%	-5.0
11903	AT3G20430.1   expressed protein   chr3:7121486-7123179 FORWARD   Aliases: MQC12.22	7.8	7.6	0.2	0.5	100.0%	-4.9
11904	AT4G13080.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endoxyloglucan transferase EXGT-A1 GI:5533309 from (Arabidopsis thaliana)   chr4:7626609-7628364 REVERSE   Aliases: F25G13.170, F25G13_170	3.0	3.1	-0.1	-0.5	100.0%	-5.2
11905	AT3G62580.1   expressed protein   chr3:23157804-23159326 FORWARD   Aliases: T12C14.280	8.5	8.0	0.6	0.5	100.0%	-4.4
11906	NA	11.6	11.5	0.1	0.5	100.0%	-6.0
11907	AT1G43760.1   expressed protein   chr1:16531320-16533505 REVERSE   Aliases: F2J6.14	3.1	3.0	0.1	0.5	100.0%	-5.2
11908	AT5G40650.1   Symbol: SDH2 2	9.4	9.6	-0.3	-0.5	100.0%	-4.8
11909	AT1G09500.3   similar to cinnamyl-alcohol dehydrogenase family / CAD family [Arabidopsis thaliana] (TAIR:At1g09510.1); similar to NADPH-dependent cinnamyl alcohol dehydrogenase [Quercus suber] (GB:AAQ88099.1); similar to aldehyde reductase [Vigna radiata] (GB:AAD53967.1)   chr1:3066755-3068334 FORWARD   Aliases: F14J9.16, F14J9_16	2.6	2.7	-0.1	-0.5	100.0%	-5.3
11910	AT2G16800.1   high-affinity nickel-transport family protein, contains Pfam domain, PF03824: High-affinity nickel-transport protein   chr2:7292820-7294447 FORWARD   Aliases: T24I21.21, T24I21_21	9.2	9.4	-0.1	-0.5	100.0%	-4.9
11911	AT2G22475.2   GRAM domain-containing protein / ABA-responsive protein-related, similar to ABA-responsive protein (Hordeum vulgare) GI:4103635; contains Pfam profile PF02893: GRAM domain   chr2:9548481-9552089 FORWARD   Aliases: None	7.5	7.4	0.2	0.5	100.0%	-4.8
11912	AT1G11970.1   hypothetical protein   chr1:4044368-4044667 FORWARD   Aliases: F12F1.16, F12F1_16	2.6	2.6	0.1	0.5	100.0%	-5.5
11913	AT4G14870.1   expressed protein   chr4:8517187-8517897 FORWARD   Aliases: DL3475W, FCAALL.408	5.9	6.1	-0.2	-0.5	100.0%	-4.9
11914	AT2G01690.2   expressed protein   chr2:308701-313804 REVERSE   Aliases: T8O11.14, T8O11_14	3.8	4.1	-0.3	-0.5	100.0%	-4.7
11915	AT3G05100.1   expressed protein   chr3:1424102-1426006 FORWARD   Aliases: T12H1.6, T12H1_6	4.0	4.2	-0.2	-0.5	100.0%	-4.7
11916	AT4G13580.1   disease resistance-responsive family protein, contains similarity to pathogenesis-related protein (Pisum sativum) gi:4585273:gb:AAD25355	3.6	3.9	-0.3	-0.5	100.0%	-4.1
11917	AT3G18670.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr3:6424141-6426477 REVERSE   Aliases: MVE11.3	3.0	3.1	-0.1	-0.5	100.0%	-5.2
11918	AT1G57600.1   membrane bound O-acyl transferase (MBOAT) family protein, low similarity to skinny hedgehog (Drosophila melanogaster) GI:15420842; contains Pfam profile PF03062: MBOAT family   chr1:21334255-21338392 REVERSE   Aliases: T8L23.7, T8L23_7	5.9	6.1	-0.2	-0.5	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11919	AT2G40680.1   hypothetical protein   chr2:16979907-16980797 FORWARD   Aliases: T7D17.14, T7D17_14	2.6	2.4	0.2	0.5	100.0%	-4.8
11920	AT1G80830.1   Symbol: NRAMP1	9.1	9.3	-0.2	-0.5	100.0%	-5.2
11921	AT1G29480.1   hypothetical protein   chr1:10317922-10318697 FORWARD   Aliases: F15D2.6, F15D2_6	2.2	2.2	-0.0	-0.5	100.0%	-5.9
11922	AT2G32450.1   calcium-binding EF hand family protein, low similarity to O-linked GlcNAc transferase (Homo sapiens) GI:2266994; contains Pfam profiles PF00036: EF hand, PF00515: TPR Domain   chr2:13785526-13788335 FORWARD   Aliases: T32F6.3, T32F6_3	3.8	3.6	0.1	0.5	100.0%	-5.0
11923	AT3G09470.2   expressed protein   chr3:2911521-2914505 REVERSE   Aliases: AT3G09460, F11F8.4	6.4	6.6	-0.3	-0.5	100.0%	-4.1
11924	AT5G11030.1   Symbol: ALF4   expressed protein   chr5:3490834-3495095 REVERSE   Aliases: ABERRANT LATERAL ROOT FORMATION 4, T5K6.20, T5K6_20	4.5	4.7	-0.2	-0.5	100.0%	-4.7
11925	AT1G04420.1   aldo/keto reductase family protein, Similar to SP:Q46933 Tas protein {Escherichia coli}, Babesia aldo-keto reductase SP:P40690; contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:1191607-1193883 FORWARD   Aliases: F19P19.12, F19P19_12	7.5	7.8	-0.2	-0.5	100.0%	-4.2
11926	AT2G28605.1   expressed protein   chr2:12261965-12262914 FORWARD   Aliases: T8O18.1, T8O18_1	3.0	2.9	0.1	0.5	100.0%	-5.3
11927	AT2G16580.1   auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR21 (GI:10185818) (Tulipa gesneriana)   chr2:7191504-7194050 REVERSE   Aliases: F1P15.4, F1P15_4	3.0	3.1	-0.1	-0.5	100.0%	-5.1
11928	AT1G02475.1   expressed protein   chr1:513916-515343 REVERSE   Aliases: None	6.4	6.2	0.2	0.5	100.0%	-4.4
11929	AT1G72310.1   Symbol: ATL3   zinc finger (C3HC4-type RING finger) family protein (ATL3), identical to RING-H2 zinc finger protein (ATL3) GB:AF132013 (Arabidopsis thaliana)   chr1:27229559-27231207 FORWARD   Aliases: RING H2 ZINC FINGER PROTEIN ATL3, T9N14.21	6.8	7.0	-0.2	-0.5	100.0%	-4.7
11930	AT1G27430.1   GYF domain-containing protein, contains Pfam profile: PF02213 GYF domain	4.8	4.6	0.2	0.5	100.0%	-4.9
11931	AT5G06170.1   sucrose transporter, putative / sucrose-proton symporter, putative, similar to sucrose-proton symporter SUC1 (Arabidopsis thaliana) GI:407094, sucrose transporter (Arabidopsis thaliana) GI:12057172; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:1869792-1871720 FORWARD   Aliases: MBL20.5, MBL20_5	3.6	3.4	0.2	0.5	100.0%	-5.0
11932	AT1G64940.1   Symbol: CYP89A6   cytochrome P450, putative, similar to cytochrome p450 GI:438242 from (Solanum melongena)   chr1:24127452-24128987 FORWARD   Aliases: F13O11.24, F13O11_24	4.0	3.8	0.2	0.5	100.0%	-5.3
11933	AT5G13710.1   Symbol: SMT1   sterol 24-C-methyltransferase, putative, similar to SP:P25087 Sterol 24-C-methyltransferase, Delta(24)-sterol C- methyltransferase, Saccharomyces cerevisiae   chr5:4423698-4427050 REVERSE   Aliases: CEPHALOPOD, CPH, MSH12.18, MSH12_18, SAM:CYCLOARTENOL C24 METHYLTRANSFERASE, STEROL METHYLTRANSFERASE 1	9.4	9.2	0.2	0.5	100.0%	-4.9
11934	AT5G07200.1   Symbol: YAP169	2.4	2.5	-0.1	-0.5	100.0%	-5.5
11935	AT4G16120.1   Symbol: ATSEB1	5.8	6.0	-0.3	-0.5	100.0%	-4.5
11936	AT2G40900.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575; contains Pfam profile PF00892: Integral membrane protein   chr2:17070220-17072747 REVERSE   Aliases: T20B5.10, T20B5_10	5.9	5.7	0.2	0.5	100.0%	-4.7
11937	AT2G46960.2   Symbol: CYP709B1   cytochrome P450 family protein, similar to cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus); contains Pfam profile: PF00067: Cytochrome P450; supported by cDNA: gi_13605860_gb_AF367329.1_AF367329   chr2:19299118-19301329 REVERSE   Aliases: F14M4.21	2.3	2.3	-0.1	-0.5	100.0%	-5.7
11938	AT4G08602.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g43205.1)   chr4:5489256-5489971 REVERSE   Aliases: None	2.5	2.6	-0.1	-0.5	100.0%	-5.0
11939	AT3G24540.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:8952910-8955628 FORWARD   Aliases: MOB24.4	2.8	2.6	0.2	0.5	100.0%	-5.1
11940	AT2G22360.1   DNAJ heat shock family protein, similar to SP:Q9S5A3 Chaperone protein dnaJ {Listeria monocytogenes}; contains Pfam profiles PF00226 DnaJ domain, PF01556 DnaJ C terminal region, PF00684 DnaJ central domain (4 repeats)   chr2:9504675-9507695 FORWARD   Aliases: F14M13.24, F14M13_24	5.0	4.8	0.2	0.5	100.0%	-4.7
11941	AT5G11250.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:3587979-3591961 REVERSE   Aliases: F2I11.140, F2I11_140	3.1	3.2	-0.1	-0.5	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11942	AT2G27410.1   expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)   chr2:11731724-11732763 REVERSE   Aliases: F12K2.1, F12K2_1	2.7	2.6	0.1	0.5	100.0%	-5.3
11943	AT5G63440.2   expressed protein, contains Pfam PF02594: Uncharacterized ACR, YggU family COG1872   chr5:25423551-25425631 FORWARD   Aliases: MLE2.7, MLE2_7	4.5	4.4	0.1	0.5	100.0%	-5.1
11944	AT5G13400.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:4295757-4299108 REVERSE   Aliases: T22N19.50, T22N19_50	3.0	2.9	0.1	0.5	100.0%	-5.2
11945	AT4G39570.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:18384094-18385538 REVERSE   Aliases: F23K16.200, F23K16_200	5.8	5.6	0.2	0.5	100.0%	-4.9
11946	AT4G16400.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g13175.1)   chr4:9260587-9263019 FORWARD   Aliases: DL4230W, FCAALL.356	4.5	4.2	0.2	0.5	100.0%	-4.4
11947	AT1G79250.1   protein kinase, putative, similar to viroid symptom modulation protein/dual-specificity protein kinase (Lycopersicon esculentum) gi:7672777:gb:AAF66637   chr1:29815034-29817111 REVERSE   Aliases: YUP8H12R.15, YUP8H12R_15	3.5	3.4	0.1	0.5	100.0%	-5.0
11948	AT4G37080.2   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr4:17473266-17476946 FORWARD   Aliases: AP22.58, AP22_58	4.5	4.4	0.1	0.5	100.0%	-4.8
11949	AT5G08380.1   alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative, similar to alpha-galactosidase SP:Q42656 from (Coffea arabica); contains Pfam profile PF02065: Melibiase   chr5:2694678-2697688 REVERSE   Aliases: F8L15.110, F8L15_110	9.1	8.9	0.2	0.5	100.0%	-4.5
11950	AT1G73390.3   expressed protein   chr1:27594477-27598803 REVERSE   Aliases: T9L24.40, T9L24_40	4.7	5.0	-0.2	-0.5	100.0%	-4.4
11951	AT5G07820.1   expressed protein   chr5:2498750-2500547 REVERSE   Aliases: F13G24.20, F13G24_20	3.1	3.4	-0.3	-0.5	100.0%	-4.3
11952	AT1G69440.1   Symbol: AGO7   PAZ domain-containing protein / piwi domain-containing protein, similar to SP:Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain   chr1:26104722-26108829 REVERSE   Aliases: ARGONAUTE7, F10D13.11, F10D13_11, ZIP, ZIPPY	2.6	2.6	-0.1	-0.5	100.0%	-5.2
11953	AT1G73670.1   Symbol: ATMPK15   mitogen-activated protein kinase, putative / MAPK, putative (MPK15), similar to mitogen-activated protein kinase GB:A56042 (Dictyostelium discoideum); mitogen-activated protein kinase (MAPK)(AtMPK15), PMID:12119167; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr1:27703711-27707101 FORWARD   Aliases: F25P22.9, F25P22_9	2.8	2.8	0.1	0.5	100.0%	-5.4
11954	AT1G77910.1   expressed protein, contains similarity to NADH dehydrogenase subunit 1   chr1:29301032-29301301 FORWARD   Aliases: F28K19.12, F28K19_12	2.3	2.3	0.1	0.5	100.0%	-5.8
11955	AT3G17740.1   expressed protein   chr3:6067765-6072845 REVERSE   Aliases: MIG5.4	5.0	5.2	-0.2	-0.5	100.0%	-4.7
11956	AT3G15200.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:5117496-5119067 REVERSE   Aliases: F4B12.11	3.2	3.3	-0.1	-0.5	100.0%	-5.2
11957	AT2G28780.1   expressed protein   chr2:12347111-12350498 REVERSE   Aliases: F8N16.7, F8N16_7	3.7	3.5	0.2	0.5	100.0%	-4.6
11958	AT2G39420.1   esterase/lipase/thioesterase family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379   chr2:16467442-16470111 FORWARD   Aliases: F12L6.8, F12L6_8	6.4	6.7	-0.3	-0.5	100.0%	-4.5
11959	AT1G63190.1   expressed protein   chr1:23435500-23436667 FORWARD   Aliases: F16M19.9, F16M19_9	2.1	2.1	-0.0	-0.5	100.0%	-5.9
11960	AT2G34020.1   similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At1g29020.1); similar to putative drought-induced protein RDI [Oryza sativa (japonica cultivar-group)] (GB:XP_464813.1); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048)   chr2:14378264-14380934 REVERSE   Aliases: T14G11.14, T14G11_14	2.6	2.5	0.1	0.5	100.0%	-5.7
11961	AT5G38195.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:15264140-15264559 FORWARD   Aliases: None	2.5	2.4	0.1	0.5	100.0%	-5.5
11962	AT5G09995.3   expressed protein   chr5:3125047-3126377 REVERSE   Aliases: None	3.6	3.8	-0.2	-0.5	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11963	AT4G28000.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family   chr4:13925462-13929286 FORWARD   Aliases: T13J8.110, T13J8_110	3.5	3.4	0.1	0.5	100.0%	-5.2
11964	AT1G41810.1   expressed protein   chr1:15582258-15582998 REVERSE   Aliases: T4I21.3, T4I21_3	2.6	2.5	0.1	0.5	100.0%	-5.2
11965	AT1G22280.2   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase type 2C GI:4336436 from (Lotus japonicus)   chr1:7873985-7875867 FORWARD   Aliases: T16E15.10, T16E15_10	6.9	6.7	0.2	0.5	100.0%	-4.8
11966	AT4G18490.1   hypothetical protein   chr4:10205298-10208208 FORWARD   Aliases: F28J12.150, F28J12_150	2.6	2.5	0.1	0.5	100.0%	-5.3
11967	AT5G20390.1   beta-1,3-glucanase, putative, similar to plant beta-1,3-glucanase bg4 GI:2808438 from (Arabidopsis thaliana)   chr5:6892833-6894197 REVERSE   Aliases: F5O24.280, F5O24_280	2.8	2.7	0.1	0.5	100.0%	-5.5
11968	AT3G46100.1   Symbol: ATHRS1	6.8	6.7	0.1	0.5	100.0%	-4.9
11969	AT4G34730.1   ribosome-binding factor A family protein, contains Pfam PF02033: Ribosome-binding factor A   chr4:16569401-16573685 REVERSE   Aliases: T4L20.310, T4L20_310	4.1	3.9	0.1	0.5	100.0%	-5.0
11970	AT3G57430.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:21266612-21269457 REVERSE   Aliases: T8H10.30	3.3	3.2	0.1	0.5	100.0%	-4.9
11971	AT3G23980.1   dentin sialophosphoprotein-related, contains weak similarity to Dentin sialophosphoprotein precursor (Swiss-Prot:Q9NZW4) (Homo sapiens)   chr3:8662442-8667740 REVERSE   Aliases: F14O13.17	5.1	5.2	-0.2	-0.5	100.0%	-4.7
11972	AT2G30680.1   similar to glycosyl transferase family 48 protein [Arabidopsis thaliana] (TAIR:At2g31960.1); similar to callose synthase 1 (CALS1) / 1,3-beta-glucan synthase 1 [Arabidopsis thaliana] (TAIR:At1g05570.1)   chr2:13080725-13082473 FORWARD   Aliases: T11J7.7, T11J7_7	2.4	2.5	-0.1	-0.5	100.0%	-5.4
11973	AT1G61950.1   Symbol: CPK19   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase GI:3283996 from (Nicotiana tabacum); contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048	3.0	3.0	0.1	0.5	100.0%	-5.4
11974	AT1G22420.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:7916065-7917507 REVERSE   Aliases: F12K8.23, F12K8_23	2.0	2.0	-0.1	-0.5	100.0%	-5.7
11975	AT1G63430.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profiles: PF00069 Eukaryotic protein kinase domain, PF00560 Leucine Rich Repeat; contains 1 predicted transmembrane domain   chr1:23526273-23530435 FORWARD   Aliases: F2K11.19, F2K11_19	6.0	5.8	0.2	0.5	100.0%	-4.6
11976	AT2G43210.2   UBX domain-containing protein, contains Pfam profile PF00789: UBX domain	7.4	7.2	0.2	0.5	100.0%	-4.6
11977	AT1G13630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr1:4670305-4672823 REVERSE   Aliases: F21F23.6, F21F23_6	2.3	2.4	-0.1	-0.5	100.0%	-5.7
11978	AT4G23080.1   expressed protein, predicted protein, Arabidopsis thaliana   chr4:12096797-12098899 FORWARD   Aliases: F7H19.270, F7H19_270	2.4	2.3	0.0	0.5	100.0%	-5.8
11979	AT4G26010.1   peroxidase, putative, peroxidase ATP13a - Arabidopsis thaliana, PID:e264765; identical to cDNA class III peroxidase ATP35, GI:17530565   chr4:13200602-13201950 FORWARD   Aliases: F20B18.120, F20B18_120	3.1	3.5	-0.3	-0.5	100.0%	-4.5
11980	AT5G12280.1   expressed protein   chr5:3972015-3973637 REVERSE   Aliases: None	3.0	2.9	0.1	0.5	100.0%	-5.3
11981	AT1G30000.1   glycoside hydrolase family 47 protein, similar to GI:5579331 from (Homo sapiens); contains Pfam profile PF01532: Glycosyl hydrolase family 47   chr1:10509195-10512452 REVERSE   Aliases: T1P2.10, T1P2_10	6.7	7.0	-0.3	-0.5	100.0%	-4.5
11982	AT1G79670.2   Symbol: RFO1   wall-associated kinase, putative, similar to wall-associated kinase 4 GI:3355308 from (Arabidopsis thaliana); isoform contains non-consensus AT-acceptor splice site.   chr1:29981780-29984230 REVERSE   Aliases: F20B17.27, F20B17_27, RESISTANCE TO FUSARIUM OXYSPORUM 1, WAKL22	5.0	5.2	-0.2	-0.5	100.0%	-4.7
11983	AT1G15860.1   expressed protein   chr1:5455050-5456926 FORWARD   Aliases: F7H2.19, F7H2_19	4.9	4.7	0.2	0.5	100.0%	-4.7
11984	AT1G75110.1   expressed protein   chr1:28197776-28199594 REVERSE   Aliases: F9E10.4, F9E10_4	3.7	3.8	-0.1	-0.5	100.0%	-4.9
11985	AT5G26970.1   expressed protein   chr5:9487063-9487389 REVERSE   Aliases: F2P16.230, F2P16_230	2.6	2.7	-0.1	-0.5	100.0%	-5.3
11986	AT3G49000.1   RNA polymerase III subunit RPC82 family protein, contains Pfam profile: PF05645 RNA polymerase III subunit RPC82	5.6	5.7	-0.1	-0.5	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
11987	AT3G60320.1   Symbol: P9L   expressed protein, contains Pfam profiles: PF04782: protein of unknown function (DUF632), PF04783: protein of unknown function (DUF630)   chr3:22302861-22306346 REVERSE   Aliases: F27H5.110, P9L	7.9	7.7	0.2	0.5	100.0%	-4.6
11988	AT1G10590.3   DNA-binding protein-related, contains weak similarity to G-quartet DNA binding protein 3 (Tetrahymena thermophila) gi:4583503:gb:AAD25098   chr1:3502051-3503410 REVERSE   Aliases: F20B24.1	10.2	10.1	0.1	0.5	100.0%	-5.0
11989	AT4G29190.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr4:14391944-14393379 REVERSE   Aliases: F17A13.10, F17A13_10	5.9	5.7	0.2	0.5	100.0%	-4.9
11990	AT1G61820.3   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-mannosidase enzyme (GI:17226270) (Lycopersicon esculentum)   chr1:22840043-22842280 FORWARD   Aliases: F8K4.3, F8K4_3	5.4	5.6	-0.2	-0.5	100.0%	-4.2
11991	AT1G74580.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr1:28024438-28026729 FORWARD   Aliases: F1M20.26, F1M20_26	3.2	3.3	-0.1	-0.5	100.0%	-5.1
11992	AT5G23170.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:7798414-7799451 REVERSE   Aliases: MKD15.3, MKD15_3	4.5	4.8	-0.3	-0.5	100.0%	-4.4
11993	AT2G41705.1   camphor resistance CrcB family protein, contains Pfam profile PF02537: CrcB-like protein	4.4	4.6	-0.2	-0.5	100.0%	-4.5
11994	AT4G10170.2   synaptobrevin-related family protein, similar to Vesicle-associated membrane protein 722	6.9	6.6	0.3	0.5	100.0%	-4.6
11995	AT2G02620.1   DC1 domain-containing protein / PHD finger protein-related, contains Pfam profiles PF03107: DC1 domain, weak hit to PF00628: PHD-finger   chr2:717255-719374 FORWARD   Aliases: T8K22.8, T8K22_8	3.7	3.5	0.2	0.5	100.0%	-4.9
11996	AT4G18540.1   expressed protein, ; expression supported by MPSS   chr4:10221214-10223039 REVERSE   Aliases: F28J12.200, F28J12_200	2.8	2.9	-0.1	-0.5	100.0%	-5.2
11997	AT1G50840.1   poll-like DNA polymerase, putative, similar to Poll-like DNA polymerase (Oryza sativa) GI:19912795 contains Pfam profiles PF01612: 3'-5' exonuclease, PF00476: DNA polymerase I family A	7.5	7.7	-0.2	-0.5	100.0%	-4.3
11998	AT2G47310.1   flowering time control protein-related / FCA gamma-related   chr2:19430754-19434347 FORWARD   Aliases: T8I13.15	3.2	3.3	-0.1	-0.5	100.0%	-5.4
11999	AT5G16790.1   expressed protein   chr5:5522499-5523914 REVERSE   Aliases: F5E19.130, F5E19_130	3.8	3.7	0.1	0.5	100.0%	-4.9
12000	AT1G11470.1   expressed protein   chr1:3859874-3860522 REVERSE   Aliases: T23J18.14, T23J18_14	3.3	3.2	0.1	0.5	100.0%	-4.9
12001	AT3G25540.1   Symbol: LAG1   longevity-assurance (LAG1) family protein, similar to Alternaria stem canker resistance protein (ASC1) (Lycopersicon esculentum) GI:7688742; contains Pfam profile PF03798: Longevity-assurance protein (LAG1); supporting cDNA gi:7658238:gb:AF198179.1:AF198179   chr3:9275833-9277922 FORWARD   Aliases: LAG1 HOMOLOG 1, MWL2.19	3.7	3.9	-0.2	-0.5	100.0%	-4.8
12002	AT3G51870.1   mitochondrial substrate carrier family protein, peroxisomal Ca-dependent solute carrier - Oryctolagus cuniculus, EMBL:AF004161   chr3:19254931-19257913 FORWARD   Aliases: ATEM1.12	5.0	4.8	0.2	0.5	100.0%	-4.5
12003	AT4G22300.1   phospholipase/carboxylesterase family protein, similar to acyl-protein thioesterase-1 (Homo sapiens) GI:9965372; contains Pfam profile PF02230: Phospholipase/Carboxylesterase family   chr4:11787800-11791067 REVERSE   Aliases: T10I14.130, T10I14_130	5.2	5.1	0.2	0.5	100.0%	-5.0
12004	AT4G19240.1   expressed protein   chr4:10527811-10529103 REVERSE   Aliases: T5K18.20, T5K18_20	3.0	2.9	0.1	0.5	100.0%	-5.3
12005	AT2G38540.1   Symbol: LP1   nonspecific lipid transfer protein 1 (LTP1), identical to SP:Q42589   chr2:16137428-16138252 FORWARD   Aliases: ATLTP1, LIPID TRANSFER PROTEIN 1, LTP1, T6A23.26, T6A23_26	3.6	3.5	0.1	0.5	100.0%	-5.1
12006	AT4G32280.1   Symbol: IAA29   auxin-responsive AUX/IAA family protein, contains Pfam profile: PF02309: AUX/IAA family	2.3	2.4	-0.1	-0.5	100.0%	-5.0
12007	AT1G58410.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.7	3.0	-0.2	-0.5	100.0%	-4.4
12008	AT5G57730.1   hypothetical protein   chr5:23410608-23410736 REVERSE   Aliases: MRI1.9, MRI1_9	2.5	2.5	-0.1	-0.5	100.0%	-5.8
12009	AT5G40330.1   Symbol: MYB23   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:16144953-16146883 FORWARD   Aliases: ATMYB23, MPO12.40, MPO12_40	2.5	2.6	-0.1	-0.5	100.0%	-5.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12010	AT1G53580.2   similar to hydroxyacylglutathione hydrolase, cytoplasmic / glyoxalase II (GLX2-2) [Arabidopsis thaliana] (TAIR:At3g10850.1); similar to putative glyoxalase II [Oryza sativa (japonica cultivar-group)] (GB:NP_916812.1); contains InterPro domain Beta-lactamase-like (InterPro:IPR001279)   chr1:19994943-19996898 REVERSE   Aliases: F22G10.9, T3F20.11, T3F20_11	9.4	9.7	-0.2	-0.5	100.0%	-5.1
12011	AT1G20180.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g49070.1); similar to Hypothetical protein [Oryza sativa] (GB:XP_470228.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAN87731.1); contains InterPro domain Protein of unknown function DUF677 (InterPro:IPR007749)   chr1:6996201-6997934 FORWARD   Aliases: T20H2.5, T20H2_5	2.4	2.4	-0.1	-0.5	100.0%	-5.7
12012	AT5G03120.1   expressed protein   chr5:733978-734942 FORWARD   Aliases: F15A17.150, F15A17_150	3.5	3.4	0.1	0.5	100.0%	-5.2
12013	AT4G37020.1   expressed protein   chr4:17445691-17447394 FORWARD   Aliases: AP22.69, AP22_69	5.1	5.3	-0.2	-0.5	100.0%	-4.7
12014	ATCG00330.1   Symbol: RPS14   30S chloroplast ribosomal protein S14   chrC:36938-37240 REVERSE   Aliases: RIBOSOMAL PROTEIN S14, RPS14	3.3	3.6	-0.2	-0.5	100.0%	-5.4
12015	AT1G17650.1   similar to 6-phosphogluconate dehydrogenase NAD-binding domain-containing protein [Arabidopsis thaliana] (TAIR:At3g25530.1); similar to putative gamma hydroxybutyrate dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:NP_918497.1); contains InterPro domain 6-phosphogluconate dehydrogenase, NAD binding domain (InterPro:IPR006115)   chr1:6069470-6072005 REVERSE   Aliases: F11A6.12	5.9	6.1	-0.2	-0.5	100.0%	-4.2
12016	AT2G36080.2   DNA-binding protein, putative, strong similarity to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857, RAV2 GI:3868859; contains Pfam profile PF02362: B3 DNA binding domain   chr2:15157630-15158654 REVERSE   Aliases: F9C22.1	2.6	2.7	-0.1	-0.5	100.0%	-5.1
12017	AT1G53820.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:20095159-20096091 FORWARD   Aliases: T18A20.16, T18A20_16	4.1	4.0	0.1	0.5	100.0%	-5.1
12018	AT5G66350.1   Symbol: SHI   zinc finger protein, putative (SHI), similar to lateral root primordium 1 (LRP1) (Arabidopsis thaliana) GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702); identical to cDNA putative zinc finger protein SHI (SHI) GI:4929802   chr5:26521693-26523795 REVERSE   Aliases: K1L20.13, K1L20_13, SHORT INTERNODES	2.7	2.8	-0.1	-0.5	100.0%	-5.5
12019	AT3G20220.1   auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana)   chr3:7055066-7055422 FORWARD   Aliases: MAL21.24	2.7	2.9	-0.1	-0.5	100.0%	-5.1
12020	AT3G42820.1   expressed protein, hypothetical proteins - Arabidopsis thaliana   chr3:14932025-14938020 REVERSE   Aliases: T21C14.40	3.8	3.9	-0.1	-0.5	100.0%	-5.4
12021	AT5G35250.1   expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	3.3	3.5	-0.2	-0.5	100.0%	-5.0
12022	AT2G19620.1   Ndr family protein, similar to SP:O23969 Pollen specific protein SF21 {Helianthus annuus}; contains Pfam profile PF03096: Ndr family   chr2:8493073-8495733 REVERSE   Aliases: F3P11.22, F3P11_22	4.4	4.2	0.1	0.5	100.0%	-4.8
12023	AT5G04920.1   vacuolar protein sorting 36 family protein / VPS36 family protein, contains Pfam PF04132: Vacuolar protein sorting 36   chr5:1439010-1441984 REVERSE   Aliases: MUG13.23, MUG13_23	7.8	7.5	0.3	0.5	100.0%	-4.5
12024	AT2G30770.1   Symbol: CYP71A13   cytochrome P450 71A13, putative (CYP71A13), Identical to Cytochrome P450 71A13 (SP:O49342) (Arabidopsis thaliana); similar to Cytochrome P450 (gi:5713172) (Nicotiana tabacum).   chr2:13116871-13119088 REVERSE   Aliases: T11J7.16, T11J7_16	3.1	3.2	-0.1	-0.5	100.0%	-5.0
12025	AT4G24900.1   expressed protein   chr4:12814858-12817609 FORWARD   Aliases: F13M23.40, F13M23_40	3.4	3.5	-0.1	-0.5	100.0%	-5.0
12026	AT2G22125.1   similar to C2 domain-containing protein / armadillo/beta-catenin repeat family protein [Arabidopsis thaliana] (TAIR:At1g44120.1); similar to C2 domain, putative [Oryza sativa (japonica cultivar-group)] (GB:AAX95026.1); contains InterPro domain C2 domain (InterPro:IPR000008); contains InterPro domain Armadillo repeat (InterPro:IPR000225)   chr2:9413343-9421598 FORWARD   Aliases: T16B14.2	6.8	7.1	-0.3	-0.5	100.0%	-4.5
12027	AT1G70620.2   cyclin-related, contains weak similarity to Swiss-Prot:P35662 cyclin I (Multiple-band polypeptide I) (Bos taurus)   chr1:26630297-26634767 FORWARD   Aliases: F5A18.20, F5A18_20	5.0	5.6	-0.6	-0.5	100.0%	-4.3
12028	AT5G39050.1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family   chr5:15651815-15653293 FORWARD   Aliases: MXF12.60, MXF12_60	3.2	3.1	0.1	0.5	100.0%	-5.5
12029	AT2G19660.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	2.3	-0.1	-0.5	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12030	AT4G37120.1   Symbol: SMP2   expressed protein   chr4:17486641-17489282 FORWARD   Aliases: AP22.39, AP22_39	9.1	9.3	-0.2	-0.5	100.0%	-5.2
12031	AT1G03475.1   Symbol: LIN2   coproporphyrinogen III oxidase, putative / coproporphyrinogenase, putative / coprogen oxidase, putative, similar to coproporphyrinogen III oxidase, chloroplast (precursor) from Glycine max (SP:P35055), Nicotiana tabacum (SP:Q42946), Hordeum vulgare (SP:Q42840), ESTs gb:AA586260 and dbj:D48620; contains Pfam domain coproporphyrinogen III oxidase, aerobic (PF01218)   chr1:869051-871212 REVERSE   Aliases: COPROPORPHYRINOGEN III OXIDASE, F21B7.10, LESION INITIATION 2	5.2	5.4	-0.2	-0.5	100.0%	-4.5
12032	AT1G15190.1   expressed protein   chr1:5227270-5228016 FORWARD   Aliases: F9L1.13, F9L1_13	2.6	2.7	-0.1	-0.5	100.0%	-5.5
12033	AT3G07080.1   membrane protein, contains Pfam profile: PF00892 Integral membrane protein   chr3:2241042-2243047 FORWARD   Aliases: T1B9.27	5.0	4.8	0.2	0.5	100.0%	-4.9
12034	AT2G01670.1   MutT/nudix family protein, similar to SP:Q09790 Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain	4.2	4.5	-0.3	-0.5	100.0%	-4.3
12035	AT1G11710.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3948714-3951359 FORWARD   Aliases: F25C20.14, F25C20_14	3.9	3.8	0.1	0.5	100.0%	-4.9
12036	AT1G13150.1   Symbol: CYP86C4   cytochrome P450, putative, strong similarity to gi:3313615 F21J9.9 from Arabidopsis thaliana and is a member of the PF:00067 Cytochrome P450 family   chr1:4481872-4483693 REVERSE   Aliases: F3F19.17, F3F19_17	2.9	2.8	0.1	0.5	100.0%	-5.5
12037	AT1G60870.1   expressed protein   chr1:22413137-22414159 FORWARD   Aliases: T7P1.2, T7P1_2	7.6	7.3	0.3	0.5	100.0%	-4.1
12038	AT1G20500.1   4-coumarate--CoA ligase family / 4-coumaroyl-CoA synthase family, similar to SP:Q42524 and SP:Q9S725; contains Pfam AMP-binding enzyme domain PF00501   chr1:7101474-7102905 REVERSE   Aliases: F5M15.18, F5M15_18	4.0	3.7	0.3	0.5	100.0%	-4.4
12039	AT5G19450.2   Symbol: CDPK19	7.8	7.5	0.2	0.5	100.0%	-4.7
12040	AT5G59530.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967); 1-aminocyclopropane-1-carboxylate oxidase kidney bean, PIR:T10818   chr5:24011410-24012941 REVERSE   Aliases: F2O15.26, F2O15_26	2.8	2.7	0.1	0.5	100.0%	-5.0
12041	AT4G34540.1   isoflavone reductase family protein, similar to phenylcoumaran benzylic ether reductase homolog Fi1 (Forsythia x intermedia)(GI:7578895); contains isoflavone reductase domain PF02716   chr4:16498396-16502179 FORWARD   Aliases: T4L20.120, T4L20_120	4.9	4.7	0.3	0.5	100.0%	-4.4
12042	AT3G19070.1   cell wall protein-related, similar to vegetative cell wall protein gp1 (Chlamydomonas reinhardtii) gi:12018147:gb:AAG45420;   chr3:6593779-6594983 FORWARD   Aliases: K13E13.20	2.1	2.1	0.1	0.5	100.0%	-5.5
12043	AT2G10450.1   14-3-3 protein, putative / grf15, putative, contains similarity to GF14 psi chain GI:166717, SP:P42644 from (Arabidopsis thaliana)   chr2:4027388-4027856 FORWARD   Aliases: F12P23.4, F12P23_4	3.2	3.1	0.1	0.5	100.0%	-5.4
12044	AT3G04900.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr3:1349308-1349934 REVERSE   Aliases: T9J14.15, T9J14_15	2.7	2.7	0.1	0.5	100.0%	-5.6
12045	AT4G16230.1   GDSL-motif lipase/hydrolase family protein, similar to SP:P40602 Anther-specific proline-rich protein APG precursor {Arabidopsis thaliana}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr4:9185313-9188552 FORWARD   Aliases: DL4155W, FCAALL.318	3.0	3.1	-0.1	-0.5	100.0%	-5.0
12046	AT3G13630.1   expressed protein   chr3:4456961-4458141 FORWARD   Aliases: MMM17.2	2.8	2.8	-0.1	-0.5	100.0%	-5.4
12047	AT5G43460.1   lesion inducing protein-related, similar to ORF, able to induce HR-like lesions (Nicotiana tabacum)   chr5:17477112-17478979 FORWARD   Aliases: MWF20.18, MWF20_18	10.5	10.4	0.1	0.5	100.0%	-5.7
12048	AT3G47230.1   expressed protein   chr3:17403084-17404684 REVERSE   Aliases: F13I12.280	2.6	2.6	-0.1	-0.5	100.0%	-5.5
12049	AT5G55260.1   Symbol: PPX2   serine/threonine protein phosphatase PP-X isozyme 2 (PPX2), identical to SP:P48528 Serine/threonine protein phosphatase PP-X isozyme 2 (EC 3.1.3.16) {Arabidopsis thaliana}; contains Pfam profile PF00149: Ser/Thr protein phosphatase   chr5:22433825-22436090 FORWARD   Aliases: EP128, MCO15.21, MCO15_21, PPX 2	5.7	5.5	0.2	0.5	100.0%	-4.6
12050	AT1G11750.1   Symbol: CLPP6   ATP-dependent Clp protease proteolytic subunit (ClpP), identical to ATP-dependent Clp protease proteolytic subunit GI:2827888 from (Arabidopsis thaliana); contains Pfam profile PF00574: Clp protease; contains TIGRfam profile TIGR00493: ATP-dependent Clp protease, proteolytic subunit ClpP   chr1:3967478-3969854 FORWARD   Aliases: ATP DEPENDENT CLP PROTEASE PROTEOLYTIC SUBUNIT, F25C20.10, F25C20_10, NCLPP1, NCLPP6	6.8	6.5	0.3	0.5	100.0%	-4.4
12051	AT2G27820.1   prephenate dehydratase family protein   chr2:11863845-11865365 FORWARD   Aliases: F15K20.8, F15K20_8	5.4	5.3	0.1	0.5	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12052	AT3G20880.1   zinc finger (C2H2 type) protein (WIP4), identical to WIP4 protein (Arabidopsis thaliana) gi:18376500:emb:CAC86168; contains Pfam domain, PF00096: Zinc finger, C2H2 type	3.8	3.9	-0.1	-0.5	100.0%	-5.3
12053	AT4G30930.1   Symbol: WRKY32	7.1	7.4	-0.3	-0.5	100.0%	-4.4
12054	AT5G51040.2   expressed protein, contains InterPro domain Protein of unknown function DUF339 (InterPro:IPR005631)   chr5:20767886-20769250 FORWARD   Aliases: K3K7.22, K3K7_22	10.0	10.2	-0.2	-0.5	100.0%	-5.0
12055	AT1G14930.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:20810) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:5152258-5153079 REVERSE   Aliases: F10B6.35, F10B6_35	2.8	2.7	0.1	0.5	100.0%	-5.4
12056	AT3G17600.1   Symbol: IAA31   auxin-responsive protein, putative, similar to SP:O24410 Auxin-responsive protein IAA20 (Indoleacetic acid-induced protein 20) {Arabidopsis thaliana}; contains Pfam profile: PF02309: AUX/IAA family   chr3:6020036-6021148 REVERSE   Aliases: MKP6.16	2.9	2.9	0.1	0.5	100.0%	-5.4
12057	AT1G60230.1   radical SAM domain-containing protein, contains Pfam profile PF04055: radical SAM domain protein   chr1:22215749-22218089 REVERSE   Aliases: T13D8.12, T13D8_12	5.0	4.8	0.2	0.5	100.0%	-4.3
12058	AT4G02480.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family; similar to Spastin (Swiss-Prot:Q9UBP0) (Homo sapiens) and Spastin (Fragment) (Swiss-Prot:Q9QYY8) (Mus musculus); similar to mitochondrial sorting protein 1 (MSP1) protein (TAT-binding homolog 4) (Swiss-Prot:P28737) (Saccharomyces cerevisiae)   chr4:1081759-1088846 REVERSE   Aliases: AT4G02470, T14P8.8, T14P8_8	7.0	6.7	0.2	0.5	100.0%	-5.0
12059	AT5G04500.1   glycosyltransferase family protein 47, low similarity to Exostosin-like 2, Homo sapiens (SP:Q9UBQ6), EXTL2, Mus musculus (GI:10443633)   chr5:1283469-1286360 FORWARD   Aliases: T32M21.100, T32M21_100	2.9	2.8	0.1	0.5	100.0%	-5.2
12060	AT3G28480.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Gallus gallus (GI:212530), Rattus norvegicus (GI:474940), Mus musculus (SP:Q60715); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr3:10677275-10679525 REVERSE   Aliases: MFJ20.16	8.5	8.3	0.2	0.5	100.0%	-4.5
12061	AT5G14950.1   glycosyl hydrolase family 38 protein, similar to alpha-mannosidase II SP:P27046 from (Mus musculus)   chr5:4837155-4841795 REVERSE   Aliases: F2G14.70, F2G14_70	3.5	3.7	-0.2	-0.5	100.0%	-5.0
12062	AT5G18240.5   Symbol: MYR1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:6028287-6030733 REVERSE   Aliases: MRG7.20, MRG7_20	3.1	3.2	-0.1	-0.5	100.0%	-5.1
12063	AT1G19210.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr1:6626813-6627521 REVERSE   Aliases: T29M8.8, T29M8_8	3.2	3.2	0.1	0.5	100.0%	-5.3
12064	AT4G32860.1   expressed protein   chr4:15856615-15857363 REVERSE   Aliases: T16I18.70, T16I18_70	2.4	2.3	0.1	0.5	100.0%	-5.4
12065	AT3G45490.1   expressed protein   chr3:16698051-16698823 REVERSE   Aliases: F9K21.70	3.5	3.6	-0.1	-0.5	100.0%	-5.1
12066	AT2G02250.1   Symbol: ATPP2 B2   F-box family protein / SKP1 interacting partner 3-related, contains similarity to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)	3.7	3.6	0.1	0.5	100.0%	-5.2
12067	AT5G07360.1   amidase family protein, low similarity to enantiomerase-selective amidase (Rhodococcus sp.) GI:152052; contains Pfam profile PF01425: Amidase   chr5:2326709-2330137 REVERSE   Aliases: T2I1.70, T2I1_70	5.5	5.3	0.2	0.5	100.0%	-4.5
12068	AT1G60630.1   leucine-rich repeat family protein, similar to receptor kinase GI:498278 from (Petunia integrifolia); contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr1:22338327-22340573 REVERSE   Aliases: F8A5.15, F8A5_15	2.4	2.3	0.1	0.5	100.0%	-5.5
12069	AT1G73660.1   protein kinase family protein, contains Pfam profile: PF00069 eukaryotic protein kinase domain   chr1:27695554-27700872 REVERSE   Aliases: F25P22.8, F25P22_8	4.1	4.2	-0.1	-0.5	100.0%	-4.8
12070	AT3G52820.1   purple acid phosphatase (PAP22), identical to purple acid phosphatase (PAP22)GI:20257494 from (Arabidopsis thaliana)   chr3:19584922-19587955 REVERSE   Aliases: F3C22.220	2.5	2.4	0.1	0.5	100.0%	-4.8
12071	AT2G47560.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:19519004-19519687 REVERSE   Aliases: T30B22.14	2.8	2.8	-0.1	-0.5	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12072	AT4G03480.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr4:1546022-1548869 REVERSE   Aliases: F9H3.11, F9H3_11	2.5	2.7	-0.1	-0.5	100.0%	-5.2
12073	AT1G50520.1   Symbol: CYP705A27   cytochrome P450 family protein, similar to CYTOCHROME P450 93A3 GB:O81973 from (Glycine max)   chr1:18723046-18724887 FORWARD   Aliases: F11F12.13, F11F12_13	3.5	3.6	-0.2	-0.5	100.0%	-4.5
12074	AT1G16800.1   tRNA-splicing endonuclease positive effector-related, contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease (Saccharomyces cerevisiae) gi:172574:gb:AAB63976   chr1:5745516-5755256 REVERSE   Aliases: F17F16.1, F17F16_1	4.3	4.4	-0.1	-0.5	100.0%	-5.1
12075	AT3G54230.1   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At2g16940.1); similar to putative RNA-binding protein 10 [Oryza sativa (japonica cultivar-group)] (GB:XP_464248.1); contains InterPro domain D111/G-patch domain (InterPro:IPR000467); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504); contains InterPro domain Zn-finger, Ran-binding (InterPro:IPR001876)   chr3:20084082-20091242 FORWARD   Aliases: F24B22.190	4.7	4.8	-0.2	-0.5	100.0%	-4.8
12076	AT5G61280.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr5:24660851-24662136 REVERSE   Aliases: MFB13.5, MFB13_5	2.8	2.6	0.2	0.5	100.0%	-4.8
12077	AT3G19290.1   Symbol: ABF4   ABA-responsive element-binding protein 2 (AREB2), almost identical (one amino acid) to GB:AAF27182 from (Arabidopsis thaliana); contains Pfam profile PF00170:bZIP transcription factor; identical to cDNA abscisic acid responsive elements-binding factor (ABRE) mRNA, partial cds GI:6739282   chr3:6687146-6690129 FORWARD   Aliases: ABA RESPONSIVE ELEMENT BINDING PROTEIN 2, ABRE BINDING FACTOR 4, AREB2, MVI11.7	4.8	4.5	0.2	0.5	100.0%	-4.8
12078	AT5G01340.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:143054-144719 REVERSE   Aliases: T10O8.50, T10O8_50	9.9	9.6	0.3	0.5	100.0%	-4.3
12079	AT4G20900.1   Symbol: MS5   male sterility MS5 / pollenless 3, nearly identical to male sterility MS5 (Arabidopsis thaliana) GI:3859112, pollenless3 (Arabidopsis thaliana) GI:4028970   chr4:11184114-11185855 REVERSE   Aliases: MALE STERILE 5, POLLENLESS3, T13K14.60, T13K14_60, TDM1	2.4	2.5	-0.1	-0.5	100.0%	-5.3
12080	AT3G09320.1   zinc finger (DHHC type) family protein, similar to Golgi-specific DHHC zinc finger protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain   chr3:2861749-2864251 REVERSE   Aliases: F3L24.19	5.3	5.5	-0.2	-0.5	100.0%	-4.5
12081	AT1G49380.1   cytochrome c biogenesis protein family, contains Pfam PF05140: ResB-like family; similar to CCS1 (GI:2749939) (Chlamydomonas reinhardtii); similar to Ccs1 (GI:6137102) (Synechococcus sp. PCC 6301)   chr1:18280375-18283196 FORWARD   Aliases: F13F21.19, F13F21_19	3.9	4.1	-0.2	-0.5	100.0%	-4.5
12082	AT5G12010.1   expressed protein   chr5:3877813-3879540 REVERSE   Aliases: F14F18.180, F14F18_180	7.8	8.0	-0.2	-0.5	100.0%	-5.2
12083	AT1G28550.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from (Pisum sativum)	2.2	2.3	-0.1	-0.5	100.0%	-5.6
12084	AT3G20900.1   expressed protein   chr3:7323990-7324676 REVERSE   Aliases: MFD22.2	4.4	4.2	0.2	0.5	100.0%	-4.7
12085	AT3G18570.1   glycine-rich protein / oleosin, contains similarity to Pfam profile: PF01277 Oleosin   chr3:6395866-6396612 REVERSE   Aliases: K24M9.6	2.8	2.7	0.1	0.5	100.0%	-5.3
12086	AT2G22520.1   hypothetical protein, and grail	2.8	2.9	-0.1	-0.5	100.0%	-5.1
12087	AT1G66860.1   expressed protein, similar to Hypothetical protein RP404. (Swiss-Prot:Q9ZDC7) (Rickettsia prowazekii); similar to Hypothetical protein yvdE homolog (Fragment) (Swiss-Prot:P22347) (Lactococcus lactis)   chr1:24945851-24948160 FORWARD   Aliases: F4N21.3, F4N21_3	2.6	2.7	-0.1	-0.5	100.0%	-5.5
12088	AT1G01790.1   Symbol: KEA1   K+ efflux antiporter, putative (KEA1), identical to GB:AAD01191 GI:4101473 from ( Arabidopsis thaliana); Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563   chr1:286198-291089 FORWARD   Aliases: ATKEA1, K EFFLUX ANTIPORTER 1, T1N6.21, T1N6_21	6.5	6.3	0.2	0.5	100.0%	-4.7
12089	AT5G61510.1   NADP-dependent oxidoreductase, putative, similar to zeta-crystallin homolog TED2 from Zinnia elegans (gi:531096); contains Pfam zinc-binding dehydrogenase domain PF00107   chr5:24754171-24756224 REVERSE   Aliases: K11J9.5, K11J9_5	10.2	9.9	0.2	0.5	100.0%	-4.7
12090	AT1G29330.1   Symbol: ERD2   ER lumen protein retaining receptor (ERD2) / HDEL receptor, identical to SP:P35402 ER lumen protein retaining receptor (HDEL receptor) {Arabidopsis thaliana}   chr1:10257986-10261056 REVERSE   Aliases: AERD2, ATERD2, F28N24.1	5.2	5.5	-0.3	-0.5	100.0%	-4.7
12091	AT2G42580.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr2:17735793-17738796 FORWARD   Aliases: F14N22.15, F14N22_15	5.3	5.5	-0.2	-0.5	100.0%	-5.0
12092	AT1G35663.1   hypothetical protein   chr1:13199210-13199749 REVERSE   Aliases: F15O4.65, F15O4_65	2.2	2.2	-0.1	-0.5	100.0%	-5.9
12093	AT3G13060.2   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr3:4180582-4183982 FORWARD   Aliases: MGH6.21	7.5	7.6	-0.2	-0.5	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12094	AT5G15940.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to forever young oxidoreductase GI:18138083 from ( <i>Lycopersicon esculentum</i> )   chr5:5202858-5204878 FORWARD   Aliases: F1N13.80, F1N13_80	2.7	2.8	-0.1	-0.5	100.0%	-5.5
12095	AT3G63460.2   Symbol: EMB2221   WD-40 repeat family protein, hypothetical protein contains similarity to ec31p ( <i>Oryza sativa</i> ) gi:13928450:dbj:BAB47154; contains Pfam profile PF00400: WD domain, G-beta repeat   chr3:23441619-23448319 REVERSE   Aliases: EMB2221, EMBRYO DEFECTIVE 2221, MAA21.90	4.1	4.2	-0.2	-0.5	100.0%	-5.1
12096	AT4G03120.1   proline-rich family protein, similar to U1 small nuclear ribonucleoprotein C; contains proline rich extensin domains, INTERPRO:IPR002965	4.9	5.1	-0.2	-0.5	100.0%	-4.7
12097	AT1G17950.1   Symbol: MYB52   myb family transcription factor (MYB52), similar to myb-like protein GI:6979341 from ( <i>Oryza sativa</i> )   chr1:6177610-6179282 FORWARD   Aliases: ATMYB52, BW52, F2H15.17, F2H15_17, MYB52	2.7	2.8	-0.1	-0.5	100.0%	-5.3
12098	AT2G23690.1   expressed protein   chr2:10079357-10083049 FORWARD   Aliases: F27L4.13, F27L4_13	7.3	7.0	0.2	0.5	100.0%	-4.8
12099	AT1G53010.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:19751515-19752051 FORWARD   Aliases: F8L10.17	2.2	2.1	0.1	0.5	100.0%	-5.7
12100	AT5G25920.1   expressed protein   chr5:9044209-9046000 REVERSE   Aliases: T1N24.2, T1N24_2	2.7	2.8	-0.1	-0.5	100.0%	-5.3
12101	AT4G31340.2   similar to DNA repair ATPase-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g24420.2); similar to DNA repair ATPase-related [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g24420.1); similar to unknown [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:AAO72581.1)   chr4:15205486-15209607 FORWARD   Aliases: F8F16.160, F8F16_160	7.6	7.3	0.4	0.5	100.0%	-4.8
12102	AT1G42440.1   expressed protein, contains Pfam domain, PF04950: Protein of unknown function (DUF663)   chr1:15897725-15902495 REVERSE   Aliases: F7F22.4, F7F22_4	6.0	6.1	-0.1	-0.5	100.0%	-4.8
12103	AT5G43550.1   expressed protein   chr5:17515120-17515491 FORWARD   Aliases: K9D7.5, K9D7_5	2.2	2.3	-0.1	-0.5	100.0%	-5.6
12104	AT1G66090.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:24605809-24608426 FORWARD   Aliases: F15E12.17, F15E12_17	3.1	2.9	0.1	0.5	100.0%	-5.0
12105	AT2G33870.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303742 from ( <i>Pisum sativum</i> )	2.4	2.3	0.1	0.5	100.0%	-5.7
12106	AT4G16710.2   glycosyltransferase family protein 28, low similarity to C terminus subunit of GlcA transferase from <i>Escherichia coli</i> (GI:2586169); contains Pfam profile PF04101: Glycosyltransferase family 28 C-terminal domain   chr4:9398589-9399823 FORWARD   Aliases: DL4380W, FCAALL.10	8.1	8.0	0.1	0.5	100.0%	-5.2
12107	AT1G03880.1   Symbol: CRU2   12S seed storage protein (CRB), identical to 12S seed storage protein, gi:808937 (SP:P15456) ( <i>Plant Mol Biol</i> 11:805-820 (1988)); contains Pfam profile PF00190 Cupin and Prosite 11-S plant seed storage proteins signature PS00305   chr1:985755-988145 FORWARD   Aliases: CRB, CRUCIFERIN 2, CRUCIFERIN B, F21M11.19, F21M11_19	2.5	2.4	0.1	0.5	100.0%	-5.4
12108	AT5G40930.1   Symbol: TOM20 4   mitochondrial import receptor subunit TOM20-4 / translocase of outer membrane 20 kDa subunit 4, identical to mitochondrial import receptor subunit TOM20-4 SP:P82805 from ( <i>Arabidopsis thaliana</i> )   chr5:16421688-16423224 FORWARD   Aliases: MMG1.2, MMG1_2, TOM20, TRANSLOCASE OF OUTER MEMBRANE 20 4	10.3	10.1	0.2	0.5	100.0%	-5.0
12109	AT5G42840.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.7	-0.1	-0.5	100.0%	-4.8
12110	AT3G11330.1   leucine-rich repeat family protein   chr3:3551980-3554769 REVERSE   Aliases: F11B9.22	5.4	5.6	-0.2	-0.5	100.0%	-4.7
12111	AT2G22350.1   RNase H domain-containing protein, low similarity to reverse transcriptase ( <i>Arabidopsis thaliana</i> ) GI:976278; contains Pfam profile PF00075: RNase H   chr2:9503156-9504121 FORWARD   Aliases: F14M13.25, F14M13_25	3.8	3.6	0.2	0.5	100.0%	-5.0
12112	AT2G28570.1   expressed protein   chr2:12248847-12249806 FORWARD   Aliases: T17D12.13, T17D12_13	2.9	2.5	0.3	0.5	100.0%	-4.6
12113	AT4G05190.1   Symbol: ATK5   kinesin-like protein A, putative, kinesin like protein A, <i>Arabidopsis thaliana</i> , gb:Q07970   chr4:2675136-2679480 FORWARD   Aliases: ARABIDOPSIS THALIANA KINESIN 5, C17L7.110, C17L7_110	2.3	2.4	-0.1	-0.5	100.0%	-4.9
12114	AT3G51460.1   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 ( <i>Rattus norvegicus</i> ) gi:11095248:gb:AAG29810; contains Pfam domain, PF02383: SacI homology domain; contains non-consensus AT-AC splice sites at intron 8   chr3:19103777-19108315 FORWARD   Aliases: F26O13.100	5.4	5.6	-0.2	-0.5	100.0%	-4.7
12115	AT4G35580.1   no apical meristem (NAM) family protein, similar to TIP ( <i>Arabidopsis thaliana</i> ) GI:9408601; contains Pfam profile PF02365: No apical meristem (NAM) protein   chr4:16888410-16890772 REVERSE   Aliases: F8D20.90, F8D20_90	5.2	5.1	0.2	0.5	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12116	AT1G76450.1   oxygen-evolving complex-related, SP:Q9S720; contains a PsbP domain   chr1:28689465-28691614 FORWARD   Aliases: F15M4.5	6.9	7.2	-0.2	-0.5	100.0%	-4.4
12117	AT3G62750.1   similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At4g22100.1); similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At4g27830.1); similar to glycosyl hydrolase family 1 protein [Arabidopsis thaliana] (TAIR:At4g27820.1); similar to hydroxyisourate hydrolase [Glycine max] (GB:AAL92115.1); contains InterPro domain Glycoside hydrolase, family 1 (InterPro:IPR001360)   chr3:23225347-23228021 FORWARD   Aliases: F26K9.180	2.6	2.6	0.1	0.5	100.0%	-5.2
12118	AT1G68580.2   agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain and PF05641: Agenet domain	4.5	4.2	0.2	0.5	100.0%	-4.7
12119	AT4G10730.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:6609420-6614877 REVERSE   Aliases: T12H20.4, T12H20_4	3.1	3.0	0.1	0.5	100.0%	-5.0
12120	AT4G32230.1   expressed protein   chr4:15565301-15566977 REVERSE   Aliases: F10M6.130, F10M6_130	2.5	2.6	-0.1	-0.5	100.0%	-5.4
12121	AT2G41340.1   eukaryotic rpb5 RNA polymerase subunit family protein, similar to SP:Q09191 DNA-directed RNA polymerases II 24 kDa polypeptide (EC 2.7.7.6) {Schizosaccharomyces pombe}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain   chr2:17236086-17237560 FORWARD   Aliases: F13H10.11, F13H10_11	3.1	3.0	0.1	0.5	100.0%	-4.9
12122	AT4G23880.1   expressed protein   chr4:12415729-12416460 REVERSE   Aliases: T32A16.50, T32A16_50	3.4	3.6	-0.1	-0.5	100.0%	-4.7
12123	AT5G50330.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr5:20502452-20505789 REVERSE   Aliases: MXI22.4, MXI22_4	2.8	3.0	-0.1	-0.5	100.0%	-5.0
12124	AT5G04610.1   spermidine synthase-related / putrescine aminopropyltransferase-related, contains weak similarity to Spermidine synthase 2 (EC 2.5.1.16) (Putrescine aminopropyltransferase 2) (SPDSY 2) (Swiss-Prot:O48659) (Hyoscyamus niger)   chr5:1325589-1326929 REVERSE   Aliases: T1E3.8	4.0	4.1	-0.1	-0.5	100.0%	-5.0
12125	AT1G35030.1   hypothetical protein   chr1:12808224-12809459 FORWARD   Aliases: F11O6.5, F11O6_5	2.9	3.0	-0.1	-0.5	100.0%	-5.1
12126	AT1G63750.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:23654585-23658996 FORWARD   Aliases: F24D7.6, F24D7_6	2.6	2.5	0.1	0.5	100.0%	-5.4
12127	AT2G36000.2   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr2:15124154-15125776 FORWARD   Aliases: F11F19.9, F11F19_9	3.1	3.0	0.1	0.5	100.0%	-5.3
12128	AT1G34030.1   40S ribosomal protein S18 (RPS18B), similar to ribosomal protein S18 GI:38422 from (Homo sapiens)   chr1:12370055-12371530 REVERSE   Aliases: F12G12.15, F12G12_15	10.9	11.1	-0.2	-0.5	100.0%	-4.6
12129	AT4G16210.1   enoyl-CoA hydratase/isomerase family protein, similar to 3-hydroxybutyryl-CoA dehydratase (Crotonase) from Clostridium acetobutylicum (SP:P52046), FadB1x (enoyl-CoA hydratase) from Pseudomonas putida (GI:13310130); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr4:9176688-9178036 REVERSE   Aliases: DL4145C, FCAALL.314	6.7	6.3	0.4	0.5	100.0%	-4.7
12130	AT1G56345.1   pseudouridine synthase family protein, low similarity to SP:P23851 Ribosomal large subunit pseudouridine synthase C (EC 4.2.1.70) (Pseudouridylate synthase) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF00849: RNA pseudouridylate synthase	3.8	3.7	0.1	0.5	100.0%	-5.0
12131	AT5G62600.1   transportin-SR-related, contains weak similarity to transportin-SR (GI:5052414) (Homo sapiens)   chr5:25140537-25149893 REVERSE   Aliases: K19B1.1, K19B1_1	5.7	5.9	-0.2	-0.5	100.0%	-4.8
12132	AT2G33570.1   expressed protein   chr2:14224299-14226324 FORWARD   Aliases: F4P9.34, F4P9_34	6.3	6.6	-0.3	-0.5	100.0%	-4.4
12133	AT1G35350.1   similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03250.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03240.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g14040.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At4g25350.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g26730.1); similar to putative xenotropic and polytropic murine retrovirus receptor [Oryza sativa (japonica cultivar-group)] (GB:BAD46522.1); contains InterPro domain SPX, N-terminal (InterPro:IPR004331); contains InterPro domain EXS, C-terminal (InterPro:IPR004342)   chr1:12981229-12984561 REVERSE   Aliases: T9I1.12, T9I1_12	3.6	3.9	-0.3	-0.5	100.0%	-4.2
12134	AT1G18050.1   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein, weak similarity to spliceosome-associated-protein 114 (Echinococcus multilocularis) GI:11602721; contains Pfam profile PF01805: Surp module   chr1:6209764-6211581 REVERSE   Aliases: T10F20.6	2.1	2.1	0.0	0.5	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12135	AT1G05120.1   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to SP:P79051 DNA repair protein rhp16 (RAD16 homolog) {Schizosaccharomyces pombe}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:1471623-1476066 REVERSE   Aliases: T7A14.1	3.6	3.7	-0.1	-0.5	100.0%	-5.0
12136	AT3G13890.1   Symbol: MYB26   myb family transcription factor (MYB26), similar to myb-related transcription factor Gl:1167486 from (Lycopersicon esculentum); contains myb DNA binding domain: PF0049	2.2	2.2	-0.1	-0.5	100.0%	-5.5
12137	AT3G60580.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:22404914-22406019 FORWARD   Aliases: T8B10.240	2.7	2.8	-0.1	-0.5	100.0%	-5.4
12138	AT2G20480.1   expressed protein   chr2:8837658-8838579 REVERSE   Aliases: T13C7.7, T13C7_7	3.3	3.4	-0.1	-0.5	100.0%	-5.2
12139	AT1G09790.1   phytochelatin synthetase-related, contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region   chr1:3168484-3170821 REVERSE   Aliases: F21M12.17, F21M12_17	3.8	3.6	0.2	0.5	100.0%	-4.8
12140	AT3G20320.2   mce-related family protein, contains Pfam PF02470: mce related protein   chr3:7087479-7089838 REVERSE   Aliases: MQC12.6	6.1	6.4	-0.2	-0.5	100.0%	-4.8
12141	AT3G01440.1   oxygen evolving enhancer 3 (PsbQ) family protein, photosystem II oxygen-evolving complex protein; contains Pfam profile PF05757: Oxygen evolving enhancer protein 3 (PsbQ)   chr3:168442-169625 FORWARD   Aliases: T13O15.8, T13O15_8	3.4	3.2	0.1	0.5	100.0%	-4.9
12142	AT2G29290.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12593575-12594804 FORWARD   Aliases: F16P2.33, F16P2_33	2.8	2.9	-0.1	-0.5	100.0%	-5.5
12143	AT1G25420.3   expressed protein, contains Pfam profile: PF03398 eukaryotic protein of unknown function, DUF292   chr1:8916086-8918175 FORWARD   Aliases: F2J7.16, F2J7_16	7.8	8.0	-0.2	-0.5	100.0%	-4.8
12144	AT3G53070.1   beta-galactosidase-related, contains weak similarity to beta-galactosidase (Fragaria x ananassa) gi:14970841:emb:CAC44501   chr3:19685511-19685920 FORWARD   Aliases: F8J2.240	2.6	2.5	0.1	0.5	100.0%	-5.4
12145	AT5G49470.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g06620.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g06630.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g67890.1); similar to putative MAP3K delta-1 protein kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_464691.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain PAS domain (InterPro:IPR000014); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)	3.5	3.7	-0.1	-0.5	100.0%	-4.8
12146	AT1G06210.2   VHS domain-containing protein / GAT domain-containing protein, weak similarity to SP:Q9UJY5 ADP-ribosylation factor binding protein GGA1 {Homo sapiens}; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain	5.5	5.7	-0.2	-0.5	100.0%	-4.8
12147	AT1G53230.1   Symbol: TCP3   TCP family transcription factor 3 (TCP3), identical to transcription factor 3 (TCP3) (Arabidopsis thaliana) (Gl:3243274); similar to flower development protein cycloidea (cyc3) Gl:6358611 from (Misopates orontium)   chr1:19853456-19855393 REVERSE   Aliases: F12M16.13, F12M16_13, TCP3	2.8	2.9	-0.1	-0.5	100.0%	-5.1
12148	AT2G01735.1   Symbol: RIE1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger) domain	6.3	6.1	0.2	0.5	100.0%	-4.6
12149	AT1G10710.1   expressed protein   chr1:3558424-3560408 FORWARD   Aliases: T16B5.15	2.6	2.7	-0.1	-0.5	100.0%	-5.3
12150	AT5G24460.1   expressed protein   chr5:8354702-8355877 FORWARD   Aliases: T31K7.4, T31K7_4	7.5	7.7	-0.2	-0.5	100.0%	-4.6
12151	AT3G51440.1   strictosidine synthase family protein, similar to hemomucin (Drosophila melanogaster)(Gl:1280434), strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088   chr3:19100060-19101618 FORWARD   Aliases: F26O13.80	5.6	5.4	0.2	0.5	100.0%	-4.6
12152	AT5G13990.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr5:4514570-4516894 REVERSE   Aliases: MAC12.17, MAC12_17	2.8	2.9	-0.1	-0.5	100.0%	-4.7
12153	AT4G31930.1   mitochondrial glycoprotein family protein / MAM33 family protein, similar to SUAPRGA1 (Emericella nidulans) Gl:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein   chr4:15449667-15450842 REVERSE   Aliases: F11C18.4	5.7	5.9	-0.2	-0.5	100.0%	-4.2
12154	AT1G17170.1   Symbol: ATGSTU24   glutathione S-transferase, putative, One of three repeated putative glutathione transferases. 72% identical to glutathione transferase (Arabidopsis thaliana) (gi:4006934)   chr1:5869839-5870833 FORWARD   Aliases: F20D23.13, F20D23_13	4.8	5.0	-0.2	-0.5	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12155	AT2G24640.1   ubiquitin carboxyl-terminal hydrolase family protein / zinc finger (MYND type) family protein, similar to ubiquitin-specific protease 15 (UBP15) (Arabidopsis thaliana) GI:11993475; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF01753: MYND finger	3.2	3.3	-0.1	-0.5	100.0%	-5.1
12156	AT4G22060.1   F-box family protein, contains F-box domain Pfam:PF00646	3.3	3.4	-0.1	-0.5	100.0%	-5.1
12157	AT2G05270.1   expressed protein   chr2:1920699-1921113 REVERSE   Aliases: F5G3.17, F5G3_17	2.8	3.0	-0.1	-0.5	100.0%	-5.4
12158	AT1G19700.1   homeobox-leucine zipper family protein, similar to BEL1-like homeodomain 1 (GI:13877517) (Arabidopsis thaliana); similar to homeodomain protein GI:7239157 from (Malus domestica); contains weak hit to Pfam profile PF00046: Homeobox domain   chr1:6809735-6811845 REVERSE   Aliases: F14P1.20, F14P1_20	3.7	3.6	0.1	0.5	100.0%	-5.1
12159	AT1G80140.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase GI:7381227 from (Lycopersicon esculentum); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:30151503-30153072 FORWARD   Aliases: F18B13.22, F18B13_22	3.1	3.1	0.1	0.5	100.0%	-5.2
12160	AT4G13480.1   myb family transcription factor (MYB79), contains PFASM profile: myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB79) mRNA, partial cds GI:3941511   chr4:7836671-7837680 FORWARD   Aliases: T6G15.30, T6G15_30	8.0	7.8	0.2	0.5	100.0%	-4.2
12161	AT3G63360.1   Encodes a defensin-like (DEFL) family protein.   chr3:23412232-23412566 REVERSE   Aliases: MAA21.5	3.0	2.8	0.1	0.5	100.0%	-5.2
12162	AT2G06510.2   replication protein, putative, similar to replication protein A 70kDa (Oryza sativa (japonica cultivar-group)) GI:13536993; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain   chr2:2585054-2588287 FORWARD   Aliases: T12H3.6, T12H3_6	4.7	4.9	-0.1	-0.5	100.0%	-5.0
12163	AT4G11260.1   Symbol: SGT1B   phosphatase-related, low similarity to protein phosphatase T (Saccharomyces cerevisiae) GI:897806; contains Pfam profiles PF00515: TPR Domain, PF05002: SGS domain, PF04969: CS domain   chr4:6851273-6853848 REVERSE   Aliases: ATSGT1B, EDM1, ENHANCED DOWNY MILDEW 1, ENHANCER OF TIR1 1 AUXIN RESISTANCE, ETA3, F8L21.50, F8L21_50, RPR1, SGT1A	5.5	5.1	0.4	0.5	100.0%	-4.6
12164	AT3G25750.1   F-box family protein, contains F-box domain Pfam:PF00646	2.3	2.4	-0.1	-0.5	100.0%	-5.8
12165	AT2G22590.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	3.7	3.9	-0.2	-0.5	100.0%	-4.6
12166	AT3G24150.1   expressed protein   chr3:8724168-8725919 REVERSE   Aliases: MUJ8.5	4.4	4.5	-0.1	-0.5	100.0%	-5.0
12167	AT1G51890.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19278471-19282197 REVERSE   Aliases: T14L22.10, T14L22_10	2.6	2.9	-0.2	-0.5	100.0%	-4.4
12168	AT4G21440.1   myb family transcription factor (MYB102), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr4:11418257-11419771 REVERSE   Aliases: F18E5.60	2.6	2.7	-0.1	-0.5	100.0%	-5.3
12169	AT1G42710.1   hypothetical protein   chr1:16080032-16081007 REVERSE   Aliases: F8D11.16	2.9	2.9	0.1	0.5	100.0%	-5.5
12170	AT1G76780.1   expressed protein, ; expression supported by MPSS   chr1:28821535-28827150 FORWARD   Aliases: F28O16.15, F28O16_15	3.5	3.6	-0.1	-0.5	100.0%	-5.2
12171	AT1G06340.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr1:1933296-1934013 REVERSE   Aliases: T2D23.4, T2D23_4	2.8	2.7	0.1	0.5	100.0%	-5.4
12172	AT1G74920.1   Symbol: ALDH10A8   betaine-aldehyde dehydrogenase, putative, identical to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) (Arabidopsis thaliana) SWISS-PROT:Q9S795; strong similarity to betaine aldehyde dehydrogenase (Amaranthus hypochondriacus) GI:2388710   chr1:28142686-28146405 REVERSE   Aliases: F25A4.11, F25A4_11	11.0	10.8	0.2	0.5	100.0%	-4.8
12173	AT1G36095.1   expressed protein, contains Pfam domain, PF04937: Protein of unknown function (DUF 659)   chr1:13492582-13493937 REVERSE   Aliases: F5J5.11, F5J5_11	3.0	3.0	-0.1	-0.5	100.0%	-5.7
12174	AT1G10410.1   expressed protein, similar to ESTs gb:N96021 and gb:N96863   chr1:3416686-3419640 REVERSE   Aliases: F14N23.31, F14N23_31	7.4	7.5	-0.2	-0.5	100.0%	-5.0
12175	AT1G07390.1   similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:At1g74170.1); similar to HcrVf3 protein [Malus floribunda] (GB:CAC40827.1); contains InterPro domain Leucine-rich repeat, cysteine-containing type (InterPro:IPR003885); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr1:2269891-2274813 FORWARD   Aliases: F22G5.26, F22G5_26	3.3	3.4	-0.1	-0.5	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12176	AT1G07520.1   scarecrow transcription factor family protein, similar to GB:AAD24412 from ( <i>Arabidopsis thaliana</i> ) (Plant J. 18 (1), 111-119 (1999)); contains Pfam profile: PF03514 GRAS family transcription factor   chr1:2309561-2311802 REVERSE   Aliases: F22G5.41, F22G5_41	3.6	3.5	0.1	0.5	100.0%	-5.3
12177	AT5G45980.1   Symbol: WOX8   expressed protein, similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g33880.1); similar to hypothetical protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:AAT77402.1); contains InterPro domain Homeobox (InterPro:IPR001356)   chr5:18666136-18668063 FORWARD   Aliases: MCL19.2, MCL19_2	2.4	2.5	-0.1	-0.5	100.0%	-5.5
12178	AT1G13690.1   Symbol: ATE1   RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif   chr1:4693286-4694404 FORWARD   Aliases: F21F23.13, F21F23_13, GRPE HOMOLOG	10.7	10.6	0.2	0.5	100.0%	-4.4
12179	NA	12.5	12.4	0.1	0.5	100.0%	-5.6
12180	AT1G68185.1   ubiquitin-related, similar to ubiquitin-like protein smt3/pmt3 SP:O13351 from ( <i>Fission yeast</i> )   chr1:25560121-25562179 FORWARD   Aliases: None	4.7	4.5	0.2	0.5	100.0%	-4.6
12181	AT4G12920.1   aspartyl protease family protein, low similarity to CND41, chloroplast nucleoid DNA binding protein ( <i>Nicotiana tabacum</i> ) GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease   chr4:7568283-7569452 FORWARD   Aliases: F25G13.10, F25G13_10	2.7	2.8	-0.1	-0.5	100.0%	-5.2
12182	AT4G30350.1   heat shock protein-related, contains similarity to heat shock protein 101 ( <i>Triticum aestivum</i> ) gi:6013196:gb:AAF01280   chr4:14847746-14851149 FORWARD   Aliases: F17I23.310, F17I23_310	5.0	5.3	-0.3	-0.5	100.0%	-4.3
12183	AT1G73060.1   expressed protein   chr1:27482661-27487376 FORWARD   Aliases: F3N23.26, F3N23_26	3.8	3.7	0.1	0.5	100.0%	-5.2
12184	AT3G01310.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g15070.1); similar to mKIAA0433 protein [ <i>Mus musculus</i> ] (GB:BAC97950.1); similar to hypothetical protein LOC227399 [ <i>Mus musculus</i> ] (GB:NP_776121.2); similar to hypothetical protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:BAD53244.1); similar to P0413G02.23 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:NP_916369.1); similar to PREDICTED: similar to KIAA0433 [ <i>Canis familiaris</i> ] (GB:XP_546000.1); contains InterPro domain Histidine acid phosphatase (InterPro:IPR000560)   chr3:94350-101999 REVERSE   Aliases: T22N4.6, T22N4_6, T4P13.1, T4P13_1	5.3	5.5	-0.2	-0.5	100.0%	-4.8
12185	AT3G16500.1   Symbol: PAP1   auxin-responsive AUX/IAA family protein, similar to SP:O24408:AXII_ARATH Auxin-responsive protein IAA18 ( <i>Indoleacetic acid</i> -induced protein 18) [ <i>Arabidopsis thaliana</i> ]; contains Pfam profile: PF02309: AUX/IAA family   chr3:5612506-5614416 REVERSE   Aliases: IAA26, MDC8.13, PAP1, PHYTOCHROME ASSOCIATED PROTEIN 1	6.9	7.1	-0.2	-0.5	100.0%	-4.5
12186	AT5G05930.2   guanylyl cyclase-related (GC1), similar to guanylyl cyclase (GC1) GI:21436486 from ( <i>Arabidopsis thaliana</i> ); identical to cDNA putative guanylate cyclase GI:21436486   chr5:1780013-1783379 REVERSE   Aliases: K18J17.8, K18J17_8	5.1	5.2	-0.1	-0.5	100.0%	-4.8
12187	AT1G79730.1   Symbol: ELF7   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:30005479-30008898 REVERSE   Aliases: EARLY FLOWERING 7, F19K16.29, F19K16_29	5.9	5.7	0.2	0.5	100.0%	-4.7
12188	AT5G48570.1   peptidyl-prolyl cis-trans isomerase, putative / FK506-binding protein, putative, similar to rof1 ( <i>Arabidopsis thaliana</i> ) GI:1373396   chr5:19707768-19711071 REVERSE   Aliases: K15N18.12, K15N18_12	10.1	10.3	-0.2	-0.5	100.0%	-4.7
12189	AT1G30020.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:10515858-10516331 REVERSE   Aliases: T1P2.11, T1P2_11	2.7	2.6	0.1	0.5	100.0%	-5.5
12190	AT5G25460.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr5:8863393-8865680 FORWARD   Aliases: F18G18.200, F18G18_200	2.3	2.4	-0.1	-0.5	100.0%	-5.2
12191	AT5G48370.1   thioesterase family protein, similar to SP:Q9R0X4 48 kDa acyl-CoA thioester hydrolase, mitochondrial precursor (EC 3.1.2.-) [ <i>Mus musculus</i> ]; contains Pfam profile PF03061: thioesterase family protein   chr5:19615754-19617810 REVERSE   Aliases: K23F3.9, K23F3_9	6.4	6.8	-0.4	-0.5	100.0%	-4.6
12192	AT5G52780.1   expressed protein, similar to unknown protein (pir::T04431)   chr5:21408099-21408700 REVERSE   Aliases: F6N7.27, F6N7_27	2.3	2.3	0.1	0.5	100.0%	-5.7
12193	AT5G50920.1   Symbol: CLPC   Similar to ATP-dependent Clp protease ATP-binding subunit / ClpC, almost identical to ClpC GI:2921158 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF02861: Clp amino terminal domain; contains Pfam profile PF00004: ATPase, AAA family; contains Pfam profile PF02151: UvrB/uvrC motif. Involved in protein import into the chloroplast. May provide ATP source that drives the TIC translocation machinery,   chr5:20732698-20737597 REVERSE   Aliases: ATHSP93 V, CLPC, HSP93 V, K3K7.7, K3K7_7	9.2	9.4	-0.1	-0.5	100.0%	-4.7
12194	AT3G44700.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function; expression supported by MPSS   chr3:16247330-16248723 REVERSE   Aliases: T18B22.100	2.1	2.2	-0.1	-0.5	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12195	AT5G28270.1   hypothetical protein, similar to At2g12100, At2g05450, At1g45090, At2g16180, At2g06750   chr5:10258094-10260475 REVERSE   Aliases: T8M17.40, T8M17_40	2.5	2.4	0.0	0.5	100.0%	-5.7
12196	AT4G17180.1   glycosyl hydrolase family 17 protein, similar to 3-glucanase Gl:18483232 from (Sorghum bicolor)   chr4:9646518-9648306 FORWARD   Aliases: DL4625W, FCAALL.368	4.6	4.5	0.1	0.5	100.0%	-4.7
12197	AT5G24390.1   RabGAP/TBC domain-containing protein, similar to GTPase activating protein (Yarrowia lipolytica) Gl:2370595; contains Pfam profile PF00566: TBC domain   chr5:8326003-8329466 REVERSE   Aliases: K16H17.10, K16H17_10	4.7	4.6	0.1	0.5	100.0%	-4.9
12198	AT4G14455.1   Bet1-like SNARE 1-2 / Bet1 / Sft1-like SNARE 14b / BS14b (BET12), identical to Bet1/Sft1-like SNARE BS14b (GP:14029182) {Arabidopsis thaliana}   chr4:8310336-8312243 FORWARD   Aliases: None	3.9	3.7	0.3	0.5	100.0%	-4.3
12199	AT2G29140.1   pumilio/Puf RNA-binding domain-containing protein   chr2:12538469-12542334 FORWARD   Aliases: F16P2.48, F16P2_48	3.8	4.1	-0.3	-0.5	100.0%	-4.3
12200	AT2G29200.1   pumilio/Puf RNA-binding domain-containing protein, similar to BPM (Hordeum vulgare) Gl:20513851   chr2:12556361-12560262 REVERSE   Aliases: F16P2.42, F16P2_42	3.8	4.1	-0.3	-0.5	100.0%	-4.3
12201	AT1G78530.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:29544167-29545574 REVERSE   Aliases: T30F21.14, T30F21_14	2.8	2.9	-0.2	-0.5	100.0%	-4.8
12202	AT2G26320.1   MADS-box protein (AGL33), contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr2:11212467-11213365 REVERSE   Aliases: T1D16.4, T1D16_4	3.0	3.1	-0.1	-0.5	100.0%	-5.5
12203	AT1G20260.2   vacuolar ATP synthase subunit B, putative / V-ATPase B subunit, putative / vacuolar proton pump B subunit, putative / V-ATPase 57 kDa subunit, putative, strong similarity to SP:P11574 Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar proton pump B subunit) (V-ATPase 57 kDa subunit) {Arabidopsis thaliana}; contains Pfam profiles PF00006: ATP synthase alpha/beta family nucleotide-binding domain, PF02874: ATP synthase alpha/beta family beta-barrel domain   chr1:7016701-7020611 FORWARD   Aliases: F14O10.13, F14O10_13	6.7	7.4	-0.8	-0.5	100.0%	-4.6
12204	AT1G76030.1   vacuolar ATP synthase subunit B / V-ATPase B subunit / vacuolar proton pump B subunit / V-ATPase 57 kDa subunit, identical to SP:P11574 Vacuolar ATP synthase subunit B (EC 3.6.3.14) (V-ATPase B subunit) (Vacuolar proton pump B subunit) (V-ATPase 57 kDa subunit) {Arabidopsis thaliana}   chr1:28537514-28540850 FORWARD   Aliases: T4O12.24, T4O12_24	6.7	7.4	-0.8	-0.5	100.0%	-4.6
12205	AT1G07750.1   cupin family protein, similar to legumin (11S-globulin) from Ginkgo biloba (Gl:949869), 11S globulin from Avena sativa (Gl:472867)   chr1:2404034-2405939 REVERSE   Aliases: F24B9.13, F24B9_13	8.9	9.1	-0.2	-0.5	100.0%	-4.8
12206	AT2G27450.2   Symbol: NLP1   carbon-nitrogen hydrolase family protein, low similarity to beta-alanine synthase (Drosophila melanogaster) Gl:14334063; contains Pfam profile PF00795: hydrolase, carbon-nitrogen family   chr2:11744510-11746676 REVERSE   Aliases: ATNLP1, CPA, F10A12.13, F10A12_13, N CARBAMOYLPUTRESCINE AMIDOHYDROLASE, NITRILASE LIKE PROTEIN 1	10.5	10.8	-0.3	-0.5	100.0%	-5.0
12207	AT4G01010.1   Symbol: ATCNGC13   cyclic nucleotide-regulated ion channel, putative (CNGC13), similar to CaM-regulated potassium ion channel (ACBK1) Gl:8515883 from (Arabidopsis thaliana)   chr4:434569-437242 REVERSE   Aliases: CNGC13, F3I3.1, F3I3_1	3.6	3.8	-0.2	-0.5	100.0%	-4.7
12208	AT3G44550.1   acyl CoA reductase, putative, similar to acyl CoA reductase (Simmondsia chinensis) Gl:5020215; contains Pfam profile PF03015: Male sterility protein   chr3:16149004-16151325 FORWARD   Aliases: F14L2.100	2.9	3.1	-0.2	-0.5	100.0%	-4.6
12209	AT1G33240.1   Symbol: AT GTL1   trihelix DNA-binding protein, putative, similar to GTL1 (Arabidopsis thaliana) Gl:2664198   chr1:12051451-12054526 REVERSE   Aliases: T9L6.10, T9L6_10	6.2	6.6	-0.3	-0.5	100.0%	-4.5
12210	AT3G15890.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:5374254-5376281 FORWARD   Aliases: MVC8.1	4.7	4.6	0.2	0.5	100.0%	-4.9
12211	AT4G10240.1   zinc finger (B-box type) family protein, zinc-finger protein R2931, Oryza sativa, PIR3:JE0116   chr4:6368932-6369522 REVERSE   Aliases: T9A4.2	2.4	2.5	-0.1	-0.5	100.0%	-5.5
12212	AT3G24450.1   copper-binding family protein, similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain   chr3:8880075-8881729 REVERSE   Aliases: MXP5.2	3.1	3.4	-0.3	-0.5	100.0%	-4.5
12213	AT1G06620.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (Gl:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967); contains Pfam profile: PF00671 Iron/Ascorbate oxidoreductase family   chr1:2025600-2027270 FORWARD   Aliases: F12K11.24, F12K11_24	2.6	2.5	0.1	0.5	100.0%	-4.7
12214	AT5G28190.1   hypothetical protein   chr5:10167854-10170700 REVERSE   Aliases: F26C17.6, F26C17_6	3.4	3.5	-0.1	-0.5	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12215	AT5G53340.2   similar to galactosyltransferase family protein [Arabidopsis thaliana] (TAIR:At2g25300.1); similar to putative Avr9 elicitor response protein [Oryza sativa (japonica cultivar-group)] (GB:XP_482156.1); contains InterPro domain Glycosyl transferase, family 31 (InterPro:IPR002659)   chr5:21658039-21660711 REVERSE   Aliases: K19E1.14, K19E1_14	7.2	7.3	-0.2	-0.5	100.0%	-4.9
12216	AT5G14420.4   copine-related, low similarity to SP:Q99829 Copine I {Homo sapiens}   chr5:4648115-4650793 REVERSE   Aliases: F18O22.210, F18O22_210	4.9	4.7	0.2	0.5	100.0%	-5.0
12217	AT3G07200.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:2290773-2292498 FORWARD   Aliases: T1B9.13	7.2	6.9	0.2	0.5	100.0%	-4.4
12218	AT1G20100.1   expressed protein   chr1:6969098-6970947 REVERSE   Aliases: T20H2.11, T20H2_11	7.7	7.4	0.3	0.5	100.0%	-4.6
12219	AT4G21350.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582198; contains Pfam profile PF04564: U-box domain   chr4:11356154-11357278 REVERSE   Aliases: T6K22.80, T6K22_80	4.8	4.6	0.2	0.5	100.0%	-4.6
12220	AT5G39030.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:15637296-15639716 FORWARD   Aliases: MXF12.40, MXF12_40	2.7	2.6	0.1	0.5	100.0%	-5.7
12221	AT5G67000.1   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr5:26763903-26764385 REVERSE   Aliases: K8A10.7, K8A10_7	4.1	3.8	0.3	0.5	100.0%	-4.3
12222	AT3G05330.1   cyclin family, low similarity to microtubule-binding protein TANGLED1 (Zea mays) GI:11228986; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr3:1518950-1521465 REVERSE   Aliases: T12H1.30, T12H1_30	5.6	5.3	0.3	0.5	100.0%	-3.9
12223	AT1G49220.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	2.7	2.7	-0.1	-0.5	100.0%	-5.5
12224	AT5G52980.1   expressed protein   chr5:21499386-21500889 REVERSE   Aliases: MNB8.4, MNB8_4	5.6	5.7	-0.1	-0.5	100.0%	-5.0
12225	AT5G55740.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:22579167-22581659 REVERSE   Aliases: MDF20.18, MDF20_18	3.7	3.8	-0.2	-0.5	100.0%	-4.8
12226	AT2G10940.2   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to proline-rich cell wall protein (Medicago sativa) GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family   chr2:4317494-4319185 REVERSE   Aliases: F15K19.1, F15K19_1	3.0	3.1	-0.1	-0.5	100.0%	-5.1
12227	AT4G23320.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:12189192-12191636 REVERSE   Aliases: F16G20.20	2.9	2.8	0.1	0.5	100.0%	-5.4
12228	AT2G46660.1   Symbol: CYP78A6   cytochrome P450, putative, similar to cytochrome p450 (CYP78A9)(GI:17065344) {Arabidopsis thaliana}   chr2:19160398-19162487 REVERSE   Aliases: T3A4.4, T3A4_4	3.3	3.4	-0.1	-0.5	100.0%	-5.2
12229	AT1G72610.1   Symbol: GLP1   germin-like protein (GER1), identical to germin-like protein subfamily 3 member 1 SP:P94040; contains Pfam profile: PF01072 Germin family   chr1:27342776-27343706 REVERSE   Aliases: F28P22.20, F28P22_20, GERMIN LIKE PROTEIN 1	2.8	2.7	0.1	0.5	100.0%	-5.1
12230	AT5G16210.1   HEAT repeat-containing protein, contains Pfam profile PF02985: HEAT repeat   chr5:5290870-5297977 REVERSE   Aliases: T21H19.130, T21H19_130	5.4	5.5	-0.1	-0.5	100.0%	-4.8
12231	AT2G03530.1   Symbol: UPS2   F-box family protein-related, similar to A3 protein (Swiss-Prot:Q41706)(unknown function) (Vigna unguiculata); contains 9 transmembrane domains; supported by tandem duplication of F-box family protein (GI:3805763) (TIGR_Ath1:At2g07140) (Arabidopsis thaliana)   chr2:1071987-1073559 FORWARD   Aliases: T4M8.3, T4M8_3	4.3	4.1	0.2	0.5	100.0%	-4.6
12232	AT1G80090.1   CBS domain-containing protein, low similarity to SP:Q9MYP4 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) {Sus scrofa}; contains Pfam profile PF00571: CBS domain   chr1:30134997-30136833 FORWARD   Aliases: F18B13.17, F18B13_17	3.0	2.9	0.1	0.5	100.0%	-5.3
12233	AT4G25640.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr4:13076724-13079059 REVERSE   Aliases: L73G19.20, L73G19_20	3.7	4.2	-0.4	-0.5	100.0%	-4.6
12234	AT4G21860.1   methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein, low similarity to pilin-like transcription factor (Homo sapiens) GI:5059062, SP:P14930 Peptide methionine sulfoxide reductase msrA/msrB (EC 1.8.4.6) {Neisseria gonorrhoeae}; contains Pfam profile PF01641: SelR domain   chr4:11600085-11601572 REVERSE   Aliases: T8O5.70, T8O5_70	8.7	8.5	0.2	0.5	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12235	AT1G68300.1   universal stress protein (USP) family protein, similar to ER6 protein ( <i>Lycopersicon esculentum</i> ) GI:5669654; contains Pfam profile PF00582: universal stress protein family   chr1:25602007-25603007 REVERSE   Aliases: T22E19.7, T22E19_7	10.6	10.3	0.2	0.5	100.0%	-4.8
12236	AT4G00190.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:80433-82040 REVERSE   Aliases: F6N15.23, F6N15_23	2.6	2.7	-0.1	-0.5	100.0%	-5.4
12237	AT4G13600.1   glycosyl hydrolase family protein 17, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from ( <i>Nicotiana tabacum</i> )   chr4:7911175-7912774 REVERSE   Aliases: T6G15.150, T6G15_150	2.6	2.5	0.1	0.5	100.0%	-5.2
12238	AT3G54240.1   hydrolase, alpha/beta fold family protein, low similarity to SP:P22862:ESTE_PSEFL Arylesterase (EC 3.1.1.2) (Aryl-ester hydrolase) { <i>Pseudomonas fluorescens</i> }; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr3:20091904-20093123 FORWARD   Aliases: F24B22.200	2.9	2.8	0.1	0.5	100.0%	-5.2
12239	AT1G03330.1   small nuclear ribonucleoprotein D, putative / snRNP core SM-like protein, putative / U6 snRNA-associated Sm-like protein, putative, similar to SWISS-PROT:Q9Y333 U6 snRNA-associated Sm-like protein LSm2 (Small nuclear ribonuclear protein D homolog, G7b, SnRNP core SM-like protein SM-x5) ( <i>Homo sapiens</i> )   chr1:817983-819563 REVERSE   Aliases: F15K9.7, F15K9_7	10.6	10.8	-0.2	-0.5	100.0%	-4.7
12240	AT4G23780.1   expressed protein   chr4:12386363-12386809 REVERSE   Aliases: F9D16.250, F9D16_250	2.7	2.8	-0.1	-0.5	100.0%	-5.6
12241	AT4G23820.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to polygalacturonase PG1 ( <i>Glycine max</i> ) GI:5669846; contains PF00295: Glycosyl hydrolases family 28	5.5	5.7	-0.2	-0.5	100.0%	-4.4
12242	AT1G06200.1   expressed protein   chr1:1894336-1896934 REVERSE   Aliases: F9P14.6, F9P14_6	8.3	8.0	0.3	0.5	100.0%	-4.5
12243	AT5G38895.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:15588744-15591043 FORWARD   Aliases: None	4.9	4.8	0.2	0.5	100.0%	-4.5
12244	AT5G18810.1   Symbol: SCL28   SC35-like splicing factor, 28 kD (SCL28), nearly identical to SC35-like splicing factor SCL28, 28 kD ( <i>Arabidopsis thaliana</i> ) GI:9843655; contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr5:6268720-6271327 REVERSE   Aliases: F17K4.60, F17K4_60	3.1	3.0	0.1	0.5	100.0%	-5.0
12245	AT5G19340.1   expressed protein   chr5:6515094-6516207 REVERSE   Aliases: F7K24.90, F7K24_90	3.0	2.9	0.1	0.5	100.0%	-5.4
12246	AT5G40280.1   Symbol: ERA1   protein farnesyltransferase beta subunit (ERA1), identical to GI:8347240 (SWISS-PROT:Q38920); WIGGUM mutant   chr5:16118619-16122189 FORWARD   Aliases: ATFTB, ENHANCED RESPONSE TO ABA 1, FARNESYL TRANSFERASE BETA SUBUNIT, MSN9.180, MSN9_180, WIG, WIGGUM	4.5	4.7	-0.2	-0.5	100.0%	-4.7
12247	AT1G31300.2   expressed protein, similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g19645.2); similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g19645.1); similar to unknown protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_475690.1); contains InterPro domain TRAM, LAG1 and CLN8 homology (InterPro:IPR006634)   chr1:11193616-11196293 FORWARD   Aliases: T19E23.9, T19E23_9	5.8	5.6	0.2	0.5	100.0%	-4.9
12248	AT5G50190.1   expressed protein, similar to unknown protein (pir::T08985)   chr5:20450451-20452387 REVERSE   Aliases: K6A12.5, K6A12_5	2.8	2.9	-0.1	-0.5	100.0%	-5.3
12249	AT5G07290.1   RNA recognition motif (RRM)-containing protein, Mei2-like protein - <i>Arabidopsis thaliana</i> , EMBL:D86122   chr5:2293373-2298976 FORWARD   Aliases: T28J14.230, T28J14_230	3.6	3.4	0.2	0.5	100.0%	-4.8
12250	AT2G20830.2   expressed protein, weak similarity to formiminotransferase cyclodeaminase (GI:3980064) ( <i>Gallus gallus</i> )   chr2:8975451-8977687 REVERSE   Aliases: F5H14.20, F5H14_20	7.3	7.1	0.2	0.5	100.0%	-5.1
12251	AT1G32930.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr1:11931827-11934739 REVERSE   Aliases: F9L11.10, F9L11_10	4.3	4.4	-0.1	-0.5	100.0%	-5.2
12252	AT5G53510.1   Symbol: ATOPT9	2.9	2.8	0.1	0.5	100.0%	-5.0
12253	AT3G19170.1   Zinc metalloprotease pitrilysin subfamily A. Signal peptide degrading enzyme targeted to mitochondria and chloroplasts. Expressed only in siliques and flowers   chr3:6625427-6631946 REVERSE   Aliases: MVI11.6	8.8	9.1	-0.3	-0.5	100.0%	-4.7
12254	AT3G12580.1   Symbol: HSP70   heat shock protein 70, putative / HSP70, putative, strong similarity to heat shock protein GI:425194 ( <i>Spinacia oleracea</i> )   chr3:3991268-3993798 REVERSE   Aliases: HSP70, T2E22.11	10.1	10.3	-0.2	-0.5	100.0%	-4.9
12255	AT2G37680.1   Symbol: FHY1   phytochrome A specific signal transduction component (PAT3) / far-red elongated hypocotyl protein 1 (FHY1), identical to phytochrome A specific signal transduction component PAT3 ( <i>Arabidopsis thaliana</i> ) gi:19421998:gb:AAL87850; identical to far-red elongated hypocotyl protein 1 ( <i>Arabidopsis thaliana</i> ) gi:17148773:gb:AAL35819   chr2:15808899-15812593 REVERSE   Aliases: F13M22.18, F13M22_18, PAT3	6.4	6.2	0.2	0.5	100.0%	-4.2
12256	AT5G09970.1   Symbol: CYP78A7   cytochrome P450 family protein   chr5:3111946-3114240 FORWARD   Aliases: MYH9.18, MYH9_18	2.4	2.3	0.1	0.5	100.0%	-5.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12257	AT1G56510.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:21171274-21175925 FORWARD   Aliases: F13N6.5, F13N6_5	2.9	2.8	0.1	0.5	100.0%	-5.5
12258	AT4G25270.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:12937263-12938846 REVERSE   Aliases: F24A6.110, F24A6_110	3.7	3.5	0.2	0.5	100.0%	-4.9
12259	AT1G28320.1   protease-related, similar to Protease degS (Precursor) (SP:P44947) (Haemophilus influenzae); similar to DegP protease precursor (GI:2565436) (Arabidopsis thaliana)   chr1:9920494-9924475 REVERSE   Aliases: F3H9.3, F3H9_3	5.7	5.6	0.2	0.5	100.0%	-4.7
12260	AT3G24650.1   Symbol: ABI3   abscisic acid-insensitive protein 3 (ABI3), identical to abscisic acid-insensitive protein 3 GI:16146 SP:Q01593 from (Arabidopsis thaliana), (Plant Cell 4 (10), 1251-1261 (1992))   chr3:8997399-9001070 FORWARD   Aliases: ABA INSENSITIVE 3, ABSCISIC ACID INSENSITIVE PROTEIN 3, MSD24.3	2.5	2.4	0.1	0.5	100.0%	-5.5
12261	AT1G33890.1   avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}; contains Pfam profile PF04548: AIG1 family   chr1:12308264-12309666 REVERSE   Aliases: T3M13.9, T3M13_9	2.6	2.5	0.1	0.5	100.0%	-4.9
12262	AT1G66450.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.3	3.5	-0.2	-0.5	100.0%	-4.6
12263	AT3G15090.1   oxidoreductase, zinc-binding dehydrogenase family protein, low similarity to NOGO-interacting mitochondrial protein from Mus musculus (gi:14522884); contains Pfam profile: PF00107 zinc-binding dehydrogenases   chr3:5076756-5079123 FORWARD   Aliases: K15M2.24	7.0	6.7	0.3	0.5	100.0%	-4.7
12264	AT3G09080.1   transducin family protein / WD-40 repeat family protein, contains 8 WD-40 repeats; similar to JNK-binding protein JNKBP1 (GP:6069583) (Mus musculus)   chr3:2776264-2781790 REVERSE   Aliases: MZB10.11	3.1	3.3	-0.1	-0.5	100.0%	-5.1
12265	AT1G23520.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220; expression supported by MPSS   chr1:8343560-8344664 REVERSE   Aliases: F28C11.15	2.4	2.4	0.1	0.5	100.0%	-5.7
12266	AT5G09320.1   vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein, contains similarity to Rab5 GDP/GTP exchange factor, Rabex5 (Bos taurus) gi:2558516:emb:CAA04545; contains Pfam profile PF02204: Vacuolar sorting protein 9 (VPS9) domain	3.0	2.9	0.1	0.5	100.0%	-5.5
12267	AT2G23980.1   Symbol: ATCNGC6   cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC6), identical to cyclic nucleotide and calmodulin-regulated ion channel (cngc6) GI:4581207 from (Arabidopsis thaliana)	6.6	6.7	-0.2	-0.5	100.0%	-4.7
12268	AT4G24790.1   expressed protein, ; expression supported by MPSS   chr4:12778232-12781041 FORWARD   Aliases: F6I7.13	3.1	3.1	-0.1	-0.5	100.0%	-5.2
12269	AT3G60600.3   Symbol: VAP27 1   similar to vesicle-associated membrane protein, putative / VAMP, putative [Arabidopsis thaliana] (TAIR:At2g45140.1); similar to putative vesicle-associated membrane protein-associated protein [Oryza sativa (japonica cultivar-group)] (GB:XP_480176.1); contains InterPro domain Major sperm protein (MSP) domain (InterPro:IPR000535)   chr3:22411370-22413678 FORWARD   Aliases: T4C21.10, VAMP/SYNAPTOBREVIN ASSOCIATED PROTEIN 27 1	9.4	9.2	0.2	0.5	100.0%	-4.9
12270	AT5G65240.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:26092206-26094876 REVERSE   Aliases: MQN23.19, MQN23_19	4.5	4.8	-0.4	-0.5	100.0%	-4.9
12271	AT4G23200.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:12145391-12147945 REVERSE   Aliases: F21P8.90, F21P8_90	2.4	2.5	-0.1	-0.5	100.0%	-5.5
12272	AT1G48230.1   phosphate translocator-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}   chr1:17809932-17812553 FORWARD   Aliases: F21D18.5	6.0	6.1	-0.2	-0.5	100.0%	-4.9
12273	AT2G27720.1   60S acidic ribosomal protein P2 (RPP2A)   chr2:11825568-11826655 FORWARD   Aliases: F15K20.18, F15K20_18	11.6	11.8	-0.1	-0.5	100.0%	-5.2
12274	AT2G21385.1   expressed protein   chr2:9156723-9158934 FORWARD   Aliases: None	8.1	7.9	0.2	0.5	100.0%	-4.5
12275	AT4G30030.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr4:14682216-14683490 REVERSE   Aliases: F6G3.60, F6G3_60	2.6	2.5	0.1	0.5	100.0%	-5.4
12276	AT3G01240.1   expressed protein   chr3:78383-79044 REVERSE   Aliases: T4P13.7, T4P13_7	2.2	2.3	-0.1	-0.5	100.0%	-5.6
12277	AT5G13000.1   Symbol: ATGSL12   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr5:4110298-4121430 REVERSE   Aliases: GLUCAN SYNTHASE LIKE 12, GSL12, T24H18.170, T24H18_170	9.3	9.4	-0.1	-0.5	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12278	AT1G12610.1   Symbol: DDF1   encodes a member of the DREB subfamily A-1 of ERF/AP2 transcription factor family (DDF1). The protein contains one AP2 domain. There are six members in this subfamily, including CBF1, CBF2, and CBF3. Overexpression of this gene results in delayed flowering and dwarfism, reduction of gibberellic acid biosynthesis, and increased tolerance to high levels of salt. This gene is expressed in all tissues examined, but most abundantly expressed in upper stems. Overexpression of this gene is also correlated with increased expression of GA biosynthetic genes and RD29A (a cold and drought responsive gene).   chr1:4289954-4290994 REVERSE   Aliases: DDF1, DWARF AND DELAYED FLOWERING 1, T12C24.14, T12C24_14	2.6	2.5	0.1	0.5	100.0%	-5.5
12279	AT2G10070.2   expressed protein, very low similarity to AHM1 (Triticum aestivum) GI:6691467   chr2:3824863-3826784 REVERSE   Aliases: F7B19.21, F7B19_21	2.6	2.7	-0.1	-0.5	100.0%	-5.2
12280	AT1G16080.1   expressed protein   chr1:5514311-5516012 FORWARD   Aliases: T24D18.18, T24D18_18	5.9	6.1	-0.2	-0.5	100.0%	-4.6
12281	AT3G51710.1   curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein, contains Pfam profiles: PF01453 lectin (probable mannose binding), PF00024 PAN domain   chr3:19193463-19194975 FORWARD   Aliases: T18N14.90	3.8	3.7	0.1	0.5	100.0%	-5.0
12282	AT2G12400.1   expressed protein   chr2:5012025-5015304 REVERSE   Aliases: F24C20.8, F24C20_8	6.5	6.4	0.1	0.5	100.0%	-4.9
12283	AT1G22090.1   Symbol: EMB2204   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr1:7795697-7797414 FORWARD   Aliases: EMB2204, EMBRYO DEFECTIVE 2204, F2E2.16, F2E2_16	2.8	2.7	0.1	0.5	100.0%	-5.2
12284	AT3G50420.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:18721852-18724630 REVERSE   Aliases: T20E23.20	2.7	2.8	-0.1	-0.5	100.0%	-5.2
12285	AT5G46940.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:19075395-19076041 REVERSE   Aliases: MQD22.8, MQD22_8	2.7	2.6	0.1	0.5	100.0%	-5.3
12286	AT4G23970.1   expressed protein   chr4:12445388-12445690 REVERSE   Aliases: T32A16.140, T32A16_140	2.6	2.7	-0.1	-0.5	100.0%	-5.2
12287	AT1G02390.1   Symbol: ATGPAT2/GPAT2   Encodes a member of a family of proteins with glycerol-3-phosphate acyltransferase activity.   chr1:480852-483292 FORWARD   Aliases: ATGPAT2, GPAT2, T6A9.8, T6A9_8	2.5	2.4	0.1	0.5	100.0%	-5.6
12288	AT5G49330.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA binding domain; identical to cDNA putative transcription factor (At5g49330) GI:15420625   chr5:20016178-20018604 REVERSE   Aliases: K21P3.23, K21P3_23	4.6	4.7	-0.2	-0.5	100.0%	-5.0
12289	AT4G26050.1   leucine-rich repeat family protein, contains Pfam PF00560: Leucine Rich Repeat domains;   chr4:13210468-13213443 FORWARD   Aliases: F20B18.160, F20B18_160	2.9	2.7	0.2	0.5	100.0%	-4.5
12290	AT1G72570.1   ovule development protein, putative, similar to ovule development protein AINTEGUMENTA (GI:1209099) (Arabidopsis thaliana); contains Pfam profile: PF00847 AP2 domain (2 copies); contains non-consensus TA acceptor splice site at exon 4   chr1:27335043-27337360 FORWARD   Aliases: F28P22.24, F28P22_24	2.5	2.4	0.1	0.5	100.0%	-5.5
12291	AT3G56980.1   Symbol: ORG3   basic helix-loop-helix (bHLH) family protein   chr3:21097525-21098473 REVERSE   Aliases: T8M16.8	4.7	4.9	-0.2	-0.5	100.0%	-4.2
12292	AT5G10630.1   elongation factor 1-alpha, putative / EF-1-alpha, putative, contains similarity to SWISS-PROT:Q9YAV0 elongation factor 1-alpha (EF-1-alpha) (Aeropyrum pernix)   chr5:3360174-3364531 FORWARD   Aliases: F12B17.20, F12B17_20	6.6	6.8	-0.2	-0.5	100.0%	-4.6
12293	AT5G58170.1   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor	3.5	3.6	-0.1	-0.5	100.0%	-5.4
12294	AT3G02300.1   regulator of chromosome condensation (RCC1) family protein, weak similarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	6.2	6.3	-0.2	-0.5	100.0%	-4.8
12295	AT2G04440.1   NUDIX/mutT hydrolase family protein, similar to SP:P53370 Nucleoside diphosphate-linked moiety X motif 6 {Homo sapiens}; contains Pfam profile PF00293: NUDIX domain   chr2:1541508-1542726 FORWARD   Aliases: T103.15, T103_15	3.2	3.1	0.1	0.5	100.0%	-5.3
12296	AT1G50460.1   hexokinase, putative, similar to hexokinase 1 (Spinacia oleracea) Swiss-Prot:Q9SEK3   chr1:18697352-18701327 FORWARD   Aliases: F11F12.18, F11F12_18	5.3	5.4	-0.2	-0.5	100.0%	-5.1
12297	AT2G46000.1   expressed protein   chr2:18928030-18929240 REVERSE   Aliases: F4I18.48	3.4	3.5	-0.1	-0.5	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12298	AT4G12440.2   adenine phosphoribosyltransferase, putative, strong similarity to SP:P31166 Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}; contains Pfam profile PF00156: Phosphoribosyl transferase domain   chr4:7376265-7380148 FORWARD   Aliases: T1P17.30, T1P17_30	5.9	6.0	-0.2	-0.5	100.0%	-4.5
12299	AT4G09460.1   Symbol: ATMYB6	5.8	5.9	-0.2	-0.5	100.0%	-4.7
12300	AT1G77780.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor Gl:4097946 from (Oryza sativa)   chr1:29253194-29254422 REVERSE   Aliases: T32E8.11, T32E8_11	2.1	2.0	0.0	0.5	100.0%	-5.7
12301	AT5G52360.1   actin-depolymerizing factor, putative, strong similarity to pollen specific actin-depolymerizing factor 2 (Nicotiana tabacum) Gl:22857914; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein	3.2	3.1	0.1	0.5	100.0%	-5.6
12302	AT5G01650.1   macrophage migration inhibitory factor family protein / MIF family protein, contains pfam profile: PF001187 Macrophage migration inhibitory factor   chr5:242547-244096 REVERSE   Aliases: F7A7.170, F7A7_170	10.3	10.1	0.2	0.5	100.0%	-4.6
12303	AT1G36100.1   myosin heavy chain-related, similar to hypothetical protein Gl:4263830 from (Arabidopsis thaliana) (similar to MYOSIN HEAVY CHAIN (Encephalitozoon cuniculi) Gl:19074177) (similar to MYOSIN HEAVY CHAIN (Encephalitozoon cuniculi) Gl:19074177)	2.6	2.5	0.1	0.5	100.0%	-5.5
12304	AT2G26470.1   expressed protein, contains PF02586: Uncharacterized ACR, COG2135; weak similarity to NF-M protein (Gl:205688) (Rattus norvegicus)   chr2:11266231-11269563 REVERSE   Aliases: T9J22.14, T9J22_14	3.2	3.1	0.1	0.5	100.0%	-5.2
12305	AT2G28680.1   cupin family protein, similar to legumin (11S-globulin) from Ginkgo biloba (Gl:949869), 11S globulin from Avena sativa (Gl:472867); contains a 11-S plant seed storage protein signature (PS00305)   chr2:12310040-12311876 REVERSE   Aliases: T8O18.3, T8O18_3	3.7	3.6	0.2	0.5	100.0%	-4.7
12306	AT2G37290.1   RabGAP/TBC domain-containing protein, low similarity to Rab6 GTPase activating protein, GAPCenA (Homo sapiens) Gl:12188746; contains Pfam profile PF00566: TBC domain   chr2:15664014-15668414 REVERSE   Aliases: F3G5.8, F3G5_8	2.5	2.6	-0.1	-0.5	100.0%	-5.5
12307	AT4G13760.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to SP:P35339 Exopolygalacturonase precursor (EC 3.2.1.67) (Pectinase) (Galacturan 1,4-alpha-galacturonidase) {Zea mays}; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr4:7988141-7989644 FORWARD   Aliases: F18A5.150, F18A5_150	2.3	2.4	-0.1	-0.5	100.0%	-5.7
12308	AT3G16670.1   expressed protein   chr3:5681425-5682337 FORWARD   Aliases: MGL6.14	4.0	4.3	-0.2	-0.5	100.0%	-4.6
12309	AT2G16650.1   similar to MATE efflux family protein [Arabidopsis thaliana] (TAIR:At4g21900.1); similar to OJ1656_A11.5 [Oryza sativa (japonica cultivar-group)] (GB:NP_914311.1)   chr2:7222901-7225477 REVERSE   Aliases: T24I21.6, T24I21_6	8.5	8.1	0.4	0.5	100.0%	-4.8
12310	AT5G60430.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g16650.1); similar to OJ1656_A11.5 [Oryza sativa (japonica cultivar-group)] (GB:NP_914311.1)   chr5:24318838-24320294 FORWARD   Aliases: MUF9.6, MUF9_6	8.5	8.1	0.4	0.5	100.0%	-4.8
12311	AT5G04120.1   phosphoglycerate/bisphosphoglycerate mutase family protein, low similarity to SP:P36623 Phosphoglycerate mutase (EC 5.4.2.1) {Schizosaccharomyces pombe}; contains Pfam profile PF00300: phosphoglycerate mutase family   chr5:1120024-1121776 FORWARD   Aliases: F21E1.40, F21E1_40	2.8	2.7	0.2	0.5	100.0%	-4.8
12312	AT1G66780.1   MATE efflux family protein, contains TIGRfam profile: TIGR00797: MATE efflux family protein, Pfam profile PF01554: Uncharacterized membrane protein family   chr1:24912876-24915148 FORWARD   Aliases: F4N21.9, F4N21_9	2.4	2.5	-0.1	-0.5	100.0%	-5.4
12313	AT2G18510.1   Symbol: EMB2444   pre-mRNA splicing factor, putative, similar to SP:Q15427 Splicing factor 3B subunit 4 (Spliceosome associated protein 49) (SAP 49) (SF3b50) (Pre-mRNA splicing factor SF3b 49 kDa subunit) {Homo sapiens}; contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr2:8038264-8040700 REVERSE   Aliases: EMB2444, EMBRYO DEFECTIVE 2444, F24H14.14, F24H14_14	3.9	4.1	-0.2	-0.5	100.0%	-4.7
12314	AT1G18660.4   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr1:6421109-6425872 FORWARD   Aliases: F6A14.25, F6A14_25	6.5	6.6	-0.1	-0.5	100.0%	-5.0
12315	AT1G67865.1   expressed protein   chr1:25449952-25450400 REVERSE   Aliases: None	3.8	3.7	0.1	0.5	100.0%	-5.0
12316	AT4G10250.1   Symbol: ATHSP22.0   22.0 kDa ER small heat shock protein (HSP22.0-ER), identical to endomembrane-localized small heat shock protein Gl:511795 from (Arabidopsis thaliana)   chr4:6370339-6371286 FORWARD   Aliases: ATHSP22.0, T9A4.7	3.2	3.1	0.1	0.5	100.0%	-4.9
12317	AT1G01390.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:148120-149806 REVERSE   Aliases: F6F3.19, F6F3_19	3.2	3.2	-0.1	-0.5	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12318	AT1G64860.1   Symbol: SIGA   RNA polymerase sigma subunit SigA (sigA) / sigma factor 1 (SIG1), identical to sigma factor SigA (Arabidopsis thaliana) GI:5478439, sigma factor 1 (Arabidopsis thaliana) GI:2353171, plastid RNA polymerase sigma-subunit (Arabidopsis thaliana) GI:2398851; contains Pfam profiles PF04545: Sigma-70, region 4, PF04539: Sigma-70 region 3, PF04542: Sigma-70 region 2	5.1	5.3	-0.1	-0.5	100.0%	-4.8
12319	AT3G55930.1   RNA splicing factor-related, similar to U4/U6-associated RNA splicing factor (Homo sapiens) GI:2853287   chr3:20756361-20757943 REVERSE   Aliases: F27K19.110	4.2	4.1	0.1	0.5	100.0%	-5.2
12320	AT4G31990.3   Symbol: ASP5   similar to aspartate aminotransferase, cytoplasmic isozyme 1 / transaminase A (ASP2) [Arabidopsis thaliana] (TAIR:At5g19550.1); similar to Asp aminotransferase (GB:1908424A); similar to aspartate transaminase (EC 2.6.1.1) AAT5 precursor - soybean (GB:S33528); similar to aspartate aminotransferase [Lotus corniculatus] (GB:AAC12674.1); similar to aspartate aminotransferase [Phaseolus vulgaris] (GB:AAN76499.1); similar to aspartate aminotransferase isozyme 5 [Glycine max] (GB:AAB26677.2); contains InterPro domain Aminotransferase, class I and II (InterPro:IPR004839); contains InterPro domain Aminotransferases class-I pyridoxal-phosphate-binding site (InterPro:IPR004838); contains InterPro domain Aspartate/other aminotransferase (InterPro:IPR000796)   chr4:15470767-15473859 REVERSE   Aliases: AAT3, ASPARTATE AMINOTRANSFERASE, ASPARTATE AMINOTRANSFERASE 5, ASPARTATE AMINOTRANSFERASE DEFICIENT 3, F11C18.15	10.9	11.1	-0.2	-0.5	100.0%	-4.7
12321	AT4G32190.1   centromeric protein-related, low similarity to SP:Q02224 Centromeric protein E (CENP-E protein) {Homo sapiens}   chr4:15544884-15547861 FORWARD   Aliases: F10M6.170, F10M6_170	7.2	7.4	-0.3	-0.5	100.0%	-4.8
12322	AT2G41520.2   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profiles PF00226: DnaJ domain, PF00515: TPR Domain   chr2:17324563-17330093 FORWARD   Aliases: T32G6.4, T32G6_4	3.1	3.2	-0.1	-0.5	100.0%	-5.1
12323	AT4G24010.1   Symbol: ATCSLG1   cellulose synthase family protein, similar to Zea mays cellulose synthase-5 (gi:9622882), -4 (gi:9622880)   chr4:12466401-12469770 FORWARD   Aliases: CSLG1, CSLG2, T32A16.180, T32A16_180	3.3	3.2	0.1	0.5	100.0%	-5.2
12324	AT5G45170.1   CbbY protein-related, low similarity to SP:P40119 CbbY protein, chromosomal {Alcaligenes eutrophus}   chr5:18287571-18290396 REVERSE   Aliases: K18C1.5, K18C1_5	8.3	8.5	-0.1	-0.5	100.0%	-4.8
12325	AT2G32390.2   Symbol: ATGLR3.5   similar to glutamate receptor family protein (GLR3.6) [Arabidopsis thaliana] (TAIR:At3g51480.1); similar to glutamate receptor family protein (GLR3.3) [Arabidopsis thaliana] (TAIR:At1g42540.1); similar to glutamate receptor family protein (GLR3.2) (GLUR2) [Arabidopsis thaliana] (TAIR:At4g35290.2); similar to glutamate receptor family protein (GLR3.4) [Arabidopsis thaliana] (TAIR:At1g05200.1); similar to glutamate receptor family protein (GLR3.2) (GLUR2) [Arabidopsis thaliana] (TAIR:At4g35290.1); similar to ligand gated channel-like protein [Brassica napus] (GB:AAF21901.1); similar to glutamate receptor, ionotropic kainate 5 precursor-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_919189.1); similar to putative ionotropic glutamate receptor ortholog GLR6 [Oryza sativa (japonica cultivar-group)] (GB:BAD45881.1); similar to putative ionotropic glutamate receptor homolog GLR4 [Oryza sativa (japonica cultivar-group)] (GB:XP_478449.1); similar to OSJNBa0013K16.8 [Oryza sativa (japonica cultivar-group)] (GB:XP_473671.1); contains InterPro domain Extracellular ligand-binding receptor (InterPro:IPR001828); contains InterPro domain Ionotropic glutamate receptor (InterPro:IPR001320); contains InterPro domain G-protein coupled receptors family 3 (Metabotropic glutamate receptor-like) (InterPro:IPR000337)   chr2:13755545-13758834 REVERSE   Aliases: GLR3.5, GLR6, GLUTAMATE RECEPTOR 6, T32F6.9, T32F6_9	4.1	3.9	0.1	0.5	100.0%	-4.8
12326	AT5G09570.1   expressed protein, contains Pfam domain, PF04933: Protein of unknown function (DUF657)   chr5:2970670-2972182 FORWARD   Aliases: F17I14.240, F17I14_240	5.2	5.1	0.1	0.5	100.0%	-4.8
12327	AT1G59870.1   ABC transporter family protein, similar to PDR5-like ABC transporter GI:1514643 from (Spirodela polyrhiza)   chr1:22038171-22043703 FORWARD   Aliases: F23H11.19, F23H11_19	6.1	6.5	-0.3	-0.5	100.0%	-4.5
12328	AT3G49650.1   kinesin motor protein-related, several kinesin-like proteins   chr3:18416245-18420387 REVERSE   Aliases: T9C5.240	2.7	2.8	-0.1	-0.5	100.0%	-5.2
12329	AT1G54700.1   hypothetical protein   chr1:20419565-20419936 FORWARD   Aliases: T22H22.13, T22H22_13	2.8	2.9	-0.1	-0.5	100.0%	-5.6
12330	AT1G74500.1   bHLH family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain   chr1:28001837-28002482 REVERSE   Aliases: F1M20.18, F1M20_18	2.2	2.3	-0.1	-0.5	100.0%	-5.6
12331	AT1G31080.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr1:11091813-11092880 FORWARD   Aliases: F28K20.2, F28K20_2	2.8	2.7	0.1	0.5	100.0%	-5.4
12332	AT2G32050.1   cell cycle control protein-related, contains similarity to Swiss-Prot:Q9P7C5 cell cycle control protein cwf16 (Schizosaccharomyces pombe)   chr2:13644956-13645720 REVERSE   Aliases: F22D22.20, F22D22_20	2.7	2.6	0.1	0.5	100.0%	-5.7
12333	AT1G61810.2   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase (GI:3820531) (Pinus contorta); similar to beta-glucosidase GI:804655 from (Hordeum vulgare)   chr1:22833698-22834606 FORWARD   Aliases: T13M11.19, T13M11_19	3.6	3.7	-0.2	-0.5	100.0%	-4.8
12334	AT3G42780.1   hypothetical protein, hypothetical protein MZB10.16 - Arabidopsis thaliana, EMBL:AC009326   chr3:14882201-14882731 FORWARD   Aliases: T21C14.1	2.8	3.0	-0.1	-0.5	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12335	AT1G34630.1   expressed protein   chr1:12685178-12687710 FORWARD   Aliases: F12K21.3	5.7	5.5	0.3	0.5	100.0%	-4.6
12336	AT5G54440.1   expressed protein   chr5:22117162-22125059 FORWARD   Aliases: F24B18.6, F24B18_6	7.2	7.3	-0.1	-0.5	100.0%	-5.1
12337	AT2G28410.1   expressed protein   chr2:12163207-12164006 FORWARD   Aliases: T1B3.7, T1B3_7	3.3	3.4	-0.1	-0.5	100.0%	-4.9
12338	AT2G35550.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g14685.3); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g14685.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g14685.2); similar to GAGA-binding protein [Glycine max] (GB:AAM27201.1)   chr2:14936453-14937741 FORWARD   Aliases: T32F12.7, T32F12_7	4.3	4.1	0.2	0.5	100.0%	-4.4
12339	AT1G28510.1   expressed protein   chr1:10023875-10026281 FORWARD   Aliases: F3M18.5, F3M18_5	6.3	6.5	-0.2	-0.5	100.0%	-4.8
12340	AT4G22970.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g28550.1); similar to BIMB_EMENI CELL DIVISION-ASSOCIATED PROTEIN BIMB [Aspergillus nidulans FGSC A4] (GB:EAA60576.1); similar to probable spindle pole body component bimB - Emericella nidulans (GB:A42854); contains InterPro domain Peptidase family C50 (InterPro:IPR005314)   chr4:12033448-12043583 REVERSE   Aliases: F7H19.150, F7H19_150	3.3	3.4	-0.1	-0.5	100.0%	-5.2
12341	AT2G05320.1   beta-1,2-N-acetylglucosaminyltransferase II, identical to beta-1,2-N-acetylglucosaminyltransferase II GI:10183645 from (Arabidopsis thaliana)   chr2:1936013-1937461 FORWARD   Aliases: F5G3.22, F5G3_22	4.9	4.7	0.1	0.5	100.0%	-4.9
12342	AT1G18390.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:6327456-6329928 FORWARD   Aliases: F15H18.25, F15H18_25	4.3	4.1	0.1	0.5	100.0%	-4.8
12343	AT5G27840.2   Symbol: TOPP8   serine/threonine protein phosphatase PP1 isozyme 8 (TOPP8), identical to SP:O82734 Serine/threonine protein phosphatase PP1 isozyme 8 (EC 3.1.3.16) {Arabidopsis thaliana}   chr5:9862928-9865033 REVERSE   Aliases: T1G16.170, T1G16_170	5.6	5.4	0.2	0.5	100.0%	-4.6
12344	AT1G74490.1   protein kinase, putative, similar to protein kinase (Arabidopsis thaliana) gi:2852449:dbj:BAA24695; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr1:27998361-28000392 REVERSE   Aliases: F1M20.17, F1M20_17	3.6	3.7	-0.1	-0.5	100.0%	-4.9
12345	AT1G22430.2   similar to alcohol dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At4g22110.1); similar to alcohol dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At4g22110.2); similar to alcohol dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At1g22440.1); similar to alcohol dehydrogenase ADH [Lycopersicon esculentum] (GB:AAB33480.2); contains InterPro domain Zinc-containing alcohol dehydrogenase superfamily (InterPro:IPR002085); contains InterPro domain Zinc-containing alcohol dehydrogenase (InterPro:IPR002328); contains InterPro domain NAD-binding site (InterPro:IPR000205)   chr1:7919161-7921821 FORWARD   Aliases: F12K8.22, F12K8_22	3.3	3.4	-0.1	-0.5	100.0%	-5.2
12346	AT5G25950.1   expressed protein, various predicted proteins, Arabidopsis thaliana contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr5:9057932-9059806 REVERSE   Aliases: T1N24.4, T1N24_4	2.1	2.1	-0.0	-0.5	100.0%	-5.9
12347	AT3G07710.1   expressed protein   chr3:2464342-2464779 REVERSE   Aliases: MLP3.16	2.6	2.6	0.0	0.5	100.0%	-5.8
12348	AT3G29590.1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family   chr3:11401396-11402745 REVERSE   Aliases: MTO24.5	3.8	3.7	0.2	0.5	100.0%	-4.8
12349	AT1G18400.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.6	3.8	-0.2	-0.5	100.0%	-5.0
12350	AT2G31530.1   Symbol: EMB2289   secY family protein, low similarity to SP:P31159 Preprotein translocase secY subunit {Synechococcus sp}; contains Pfam profile PF00344: eubacterial secY protein   chr2:13434485-13437541 FORWARD   Aliases: EMB2289, EMBRYO DEFECTIVE 2289, T9H9.5, T9H9_5	5.6	5.7	-0.1	-0.5	100.0%	-4.7
12351	AT5G57790.2   expressed protein   chr5:23429319-23430850 REVERSE   Aliases: MTI20.2, MTI20_2	3.5	3.6	-0.2	-0.5	100.0%	-4.8
12352	AT1G61450.1   expressed protein, contains similarity to myosin II GI:1763303 from (Schizosaccharomyces pombe); expression supported by MPSS   chr1:22676987-22677500 FORWARD   Aliases: T1F9.6, T1F9_6	2.5	2.6	-0.1	-0.5	100.0%	-5.5
12353	AT5G45810.1   Symbol: CIPK19	4.2	4.4	-0.2	-0.5	100.0%	-4.5
12354	AT4G34140.1   D111/G-patch domain-containing protein, contains Pfam PF01585: G-patch domain   chr4:16350736-16354258 FORWARD   Aliases: F28A23.100, F28A23_100	3.6	3.4	0.2	0.5	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12355	AT1G55880.2   pyridoxal-5'-phosphate-dependent enzyme, beta family protein, similar to SP:P50867 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (Aspergillus nidulans) {Emericella nidulans}; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme   chr1:20902600-20904830 REVERSE   Aliases: F14J16.13, F14J16_13	5.4	5.5	-0.1	-0.5	100.0%	-4.8
12356	AT5G09500.1   40S ribosomal protein S15 (RPS15C), ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161   chr5:2953914-2954919 REVERSE   Aliases: T5E8.300, T5E8_300	5.2	5.1	0.1	0.5	100.0%	-5.2
12357	AT2G29090.1   Symbol: CYP707A2   cytochrome P450 family protein, similar to Cytochrome P450 88A3 (SP:O23051) (Arabidopsis thaliana); similar to taxane 13-alpha-hydroxylase (GI:17148242) (Taxus cuspidata).	2.8	2.9	-0.1	-0.5	100.0%	-5.5
12358	AT4G02650.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Chain A, Calm-N N-Terminal Domain Of Clathrin Assembly Lymphoid Myeloid Leukaemia Protein, Pi(4,5)p2 Complex (GP:13399999) {Homo sapiens}; supporting cDNA gi:26451912:dbj:AK118440.1:   chr4:1156453-1158653 FORWARD   Aliases: T10P11.8, T10P11_8	4.7	5.0	-0.3	-0.5	100.0%	-4.2
12359	AT1G29510.1   auxin-responsive protein, putative, similar to auxin-induced protein 6B (SP:P33083) (Glycine max)   chr1:10322560-10323175 FORWARD   Aliases: F15D2.9, F15D2_9	2.4	2.5	-0.1	-0.5	100.0%	-5.5
12360	AT5G51380.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to F-box protein FBL2 (GI:6063090) (Homo sapiens)   chr5:20893102-20895215 FORWARD   Aliases: MFG13.9, MFG13_9	5.6	5.8	-0.2	-0.5	100.0%	-4.4
12361	AT2G05180.1   Symbol: CYP705A6   cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798) {Glycine max}   chr2:1875387-1876791 FORWARD   Aliases: F5G3.8, F5G3_8	3.2	3.0	0.2	0.5	100.0%	-5.0
12362	AT1G74360.1   leucine-rich repeat transmembrane protein kinase, putative, similar to brassinosteroid insensitive 1 GB:AAC49810 (putative receptor protein kinase); contains Pfam profiles: PF00560 Leucine Rich Repeat (17 repeats), PF00069 Eukaryotic protein kinase domain   chr1:27957892-27962176 FORWARD   Aliases: F1M20.4, F1M20_4	3.4	3.6	-0.2	-0.5	100.0%	-4.4
12363	AT2G44150.1   SET domain-containing protein (ASHH3), low similarity to huntingtin interacting protein 1 (Homo sapiens) GI:12697196; contains Pfam profile PF00856: SET domain; identical to cDNA ASH1-like protein 3 (ASHH3) partial cds GI:15488419   chr2:18265686-18268512 FORWARD   Aliases: F6E13.28	3.9	4.0	-0.1	-0.5	100.0%	-4.9
12364	AT2G03630.1   hypothetical protein   chr2:1103202-1103960 FORWARD   Aliases: F19B11.8, F19B11_8	2.2	2.2	-0.1	-0.5	100.0%	-5.5
12365	AT4G11490.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:6978843-6981543 FORWARD   Aliases: F25E4.110, F25E4_110	2.3	2.3	0.1	0.5	100.0%	-5.7
12366	AT3G05150.1   sugar transporter family protein, similar to sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:1440086-1443527 FORWARD   Aliases: T12H1.11, T12H1_11	2.9	2.8	0.1	0.5	100.0%	-5.0
12367	AT5G55850.1   Symbol: NOI   similar to nitrate-responsive NOI protein, putative [Arabidopsis thaliana] (TAIR:At5g63270.1); similar to nitrate-induced NOI protein [Zea mays] (GB:AAC03022.1); contains InterPro domain Nitrate-induced NOI (InterPro:IPR008700)   chr5:22620603-22622458 FORWARD   Aliases: MWJ3.3, MWJ3_3, NOI PROTEIN	8.8	8.7	0.2	0.5	100.0%	-4.5
12368	AT3G62960.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.3	3.2	0.1	0.5	100.0%	-5.2
12369	AT4G21610.1   Symbol: LOL2   zinc finger protein, putative, similar to zinc-finger protein Lsd1 (Arabidopsis thaliana) gi:1872521:gb:AAC49660	8.5	8.7	-0.2	-0.5	100.0%	-4.4
12370	AT1G74760.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	2.7	2.8	-0.1	-0.5	100.0%	-4.7
12371	AT5G06060.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr5:1823845-1825895 REVERSE   Aliases: K16F4.2, K16F4_2	8.0	8.2	-0.2	-0.5	100.0%	-4.5
12372	AT1G18830.1   transducin family protein / WD-40 repeat family protein, similar to Sec31p (GI:13928450)	2.7	2.6	0.1	0.5	100.0%	-5.4
12373	AT5G04080.1   expressed protein   chr5:1104706-1105389 FORWARD   Aliases: F21E1.3	3.2	2.9	0.2	0.5	100.0%	-4.7
12374	AT2G21195.2   expressed protein   chr2:9090271-9090990 FORWARD   Aliases: None	5.1	5.4	-0.3	-0.5	100.0%	-4.4
12375	AT5G41060.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr5:16452596-16454927 FORWARD   Aliases: MEE6.13, MEE6_13	4.0	4.2	-0.1	-0.5	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12376	AT5G02730.1   allergen V5/Tpx-1-related family protein, low similarity to SP:Q05968 Pathogenesis-related protein 1 precursor {Hordeum vulgare}; contains Pfam profile PF00188: SCP-like extracellular protein   chr5:615608-616225 FORWARD   Aliases: F9G14.40, F9G14_40	3.0	3.1	-0.1	-0.5	100.0%	-5.4
12377	AT4G33960.1   expressed protein   chr4:16277371-16277784 FORWARD   Aliases: F17I5.150, F17I5_150	5.0	5.2	-0.3	-0.5	100.0%	-4.3
12378	AT2G02230.1   Symbol: ATPP2 B1   similar to F-box family protein / SKP1 interacting partner 3-related [Arabidopsis thaliana] (TAIR:At2g02240.1); similar to F-box family protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_468355.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810)   chr2:590222-591649 REVERSE   Aliases: ATPP2 B1, T16F16.2, T16F16_2	9.6	9.2	0.4	0.5	100.0%	-4.3
12379	AT5G33340.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr5:12611697-12613182 FORWARD   Aliases: F19N2.60, F19N2_60	2.4	2.5	-0.1	-0.5	100.0%	-5.4
12380	AT5G10710.2   expressed protein   chr5:3379145-3382780 FORWARD   Aliases: MAJ23.70, MAJ23_70	8.3	8.1	0.2	0.5	100.0%	-4.8
12381	AT4G19990.1   similar to far-red impaired responsive protein, putative [Arabidopsis thaliana] (TAIR:At3g22170.1); similar to putative far-red impaired response protein [Oryza sativa (japonica cultivar-group)] (GB:AAP50996.1); similar to putative FAR1 protein [Oryza sativa (japonica cultivar-group)] (GB:AAT78829.1); contains InterPro domain SWIM Zn-finger (InterPro:IPR007527); contains InterPro domain Zn-finger, PMZ type (InterPro:IPR006564); contains InterPro domain FAR1 (InterPro:IPR004330)   chr4:10832858-10835710 FORWARD   Aliases: F18F4.90, F18F4_90	4.7	4.9	-0.2	-0.5	100.0%	-4.4
12382	AT1G47765.1   F-box family protein, contains F-box domain Pfam:PF00646	2.9	2.8	0.1	0.5	100.0%	-5.5
12383	AT3G48690.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr3:18047382-18049219 REVERSE   Aliases: T8P19.200	6.9	7.2	-0.2	-0.5	100.0%	-4.8
12384	AT4G33810.1   glycosyl hydrolase family 10 protein, similar to tapetum specific protein GI:3885492 from (Zea mays)   chr4:16213329-16215599 REVERSE   Aliases: T16L1.300, T16L1_300	3.5	3.7	-0.2	-0.5	100.0%	-4.7
12385	AT4G37270.1   Symbol: HMA1   cadmium/zinc-transporting ATPase, putative (HMA1), contains InterPro accession IPR001757: ATPase, E1-E2 type; identical to Potential cadmium/zinc-transporting ATPase HMA1 (EC 3.6.3.3) (EC 3.6.3.5) (Swiss-Prot:Q9M3H5) (Arabidopsis thaliana); identical to cDNA putative transcription factor (MYB73) mRNA, partial cds GI:3941503   chr4:17540484-17546478 REVERSE   Aliases: AP22.4, AP22_4	7.4	7.2	0.2	0.5	100.0%	-4.8
12386	AT1G08210.1   aspartyl protease family protein, contains Pfam profile PF00026: Eukaryotic aspartyl protease; similar to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) {Nicotiana tabacum}   chr1:2577021-2580666 REVERSE   Aliases: None	6.3	6.4	-0.2	-0.5	100.0%	-4.7
12387	AT1G14420.1   Symbol: AT59   pectate lyase family protein, similar to pectate lyase P59 SP:P15722 from (Lycopersicon esculentum)   chr1:4931774-4933400 REVERSE   Aliases: F14L17.19, F14L17_19	2.8	2.8	0.1	0.5	100.0%	-5.6
12388	AT3G49740.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:18458773-18461079 FORWARD   Aliases: T16K5.90	4.0	4.1	-0.1	-0.5	100.0%	-5.0
12389	NA	10.6	10.3	0.3	0.5	100.0%	-4.8
12390	AT4G19010.1   4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein, similar to 4CL from Pinus taeda, gi:515503, gi:1143308; contains Pfam AMP-binding enzyme domain PF00501   chr4:10411501-10414260 REVERSE   Aliases: F13C5.180, F13C5_180	3.9	3.8	0.1	0.5	100.0%	-4.8
12391	NA	2.3	2.3	-0.0	-0.5	100.0%	-6.1
12392	AT4G28090.1   Symbol: SKS10   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr4:13961894-13964235 REVERSE   Aliases: SKS10, T13J8.200, T13J8_200	2.7	2.6	0.1	0.5	100.0%	-5.2
12393	AT5G03660.1   expressed protein, low similarity to outer surface protein F (Borrelia burgdorferi) GI:466482; contains Pfam profile PF04949: Family of unknown function (DUF662)   chr5:937976-940057 FORWARD   Aliases: F17C15.80, F17C15_80	9.0	9.2	-0.3	-0.5	100.0%	-4.7
12394	AT2G39440.1   expressed protein   chr2:16471796-16477549 REVERSE   Aliases: F12L6.10, F12L6_10	3.8	3.9	-0.1	-0.5	100.0%	-5.1
12395	AT4G24660.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, hypothetical protein T8K22.16, Arabidopsis thalianachromosome II BAC T8K22, PATX:G3184285   chr4:12724753-12725647 REVERSE   Aliases: F22K18.140, F22K18_140	3.3	3.2	0.1	0.5	100.0%	-5.1
12396	AT4G03370.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:1478077-1478964 REVERSE   Aliases: F4C21.32, F4C21_32	2.7	2.6	0.1	0.5	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12397	AT2G20750.1   Symbol: ATEXPB1   beta-expansin, putative (EXPB1), identical to beta-expansin (Arabidopsis thaliana) gi:2224913:gb:AAB61709; similar to SP:O04701 major pollen allergen, Bermuda grass (Cynodon dactylon); beta-expansin gene family, PMID:11641069   chr2:8948202-8949768 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN B1, ATEXPB1, ATHEXP BETA 1.5, EXPB1, F5H14.28, F5H14_28	2.4	2.3	0.1	0.5	100.0%	-5.4
12398	AT2G43710.2   Symbol: SSI2   acyl-(acyl-carrier-protein) desaturase / stearyl-ACP desaturase (SSI2), identical to gi:15149310; contains Pfam profile PF03405: Fatty acid desaturase; identical to cDNA stearyl ACP desaturase (SSI2), SSI2-FAB2 allele, GI:15149309   chr2:18127039-18129966 FORWARD   Aliases: F18O19.18, FAB2	9.2	9.4	-0.2	-0.5	100.0%	-4.6
12399	AT5G11080.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr5:3517450-3519450 REVERSE   Aliases: T5K6.70, T5K6_70	3.2	3.1	0.1	0.5	100.0%	-5.3
12400	AT3G24503.1   Symbol: ALDH2C4   aldehyde dehydrogenase (ALDH1a), identical to aldehyde dehydrogenase ALDH1a (Arabidopsis thaliana) gi:20530143:gb:AAM27004   chr3:8919567-8923074 REVERSE   Aliases: ALDH1A, REDUCED EPIDERMAL FLUORESCENCE1, REF1	6.7	6.6	0.2	0.5	100.0%	-4.6
12401	AT1G02080.1   transcriptional regulator-related, contains Pfam PF04054: CCR4-Not complex component, Not1; contains TIGRFAM TIGR01612: reticulocyte binding protein; similar to General negative regulator of transcription subunit 1 (SP:P25655) {Saccharomyces cerevisiae}; Location of ESTs gb:T44328 and gb:AA395265   chr1:373694-386820 FORWARD   Aliases: T7I23.15, T7I23_15	7.7	7.9	-0.2	-0.5	100.0%	-4.7
12402	AT4G29590.1   expressed protein   chr4:14512555-14514449 REVERSE   Aliases: T16L4.100, T16L4_100	7.9	7.6	0.3	0.5	100.0%	-4.4
12403	AT2G34190.1   xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family   chr2:14443888-14446595 FORWARD   Aliases: F13P17.3, F13P17_3	5.6	5.7	-0.1	-0.5	100.0%	-4.8
12404	AT1G34480.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr1:12607254-12609062 FORWARD   Aliases: F12K21.20, F12K21_20	2.3	2.3	-0.1	-0.5	100.0%	-5.8
12405	AT5G42370.1   expressed protein   chr5:16956367-16958953 REVERSE   Aliases: MDH9.6, MDH9_6	6.1	5.9	0.2	0.5	100.0%	-4.2
12406	AT1G13540.1   expressed protein   chr1:4635471-4636705 REVERSE   Aliases: F13B4.29, F13B4_29	2.7	2.8	-0.1	-0.5	100.0%	-5.6
12407	AT5G04240.1   Symbol: ELF6   similar to zinc finger (C2H2 type) family protein / transcription factor jumonji (jmi) family protein [Arabidopsis thaliana] (TAIR:At3g48430.1); similar to putative zinc finger protein [Oryza sativa (japonica cultivar-group)] (GB:XP_463579.1); contains InterPro domain Transcription factor jumonji, JmjN (InterPro:IPR003349); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087); contains InterPro domain Transcription factor jumonji, jmiC (InterPro:IPR003347)   chr5:1169545-1174858 FORWARD   Aliases: EARLY FLOWERING 6, F21E1.160, F21E1_160	6.2	6.4	-0.2	-0.5	100.0%	-5.0
12408	AT4G21650.1   subtilase family protein, contains Pfam domain, PF00082: Subtilase family; contains Pfam domain, PF02225: protease associated (PA) domain   chr4:11501210-11504690 REVERSE   Aliases: F17L22.110, F17L22_110	2.8	2.9	-0.1	-0.5	100.0%	-5.6
12409	AT4G03610.1   phosphonate metabolism protein-related, weak similarity to PhnP protein. (Swiss-Prot:P16692) (Escherichia coli)   chr4:1605037-1606857 FORWARD   Aliases: T5L23.10, T5L23_10	4.4	4.6	-0.1	-0.5	100.0%	-4.8
12410	AT3G63100.1   glycine-rich protein   chr3:23326462-23327144 REVERSE   Aliases: T20O10.200	4.2	4.2	0.1	0.5	100.0%	-5.1
12411	ATCG01070.1   Symbol: NDHE   NADH dehydrogenase ND4L   chrC:117804-118109 REVERSE   Aliases: NDHE	4.6	5.2	-0.6	-0.5	100.0%	-4.3
12412	AT1G17250.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-0B (Lycopersicon esculentum) gi:3894387:gb:AAC78593   chr1:5901162-5903432 REVERSE   Aliases: F20D23.5, F20D23_5	2.5	2.6	-0.1	-0.5	100.0%	-4.9
12413	AT5G28510.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase 1 (GI:12043529) (Arabidopsis thaliana)   chr5:10481045-10484026 REVERSE   Aliases: T26D3.6, T26D3_6	3.1	3.0	0.1	0.5	100.0%	-5.3
12414	AT3G56590.1   hydroxyproline-rich glycoprotein family protein   chr3:20975888-20978654 FORWARD   Aliases: None	4.9	4.8	0.2	0.5	100.0%	-4.8
12415	AT1G71870.1   MATE efflux family protein, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:27036118-27038557 REVERSE   Aliases: F14O23.25, F14O23_25	3.8	3.6	0.2	0.5	100.0%	-4.7
12416	AT4G22000.1   expressed protein   chr4:11659650-11660916 REVERSE   Aliases: F1N20.100, F1N20_100	9.1	9.3	-0.2	-0.5	100.0%	-4.6
12417	AT1G12880.1   MutT/nudix family protein, similar to diphosphoinositol polyphosphate phosphohydrolase (Homo sapiens) GI:3978224; contains Pfam profile PF00293: NUDIX domain   chr1:4389749-4391149 FORWARD   Aliases: F13K23.14, F13K23_14	3.5	3.9	-0.5	-0.5	100.0%	-4.3
12418	AT2G18680.1   expressed protein   chr2:8101976-8102861 FORWARD   Aliases: MSF3.6, MSF3_6	3.5	3.4	0.1	0.5	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12419	AT1G65610.1   endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-1,4-beta-glucanase GI:2065530 from (Lycopersicon esculentum)   chr1:24395342-24399023 REVERSE   Aliases: F5I14.14, F5I14_14	3.5	3.3	0.2	0.5	100.0%	-4.3
12420	AT5G09360.1   laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)(GI:13661201)   chr5:2906427-2908659 REVERSE   Aliases: T5E8.160, T5E8_160	3.0	3.1	-0.1	-0.5	100.0%	-5.3
12421	AT5G62800.1   seven in absentia (SINA) family protein, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr5:25235889-25237193 FORWARD   Aliases: MQB2.12, MQB2_12	4.0	3.8	0.2	0.5	100.0%	-4.7
12422	AT1G21580.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:7560554-7565792 REVERSE   Aliases: F24J8.17, F24J8_17	2.3	2.4	-0.1	-0.5	100.0%	-5.7
12423	AT2G39470.2   similar to photosystem II reaction center PsbP family protein [Arabidopsis thaliana] (TAIR:At3g55330.1); similar to putative oxygen evolving complex protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54142.1); contains InterPro domain Photosystem II reaction center protein PsbP (InterPro:IPR002683)	2.4	2.4	-0.1	-0.5	100.0%	-5.6
12424	AT4G22380.1   ribosomal protein L7Ae/L30e/S12e/Gadd45 family protein, Similar to NHP2/L7Ae family proteins, see SWISSPROT:P32495 and PMID:2063628.   chr4:11812053-11812934 REVERSE   Aliases: F7K2.1	5.4	5.6	-0.2	-0.5	100.0%	-4.6
12425	AT2G12190.1   cytochrome P450, putative   chr2:4898724-4900427 REVERSE   Aliases: F23M2.31, F23M2_31	2.6	2.7	-0.1	-0.5	100.0%	-5.4
12426	AT5G56980.1   expressed protein, non-consensus CG donor splice site at exon 1, GA donor splice site at exon 3   chr5:23073306-23074968 REVERSE   Aliases: MHM17.10, MHM17_10	3.7	3.5	0.2	0.5	100.0%	-4.6
12427	AT1G33470.2   RNA recognition motif (RRM)-containing protein, similar to RRM-containing protein SEB-4 (Xenopus laevis) GI:8895698; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:12144524-12147188 FORWARD   Aliases: F10C21.14, F10C21_14	3.5	3.4	0.1	0.5	100.0%	-4.8
12428	AT2G32980.1   expressed protein   chr2:14004459-14006905 REVERSE   Aliases: T21L14.8, T21L14_8	6.8	7.2	-0.4	-0.5	100.0%	-4.6
12429	AT2G19280.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:8369517-8371835 FORWARD   Aliases: F27F23.8, F27F23_8	3.4	3.4	-0.1	-0.5	100.0%	-5.3
12430	AT3G23640.1   glycosyl hydrolase family 31 protein, similar to alpha-glucosidase II from SP:Q9F234 (Bacillus thermoamyloliquefaciens); contains Pfam profile: PF01055 Glycosyl hydrolases family 31   chr3:8501935-8509591 FORWARD   Aliases: MDB19.14	9.6	9.6	-0.1	-0.5	100.0%	-5.2
12431	AT1G15590.1   hypothetical protein   chr1:5367369-5368418 FORWARD   Aliases: T16N11.26, T16N11_26	2.7	2.6	0.1	0.5	100.0%	-5.3
12432	AT4G36410.1   Symbol: UBC17   ubiquitin-conjugating enzyme 17 (UBC17), E2; identical to gi:2801446   chr4:17201930-17202988 FORWARD   Aliases: AP22.89, AP22_89, UBIQUITIN CONJUGATING ENZYME 17	3.9	3.8	0.2	0.5	100.0%	-4.4
12433	AT4G24920.1   protein transport protein SEC61 gamma subunit, putative, similar to Swiss-Prot:Q19967 protein transport protein SEC61 gamma subunit (Caenorhabditis elegans)   chr4:12819521-12820746 REVERSE   Aliases: F13M23.60, F13M23_60	8.7	8.9	-0.2	-0.5	100.0%	-4.5
12434	ATCG01050.1   Symbol: NDHD   Represents a plastid-encoded subunit of a NAD(P)H dehydrogenase complex.	4.5	5.0	-0.5	-0.5	100.0%	-4.6
12435	AT4G23470.3   similar to proline-rich family protein [Arabidopsis thaliana] (TAIR:At1g63830.2); similar to proline-rich family protein [Arabidopsis thaliana] (TAIR:At1g63830.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468591.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr4:12249081-12251406 FORWARD   Aliases: F16G20.170, F16G20_170	5.3	5.6	-0.3	-0.5	100.0%	-4.7
12436	AT5G14720.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:4747934-4753595 REVERSE   Aliases: T9L3.20, T9L3_20	2.6	2.7	-0.1	-0.5	100.0%	-5.4
12437	AT3G62400.2   expressed protein, cytochrome c oxidase subunit 5c - Oryza sativa, EMBL:AB027123	11.2	11.3	-0.1	-0.5	100.0%	-5.4
12438	AT3G56510.2   similar to unnamed protein product [Yarrowia lipolytica CLIB99] (GB:CAG82708.1)   chr3:20954907-20957640 REVERSE   Aliases: T5P19.160	9.2	9.3	-0.1	-0.5	100.0%	-4.8
12439	AT1G14650.1   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein / ubiquitin family protein, similar to SP:Q15459 Splicing factor 3 subunit 1 (Spliceosome associated protein 114) {Homo sapiens}; contains Pfam profiles PF00240: Ubiquitin family, PF01805: Surp module   chr1:5027657-5030787 FORWARD   Aliases: T5E21.13, T5E21_13	3.8	3.8	-0.1	-0.5	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12440	AT1G03290.1   expressed protein, ESTs gb:H36966, gb:R65511, gb:T42324 and gb:T20569 come from this gene   chr1:807970-810690 FORWARD   Aliases: F15K9.11, F15K9_11	7.9	7.7	0.1	0.5	100.0%	-4.7
12441	AT1G80280.1   hydrolase, alpha/beta fold family protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold   chr1:30188433-30191478 REVERSE   Aliases: F5I6.3, F5I6_3	3.7	3.8	-0.2	-0.5	100.0%	-4.8
12442	AT5G48130.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr5:19533517-19535676 FORWARD   Aliases: MIF21.2, MIF21_2	2.8	2.9	-0.1	-0.5	100.0%	-5.3
12443	AT4G32020.1   expressed protein, NuLL   chr4:15487950-15489456 FORWARD   Aliases: F10N7.170, F10N7_170	2.6	2.2	0.4	0.5	100.0%	-4.4
12444	AT1G71770.1   Symbol: PAB5   polyadenylate-binding protein 5 (PABP5), identical to GB:Q05196 from (Arabidopsis thaliana)   chr1:26994170-26997109 REVERSE   Aliases: F14O23.15, F14O23_15, POLY(A) BINDING PROTEIN	4.5	4.7	-0.2	-0.5	100.0%	-4.5
12445	AT5G15320.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:4977541-4978897 FORWARD   Aliases: F8M21.210, F8M21_210	10.3	10.2	0.1	0.5	100.0%	-4.9
12446	AT1G62700.1   Symbol: ANAC026   no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.4	2.5	-0.1	-0.5	100.0%	-5.5
12447	AT1G57650.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr1:21354956-21357647 FORWARD   Aliases: T8L23.12, T8L23_12	3.0	3.1	-0.1	-0.5	100.0%	-5.6
12448	AT3G06020.1   expressed protein, ; expression supported by MPSS   chr3:1813273-1814175 FORWARD   Aliases: F2O10.2, F2O10_2	6.2	6.0	0.1	0.5	100.0%	-4.6
12449	AT5G49890.1   Symbol: CLC C   chloride channel protein (CLC-c), identical to gi:1742956   chr5:20305346-20309576 REVERSE   Aliases: ATCLC C, CHLORIDE CHANNEL C, K9P8.3, K9P8_3	3.7	4.0	-0.3	-0.5	100.0%	-4.5
12450	AT3G42050.1   vacuolar ATP synthase subunit H family protein, identical to probable vacuolar ATP synthase subunit H (EC 3.6.3.14)(V-ATPase H subunit) (Vacuolar proton pump H subunit) (Vacuolar proton pump subunit SFD) SP:Q9LX65 from (Arabidopsis thaliana); contains Pfam PF03224: V-ATPase subunit H   chr3:14239482-14244216 REVERSE   Aliases: F4M19.10	8.8	9.1	-0.3	-0.5	100.0%	-4.8
12451	AT1G04860.1   Symbol: UBP2   ubiquitin-specific protease 2 (UBP2), identical to GI:11993463   chr1:1369053-1373097 REVERSE   Aliases: F13M7.15, F13M7_15, UBIQUITIN SPECIFIC PROTEASE 2	5.3	5.4	-0.1	-0.5	100.0%	-5.0
12452	AT3G21640.1   Symbol: TWD1   FKBP-type peptidyl-prolyl cis-trans isomerase family protein, similar to rof1 (Arabidopsis thaliana) GI:1354207; contains Pfam profile: PF00254 FKBP-type peptidyl-prolyl cis-trans isomerases   chr3:7618937-7621484 REVERSE   Aliases: ATFKBP42, MIL23.21, TWISTED DWARF 1, UCU2, ULTRACURVATA 2	6.1	6.4	-0.2	-0.5	100.0%	-4.6
12453	AT4G33490.1   similar to nucellin protein, putative [Arabidopsis thaliana] (TAIR:At1g44130.1); similar to nucellin-like aspartic protease [Oryza sativa (japonica cultivar-group)] (GB:AA23257.1); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461)	4.3	4.2	0.1	0.5	100.0%	-4.8
12454	AT5G17260.1   Symbol: ANAC086   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr5:5675325-5677914 REVERSE   Aliases: ANAC086, MKP11.11, MKP11_11	2.7	2.6	0.1	0.5	100.0%	-5.4
12455	AT5G44990.1   expressed protein   chr5:18180597-18181995 FORWARD   Aliases: K21C13.18, K21C13_18	2.3	2.4	-0.1	-0.5	100.0%	-5.3
12456	AT2G43570.1   chitinase, putative, similar to chitinase class IV GI:722272 from (Brassica napus)   chr2:18083301-18084539 REVERSE   Aliases: F18O19.32	3.8	4.0	-0.2	-0.5	100.0%	-4.5
12457	AT1G12850.1   phosphoglycerate/bisphosphoglycerate mutase family protein, similar to XY4 protein (Silene vulgaris) GI:21386788; contains Pfam profile PF00300: phosphoglycerate mutase family   chr1:4379705-4381610 REVERSE   Aliases: F13K23.10, F13K23_10	6.3	6.0	0.3	0.5	100.0%	-4.9
12458	AT4G24030.1   expressed protein   chr4:12486257-12486643 REVERSE   Aliases: T19F6.20, T19F6_20	3.7	3.5	0.2	0.5	100.0%	-4.6
12459	AT2G28070.1   ABC transporter family protein   chr2:11963509-11966859 FORWARD   Aliases: F24D13.14, F24D13_14	4.8	4.9	-0.1	-0.5	100.0%	-5.0
12460	AT3G61550.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 zinc finger protein ATL6 (Arabidopsis thaliana) GI:4928403; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)	3.9	3.8	0.1	0.5	100.0%	-5.3
12461	AT3G56600.1   phosphatidylinositol 3- and 4-kinase family protein, low similarity to 55 kDa type II phosphatidylinositol 4-kinase (Rattus norvegicus) GI:13660755; contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase	2.9	2.8	0.1	0.5	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12462	AT1G54830.3   CCAAT-box binding transcription factor Hap5a, putative, similar to heme activated protein GI:6289057 from (Arabidopsis thaliana) GI:14577940 CCAAT-binding protein subunit HAP5 {Hypocrea jecorina} similar to Transcription factor GB:CAA74053 GI:2398533 from (Arabidopsis thaliana) similarity to transcription factor Hap5a similar to transcription factor Hap5a (Arabidopsis thaliana)(GI:6523090)	8.3	8.1	0.2	0.5	100.0%	-4.7
12463	AT4G10420.1   expressed protein   chr4:6453414-6454205 REVERSE   Aliases: F7L13.3	2.7	2.8	-0.1	-0.5	100.0%	-5.4
12464	AT5G05070.1   similar to zinc finger (DHHC type) family protein [Arabidopsis thaliana] (TAIR:At2g40990.1); similar to putative zisp [Oryza sativa (japonica cultivar-group)] (GB:BAD88184.1); contains InterPro domain Zn-finger, DHHC type (InterPro:IPR001594)   chr5:1496856-1498545 FORWARD   Aliases: MUG13.7, MUG13_7	2.3	2.2	0.1	0.5	100.0%	-5.3
12465	AT1G31670.1   copper amine oxidase, putative, similar to amine oxidase (copper-containing) precursor (Pisum sativum) SWISS-PROT:Q43077	2.8	2.7	0.1	0.5	100.0%	-4.9
12466	AT3G52270.1   expressed protein   chr3:19398158-19399865 REVERSE   Aliases: T25B15.40	3.1	3.0	0.1	0.5	100.0%	-5.3
12467	AT1G07090.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr1:2173951-2174893 REVERSE   Aliases: F10K1.20, F10K1_20	4.8	4.7	0.1	0.5	100.0%	-5.1
12468	AT2G45930.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr2:18908465-18909871 REVERSE   Aliases: F4I18.9	3.2	3.3	-0.1	-0.5	100.0%	-5.4
12469	AT4G33450.1   myb family transcription factor (MYB69), contains PFAM profile: Myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB69) mRNA, partial cds GI:3941495   chr4:16095395-16096606 REVERSE   Aliases: F17M5.210, F17M5_210	2.7	2.8	-0.1	-0.5	100.0%	-5.6
12470	AT3G55530.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:20606115-20608552 REVERSE   Aliases: T22E16.190	4.3	4.2	0.1	0.5	100.0%	-4.9
12471	AT1G06170.2   basic helix-loop-helix (bHLH) family protein, contains Pfam profile:PF00010 helix-loop-helix DNA-binding domain   chr1:1884980-1886723 REVERSE   Aliases: F9P14.3, F9P14_3	2.5	2.5	0.0	0.5	100.0%	-5.9
12472	AT4G30960.1   Symbol: CIPK6   CBL-interacting protein kinase 6 (CIPK6), identical to CBL-interacting protein kinase 6 (Arabidopsis thaliana) gi:9280634:gb:AAF86505   chr4:15067059-15069016 FORWARD   Aliases: CBL INTERACTING PROTEIN KINASE 6, F6I18.130, F6I18_130	7.1	7.3	-0.2	-0.5	100.0%	-4.7
12473	AT1G09415.1   NPR1/NIM1-interacting protein 3 (NIMIN-3), identical to NIMIN-3 protein (Arabidopsis thaliana) GI:12057158, cDNA NIMIN-3 protein (nimin-3 gene)GI:12057157   chr1:3037756-3038390 REVERSE   Aliases: None	7.2	7.4	-0.2	-0.5	100.0%	-4.5
12474	AT2G23840.1   HNH endonuclease domain-containing protein, contains Pfam profile PF01844: HNH endonuclease   chr2:10160877-10162680 REVERSE   Aliases: T29E15.4, T29E15_4	3.1	3.0	0.1	0.5	100.0%	-5.2
12475	AT2G39620.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:16526046-16528556 REVERSE   Aliases: F12L6.28, F12L6_28	3.0	3.1	-0.1	-0.5	100.0%	-5.4
12476	AT5G19480.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g12230.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAF96846.1); contains domain LYS_RICH (PS50318)   chr5:6571503-6573455 FORWARD   Aliases: F7K24.230, F7K24_230	7.0	7.4	-0.4	-0.5	100.0%	-4.7
12477	AT5G09440.1   phosphate-responsive protein, putative, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr5:2938348-2939462 FORWARD   Aliases: T5E8.240, T5E8_240	6.3	5.9	0.4	0.5	100.0%	-4.6
12478	AT1G58120.1   expressed protein   chr1:21524066-21526122 FORWARD   Aliases: T15M6.13	3.2	3.3	-0.1	-0.5	100.0%	-5.0
12479	AT5G19840.1   transcription factor jumonji (jmc) domain-containing protein, low similarity to PASS1 (Homo sapiens) GI:21591407; contains Pfam profile PF02373: jmc domain   chr5:6705374-6709794 FORWARD   Aliases: T29J13.260, T29J13_260	2.4	2.4	-0.1	-0.5	100.0%	-5.3
12480	AT5G54530.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:22169951-22171651 FORWARD   Aliases: MRB17.3, MRB17_3	3.4	3.6	-0.2	-0.5	100.0%	-4.5
12481	AT1G08930.2   Symbol: ERD6   similar to sugar transporter, putative [Arabidopsis thaliana] (TAIR:At1g08920.1); similar to integral membrane protein [Beta vulgaris] (GB:AAB53155.1); contains InterPro domain Sugar transporter superfamily (InterPro:IPR005829); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sugar transporter (InterPro:IPR003663)   chr1:2873468-2877273 FORWARD   Aliases: ERD6, F7G19.19, F7G19_19	4.4	4.2	0.2	0.5	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12482	AT5G11280.1   expressed protein   chr5:3597258-3598515 FORWARD   Aliases: F2I11.170, F2I11_170	6.0	5.7	0.4	0.5	100.0%	-4.7
12483	AT5G45000.1   similar to disease resistance protein (TIR class), putative [Arabidopsis thaliana] (TAIR:At1g51280.1); similar to R 8 protein [Glycine max] (GB:AAO23077.1); similar to nematode resistance-like protein [Solanum tuberosum] (GB:AAP44391.1); contains InterPro domain TIR domain (InterPro:IPR000157)   chr5:18182654-18184420 FORWARD   Aliases: K21C13.19, K21C13_19	3.1	2.9	0.2	0.5	100.0%	-4.8
12484	AT1G44910.1   similar to FF domain-containing protein / WW domain-containing protein [Arabidopsis thaliana] (TAIR:At3g19670.1); similar to formin binding protein 3-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87484.1); contains InterPro domain FF domain (InterPro:IPR002713); contains InterPro domain WW/Rsp5/WWP domain (InterPro:IPR001202)   chr1:16978044-16985405 FORWARD   Aliases: F27F5.2	5.9	6.4	-0.5	-0.5	100.0%	-4.5
12485	AT1G06380.1   ribosomal protein-related, similar to PBK1 protein (GI:3668141) {Homo sapiens}; weakly similar to 60S ribosomal protein L10a. (SP:Q963B6) (Fall armyworm) {Spodoptera frugiperda}   chr1:1945123-1946075 FORWARD   Aliases: T2D23.8, T2D23_8	5.0	5.1	-0.1	-0.5	100.0%	-4.6
12486	AT5G48840.1   pantoate-beta-alanine ligase, putative, similar to pantoate--beta-alanine ligase (Lotus japonicus) GI:2292921; contains Pfam profile PF02569: pantoate--beta-alanine ligase   chr5:19820797-19822303 REVERSE   Aliases: K24G6.18, K24G6_18	7.1	7.3	-0.2	-0.5	100.0%	-4.7
12487	AT5G18970.1   AWPM-19-like membrane family protein, contains Pfam profile: PF05512 AWPM-19-like family	3.0	2.8	0.3	0.5	100.0%	-4.3
12488	AT3G25860.1   Symbol: LTA2   dihydrolipoamide S-acetyltransferase (LTA2), identical to dihydrolipoamide S-acetyltransferase (LTA2) (Arabidopsis thaliana) GI:5881963   chr3:9461797-9464024 FORWARD   Aliases: DIHYDROLIPOAMIDE S ACETYLTRANSFERASE, MPE11.6, PLASTID E2 SUBUNIT OF PYRUVATE DECARBOXYLASE, PLE2	8.6	9.0	-0.4	-0.5	100.0%	-4.4
12489	AT2G40220.1   Symbol: ABI4   encodes a member of the DREB subfamily A-3 of ERF/AP2 transcription factor family (ABI4). The protein contains one AP2 domain. There is only one member in this family. Involved in abscisic acid (ABA) signal transduction, ABA-mediated glucose response, and hexokinase-dependent sugar responses.   chr2:16803677-16804663 REVERSE   Aliases: ABA INSENSITIVE 4, ABSCISIC ACID INSENSITIVE PROTEIN 4, GIN6, GLUCOSE INSENSITIVE 6, IMPAIRED SUCROSE INDUCTION 3, ISI3, SALOBREN??O 5, SAN5, SIS5, SUCROSE UNCOUPLED 6, SUCROSE UNCOUPLED 6, SUGAR INSENSITIVE 5, SUN6, T7M7.16	3.4	3.3	0.1	0.5	100.0%	-5.3
12490	AT3G52240.1   expressed protein   chr3:19383880-19386858 REVERSE   Aliases: T25B15.10	4.4	4.3	0.1	0.5	100.0%	-4.9
12491	AT3G18165.1   expressed protein, similar to DAM1 (GI:3985930) (Homo sapiens); contains Pfam profile PF05700: Breast carcinoma amplified sequence 2 (BCAS2)   chr3:6223194-6225378 FORWARD   Aliases: None	5.6	5.4	0.2	0.5	100.0%	-4.7
12492	AT1G19120.1   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to U6 snRNA-associated Sm-like protein LSm1 (Small nuclear ribonuclear CaSm, Cancer-associated Sm-like) (Homo sapiens) SWISS-PROT:O15116   chr1:6608112-6609338 FORWARD   Aliases: F14D16.28, F14D16_28	6.7	6.9	-0.2	-0.5	100.0%	-4.8
12493	AT4G18080.1   expressed protein   chr4:10033222-10033947 REVERSE   Aliases: F15J5.50, F15J5_50	3.3	3.2	0.1	0.5	100.0%	-5.3
12494	AT5G59190.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo)   chr5:23903081-23905899 FORWARD   Aliases: MNC17.18, MNC17_18	3.4	3.5	-0.1	-0.5	100.0%	-5.1
12495	AT1G02660.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr1:571955-574981 REVERSE   Aliases: T14P4.6, T14P4_6	3.9	3.8	0.1	0.5	100.0%	-5.0
12496	AT5G43020.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:17272540-17274970 REVERSE   Aliases: MMG4.2, MMG4_2	2.8	2.9	-0.1	-0.5	100.0%	-5.2
12497	AT5G36910.1   Symbol: THI2.2.2   thionin (THI2.2), identical to thionin (Arabidopsis thaliana) gi:1181533:gb:AAC41679	3.2	3.4	-0.2	-0.5	100.0%	-5.0
12498	AT1G57850.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:21430355-21431014 FORWARD   Aliases: F12K22.22, F12K22_22	2.7	2.6	0.1	0.5	100.0%	-5.4
12499	AT4G00630.1   Symbol: KEA2   K+ efflux antiporter, putative (KEA2), Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563; similar to SWISS-PROT:SPP03819 Glutathione-regulated potassium-efflux system protein kefC (K+)/H(+) antiporter (Escherichia coli)   chr4:261655-265958 REVERSE   Aliases: ATKEA2, F6N23.15, F6N23_15	8.5	8.7	-0.1	-0.5	100.0%	-5.0
12500	AT1G18590.1   sulfotransferase family protein, similar to SP:P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) {Flaveria chloraefolia}; contains Pfam profile PF00685: Sulfotransferase domain   chr1:6398572-6399934 FORWARD   Aliases: F25I16.7, F25I16_7	4.2	4.3	-0.1	-0.5	100.0%	-4.9
12501	AT1G35515.1   Symbol: HOS10/MYB8   myb family transcription factor (MYB8), similar to DNA-binding protein GB:AAA98761 GI:1020155 from (Arabidopsis thaliana)   chr1:13077904-13080243 FORWARD   Aliases: HIGH RESPONSE TO OSMOTIC STRESS 10	4.3	4.1	0.1	0.5	100.0%	-5.2
12502	AT3G17030.1   expressed protein   chr3:5804515-5808468 REVERSE   Aliases: K14A17.10	4.2	4.4	-0.1	-0.5	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12503	AT5G10620.1   expressed protein, contains Pfam profile PF02590: Uncharacterized ACR, COG1576   chr5:3355467-3356616 REVERSE   Aliases: F12B17.30, F12B17_30	5.2	5.0	0.2	0.5	100.0%	-4.4
12504	AT2G22100.1   RNA recognition motif (RRM)-containing protein, similar to UBPI interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains Pfam profile: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain)   chr2:9399290-9400642 REVERSE   Aliases: T16B14.5, T16B14_5	5.4	5.3	0.1	0.5	100.0%	-5.0
12505	AT1G69320.1   Symbol: CLE10   CLE10, putative, CLAVATA3/ESR-Related 10 (CLE10)   chr1:26065525-26066177 FORWARD   Aliases: CLAVATA3/ESR RELATED 10, F10D13.2, F10D13_2	2.0	2.1	-0.1	-0.5	100.0%	-5.2
12506	AT5G64040.2   Symbol: PSI N   similar to photosystem I subunit N [Hordeum vulgare subsp. vulgare] (GB:CAA47056.1); contains InterPro domain Photosystem I reaction centre subunit N (InterPro:IPR008796)   chr5:25645814-25646841 REVERSE   Aliases: MHJ24.2, MHJ24_2	8.2	7.9	0.3	0.5	100.0%	-4.3
12507	AT3G52060.2   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr3:19321511-19323264 REVERSE   Aliases: F4F15.170	4.7	4.9	-0.2	-0.5	100.0%	-4.2
12508	AT4G29490.1   Xaa-Pro dipeptidase, putative / prolidase, putative / imidodipeptidase, putative, similar to SP:P12955 Xaa-Pro dipeptidase (EC 3.4.13.9) (X-Pro dipeptidase) (Proline dipeptidase) (Prolidase) (Imidodipeptidase) {Homo sapiens}; contains Pfam profiles PF00557: metallopeptidase family M24, PF05195: Aminopeptidase P, N-terminal domain   chr4:14487906-14490162 FORWARD   Aliases: F17A13.310, F17A13_310	3.9	3.8	0.2	0.5	100.0%	-4.7
12509	AT3G06300.1   Symbol: AT P4H 2   Encodes a prolyl-4 hydroxylase that can hydroxylate poly(L-proline)and other proline rich peptides, including those with sequences corresponding to those in arabinogalactan proteins and extensins.	6.4	6.0	0.4	0.5	100.0%	-4.7
12510	AT1G33830.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to AIG1 protein SP:P54120 (Arabidopsis thaliana); contains Pfam profile: PF00735 cell division protein (members of this family bind GTP)   chr1:12279927-12281386 REVERSE   Aliases: F14M2.25, F14M2_25	2.2	2.3	-0.0	-0.5	100.0%	-5.9
12511	AT3G52450.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain   chr3:19451717-19453361 REVERSE   Aliases: F22O6.170	7.1	7.0	0.2	0.5	100.0%	-4.8
12512	AT3G31350.1   expressed protein   chr3:12705066-12705701 FORWARD   Aliases: T22B15.44	2.0	1.9	0.1	0.5	100.0%	-5.6
12513	AT2G46530.3   Symbol: ARF11   similar to transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related [Arabidopsis thaliana] (TAIR:At3g61830.1); similar to auxin-responsive factor (ARF9) [Arabidopsis thaliana] (TAIR:At4g23980.1); similar to OSJNBa0064D20.11 [Oryza sativa (japonica cultivar-group)] (GB:CAE04227.2); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340); contains InterPro domain AUX/IAA protein (InterPro:IPR003311)   chr2:19112184-19115403 FORWARD   Aliases: AUXIN RESPONSE FACTOR 11, F11C10.34	3.0	2.9	0.1	0.5	100.0%	-5.1
12514	AT1G71490.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:26936567-26939487 REVERSE   Aliases: F26A9.13	3.4	3.2	0.1	0.5	100.0%	-4.9
12515	AT5G20560.1   beta-1,3-glucanase, putative, similar to plant beta-1,3-glucanase genes bg4 GI:2808438 from (Arabidopsis thaliana)   chr5:6955370-6956383 FORWARD   Aliases: F7C8.150, F7C8_150	2.6	2.6	0.1	0.5	100.0%	-5.6
12516	AT2G36980.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:15538240-15540117 FORWARD   Aliases: T1J8.16, T1J8_16	3.1	3.3	-0.1	-0.5	100.0%	-5.0
12517	AT3G58190.1   LOB domain protein 29 / lateral organ boundaries domain protein 29 (LBD29), identical to SP:Q9M2J7 LOB domain protein 29 {Arabidopsis thaliana}; supported by full-length cDNA gi:17227167   chr3:21559461-21560535 REVERSE   Aliases: F9D24.100	3.4	3.5	-0.1	-0.5	100.0%	-5.2
12518	NA	8.0	7.8	0.3	0.5	100.0%	-4.9
12519	AT3G13960.1   Symbol: AtGRF5	2.1	2.2	-0.1	-0.5	100.0%	-5.9
12520	AT5G22990.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:7691497-7692471 REVERSE   Aliases: MRN17.22, MRN17_22	2.1	2.1	-0.1	-0.5	100.0%	-6.0
12521	AT2G17350.1   expressed protein   chr2:7552620-7553456 REVERSE   Aliases: F5J6.11, F5J6_11	8.3	8.1	0.2	0.5	100.0%	-4.7
12522	AT5G13280.1   Symbol: AK LYS1   aspartate kinase, identical to aspartate kinase (Arabidopsis thaliana) GI:4376158   chr5:4249441-4252839 FORWARD   Aliases: AK, ASPARTATE KINASE, T31B5.100, T31B5_100	10.2	10.4	-0.2	-0.5	100.0%	-4.6
12523	AT3G02240.1   expressed protein   chr3:418522-419158 FORWARD   Aliases: F14P3.11, F14P3_11	3.1	3.3	-0.2	-0.5	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12524	AT5G40370.1   glutaredoxin, putative, similar to glutaredoxin (Ricinus communis) SWISS-PROT:P55143   chr5:16164833-16166382 REVERSE   Aliases: MPO12.80, MPO12_80	13.0	13.1	-0.1	-0.5	100.0%	-5.0
12525	AT2G19270.1   expressed protein   chr2:8367271-8369006 REVERSE   Aliases: F27F23.7, F27F23_7	8.2	8.4	-0.1	-0.5	100.0%	-5.5
12526	AT4G17990.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr4:9984524-9988265 REVERSE   Aliases: T6K21.170, T6K21_170	3.2	3.3	-0.2	-0.5	100.0%	-5.0
12527	AT4G14080.1   glycosyl hydrolase family 17 protein / anther-specific protein (A6), identical to probable glucan endo-1,3-beta-glucosidase A6 precursor SP:Q06915 from (Arabidopsis thaliana)   chr4:8118535-8120353 REVERSE   Aliases: DL3080C, FCAALL.82	2.2	2.2	0.1	0.5	100.0%	-5.6
12528	AT3G10680.1   heat shock protein-related, contains weak similarity to Pfam profile PF00011: Hsp20/alpha crystallin family   chr3:3337778-3339350 FORWARD   Aliases: T7M13.24	3.6	3.8	-0.1	-0.5	100.0%	-4.6
12529	AT3G60120.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; similar to anther-specific protein ATA27 (GI:2746341) (Arabidopsis thaliana)   chr3:22217322-22219927 FORWARD   Aliases: T2O9.100	3.4	3.5	-0.1	-0.5	100.0%	-5.1
12530	AT5G50360.1   expressed protein   chr5:20522406-20523564 REVERSE   Aliases: MXI22.7, MXI22_7	6.6	6.4	0.2	0.5	100.0%	-4.3
12531	AT1G72840.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:27412963-27417284 REVERSE   Aliases: F3N23.4, F3N23_4	2.4	2.5	-0.1	-0.5	100.0%	-5.1
12532	AT5G07530.1   Symbol: GRP17   glycine-rich protein (GRP17), olesin; glycine-rich protein 17 (GRP17) PMID:11431566; function: pollen recognition (PMID:10655594)   chr5:2382469-2384511 REVERSE   Aliases: ATGRP 7, ATGRP17, T2I1.240, T2I1_240	5.5	5.1	0.4	0.5	100.0%	-4.5
12533	AT4G12010.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:7197205-7201387 REVERSE   Aliases: F16J13.80, F16J13_80	3.0	3.2	-0.1	-0.5	100.0%	-4.7
12534	AT5G06530.3   similar to ABC transporter family protein [Arabidopsis thaliana] (TAIR:At3g52310.1); similar to putative ABC transporter AbcG1 [Oryza sativa (japonica cultivar-group)] (GB:XP_480256.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain ABC transporter (InterPro:IPR003439); contains InterPro domain ATP/GTP-binding site motif A (P-loop) (InterPro:IPR001687)   chr5:1989748-1994825 REVERSE   Aliases: F15M7.6, F15M7_6	3.3	3.2	0.1	0.5	100.0%	-5.0
12535	AT1G11760.1   expressed protein, weak similarity to Pfam PF01648: 4'-phosphopantetheinyl transferase superfamily   chr1:3970545-3973295 REVERSE   Aliases: F25C20.9, F25C20_9	3.2	3.3	-0.1	-0.5	100.0%	-5.3
12536	AT3G46570.1   glycosyl hydrolase family 17 protein, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum)   chr3:17156782-17157852 REVERSE   Aliases: F12A12.90	2.4	2.4	0.1	0.5	100.0%	-5.4
12537	AT2G07630.1   expressed protein   chr2:3208707-3210806 REVERSE   Aliases: F9A16.16, F9A16_16	2.0	2.1	-0.0	-0.5	100.0%	-6.2
12538	AT1G50570.2   similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g55530.2); similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g55530.3); similar to C2 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g55530.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:NP_911888.1); contains InterPro domain C2 domain (InterPro:IPR000008)   chr1:18729489-18731538 REVERSE   Aliases: F11F12.11	6.5	6.8	-0.3	-0.5	100.0%	-4.5
12539	AT5G53670.1   hypothetical protein, similar to unknown protein (pir :T17429)   chr5:21814223-21814957 FORWARD   Aliases: MGN6.1, MGN6_1	2.9	2.8	0.1	0.5	100.0%	-5.3
12540	AT5G38210.1   serine/threonine protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290   chr5:15278235-15282860 FORWARD   Aliases: MXA21.10, MXA21_10	3.3	3.4	-0.1	-0.5	100.0%	-4.9
12541	AT3G01180.1   glycogen synthase, putative, similar to glycogen synthase Q43847 from (Solanum tuberosum)   chr3:62252-65852 REVERSE   Aliases: T4P13.13, T4P13_13	6.8	6.5	0.3	0.5	100.0%	-4.6
12542	AT3G30250.1   expressed protein   chr3:11893238-11893911 REVERSE   Aliases: MIL15.16	2.4	2.6	-0.1	-0.5	100.0%	-5.2
12543	AT4G22600.1   expressed protein   chr4:11900222-11901043 REVERSE   Aliases: F7K2.180, F7K2_180	3.1	3.2	-0.1	-0.5	100.0%	-5.2
12544	AT1G79340.1   latex-abundant protein, putative (AMC7) / caspase family protein, similar to latex-abundant protein (Hevea brasiliensis) gb:AAD13216; contains Pfam domain, PF00656: ICE-like protease (caspase) p20 domain   chr1:29847668-29849531 FORWARD   Aliases: YUP8H12R.4, YUP8H12R_4	6.5	6.7	-0.2	-0.5	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12545	AT1G58290.1   Symbol: HEMA1   glutamyl-tRNA reductase 1 / GluTR (HEMA1), identical to glutamyl-tRNA reductase 1, chloroplast (SP:P42804)   chr1:21627391-21629865 REVERSE   Aliases: F19C14.9, F19C14_9	6.0	6.2	-0.2	-0.5	100.0%	-4.7
12546	AT1G13195.1   zinc finger (C3HC4-type RING finger) family protein, similar to MTD2 (Medicago truncatula) GI:9294812; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:4501081-4503588 REVERSE   Aliases: None	6.0	5.8	0.2	0.5	100.0%	-4.7
12547	AT5G46460.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:18857532-18859625 FORWARD   Aliases: K1111.5, K1111_5	3.7	3.9	-0.2	-0.5	100.0%	-4.7
12548	AT3G03310.1   lecithin:cholesterol acyltransferase family protein / LACT family protein, weak similarity to LCAT-like lysophospholipase (LLPL) (Homo sapiens) GI:4589720; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)   chr3:778711-781587 REVERSE   Aliases: T21P5.27, T21P5_27	6.5	6.7	-0.2	-0.5	100.0%	-4.6
12549	AT5G10820.1   integral membrane transporter family protein, contains 11 transmembrane domains; similar to folate/methotrexate transporter FT1 (GI:5813863) {Leishmania donovani}; lignostilbene-alpha,beta-dioxygenase gene, Synechococcus PCC7942, EMBL:AF055873   chr5:3420838-3423222 REVERSE   Aliases: T30N20.90, T30N20_90	7.4	7.6	-0.1	-0.5	100.0%	-4.7
12550	AT5G67150.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:26812997-26814538 REVERSE   Aliases: K21H1.11, K21H1_11	7.9	8.1	-0.2	-0.5	100.0%	-4.8
12551	AT2G18590.1   transporter-related, low similarity to spinster membrane proteins from (Drosophila melanogaster) GI:12003976, GI:12003972, GI:12003974, GI:12003970; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:8077433-8079948 FORWARD   Aliases: F24H14.6, F24H14_6	5.2	5.0	0.2	0.5	100.0%	-5.0
12552	AT1G43040.1   auxin-responsive protein, putative, similar to auxin-induced protein (SP:P33079) (GI:416693) (Glycine max)   chr1:16186649-16186963 FORWARD   Aliases: F2H10.1, F2H10_1	2.8	2.7	0.1	0.5	100.0%	-5.0
12553	AT4G39900.1   expressed protein   chr4:18508364-18510547 REVERSE   Aliases: T5J17.70, T5J17_70	6.0	5.7	0.2	0.5	100.0%	-4.6
12554	AT1G69570.1   Dof-type zinc finger domain-containing protein, nearly identical to H-protein promoter binding factor-2b (Arabidopsis thaliana) GI:3386548   chr1:26165191-26166927 REVERSE   Aliases: F10D13.20, F10D13_20	6.4	6.1	0.3	0.5	100.0%	-4.1
12555	AT5G03640.1   protein kinase family protein, contains serine/threonine protein kinase domain, INTERPRO:IPR002290   chr5:927914-930780 FORWARD   Aliases: F17C15.60, F17C15_60	2.6	2.7	-0.1	-0.5	100.0%	-4.9
12556	AT2G20625.1   expressed protein   chr2:8903235-8904299 REVERSE   Aliases: F23N11.15, F23N11_15	2.8	3.0	-0.2	-0.5	100.0%	-4.6
12557	AT5G09550.1   Rab GDP dissociation inhibitor, putative, strong similarity to GDP dissociation inhibitor protein OsGDI1 (Oryza sativa) GI:2384758; contains Pfam profile PF00996: GDP dissociation inhibitor   chr5:2964554-2966728 FORWARD   Aliases: F17I14.260, F17I14_260	2.9	2.8	0.1	0.5	100.0%	-5.1
12558	NA	12.3	12.2	0.1	0.5	100.0%	-6.0
12559	AT5G44360.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr5:17889151-17890925 REVERSE   Aliases: K9L2.15, K9L2_15	2.7	2.7	-0.1	-0.5	100.0%	-5.5
12560	AT1G27080.1   proton-dependent oligopeptide transport (POT) family protein, similar to nitrate transporter NRT1-5 (Glycine max) GI:11933414; contains Pfam profile PF00854: POT family	3.3	3.4	-0.1	-0.5	100.0%	-4.9
12561	AT5G64280.1   oxoglutarate/malate translocator, putative, similar to SWISS-PROT:Q41364 2-oxoglutarate/malate translocator, chloroplast precursor (Spinach){Spinacia oleracea}   chr5:25728295-25730699 REVERSE   Aliases: MSJ1.12, MSJ1_12	5.4	5.3	0.1	0.5	100.0%	-4.8
12562	AT1G14080.1   Symbol: FUT6   xyloglucan fucosyltransferase, putative (FUT6), nearly identical to SP:Q9XI80 Probable fucosyltransferase 6 (EC 2.4.1.-) (AtFUT6) {Arabidopsis thaliana}; similar to xyloglucan fucosyltransferase GI:5231145 from (Arabidopsis thaliana)   chr1:4822525-4824411 FORWARD   Aliases: ATFUT6, F7A19.16, F7A19_16	2.7	2.5	0.2	0.5	100.0%	-4.4
12563	AT1G55990.1   glycine-rich protein, predicted proteins, Arabidopsis thaliana   chr1:20946152-20946616 REVERSE   Aliases: F14J16.30, F14J16_30	2.7	2.7	-0.1	-0.5	100.0%	-5.4
12564	AT2G13620.1   Symbol: ATCHX15   cation/hydrogen exchanger, putative (CHX15), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr2:5685088-5687703 FORWARD   Aliases: CHX15, T10F5.16, T10F5_16	3.5	3.6	-0.1	-0.5	100.0%	-5.4
12565	ATMG01330.1   Symbol: ORF107H   hypothetical protein   chrM:329082-329465 REVERSE   Aliases: ORF107H	2.9	2.7	0.2	0.5	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12566	AT5G07780.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr5:2479708-2482834 FORWARD   Aliases: MXM12.2, MXM12_2	2.9	2.7	0.2	0.5	100.0%	-4.4
12567	AT3G21550.1   expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679)   chr3:7591489-7592328 REVERSE   Aliases: MIL23.12	3.5	3.2	0.2	0.5	100.0%	-4.3
12568	AT5G57800.1   Symbol: WAX2   CER1 protein, putative (WAX2), similar to maize glossy1 homolog GI:2213643 from (Oryza sativa); contains Pfam profile PF01598: Sterol desaturase	4.3	4.1	0.1	0.5	100.0%	-5.0
12569	AT3G07880.1   Rho GDP-dissociation inhibitor family protein, similar to SP:P52565 Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) {Homo sapiens}; contains Pfam profile PF02115: RHO protein GDP dissociation inhibitor   chr3:2513977-2515828 FORWARD   Aliases: F17A17.22	9.0	8.8	0.2	0.5	100.0%	-4.9
12570	AT5G37230.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 finger protein RHA3b, Arabidopsis thaliana, PIR:T41745 (gi:3790575); contains Pfam domain zinc finger, C3HC4 type (RING finger) PF00097   chr5:14752384-14753010 FORWARD   Aliases: MNJ8.2, MNJ8_2	2.7	2.5	0.1	0.5	100.0%	-4.8
12571	AT3G53940.1   mitochondrial substrate carrier family protein   chr3:19981997-19984747 REVERSE   Aliases: F5K20.240	4.2	4.0	0.1	0.5	100.0%	-4.6
12572	AT3G63270.1   expressed protein   chr3:23386592-23388448 REVERSE   Aliases: F16M2.120	3.0	3.0	0.1	0.5	100.0%	-5.3
12573	AT1G09460.1   glucan endo-1,3-beta-glucosidase-related, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum)   chr1:3053903-3055273 FORWARD   Aliases: F14J9.12, F14J9_12	3.2	3.2	0.1	0.5	100.0%	-5.3
12574	AT4G14720.1   expressed protein   chr4:8431968-8435070 REVERSE   Aliases: DL3400C, FCAALL.297	5.7	6.0	-0.3	-0.5	100.0%	-4.7
12575	AT3G12600.1   MutT/nudix family protein, contains Pfam profile PF00293: NUDIX domain   chr3:4004590-4006205 FORWARD   Aliases: T2E22.9, T2E22_9	7.4	7.3	0.1	0.5	100.0%	-4.8
12576	AT3G05460.1   sporozoite surface protein-related, contains weak similarity to Sporozoite surface protein 2 precursor (Swiss-Prot:Q01443) (Plasmodium berghei yoelii)   chr3:1577806-1578740 FORWARD   Aliases: F22F7.9, F22F7_9	3.7	3.7	0.1	0.5	100.0%	-5.3
12577	AT3G51970.1   long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis   chr3:19295398-19296499 FORWARD   Aliases: F4F15.80	2.5	2.4	0.1	0.5	100.0%	-5.5
12578	AT2G32680.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780	3.1	3.1	0.1	0.5	100.0%	-5.2
12579	AT4G20870.1   fatty acid hydroxylase, putative, similar to fatty acid hydroxylase Fah1p GB:AF021804 GI:2736147 from (Arabidopsis thaliana)   chr4:11174597-11175889 REVERSE   Aliases: T13K14.30, T13K14_30	4.6	4.9	-0.3	-0.5	100.0%	-4.9
12580	AT1G01030.1   DNA-binding protein, putative, similar to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857, RAV2 GI:3868859; contains Pfam profile PF02362: B3 DNA binding domain   chr1:11649-13611 REVERSE   Aliases: T25K16.3, T25K16_3	2.8	2.9	-0.1	-0.5	100.0%	-5.4
12581	AT4G09680.1   expressed protein   chr4:6116759-6123301 FORWARD   Aliases: F17A8.30, F17A8_30	4.9	5.0	-0.1	-0.5	100.0%	-5.0
12582	AT5G18960.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282   chr5:6330558-6333073 FORWARD   Aliases: F17K4.210, F17K4_210	3.1	3.2	-0.1	-0.5	100.0%	-5.0
12583	AT1G04390.1   expressed protein   chr1:1179362-1183703 REVERSE   Aliases: F19P19.16, F19P19_16	3.3	3.4	-0.1	-0.5	100.0%	-4.8
12584	AT1G33750.1   terpene synthase/cyclase family protein, similar to DELTA-CADINENE SYNTHASE ISOZYME A GB:Q43714 from (Gossypium arboreum)   chr1:12233749-12236456 FORWARD   Aliases: F14M2.13, F14M2_13	2.8	2.7	0.1	0.5	100.0%	-5.2
12585	AT5G35640.1   hypothetical protein, contains Pfam profile PF04396: Protein of unknown function, DUF537	3.0	3.1	-0.1	-0.5	100.0%	-5.2
12586	AT3G52160.1   beta-ketoacyl-CoA synthase family protein, beta-ketoacyl-CoA synthase - Simmondsia chinensis,PID:g1045614   chr3:19355950-19357591 REVERSE   Aliases: F4F15.270	3.2	3.1	0.1	0.5	100.0%	-5.2
12587	AT3G43170.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr3:15183136-15183742 REVERSE   Aliases: F7K15.20	2.3	2.2	0.1	0.5	100.0%	-5.6
12588	AT1G02813.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:620678-621289 FORWARD   Aliases: None	2.3	2.4	-0.1	-0.5	100.0%	-5.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12589	AT1G36230.1   hypothetical protein   chr1:13612197-13615263 REVERSE   Aliases: F15C21.12, F15C21_12	3.4	3.5	-0.1	-0.5	100.0%	-5.1
12590	AT3G21510.1   Symbol: AHP1   two-component phosphorelay mediator 3 (HP3), identical to ATHP3 (Arabidopsis thaliana) GI:4156245   chr3:7578181-7579603 REVERSE   Aliases: ATHP3, HISTIDINE CONTAINING PHOSPHOTRANSMITTER 3, MIL23.7	3.8	4.0	-0.2	-0.5	100.0%	-4.3
12591	AT5G46370.1   Symbol: KCO2   outward rectifying potassium channel, putative (KCO2), identical to KCO2 protein (Arabidopsis thaliana) gi:6686780:emb:CAB64717; similar to kco1 (Arabidopsis thaliana) gi:2230761:emb:CAA69158; member of the 2 pore, 4 transmembrane (2P/4TM) K+ channel family, PMID:11500563	3.6	3.5	0.1	0.5	100.0%	-5.1
12592	AT3G59130.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	2.8	0.1	0.5	100.0%	-5.4
12593	AT3G09540.1   pectate lyase family protein, similar to style development-specific protein 9612 SP:P24396 from (Lycopersicon esculentum)   chr3:2928875-2931234 REVERSE   Aliases: F11F8.12	3.9	3.7	0.2	0.5	100.0%	-4.5
12594	AT3G62980.1   Symbol: TIR1   transport inhibitor response 1 (TIR1) (FBL1), E3 ubiquitin ligase SCF complex F-box subunit; identical to transport inhibitor response 1 GI:2352492 from (Arabidopsis thaliana)   chr3:23284091-23287350 REVERSE   Aliases: T20O10.80, TRANSPORT INHIBITOR RESPONSE 1	5.2	5.1	0.1	0.5	100.0%	-4.9
12595	AT2G34250.2   similar to protein transport protein sec61, putative [Arabidopsis thaliana] (TAIR:At1g78720.1); similar to protein transport protein sec61, putative [Arabidopsis thaliana] (TAIR:At1g29310.1); similar to hypothetical protein DDB0206262 [Dictyostelium discoideum] (GB:EAL68044.1); similar to putative Sec61; signal peptide plus 9 transmembrane domain-containing protein [Cryptosporidium parvum] (GB:EAK90569.1); similar to Sec61p [Triticum aestivum] (GB:AAF80449.1); similar to putative Sec61 alpha form 2 [Oryza sativa (japonica cultivar-group)] (GB:BAD28481.1); similar to Sec61 alpha subunit [Hordeum vulgare] (GB:AAK94784.1); contains InterPro domain SecY protein (InterPro:IPR002208)   chr2:14469180-14471947 FORWARD   Aliases: F13P17.9, F13P17_9	7.7	7.9	-0.2	-0.5	100.0%	-5.1
12596	AT1G43790.1   expressed protein   chr1:16578335-16578857 FORWARD   Aliases: F28H19.19, F28H19_19	4.7	4.9	-0.2	-0.5	100.0%	-4.2
12597	AT1G23200.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr1:8227167-8229571 FORWARD   Aliases: F26F24.2	3.0	2.9	0.1	0.5	100.0%	-5.2
12598	AT4G22360.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr4:11807672-11810129 FORWARD   Aliases: T10I14.190, T10I14_190	4.5	4.4	0.1	0.5	100.0%	-4.9
12599	AT5G43520.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.8	-0.3	-0.5	100.0%	-4.1
12600	AT2G14460.1   expressed protein   chr2:6161575-6162086 REVERSE   Aliases: T13P21.16, T13P21_16	7.2	6.9	0.3	0.5	100.0%	-4.7
12601	AT4G15520.1   tRNA/rRNA methyltransferase (SpoU) family protein, similar to SP:P19396 tRNA (Guanosine-2'-O-)-methyltransferase (EC 2.1.1.34) {Escherichia coli O157:H7}; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family; contains non_consensus donor splice site TA at exon 4   chr4:8862813-8864616 FORWARD   Aliases: DL3800W, FCAALL.322	6.6	6.4	0.2	0.5	100.0%	-4.5
12602	AT4G07515.1   expressed protein   chr4:4314954-4315507 REVERSE   Aliases: None	3.2	3.3	-0.1	-0.5	100.0%	-5.3
12603	AT2G17000.1   mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, contains Pfam profile PF00924: Mechanosensitive ion channel   chr2:7395975-7399187 REVERSE   Aliases: F6P23.16, F6P23_16	2.2	2.1	0.1	0.5	100.0%	-6.0
12604	AT1G07540.1   Symbol: TRFL2   telomere-binding protein, putative, similar to telomere binding protein TBP1 (Nicotiana glutinosa) gi:23664357:gb:AAN39330   chr1:2318430-2321045 REVERSE   Aliases: F22G5.8, F22G5_8, TRF LIKE 2	2.8	2.9	-0.1	-0.5	100.0%	-5.1
12605	AT5G45940.1   MutT/nudix family protein, contains Pfam profile PF00293: NUDIX domain   chr5:18646279-18647884 REVERSE   Aliases: K15I22.14, K15I22_14	4.7	4.9	-0.2	-0.5	100.0%	-4.7
12606	AT3G43720.2   similar to protease inhibitor/seed storage/lipid transfer protein (LTP) family protein [Arabidopsis thaliana] (TAIR:At2g27130.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAT77287.1); contains InterPro domain Plant lipid transfer/seed storage/trypsin-alpha amylase inhibitor (InterPro:IPR003612)   chr3:15626378-15628135 REVERSE   Aliases: T28A8.10	3.2	3.3	-0.1	-0.5	100.0%	-5.4
12607	AT2G44860.1   60S ribosomal protein L24, putative   chr2:18507444-18509617 REVERSE   Aliases: T13E15.13	10.0	10.2	-0.2	-0.5	100.0%	-4.9
12608	AT1G48120.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.8	3.7	0.1	0.5	100.0%	-5.1
12609	AT4G16240.1   expressed protein   chr4:9192351-9192583 REVERSE   Aliases: DL4160C, FCAALL.320	10.5	10.7	-0.2	-0.5	100.0%	-4.9
12610	AT1G77210.1   sugar transporter, putative, similar to monosaccharide transporter PaMst-1 (Picea abies) GI:2258137, sugar carrier protein GI:169735 from (Ricinus communis), glucose transporter (Saccharum hybrid cultivar H65-7052) GI:347855; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:29013833-29015983 REVERSE   Aliases: T14N5.7, T14N5_7	3.1	3.0	0.1	0.5	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12611	AT1G23400.1   expressed protein   chr1:8312065-8314733 REVERSE   Aliases: F26F24.27, F26F24_27	4.4	4.5	-0.1	-0.5	100.0%	-5.0
12612	AT1G75830.1   Symbol: LCR67/PDF1.1   plant defensin-fusion protein, putative (PDF1.1), identical to SP:P30224 Cysteine-rich antifungal protein 1 precursor (AFP1) (Anther-specific protein S18 homolog) {Arabidopsis thaliana}   chr1:28476022-28476552 FORWARD   Aliases: LCR67, Low molecular weight cysteine rich 67, PDF1.1, T4O12.7, T4O12_7	2.9	2.8	0.1	0.5	100.0%	-5.5
12613	AT5G62770.1   expressed protein   chr5:25227721-25228833 FORWARD   Aliases: MQB2.9, MQB2_9	3.3	3.2	0.1	0.5	100.0%	-5.2
12614	AT5G16720.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr5:5494231-5496813 FORWARD   Aliases: F5E19.60, F5E19_60	4.3	4.2	0.1	0.5	100.0%	-5.0
12615	AT2G41160.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627: UBA/TS-N domain   chr2:17163107-17165936 REVERSE   Aliases: T3K9.7, T3K9_7	4.1	4.3	-0.1	-0.5	100.0%	-4.9
12616	AT5G55580.1   mitochondrial transcription termination factor family protein / mTERF family protein, weak similarity to mtDBP protein (Paracentrotus lividus) GI:4584695; contains Pfam profile PF02536: mTERF   chr5:22532666-22535155 FORWARD   Aliases: MDF20.2, MDF20_2	2.9	3.0	-0.1	-0.5	100.0%	-5.4
12617	AT2G35910.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 zinc finger protein ATL6 (Arabidopsis thaliana) GI:4928403; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:15080011-15081160 REVERSE   Aliases: F11F19.18, F11F19_18	2.7	2.8	-0.1	-0.5	100.0%	-4.7
12618	AT4G21340.1   ethylene-responsive protein-related, contains similarity to ethylene-inducible ER33 protein (Lycopersicon esculentum) gi:5669656:gb:AAD46413   chr4:11352996-11354787 FORWARD   Aliases: T6K22.70, T6K22_70	2.3	2.4	-0.1	-0.5	100.0%	-5.3
12619	AT1G71440.1   Symbol: PFI   tubulin folding cofactor E / Pfifferling (PFI), almost identical to tubulin folding cofactor E (Pfifferling; PFI) GI:20514267 from (Arabidopsis thaliana); identical to cDNA tubulin folding cofactor E, GI:20514266   chr1:26924125-26928048 REVERSE   Aliases: F3I17.21, F3I17_21, PFIFFERLING, TFC E, TUBULIN FOLDING COFACTOR E	6.6	6.7	-0.2	-0.5	100.0%	-4.8
12620	AT1G12820.1   Symbol: IPS1   transport inhibitor response protein, putative, E3 ubiquitin ligase SCF complex F-box subunit; similar to transport inhibitor response 1 GI:2352492 from (Arabidopsis thaliana)   chr1:4368548-4371291 REVERSE   Aliases: F13K23.7, F13K23_7	6.4	6.5	-0.1	-0.5	100.0%	-4.8
12621	AT2G45270.1   glycoprotease M22 family protein, similar to SP:P36175 O-sialoglycoprotein endopeptidase (EC 3.4.24.57) (Glycoprotease) {Pasteurella haemolytica}; contains Pfam profile PF00814: Glycoprotease family   chr2:18673622-18676947 FORWARD   Aliases: F4L23.22	5.7	5.9	-0.2	-0.5	100.0%	-4.5
12622	AT4G38530.1   Symbol: ATPLC1	3.0	2.9	0.1	0.5	100.0%	-5.1
12623	AT5G23570.1   Symbol: SGS3   XS domain-containing protein / XS zinc finger domain-containing protein-related, contains Pfam profiles PF03468: XS domain, weak hit to PF03470: XS zinc finger domain   chr5:7943127-7946053 FORWARD   Aliases: MQM1.17, MQM1_17, SUPPRESSOR OF GENE SILENCING 3	4.2	4.4	-0.2	-0.5	100.0%	-4.7
12624	AT1G63100.1   scarecrow transcription factor family protein, similar to GI:1497987 from (Arabidopsis thaliana) (Cell (1996) In press)   chr1:23403056-23405032 REVERSE   Aliases: F16M19.21, F16M19_21	6.6	6.4	0.2	0.5	100.0%	-5.0
12625	AT2G01860.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:388054-390248 FORWARD   Aliases: T23K3.5, T23K3_5	4.0	4.1	-0.1	-0.5	100.0%	-4.8
12626	AT2G18620.1   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative, similar to gi:413730 to geranylgeranyl pyrophosphate synthase, chloroplast precursor GB:P34802 from (Arabidopsis thaliana) synonymous with farnesyltranstransferase   chr2:8085370-8086442 FORWARD   Aliases: F24H14.3, F24H14_3	3.5	3.6	-0.1	-0.5	100.0%	-5.2
12627	AT5G48410.1   Symbol: ATGLR1.3   glutamate receptor family protein (GLR1.3), plant glutamate receptor family, PMID:11379626   chr5:19637493-19640651 FORWARD   Aliases: GLR1.3, MJE7.4, MJE7_4	2.7	2.6	0.1	0.5	100.0%	-5.2
12628	AT1G28690.1   pentatricopeptide (PPR) repeat-containing protein, contains six TIGRFAM TIGR00756: pentatricopeptide repeat domains; contains five Pfam PF01535: PPR repeats   chr1:10080028-10081590 REVERSE   Aliases: F1K23.11, F1K23_11	2.8	2.7	0.1	0.5	100.0%	-5.7
12629	AT2G38730.1   peptidyl-prolyl cis-trans isomerase, putative / cyclophilin, putative / rotamase, putative, similar to cyclophilin (Homo sapiens) gi:3647230:gb:AAC60793	7.0	7.4	-0.4	-0.5	100.0%	-4.2
12630	AT1G66370.1   Symbol: MYB113	3.0	3.2	-0.1	-0.5	100.0%	-5.1
12631	AT2G41600.2   expressed protein   chr2:17352455-17353793 REVERSE   Aliases: T32G6.12, T32G6_12	5.6	5.8	-0.2	-0.5	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12632	AT5G19710.1   hypothetical protein, HPT phosphotransmitter - Arabidopsis thaliana, EMBL:AB041766   chr5:6664747-6666109 REVERSE   Aliases: T29J13.130, T29J13_130	2.2	2.2	-0.0	-0.5	100.0%	-5.9
12633	AT3G07910.1   expressed protein   chr3:2523163-2524171 REVERSE   Aliases: F17A17.25	10.0	10.2	-0.1	-0.5	100.0%	-4.9
12634	AT4G13790.1   auxin-responsive protein, putative, similar to small auxin up RNA (SAUR-AC1) (SP:S70188) (Arabidopsis thaliana)   chr4:7999710-8000218 REVERSE   Aliases: F18A5.180, F18A5_180	3.1	3.0	0.0	0.5	100.0%	-5.9
12635	AT5G04650.1   hypothetical protein, predicted protein, Arabidopsis thaliana   chr5:1334404-1334957 FORWARD   Aliases: T1E3.10, T1E3_10	4.5	4.3	0.3	0.5	100.0%	-4.7
12636	AT1G64410.1   expressed protein   chr1:23930056-23935866 REVERSE   Aliases: F15H21.18, F15H21_18	3.8	4.1	-0.2	-0.5	100.0%	-5.0
12637	AT5G66670.1   hypothetical protein, contains Pfam:PF05055: Protein of unknown function (DUF677)   chr5:26628700-26629926 REVERSE   Aliases: MSN2.5, MSN2_5	3.3	3.1	0.2	0.5	100.0%	-5.1
12638	AT3G59260.1   pirin, putative, similar to SP:O00625 Pirin {Homo sapiens}; contains Pfam profile PF02678: Pirin	2.5	2.4	0.1	0.5	100.0%	-5.5
12639	AT3G05110.1   expressed protein   chr3:1426303-1427725 REVERSE   Aliases: T12H1.7, T12H1_7	2.8	2.7	0.1	0.5	100.0%	-5.8
12640	AT2G36750.1   Symbol: UGT72C1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:15417541-15419117 REVERSE   Aliases: F13K3.15, F13K3_15, UGT72C1	2.8	2.7	0.1	0.5	100.0%	-5.2
12641	AT1G75240.1   zinc finger homeobox family protein / ZF-HD homeobox family protein   chr1:28244735-28246417 FORWARD   Aliases: F22H5.4, F22H5_4	3.6	3.5	0.1	0.5	100.0%	-4.8
12642	AT2G38670.1   ethanolamine-phosphate cytidyltransferase, putative / phosphorylethanolamine transferase, putative / CTP:phosphoethanolamine cytidyltransferase, putative, similar to SP:Q99447 Ethanolamine-phosphate cytidyltransferase (EC 2.7.7.14) {Homo sapiens}; contains Pfam profile PF01467: Cytidyltransferase   chr2:16175945-16178996 FORWARD   Aliases: T6A23.13, T6A23_13	7.4	7.7	-0.3	-0.5	100.0%	-4.6
12643	AT5G27600.1   Symbol: LACS7   AMP-binding protein, putative, similar to AMP-binding protein (MF39P) gi:1617274 from Brassica napus, long-chain-fatty-acid--CoA ligase - Brassica napus, EMBL:Z72152; contains Pfam AMP-binding enzyme domain PF00501   chr5:9742619-9747008 FORWARD   Aliases: F15A18.60, F15A18_60, LONG CHAIN ACYL COA SYNTHETASE 7	6.0	6.1	-0.2	-0.5	100.0%	-4.8
12644	AT3G51820.1   chlorophyll synthetase, putative, identical to gi:972938 putative chlorophyll synthetase from Arabidopsis thaliana   chr3:19226980-19230027 REVERSE   Aliases: ATEM1.7, ATG4	10.3	10.1	0.2	0.5	100.0%	-4.4
12645	AT2G35360.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr2:14896128-14897922 REVERSE   Aliases: T32F12.26, T32F12_26	4.2	4.4	-0.1	-0.5	100.0%	-5.1
12646	AT4G16990.4   similar to disease resistance protein (TIR-NBS-LRR class), putative [Arabidopsis thaliana] (TAIR:At4g16940.1); similar to disease resistance protein (TIR-NBS-LRR class), putative [Arabidopsis thaliana] (TAIR:At4g16960.1); similar to disease resistance-like protein [Brassica napus] (GB:AAG40141.1); contains InterPro domain NB-ARC domain (InterPro:IPR002182); contains InterPro domain ATP/GTP-binding site motif A (P-loop) (InterPro:IPR001687); contains InterPro domain Disease resistance protein (InterPro:IPR000767)   chr4:9560154-9565574 FORWARD   Aliases: DL4525W, FCAALL.324	2.5	2.4	0.1	0.5	100.0%	-5.5
12647	AT1G22270.1   expressed protein, contains Pfam domain PF03966: Protein of unknown function (DUF343)   chr1:7865482-7866128 FORWARD   Aliases: T16E15.11, T16E15_11	8.7	8.5	0.2	0.5	100.0%	-4.5
12648	AT5G38320.1   expressed protein, ; expression supported by MPSS   chr5:15333390-15334028 REVERSE   Aliases: MSI17.5, MSI17_5	2.5	2.5	-0.1	-0.5	100.0%	-5.5
12649	AT2G24830.1   zinc finger (CCCH-type) family protein / D111/G-patch domain-containing protein, contains Pfam profiles PF01585: G-patch domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:10583408-10586309 REVERSE   Aliases: F27C12.25, F27C12_25	8.7	8.9	-0.2	-0.5	100.0%	-5.0
12650	AT1G17830.1   expressed protein   chr1:6135796-6138425 REVERSE   Aliases: F2H15.6, F2H15_6	2.9	3.0	-0.1	-0.5	100.0%	-5.0
12651	AT3G57830.1   leucine-rich repeat transmembrane protein kinase, putative, several receptor-like protein kinases   chr3:21430494-21433523 FORWARD   Aliases: T10K17.40	2.5	2.6	-0.1	-0.5	100.0%	-5.5
12652	AT2G23610.1   esterase, putative, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:10051259-10053612 REVERSE   Aliases: F26B6.26, F26B6_26	9.4	9.0	0.4	0.5	100.0%	-4.6
12653	AT4G10970.3   expressed protein   chr4:6719203-6722198 REVERSE   Aliases: F25I24.180, F25I24_180	7.5	7.3	0.1	0.5	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12654	AT1G18260.1   suppressor of lin-12-like protein-related / sel-1 protein-related, similar to Sel-1 homolog precursor (Suppressor of lin-12-like protein) (Sel-1L)(SP:Q9UBV2) {Homo sapiens}   chr1:6278841-6282071 REVERSE   Aliases: T10O22.22, T10O22_22	7.8	8.0	-0.3	-0.5	100.0%	-4.6
12655	AT5G19460.1   MutT/nudix family protein, similar to SP:P41888 Thiamine pyrophosphokinase (EC 2.7.6.2) (TPK) (Thiamine kinase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain	4.5	4.3	0.2	0.5	100.0%	-4.3
12656	AT5G19470.1   MutT/nudix family protein, similar to SP:P41888 Thiamine pyrophosphokinase (EC 2.7.6.2) (TPK) (Thiamine kinase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain	4.5	4.3	0.2	0.5	100.0%	-4.3
12657	AT1G13920.1   remorin family protein, contains Pfam domain, PF03763: Remorin, C-terminal region   chr1:4758185-4759751 FORWARD   Aliases: F16A14.13	2.9	2.8	0.1	0.5	100.0%	-4.7
12658	AT5G14400.1   Symbol: CYP724A1   similar to steroid 22-alpha-hydroxylase (CYP90B1) (DWF4) [Arabidopsis thaliana] (TAIR:At3g50660.1); similar to OSJNBa0016O02.25 [Oryza sativa (japonica cultivar-group)] (GB:XP_472820.1); contains InterPro domain E-class P450, group I (InterPro:IPR002401); contains InterPro domain Cytochrome P450 (InterPro:IPR001128)   chr5:4643524-4646385 FORWARD   Aliases: F18O22.190, F18O22_190	3.3	3.4	-0.1	-0.5	100.0%	-5.0
12659	AT5G44930.2   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr5:18157457-18159371 REVERSE   Aliases: K21C13.11, K21C13_11	3.1	3.2	-0.1	-0.5	100.0%	-5.3
12660	AT1G64670.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoate hydrolase (Pseudomonas putida) GI:2822275; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:24034483-24037218 REVERSE   Aliases: F1N19.24, F1N19_24	2.3	2.3	-0.1	-0.5	100.0%	-5.5
12661	AT5G15570.1   expressed protein, hypothetical protein F14P3.19 - Arabidopsis thaliana, EMBL:AC009755   chr5:5066854-5067999 FORWARD   Aliases: T20K14.180, T20K14_180	3.9	4.1	-0.2	-0.5	100.0%	-4.9
12662	AT4G21890.1   expressed protein   chr4:11611855-11612915 REVERSE   Aliases: T8O5.100, T8O5_100	3.5	3.4	0.1	0.5	100.0%	-5.2
12663	AT4G03390.1   leucine-rich repeat transmembrane protein kinase, putative, similar to Z. mays leucine-rich repeat transmembrane protein kinase LRRTPK 1, GenBank accession number AF023164   chr4:1490465-1495102 REVERSE   Aliases: F4C21.35, F4C21_35	6.6	6.5	0.2	0.5	100.0%	-4.8
12664	AT5G15110.1   pectate lyase family protein, similar to pectate lyase P59 SP:P15722 from (Lycopersicon esculentum)   chr5:4895969-4897685 FORWARD   Aliases: F2G14.230, F2G14_230	2.3	2.3	-0.1	-0.5	100.0%	-5.4
12665	AT1G20530.1   expressed protein   chr1:7108360-7110367 REVERSE   Aliases: F5M15.15, F5M15_15	3.3	3.2	0.1	0.5	100.0%	-5.2
12666	AT4G15510.3   similar to photosystem II reaction center PsbP family protein [Arabidopsis thaliana] (TAIR:At3g55330.1); similar to photosystem II oxygen-evolving complex 23K protein PsbP homolog [Thermosynechococcus elongatus BP-1] (GB:NP_682865.1); contains InterPro domain Photosystem II reaction center protein PsbP (InterPro:IPR002683)   chr4:8860717-8862656 FORWARD   Aliases: DL3795W, FCAALL.88	3.4	3.6	-0.1	-0.5	100.0%	-4.8
12667	AT1G15640.1   expressed protein   chr1:5379072-5380022 FORWARD   Aliases: T16N11.15, T16N11_15	3.9	3.7	0.2	0.5	100.0%	-4.7
12668	AT1G69660.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr1:26203286-26204266 REVERSE   Aliases: F24J1.26	3.0	2.9	0.1	0.5	100.0%	-5.3
12669	AT3G56150.1   Symbol: EIF3C   eukaryotic translation initiation factor 3 subunit 8 / eIF3 p110 / eIF3c / p105 (TIF3C1), nearly identical to SP:O49160 Eukaryotic translation initiation factor 3 subunit 8 (eIF3 p110) (eIF3c) (p105) {Arabidopsis thaliana}   chr3:20844563-20848136 REVERSE   Aliases: ATEIF3C 1, ATTIF3C1, EIF3C 1, EUKARYOTIC TRANSLATION INITIATION FACTOR 3, EUKARYOTIC TRANSLATION INITIATION FACTOR 3 SUBUNIT 8, F18O21.110, TIF3C1	6.4	6.6	-0.2	-0.5	100.0%	-5.0
12670	AT3G25970.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:9501353-9503293 REVERSE   Aliases: MPE11.14	3.4	3.4	0.1	0.5	100.0%	-5.5
12671	AT2G33980.1   MutT/nudix family protein, similar to coenzyme A diphosphatase (Mus musculus) GI:12746410; contains Pfam profile PF00293: NUDIX domain   chr2:14356843-14366919 REVERSE   Aliases: T14G11.10, T14G11_10	2.4	2.4	0.1	0.5	100.0%	-5.7
12672	AT2G44380.1   DC1 domain-containing protein, highly similar to GP:2435515:AF024504; contains Pfam profile PF03107: DC1 domain   chr2:18330666-18331504 REVERSE   Aliases: F4I1.19	3.1	3.3	-0.2	-0.5	100.0%	-4.2
12673	AT4G00280.1   expressed protein   chr4:122409-122851 REVERSE   Aliases: A_IG005I10.10, A_IG005I10_10, F5I10.10, F5I10_10	4.0	4.1	-0.1	-0.5	100.0%	-5.4
12674	ATCG00690.1   Symbol: PSBT   photosystem II protein T. Encodes the chlorophyll a apoprotein CP47.   chrC:74082-74183 FORWARD   Aliases: PSBT	4.1	5.2	-1.1	-0.5	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12675	AT5G53140.1   protein phosphatase 2C, putative / PP2C, putative   chr5:21565701-21569696 FORWARD   Aliases: MFH8.8, MFH8_8	5.1	4.6	0.5	0.5	100.0%	-4.8
12676	AT2G36570.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:15342575-15345006 FORWARD   Aliases: F1O11.20, F1O11_20	3.8	3.7	0.1	0.5	100.0%	-5.3
12677	AT4G01900.1   Symbol: GLB1   P II nitrogen sensing protein (GLB I), identical to P II nitrogen sensing protein GLB I (GI:7268574) (Arabidopsis thaliana); similar to nitrogen regulatory protein P-II (PII signal transducing protein) (SP:O30794) {Nostoc punctiforme}   chr4:821685-823510 FORWARD   Aliases: P11, PII PROTEIN, T7B11.16, T7B11_16	4.9	5.2	-0.3	-0.5	100.0%	-4.7
12678	AT2G22990.5   Symbol: SNG1   sinapoylglucose:malate sinapoyltransferase (SNG1), similar to serine carboxypeptidase I precursor (SP:P37890) (Oryza sativa); contains Pfam profile PF00450: Serine carboxypeptidase; identical to cDNA sinapoylglucose:malate sinapoyltransferase (SNG1) GI:8699618   chr2:9793396-9797259 FORWARD   Aliases: MALATE SINAPOYLTRANSFERASE, SCPL8, SINAPOYL GLUCOSE ACCUMULATOR 1, SINAPOYLGLUCOSE 1, T20K9.18	2.3	2.3	0.0	0.5	100.0%	-5.9
12679	AT5G51280.1   DEAD-box protein abstrakt, putative   chr5:20858474-20861032 FORWARD   Aliases: MWD22.23, MWD22_23	8.6	8.8	-0.2	-0.5	100.0%	-4.8
12680	AT1G11250.1   Symbol: SYP125	3.9	4.1	-0.1	-0.5	100.0%	-5.1
12681	AT1G19640.1   Symbol: JMT   S-adenosyl-L-methionine:jasmonic acid carboxyl methyltransferase (JMT), nearly identical to gi:13676829   chr1:6788876-6791837 REVERSE   Aliases: F14P1.3, F14P1_3, JASMONIC ACID CARBOXYL METHYLTRANSFERASE	4.9	4.6	0.2	0.5	100.0%	-4.2
12682	AT4G07390.1   PQ-loop repeat family protein / transmembrane family protein, similar to SP:Q60441 Mannose-P-dolichol utilization defect 1 protein (Suppressor of Lec15 and Lec35 glycosylation mutation) {Cricetulus griseus}, Lec35 protein (Cricetulus griseus) GI:9858721; contains Pfam profile PF04193: PQ loop repeat   chr4:4195677-4197568 FORWARD   Aliases: F28D6.6, F28D6_6	6.9	7.1	-0.2	-0.5	100.0%	-4.7
12683	AT1G77380.1   Symbol: AAP3   amino acid carrier, putative / amino acid permease, putative, strong similarity to amino acid carrier GI:3293031 from (Ricinus communis); contains Pfam profile PF01490: Transmembrane amino acid transporter protein; identical to cDNA AAP3 (Amino Acid Permease) GI:3970651   chr1:29079782-29082284 REVERSE   Aliases: F2P24.9, F2P24_9	9.9	9.7	0.2	0.5	100.0%	-4.7
12684	AT5G23860.1   Symbol: TUB8   tubulin beta-8 chain (TUB8) (TUBB8), identical to SP:P29516 Tubulin beta-8 chain {Arabidopsis thaliana}; supporting cDNA gi:15451225:gb:AY054693.1:   chr5:8042886-8044822 FORWARD   Aliases: None	3.0	2.9	0.1	0.5	100.0%	-5.0
12685	AT3G14490.1   terpene synthase/cyclase family protein, contains Pfam profile: PF01397 terpene synthase family   chr3:4863638-4865956 REVERSE   Aliases: MOA2.12	2.4	2.5	-0.1	-0.5	100.0%	-5.5
12686	AT1G11190.1   Symbol: BFN1   bifunctional nuclease (BFN1), identical to bifunctional nuclease bfn1 (Arabidopsis thaliana) gi:4099831:gb:AAD00693   chr1:3750066-3752780 REVERSE   Aliases: BIFUNCTIONAL NUCLEASE I, T28P6.14, T28P6_14	3.8	4.0	-0.2	-0.5	100.0%	-4.5
12687	AT5G23630.1   ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein, similar to SP:O14072 Cation-transporting ATPase 4 (EC 3.6.3.-) {Schizosaccharomyces pombe}; contains InterPro accession IPR001757: ATPase, E1-E2 type; contains Pfam profile PF00702: haloacid dehalogenase-like hydrolase   chr5:7960654-7967647 REVERSE   Aliases: MQM1.11, MQM1_11	6.6	6.8	-0.2	-0.5	100.0%	-4.9
12688	AT4G33290.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.9	3.0	-0.1	-0.5	100.0%	-5.4
12689	AT1G64510.1   ribosomal protein S6 family protein, similar to plastid ribosomal protein S6 precursor GB:AAF64311 GI:7582401 from (Spinacia oleracea)   chr1:23958466-23959914 REVERSE   Aliases: F1N19.8, F1N19_8	6.4	6.7	-0.4	-0.5	100.0%	-4.3
12690	ATCG00040.1   Symbol: MATK   Encodes a maturase located in the trnK intron in the chloroplast genome.	10.1	10.6	-0.4	-0.5	100.0%	-4.9
12691	AT2G13630.1   F-box family protein-related, contains TIGRFAM TIGR01640 : F-box protein interaction domain; similar to F-box protein Fbx8 (GI:6164735) (Homo sapiens)   chr2:5691620-5692513 REVERSE   Aliases: T10F5.17, T10F5_17	3.0	3.1	-0.1	-0.5	100.0%	-5.3
12692	AT1G34540.1   Symbol: CYP94D1   cytochrome P450 family protein, similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:O81117) {Vicia sativa}; contains Pfam profile: PF00067 cytochrome P450   chr1:12637032-12638528 FORWARD   Aliases: F12K21.15, F12K21_15	2.9	2.8	0.1	0.5	100.0%	-5.0
12693	AT3G25810.1   myrcene/ocimene synthase, putative, similar to GI:9957293; contains Pfam profile: PF01397 terpene synthase family   chr3:9432042-9435081 FORWARD   Aliases: K13N2.7	2.4	2.5	-0.1	-0.5	100.0%	-5.6
12694	AT3G60980.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:22576284-22577720 REVERSE   Aliases: T27I15.70	6.3	6.4	-0.1	-0.5	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12695	AT1G10310.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short-chain dehydrogenase/reductase (SDR) superfamily   chr1:3381605-3383916 REVERSE   Aliases: F14N23.19, F14N23_19	8.3	8.4	-0.1	-0.5	100.0%	-4.6
12696	AT5G36270.1   dehydroascorbate reductase, putative, similar to dehydroascorbate reductase {Spinacia oleracea} gi:10952511 gb:AF195783, PMID:11148269   chr5:14310161-14310814 FORWARD   Aliases: T30G6.13, T30G6_13	4.3	4.1	0.2	0.5	100.0%	-4.5
12697	AT3G06640.1   protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108   chr3:2074544-2078323 REVERSE   Aliases: T8E24.12	4.0	3.9	0.1	0.5	100.0%	-5.0
12698	AT1G26870.1   Symbol: ANAC009   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to GB:AAD22369, NAM stands for No Apicla Meristem   chr1:9312843-9314970 FORWARD   Aliases: ANAC009, T2P11.6, T2P11_6	2.0	2.0	0.0	0.5	100.0%	-6.1
12699	AT1G54180.1   expressed protein   chr1:20231364-20232186 FORWARD   Aliases: F15I1.28, F15I1_28	3.0	2.9	0.1	0.5	100.0%	-5.4
12700	AT4G16470.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:9287884-9289485 REVERSE   Aliases: DL4260C, FCAALL.374	4.2	4.4	-0.1	-0.5	100.0%	-4.9
12701	AT2G46225.1   Symbol: ABI1L1	3.9	4.0	-0.1	-0.5	100.0%	-4.7
12702	AT4G04480.1   expressed protein   chr4:2229647-2230843 FORWARD   Aliases: T26N6.8, T26N6_8	3.1	3.0	0.1	0.5	100.0%	-5.1
12703	AT5G35450.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.6	3.5	0.1	0.5	100.0%	-5.0
12704	AT1G29600.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:10344032-10345637 FORWARD   Aliases: F15D2.17, F15D2_17	2.4	2.3	0.1	0.5	100.0%	-5.3
12705	AT4G37770.1   Symbol: ACS8   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to 1-aminocyclopropane-1-carboxylate synthase, Arabidopsis thaliana, GI:940370 (S71174)   chr4:17752216-17753919 FORWARD   Aliases: T28I19.50, T28I19_50	3.5	3.7	-0.2	-0.5	100.0%	-4.9
12706	AT5G64780.1   expressed protein, similar to unknown protein (pir::T04031)   chr5:25917785-25919351 REVERSE   Aliases: MVP7.11, MVP7_11	4.0	3.9	0.1	0.5	100.0%	-4.8
12707	AT2G37780.1   DC1 domain-containing protein, contains Pfam PF03107: DC1 domain	2.4	2.4	0.1	0.5	100.0%	-5.4
12708	AT5G41240.1   Symbol: ATGSTT2   glutathione S-transferase, putative, similar to glutathione S-transferase, GST 10b GB:CAA10662 (Arabidopsis thaliana) 37349.   chr5:16515383-16518086 REVERSE   Aliases: GST10B, K1O13.3, K1O13_3	2.7	2.6	0.1	0.5	100.0%	-5.4
12709	AT1G59790.1   cullin-related, low similarity to Hs-CUL-1 (Homo sapiens) GI:1381142   chr1:22005169-22007050 FORWARD   Aliases: F23H11.11, F23H11_11	3.4	3.3	0.1	0.5	100.0%	-5.3
12710	AT3G09530.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr3:2926308-2928221 FORWARD   Aliases: F11F8.11	2.9	2.9	0.1	0.5	100.0%	-5.2
12711	AT5G11420.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr5:3644599-3647296 FORWARD   Aliases: F15N18.10, F15N18_10	4.0	3.9	0.1	0.5	100.0%	-4.9
12712	AT3G45120.1   expressed protein   chr3:16522715-16523035 REVERSE   Aliases: T14D3.60	3.8	4.0	-0.3	-0.5	100.0%	-4.3
12713	AT1G06270.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:1918087-1919746 REVERSE   Aliases: F9P14.13, F9P14_13	4.8	5.0	-0.1	-0.5	100.0%	-5.0
12714	AT3G29200.1   Symbol: CM1   chorismate mutase, chloroplast (CM1), identical to chorismate mutase GB:Z26519 (SP:P42738) (Arabidopsis thaliana)	5.8	5.7	0.2	0.5	100.0%	-4.8
12715	AT1G06590.1   expressed protein   chr1:2016307-2024643 REVERSE   Aliases: F12K11.7, F12K11_7	3.7	3.8	-0.1	-0.5	100.0%	-5.1
12716	AT3G28170.1   hypothetical protein   chr3:10499598-10501597 FORWARD   Aliases: MIG10.7	3.9	4.0	-0.1	-0.5	100.0%	-5.2
12717	AT5G12440.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr5:4035295-4038798 REVERSE   Aliases: None	3.4	3.3	0.1	0.5	100.0%	-4.9
12718	NA	2.6	2.6	0.1	0.5	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12719	AT4G13000.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:7598090-7599254 REVERSE   Aliases: F25G13.90, F25G13_90	3.4	3.5	-0.1	-0.5	100.0%	-5.5
12720	AT1G08315.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr1:2620334-2621542 REVERSE   Aliases: None	6.1	5.9	0.1	0.5	100.0%	-4.9
12721	AT5G47455.6   expressed protein   chr5:19267950-19269591 FORWARD   Aliases: None	4.4	4.5	-0.2	-0.5	100.0%	-4.7
12722	AT3G11600.1   expressed protein, weak similarity to B-type cyclin (GI:849074) (Nicotiana tabacum)   chr3:3667235-3667985 FORWARD   Aliases: F24K9.6	3.1	3.4	-0.2	-0.5	100.0%	-4.1
12723	AT1G17020.1   Symbol: SRG1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase (Petunia x hybrida)(GI:311658), leucoanthocyanidin dioxygenase (Malus domestica)(SP:P51091); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:5820217-5822006 FORWARD   Aliases: ATSRG1, F20D23.28, F20D23_28, SENESCENCE RELATED GENE 1	2.7	2.7	0.1	0.5	100.0%	-5.5
12724	AT3G61040.2   Symbol: CYP76C7   cytochrome P450 family protein, similar to cytochrome P450 monooxygenase - Arabidopsis thaliana, EMBL:D78600   chr3:22605384-22607100 REVERSE   Aliases: T27I15.130	3.2	3.3	-0.1	-0.5	100.0%	-5.1
12725	AT4G08290.2   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr4:5238924-5241027 FORWARD   Aliases: T12G13.130, T12G13_130	3.9	3.4	0.5	0.5	100.0%	-4.5
12726	AT4G26330.1   subtilase family protein, contains similarity to SBT1, a subtilase from tomato plants GI:1771160 from (Lycopersicon esculentum)   chr4:13320417-13323470 FORWARD   Aliases: T25K17.140, T25K17_140	3.1	3.2	-0.1	-0.5	100.0%	-5.2
12727	AT1G06980.1   expressed protein, similar to hypothetical protein GI:2347189 from (Arabidopsis thaliana)   chr1:2143030-2143820 REVERSE   Aliases: F10K1.30, F10K1_30	3.0	3.1	-0.1	-0.5	100.0%	-5.6
12728	AT1G55530.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:20732848-20734923 REVERSE   Aliases: T5A14.7, T5A14_7	7.7	7.9	-0.2	-0.5	100.0%	-4.7
12729	AT3G26280.1   Symbol: CYP71B4   cytochrome P450 family protein, identical to cytochrome P450 monooxygenase (CYP71B4) GB:D78603 (Arabidopsis thaliana) (Plant Mol. Biol. 37 (1), 39-52 (1998))	2.7	2.8	-0.1	-0.5	100.0%	-5.5
12730	AT5G51570.1   band 7 family protein, similar to hypersensitive-induced response protein (Zea mays) GI:7716468; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr5:20966652-20968723 FORWARD   Aliases: K17N15.12, K17N15_12	9.5	9.2	0.4	0.5	100.0%	-4.5
12731	AT5G01150.1   hypothetical protein, contains Pfam profile PF05056: Protein of unknown function (DUF674)   chr5:51987-53648 FORWARD   Aliases: F7J8.130, F7J8_130	2.2	2.3	-0.1	-0.5	100.0%	-5.6
12732	AT5G58210.3   hydroxyproline-rich glycoprotein family protein   chr5:23569339-23571572 FORWARD   Aliases: MCK7.8, MCK7_8	4.2	4.1	0.1	0.5	100.0%	-5.0
12733	AT3G08500.1   Symbol: MYB83   myb family transcription factor (MYB83), contains Pfam profile: PF00249: Myb-like DNA-binding domain   chr3:2576964-2578078 REVERSE   Aliases: T8G24.3	2.4	2.4	0.1	0.5	100.0%	-5.7
12734	AT2G42860.1   expressed protein   chr2:17840842-17842190 FORWARD   Aliases: F7D19.14, F7D19_14	2.6	2.7	-0.1	-0.5	100.0%	-5.2
12735	AT5G53370.1   pectinesterase family protein   chr5:21666758-21668819 REVERSE   Aliases: ATPMEPCRF, K19E1.17, K19E1_17	7.5	7.1	0.4	0.5	100.0%	-4.4
12736	AT5G45400.1   replication protein, putative, similar to replication protein A 70kDa (Oryza sativa (japonica cultivar-group)) GI:13536993; contains InterPro entry IPR004365: OB-fold nucleic acid binding domain, PF04057: Replication factor-A protein 1, N-terminal domain   chr5:18416217-18418871 FORWARD   Aliases: MFC19.7, MFC19_7	2.9	3.0	-0.1	-0.5	100.0%	-5.4
12737	AT2G02630.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.9	-0.1	-0.5	100.0%	-5.0
12738	AT1G54520.1   expressed protein   chr1:20367115-20369706 FORWARD   Aliases: F20D21.34, F20D21_34	7.9	8.2	-0.2	-0.5	100.0%	-4.7
12739	AT4G34690.1   expressed protein   chr4:16555468-16556102 REVERSE   Aliases: T4L20.270, T4L20_270	2.5	2.6	-0.1	-0.5	100.0%	-5.2
12740	AT3G59020.2   similar to importin beta-2 subunit family protein [Arabidopsis thaliana] (TAIR:At2g31660.1); similar to putative Importin 7<Ran-binding protein 7 [Oryza sativa (japonica cultivar-group)] (GB:XP_465609.1); contains InterPro domain Importin-beta, N-terminal (InterPro:IPR001494)   chr3:21821237-21828532 REVERSE   Aliases: F17J16.70	4.8	5.3	-0.4	-0.5	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12741	AT1G26880.1   60S ribosomal protein L34 (RPL34A), identical to GB:Q42351, location of EST 105E2T7, gb:T22624   chr1:9315370-9316716 REVERSE   Aliases: T2P11.7, T2P11_7	10.3	10.5	-0.2	-0.5	100.0%	-4.6
12742	AT5G09330.1   Symbol: ANAC082   no apical meristem (NAM) family protein, similar to NAC1 (GI:7716952)	7.4	7.5	-0.1	-0.5	100.0%	-4.9
12743	AT5G67460.1   glycosyl hydrolase family protein 17, similar to beta-1,3-glucanase GI:6714534 from (Salix gilgiana)   chr5:26938810-26940500 REVERSE   Aliases: K9I9.2, K9I9_2	3.7	3.8	-0.1	-0.5	100.0%	-4.8
12744	AT1G67570.1   expressed protein   chr1:25328826-25331469 FORWARD   Aliases: F12B7.12, F12B7_12	4.8	4.9	-0.1	-0.5	100.0%	-4.9
12745	NA	2.3	2.4	-0.1	-0.5	100.0%	-6.0
12746	AT1G09550.1   pectinacylesterase, putative, similar to pectinacylesterase precursor GI:1431629 from (Vigna radiata)   chr1:3089735-3092329 REVERSE   Aliases: F14J9.21, F14J9_21	2.5	2.6	-0.1	-0.5	100.0%	-5.3
12747	AT1G54280.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Homo sapiens (SP:O43520), Mus musculus (SP:P70704); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:20266433-20270960 REVERSE   Aliases: F20D21.10, F20D21_10	3.1	3.1	-0.1	-0.5	100.0%	-5.5
12748	AT3G43220.1   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248:gb:AAG29810; contains Pfam domain, PF02383: SacI homology domain; identical to SAC domain protein 3 (SAC3) GI:31415722   chr3:15207851-15214050 REVERSE   Aliases: F7K15.70	6.2	6.3	-0.1	-0.5	100.0%	-5.0
12749	AT5G19680.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr5:6649610-6651937 FORWARD   Aliases: T29J13.100, T29J13_100	6.8	7.0	-0.3	-0.5	100.0%	-4.7
12750	AT3G21170.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr3:7419982-7421166 FORWARD   Aliases: MXL8.1	4.0	3.8	0.2	0.5	100.0%	-4.8
12751	AT4G15110.1   Symbol: CYP97B3   cytochrome P450 97B3, putative (CYP97B3), identical to Cytochrome P450 97B3 (SP:O23365) (Arabidopsis thaliana)   chr4:8629770-8633030 REVERSE   Aliases: DL3600C, FCAALL.208	7.1	7.2	-0.1	-0.5	100.0%	-4.8
12752	AT5G18190.1   protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain   chr5:6009969-6013726 REVERSE   Aliases: MRG7.15, MRG7_15	4.6	4.7	-0.2	-0.5	100.0%	-4.9
12753	AT3G21590.1   senescence/dehydration-associated protein-related, similar to senescence-associated protein 12 (Hemerocallis hybrid cultivar) gi:3551958:gb:AAC34857; similar to early-responsive to dehydration stress ERD7 protein (Arabidopsis thaliana) gi:15320412:dbj:BAB63916   chr3:7604558-7605796 REVERSE   Aliases: MIL23.16	3.0	2.9	0.1	0.5	100.0%	-5.4
12754	AT1G05200.2   Symbol: ATGLR3.4   similar to glutamate receptor family protein (GLR3.6) [Arabidopsis thaliana] (TAIR:At3g51480.1); similar to glutamate receptor family protein (GLR3.5) [Arabidopsis thaliana] (TAIR:At2g32390.1); similar to glutamate receptor family protein (GLR3.3) [Arabidopsis thaliana] (TAIR:At1g42540.1); similar to glutamate receptor family protein (GLR3.2) (GLUR2) [Arabidopsis thaliana] (TAIR:At4g35290.2); similar to glutamate receptor family protein (GLR3.1) (GLR2) [Arabidopsis thaliana] (TAIR:At2g17260.1); similar to glutamate receptor, ionotropic kainate 5 precursor-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_919189.1); similar to putative ionotropic glutamate receptor ortholog GLR6 [Oryza sativa (japonica cultivar-group)] (GB:BAD45881.1); similar to GLR31_ARATH Glutamate receptor 3.1 precursor (Ligand-gated ion channel 3.1) (AtGLR2) (GB:Q7XJL2); similar to putative ionotropic glutamate receptor homolog GLR4 [Oryza sativa (japonica cultivar-group)] (GB:XP_478449.1); similar to OSJNBa0013K16.8 [Oryza sativa (japonica cultivar-group)] (GB:XP_473671.1); contains InterPro domain Metabotropic gamma-aminobutyric acid receptor, type B (InterPro:IPR002455); contains InterPro domain Extracellular ligand-binding receptor (InterPro:IPR001828); contains InterPro domain Ionotropic glutamate receptor (InterPro:IPR001320)   chr1:1504959-1509151 FORWARD   Aliases: GLR3.4, GLUR3, LIGAND GATED CHANNEL LIKE PROTEIN PRECURSOR, YUP8H12.19, YUP8H12_19	3.1	3.3	-0.1	-0.5	100.0%	-4.9
12755	AT2G02160.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:553109-556082 REVERSE   Aliases: F5O4.7, F5O4_7	8.7	9.2	-0.5	-0.5	100.0%	-4.9
12756	AT1G16860.1   merozoite surface protein-related, contains weak similarity to merozoite surface protein (Plasmodium falciparum) gi:12043655:gb:AAG47601	4.1	4.3	-0.1	-0.5	100.0%	-4.6
12757	AT3G49900.1   BTB/POZ domain-containing protein, contains BTB/POZ domain, INTERPRO:IPR000210   chr3:18511620-18513599 REVERSE   Aliases: T16K5.250	3.1	3.1	0.1	0.5	100.0%	-5.2
12758	AT3G29250.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to 3-beta-hydroxysteroiddehydrogenase GI:15983819 from (Digitalis lanata); contains Pfam profile: PF00106 short chain dehydrogenase   chr3:11195004-11200309 REVERSE   Aliases: MXO21.10	3.0	3.2	-0.3	-0.5	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12759	AT5G02920.1   F-box family protein, low similarity to ribosomal RNA apurinic site specific lyase (Triticum aestivum) GI:6505722; contains F-box domain Pfam:PF00646   chr5:680539-681775 FORWARD   Aliases: F9G14.230, F9G14_230	2.6	2.7	-0.1	-0.5	100.0%	-5.3
12760	AT4G03153.1   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia)   chr4:1394845-1395588 REVERSE   Aliases: None	2.1	2.2	-0.1	-0.5	100.0%	-5.6
12761	AT2G38660.2   similar to tetrahydrofolate dehydrogenase/cyclohydrolase, putative [Arabidopsis thaliana] (TAIR:At4g00620.1); similar to plastid 5,10-methylene-tetrahydrofolate dehydrogenase [Prototheca wickerhamii] (GB:AAV65369.1); contains InterPro domain Tetrahydrofolate dehydrogenase/cyclohydrolase (InterPro:IPR000672)   chr2:16173036-16175405 FORWARD   Aliases: T6A23.14, T6A23_14	6.7	6.6	0.1	0.5	100.0%	-4.8
12762	AT1G11600.1   Symbol: CYP77B1   cytochrome P450, putative, similar to cytochrome P450 77A2 (CYPLXXVIIA2) (P-450EG5) (Solanum melongena) and cytochrome P450 77A3 (SP:O48928) (Glycine max); is a member of the PF:00067 Cytochrome P450 family. ESTs gb:Z30775 and gb:Z30776 come from this gene   chr1:3902012-3903778 FORWARD   Aliases: F25C20.25, F25C20_25	3.4	3.3	0.1	0.5	100.0%	-5.1
12763	AT1G34780.1   Symbol: ATAPRL4   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily. This protein also belongs to the adenosine 5'-phosphosulfate reductase-like (APRL) group.   chr1:12748549-12750361 REVERSE   Aliases: APR LIKE 4, ATAPRL4, F11O6.7, F11O6_7	3.2	3.1	0.1	0.5	100.0%	-5.2
12764	AT2G27900.2   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54889.1)   chr2:11884507-11893090 FORWARD   Aliases: AT2G27890, AT2G27910, T1E2.18, T1E2_18	4.0	4.1	-0.1	-0.5	100.0%	-5.4
12765	AT1G32600.1   F-box family protein-related, contains TIGRFAM TIGR01640 : F-box protein interaction domain; identical to hypothetical protein GB:AAF25964 GI:6714268 from (Arabidopsis thaliana)   chr1:11794782-11795663 FORWARD   Aliases: F6N18.20, F6N18_20	2.6	2.7	-0.1	-0.5	100.0%	-5.7
12766	AT5G41040.2   transferase family protein, similar to hypersensitivity-related gene product HSR201 - Nicotiana tabacum, EMBL:X95343; contains Pfam transferase family domain PF00248   chr5:16448619-16450533 FORWARD   Aliases: MEE6.11, MEE6_11	2.7	2.9	-0.2	-0.5	100.0%	-4.2
12767	AT5G52670.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:21380954-21381460 FORWARD   Aliases: F6N7.16, F6N7_16	2.8	3.0	-0.2	-0.5	100.0%	-4.7
12768	AT2G03770.1   sulfotransferase family protein, similar to steroid sulfotransferase 3 (Brassica napus) GI:3420008; contains Pfam profile PF00685: Sulfotransferase domain   chr2:1150868-1151842 REVERSE   Aliases: F19B11.22, F19B11_22	2.7	2.8	-0.1	-0.5	100.0%	-5.3
12769	AT5G49530.1   SIN-like family protein, low similarity to Sex-lethal interactor (Drosophila melanogaster) GI:6049274; contains Pfam profile PF04801: Sin-like protein conserved region   chr5:20117805-20121673 FORWARD   Aliases: K6M13.8, K6M13_8	8.5	8.7	-0.2	-0.5	100.0%	-5.0
12770	AT1G09840.4   similar to shaggy-related protein kinase kappa, putative / ASK-kappa, putative [Arabidopsis thaliana] (TAIR:At1g57870.1); similar to shaggy-related protein kinase 3 [Physcomitrella patens] (GB:AAQ23113.1); similar to shaggy-related protein kinase 2 [Physcomitrella patens] (GB:AAQ23112.1); similar to putative protein kinase [Oryza sativa (japonica cultivar-group)] (GB:AAT77026.1); similar to putative salt-inducible protein kinase [Zea mays] (GB:AAU43771.1); similar to shaggy-related protein kinase 1 [Physcomitrella patens] (GB:AAQ23106.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:3195826-3200293 REVERSE   Aliases: F21M12.23, F21M12_23	5.8	5.9	-0.2	-0.5	100.0%	-4.8
12771	AT4G32030.2   expressed protein   chr4:15490778-15493342 FORWARD   Aliases: F10N7.160, F10N7_160	3.1	3.2	-0.2	-0.5	100.0%	-5.0
12772	AT2G15020.1   expressed protein, and genefinder   chr2:6498516-6500434 REVERSE   Aliases: T15J14.6, T15J14_6	3.0	2.9	0.1	0.5	100.0%	-5.3
12773	AT5G07450.1   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr5:2358353-2359309 REVERSE   Aliases: T2I1.160, T2I1_160	2.9	3.0	-0.1	-0.5	100.0%	-4.8
12774	AT1G04980.1   Symbol: ATPDIL2 2   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	5.9	6.1	-0.1	-0.5	100.0%	-4.7
12775	AT1G52840.1   expressed protein   chr1:19678208-19679779 FORWARD   Aliases: F14G24.11, F14G24_11	2.2	2.2	-0.1	-0.5	100.0%	-5.5
12776	AT2G39060.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr2:16313766-16315328 REVERSE   Aliases: T7F6.23, T7F6_23	4.2	4.1	0.1	0.5	100.0%	-4.8
12777	AT2G04025.1   expressed protein   chr2:1276774-1277731 REVERSE   Aliases: F3C11.1, F3C11_1	2.6	2.6	-0.1	-0.5	100.0%	-5.5
12778	AT2G02690.1   expressed protein   chr2:749935-751899 FORWARD   Aliases: T20F6.17	3.0	3.2	-0.2	-0.5	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12779	AT5G09880.1   RNA recognition motif (RRM)-containing protein   chr5:3081458-3085255 REVERSE   Aliases: MYH9.9, MYH9_9	6.4	6.6	-0.2	-0.5	100.0%	-4.8
12780	AT3G49770.1   expressed protein   chr3:18471875-18472861 REVERSE   Aliases: T16K5.120	3.4	3.5	-0.1	-0.5	100.0%	-5.1
12781	AT5G08390.1   transducin family protein / WD-40 repeat family protein, similar to katanin p80 subunit (Strongylocentrotus purpuratus) GI:3005601; contains Pfam profile PF00400: WD domain, G-beta repeat   chr5:2699358-2706765 FORWARD   Aliases: F8L15.120, F8L15_120	5.4	5.3	0.1	0.5	100.0%	-4.8
12782	AT5G65800.1   Symbol: ACS5   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to ACC synthases from Arabidopsis thaliana (GI:940370), Lycopersicon esculentum (GI:508609), Cucumis sativus (GI:3641649)	2.7	2.7	0.1	0.5	100.0%	-5.6
12783	AT5G55590.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:22537137-22538925 FORWARD   Aliases: MDF20.3, MDF20_3	3.4	3.2	0.2	0.5	100.0%	-4.6
12784	AT5G40050.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.5	-0.1	-0.5	100.0%	-5.7
12785	AT5G65090.1   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr5:26021422-26024077 FORWARD   Aliases: MQN23.2, MQN23_2	2.4	2.7	-0.2	-0.5	100.0%	-4.1
12786	AT1G62860.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr1:23278341-23280142 REVERSE   Aliases: F16P17.1, F16P17_1	6.5	6.6	-0.1	-0.5	100.0%	-5.2
12787	AT1G08520.1   Symbol: PDE166	7.1	7.2	-0.1	-0.5	100.0%	-5.0
12788	AT3G47170.1   transferase family protein, low similarity to 10-deacetyl baccatin III-10-O-acetyl transferase Taxus cuspidata GI:6746554; contains Pfam profile PF02458 transferase family   chr3:17379657-17381479 REVERSE   Aliases: F13I12.220	3.2	3.1	0.1	0.5	100.0%	-5.3
12789	AT5G16060.1   expressed protein   chr5:5246125-5247434 FORWARD   Aliases: F1N13.200, F1N13_200	11.5	11.6	-0.1	-0.5	100.0%	-4.8
12790	AT3G45780.2   Symbol: PHOT1   similar to protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) [Arabidopsis thaliana] (TAIR:At5g58140.1); similar to protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) [Arabidopsis thaliana] (TAIR:At5g58140.2); similar to protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) [Arabidopsis thaliana] (TAIR:At5g58140.3); similar to protein kinase family protein / non phototropic hypocotyl 1-like protein (NPL1) [Arabidopsis thaliana] (TAIR:At5g58140.4); similar to phototropin [Vicia faba] (GB:BAC23099.1); similar to phototropin 1 [Pisum sativum] (GB:AAM15725.1); similar to phototropin-like protein PsPK4 [Pisum sativum] (GB:AAB41023.2); similar to phototropin [Vicia faba] (GB:BAC23098.1); similar to phototropin [Phaseolus vulgaris] (GB:BAD89966.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain PAS domain (InterPro:IPR000014); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain PAC motif (InterPro:IPR001610)   chr3:16829428-16835195 FORWARD   Aliases: F16L2.3, JK224, NONPHOTOTROPIC HYPOCOTYL 1, NPH1, PHOTOTROPIN, ROOT PHOTOTROPISM 1, RPT1	3.5	3.6	-0.1	-0.5	100.0%	-5.4
12791	AT2G45620.1   nucleotidyltransferase family protein, low similarity to SP:O13833: Caffeine-induced death protein 1 {Schizosaccharomyces pombe}; contains Pfam profiles PF03828: PAP/25A associated domain, PF01909: Nucleotidyltransferase domain   chr2:18799938-18802978 FORWARD   Aliases: F17K2.15	6.2	6.0	0.2	0.5	100.0%	-4.7
12792	AT5G55680.1   glycine-rich protein   chr5:22564961-22565587 REVERSE   Aliases: MDF20.12, MDF20_12	5.4	5.2	0.2	0.5	100.0%	-4.9
12793	AT3G49280.1   hypothetical protein   chr3:18281010-18281919 FORWARD   Aliases: F2K15.140	2.7	2.6	0.1	0.5	100.0%	-5.1
12794	AT4G11360.1   Symbol: RHA1B   zinc finger (C3HC4-type RING finger) family protein (RHA1b), identical to RING-H2 finger protein RHA1b (Arabidopsis thaliana) GI:3790567   chr4:6906009-6906754 FORWARD   Aliases: F8L21.150, F8L21_150, RING H2 FINGER PROTEIN RHA1B	4.8	4.6	0.2	0.5	100.0%	-4.6
12795	AT1G52820.1   2-oxoglutarate-dependent dioxygenase, putative, similar to AOP1 (Arabidopsis lyrata)(GI:16118889); contains Pfam profile PF03171: 2OG-Fe(II) oxygenase superfamily domain   chr1:19672851-19674095 FORWARD   Aliases: F14G24.9, F14G24_9	2.3	2.3	-0.1	-0.5	100.0%	-5.6
12796	AT2G02650.1   reverse transcriptase-related, similar to reverse transcriptase (Arabidopsis thaliana) GI:976278	2.3	2.3	0.1	0.5	100.0%	-5.5
12797	AT5G55000.2   Symbol: FIP2   potassium channel tetramerisation domain-containing protein / pentapeptide repeat-containing protein, contains Pfam profiles PF02214: K+ channel tetramerisation domain, PF00805: Pentapeptide repeats (8 copies)   chr5:22335536-22338973 FORWARD   Aliases: MBG8.27, MBG8_27	9.7	9.4	0.3	0.5	100.0%	-4.6
12798	AT5G11530.1   Symbol: EMF1   embryonic flower 1 (EMF1), identical to embryonic flower 1 (Arabidopsis thaliana) GI:15430697   chr5:3697141-3701549 FORWARD   Aliases: EMBRYONIC FLOWER 1, F15N18.120, F15N18_120	3.2	3.5	-0.3	-0.5	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12799	AT4G27640.1   importin beta-2 subunit family protein, low similarity to importin 4 GI:18700635 from (Homo sapiens)   chr4:13797664-13803069 REVERSE   Aliases: T29A15.130, T29A15_130	3.7	3.7	0.1	0.5	100.0%	-5.3
12800	AT5G60170.1   RNA recognition motif (RRM)-containing protein, low similarity to transcriptional repressor Not4-Np (Homo sapiens) GI:6856207; contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif)   chr5:24245715-24250095 FORWARD   Aliases: F15L12.6, F15L12_6	3.9	3.8	0.1	0.5	100.0%	-5.1
12801	AT1G05190.1   Symbol: EMB2394   ribosomal protein L6 family protein, Similar to Mycobacterium RlpF (gb:Z84395). ESTs gb:T75785,gb:R30580,gb:T04698 come from this gene   chr1:1502343-1503826 REVERSE   Aliases: EMB2394, EMBRYO DEFECTIVE 2394, YUP8H12.20, YUP8H12_20	6.8	7.1	-0.3	-0.5	100.0%	-4.4
12802	AT5G58280.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:23584564-23585896 FORWARD   Aliases: MCK7.15, MCK7_15	3.0	2.9	0.1	0.5	100.0%	-5.2
12803	AT4G32290.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr4:15589680-15591170 REVERSE   Aliases: F10M6.70, F10M6_70	4.4	4.5	-0.2	-0.5	100.0%	-4.7
12804	AT3G52290.1   calmodulin-binding family protein, similar to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:19404797-19407381 FORWARD   Aliases: T25B15.60	3.4	3.5	-0.1	-0.5	100.0%	-5.1
12805	AT1G27040.2   nitrate transporter, putative, contains Pfam profile: PF00854 POT family; similar to nitrate transporter (NTL1) GI:3377517 (Arabidopsis thaliana)   chr1:9386771-9389901 REVERSE   Aliases: T7N9.10, T7N9_10	3.0	2.9	0.1	0.5	100.0%	-5.0
12806	AT2G37130.1   peroxidase 21 (PER21) (P21) (PRXR5), identical to SP:Q42580 Peroxidase 21 precursor (EC 1.11.1.7) (Atperox P21) (PRXR5) (ATP2a/ATP2b) {Arabidopsis thaliana}   chr2:15605000-15607137 REVERSE   Aliases: T2N18.11, T2N18_11	4.1	3.8	0.3	0.5	100.0%	-4.7
12807	AT3G14205.1   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248;gb:AAG29810; contains Pfam domain, PF02383: Sac1 homology domain; identical to SAC domain protein 2 (SAC2) GI:31415720   chr3:4715755-4720958 REVERSE   Aliases: None	5.9	6.1	-0.3	-0.5	100.0%	-4.8
12808	AT1G61070.1   Symbol: LCR66/PDF2.4   plant defensin-fusion protein, putative (PDF2.4), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); contains gamma-thionin domain   chr1:22495398-22496207 REVERSE   Aliases: LCR66, Low molecular weight cysteine rich 66, PDF2.4, T7P1.20, T7P1_20	4.0	3.9	0.1	0.5	100.0%	-5.2
12809	AT1G56650.1   Symbol: PAP1   myb family transcription factor (MYB75), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA putative transcription factor (MYB75) GI:3941507   chr1:21237260-21238801 REVERSE   Aliases: F25P12.92, F25P12_92, MYB75, PRODUCTION OF ANTHOCYANIN PIGMENT 1	2.4	2.3	0.1	0.5	100.0%	-5.3
12810	AT3G32960.1   hypothetical protein   chr3:13503390-13504128 FORWARD   Aliases: T13O13.4	2.3	2.2	0.1	0.5	100.0%	-5.7
12811	AT1G20400.1   myosin heavy chain-related   chr1:7072182-7075828 REVERSE   Aliases: F5M15.25, F5M15_25	2.8	2.8	0.1	0.5	100.0%	-5.2
12812	AT4G33330.1   similar to glycogenin glucosyltransferase (glycogenin)-related [Arabidopsis thaliana] (TAIR:At3g18660.1); similar to P0018C10.26 [Oryza sativa (japonica cultivar-group)] (GB:NP_915047.1); similar to glycogenin-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81673.1); similar to putative glycogenin [Oryza sativa (japonica cultivar-group)] (GB:XP_475247.1); similar to secondary cell wall-related glycosyltransferase family 8 [Populus tremula x Populus tremuloides] (GB:AAX33317.1); contains InterPro domain Glycosyl transferase, family 8 (InterPro:IPR002495)   chr4:16060016-16063074 REVERSE   Aliases: F17M5.90, F17M5_90	3.3	3.4	-0.2	-0.5	100.0%	-5.0
12813	AT4G24120.1   similar to oligopeptide transporter OPT family protein [Arabidopsis thaliana] (TAIR:At1g48370.1); similar to transporter, putative [Arabidopsis thaliana] (TAIR:At5g53550.1); similar to oligopeptide transporter OPT family protein [Arabidopsis thaliana] (TAIR:At1g65730.1); similar to transporter, putative [Arabidopsis thaliana] (TAIR:At5g24380.1); similar to oligopeptide transporter OPT family protein [Arabidopsis thaliana] (TAIR:At3g27020.1); similar to OSJNBb0103108.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_473374.1); similar to putative iron-phytosiderophore transporter protein yellow stripe 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_467066.1); similar to iron transport protein 1 [Oryza sativa] (GB:AAS49493.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD90812.1); similar to iron-phytosiderophore transporter protein yellow stripe 1 [Zea mays] (GB:AAG17016.2); contains InterPro domain Oligopeptide transporter OPT superfamily (InterPro:IPR004813)   chr4:12524501-12527351 FORWARD   Aliases: T19F6.110, T19F6_110	4.6	4.5	0.2	0.5	100.0%	-4.6
12814	AT3G30840.1   expressed protein   chr3:12590931-12591505 REVERSE   Aliases: MJ16.20	2.7	2.7	0.1	0.5	100.0%	-5.5
12815	AT3G48420.1   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:P95649 CbbY protein {Rhodobacter sphaeroides}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr3:17940632-17942686 FORWARD   Aliases: T29H11.1	6.9	6.6	0.3	0.5	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12816	AT4G10490.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to naringenin,2-oxoglutarate 3-dioxygenase (Dianthus caryophyllus)(SP:Q05964), hyoscyamine 6 beta-hydroxylase (Atropa belladonna)(gi:4996123); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr4:6483863-6485356 FORWARD   Aliases: F7L13.70, F7L13_70	2.3	2.4	-0.1	-0.5	100.0%	-5.7
12817	AT3G12980.1   histone acetyltransferase 5 (HAC5), identical to HAC5 (GI:21105780) (Arabidopsis thaliana); similar to CREB-binding protein GB:S39162 from (Homo sapiens)   chr3:4146926-4154902 FORWARD   Aliases: MGH6.20	4.6	4.4	0.1	0.5	100.0%	-4.9
12818	AT3G14960.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr3:5035903-5038014 REVERSE   Aliases: K15M2.10	5.3	5.1	0.2	0.5	100.0%	-4.7
12819	AT3G05790.1   Lon protease, putative, similar to Lon protease homolog 2 SP:P93655   chr3:1720160-1725188 REVERSE   Aliases: F10A16.8, F10A16_8	2.6	2.5	0.1	0.5	100.0%	-5.1
12820	AT2G23570.1   hydrolase, alpha/beta fold family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393	3.0	3.1	-0.1	-0.5	100.0%	-5.3
12821	AT3G58750.1   citrate synthase, glyoxysomal, putative, strong similarity to SP:P49299 Citrate synthase, glyoxysomal precursor {Cucurbita maxima}; contains Pfam profile PF00285: Citrate synthase   chr3:21735291-21738667 REVERSE   Aliases: T20N10.100	5.7	5.9	-0.2	-0.5	100.0%	-4.7
12822	AT2G07140.1   F-box family protein, contains Pfam:PF00646 F-box domain ; contains TIGRFAM TIGR01640: F-box protein interaction domain ; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr2:2957558-2958712 FORWARD   Aliases: T25N22.10, T25N22_10	3.8	4.1	-0.3	-0.5	100.0%	-4.0
12823	AT5G28020.5   Symbol: ATCYSD2   similar to cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative [Arabidopsis thaliana] (TAIR:At5g28030.1); similar to cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative [Arabidopsis thaliana] (TAIR:At5g28030.2); similar to cysteine synthase [Nicotiana glauca] (GB:AAR18402.1); contains InterPro domain Pyridoxal-5'-phosphate-dependent enzyme, beta family (InterPro:IPR001926)   chr5:10026191-10027872 REVERSE   Aliases: CYSTEINE SYNTHASE, F15F15.90, F15F15_90	4.0	4.2	-0.2	-0.5	100.0%	-4.6
12824	AT1G30120.1   Symbol: PDH E1 BETA   pyruvate dehydrogenase E1 component beta subunit, chloroplast, identical to pyruvate dehydrogenase E1 beta subunit (Arabidopsis thaliana) GI:2454184; identical to cDNA pyruvate dehydrogenase E1 beta subunit mRNA, nuclear gene encoding plastid protein GI:2454183   chr1:10584144-10586615 REVERSE   Aliases: PYRUVATE DEHYDROGENASE E1 BETA	8.7	8.9	-0.2	-0.5	100.0%	-4.9
12825	AT1G15930.2   40S ribosomal protein S12 (RPS12A), similar to 40S ribosomal protein S12 GI:4263712 from (Arabidopsis thaliana)   chr1:5471431-5472978 FORWARD   Aliases: T24D18.3, T24D18_3	12.4	12.3	0.1	0.5	100.0%	-5.3
12826	AT1G30860.1   expressed protein   chr1:10986677-10989227 REVERSE   Aliases: T17H7.18	4.8	4.6	0.2	0.5	100.0%	-4.9
12827	AT2G25690.2   similar to senescence-associated protein-related [Arabidopsis thaliana] (TAIR:At5g11460.1); similar to putative senescence-associated protein [Oryza sativa (japonica cultivar-group)] (GB:XP_469171.1); contains InterPro domain Protein of unknown function DUF581 (InterPro:IPR007650)   chr2:10947174-10949040 REVERSE   Aliases: F3N11.14, F3N11_14	3.3	3.4	-0.1	-0.5	100.0%	-5.1
12828	AT5G44900.1   similar to Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana] (TAIR:At5g45000.1); similar to putative TIR-NBS type R protein 4 [Malus baccata] (GB:AAQ93074.1); similar to nematode resistance-like protein [Solanum tuberosum] (GB:AAP44392.1); contains InterPro domain TIR domain (InterPro:IPR000157)   chr5:18152673-18153665 FORWARD   Aliases: K21C13.8, K21C13_8	2.9	2.8	0.1	0.5	100.0%	-4.8
12829	AT4G17750.1   Symbol: HSF1   heat shock factor protein 1 (HSF1) / heat shock transcription factor 1 (HSTF1), identical to heat shock transcription factor 1 (HSF1) SP:P41151 from (Arabidopsis thaliana) ;contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr4:9869831-9871616 REVERSE   Aliases: ARABIDOPSIS HEAT SHOCK FACTOR 1, ATHSF1, ATHSFA1A, DL4910C, FCAALL.107, HEAT SHOCK FACTOR, HSFA1A	3.9	4.1	-0.2	-0.5	100.0%	-4.9
12830	AT1G19370.1   expressed protein   chr1:6692755-6694925 REVERSE   Aliases: F18O14.9, F18O14_9	5.8	5.9	-0.1	-0.5	100.0%	-4.9
12831	AT2G27350.5   similar to SEC-C motif-containing protein / OTU-like cysteine protease family protein [Arabidopsis thaliana] (TAIR:At5g67170.2); similar to SEC-C motif-containing protein / OTU-like cysteine protease family protein [Arabidopsis thaliana] (TAIR:At5g67170.1); similar to PREDICTED: similar to hypothetical protein [Canis familiaris] (GB:XP_538031.1); contains InterPro domain OTU-like cysteine protease (InterPro:IPR003323)   chr2:11706627-11711326 REVERSE   Aliases: F12K2.7, F12K2_7	6.4	6.5	-0.1	-0.5	100.0%	-5.1
12832	AT1G59630.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; similar to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana) contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain;   chr1:21910842-21911620 REVERSE   Aliases: T30E16.20, T30E16_20	2.6	2.5	0.1	0.5	100.0%	-5.5
12833	AT2G37740.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:15834784-15835698 REVERSE   Aliases: T8P21.34	2.9	3.0	-0.1	-0.5	100.0%	-5.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12834	AT4G00530.1   expressed protein   chr4:233030-233553 REVERSE   Aliases: F6N23.20, F6N23_20	3.8	3.7	0.1	0.5	100.0%	-4.8
12835	AT2G03880.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:1181534-1183700 FORWARD   Aliases: T18C20.8, T18C20_8	2.4	2.5	-0.1	-0.5	100.0%	-5.7
12836	AT5G04040.1   patatin-related, contains Patatin domain PF01734	6.0	6.1	-0.1	-0.5	100.0%	-4.6
12837	AT3G23760.1   expressed protein   chr3:8562836-8564677 REVERSE   Aliases: MYM9.10	5.1	4.9	0.2	0.5	100.0%	-4.2
12838	AT3G42160.1   pectinesterase-related, contains weak similarity to Swiss-Prot:Q96575 pectinesterase 2 precursor	2.5	2.5	-0.1	-0.5	100.0%	-5.4
12839	AT5G37740.1   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr5:15009295-15010901 FORWARD   Aliases: K12B20.22, K12B20_22	6.0	5.8	0.3	0.5	100.0%	-4.8
12840	AT5G59420.1   oxysterol-binding family protein, similar to SP:P16258 Oxysterol-binding protein 1 {Oryctolagus cuniculus}; contains Pfam profile PF01237: Oxysterol-binding protein   chr5:23978806-23982050 FORWARD   Aliases: F2O15.17, F2O15_17	9.3	9.5	-0.2	-0.5	100.0%	-5.1
12841	AT3G11690.1   expressed protein   chr3:3694994-3696484 FORWARD   Aliases: T19F11.9	4.3	4.1	0.1	0.5	100.0%	-4.5
12842	AT2G37970.1   SOUL heme-binding family protein, weak similarity to SOUL protein (Mus musculus) GI:4886906; contains Pfam profile PF04832: SOUL heme-binding protein   chr2:15898050-15898921 FORWARD   Aliases: T8P21.12, T8P21_12	8.2	8.0	0.2	0.5	100.0%	-4.6
12843	AT5G35900.1   LOB domain family protein / lateral organ boundaries domain family protein (LBD35), identical to SP:Q9FFL3 Putative LOB domain protein 35 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis thaliana	2.0	2.1	-0.0	-0.5	100.0%	-5.9
12844	AT3G50990.1   similar to peroxidase 72 (PER72) (P72) (PRXR8) [Arabidopsis thaliana] (TAIR:At5g66390.1); similar to putative peroxidase [Oryza sativa (japonica cultivar-group)] (GB:NP_918204.1); contains InterPro domain Haem peroxidase (InterPro:IPR002016); contains InterPro domain Plant peroxidase (InterPro:IPR000823)   chr3:18954117-18955586 FORWARD   Aliases: F24M12.30	2.8	2.7	0.1	0.5	100.0%	-5.4
12845	AT5G17700.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr5:5830617-5833903 REVERSE   Aliases: MVA3.5, MVA3_5	2.9	2.8	0.1	0.5	100.0%	-5.2
12846	AT5G28240.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr5:10216257-10216787 FORWARD   Aliases: T8M17.10, T8M17_10	2.7	2.8	-0.1	-0.5	100.0%	-5.4
12847	AT5G19860.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:6714266-6715877 REVERSE   Aliases: T29J13.3	9.1	8.8	0.3	0.5	100.0%	-4.7
12848	AT5G45360.1   F-box family protein, similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250	7.8	7.6	0.2	0.5	100.0%	-4.8
12849	AT1G76560.1   CP12 domain-containing protein, contains Pfam domain PF02672: CP12 domain   chr1:28733147-28733747 FORWARD   Aliases: F14G6.16, F14G6_16	7.0	6.8	0.2	0.5	100.0%	-4.6
12850	AT3G17190.1   hypothetical protein   chr3:5867398-5867954 FORWARD   Aliases: MCE21.3	2.5	2.6	-0.1	-0.5	100.0%	-5.8
12851	AT3G06220.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr3:1883678-1884726 REVERSE   Aliases: F28L1.16, F28L1_16	2.7	2.6	0.1	0.5	100.0%	-5.4
12852	AT1G22640.1   Symbol: MYB3   myb family transcription factor (MYB4), similar to myb-related protein GI:1020155 from (Arabidopsis thaliana)   chr1:8006186-8007417 FORWARD   Aliases: ATMYB3, T22J18.19, T22J18_19, TRANSCRIPTION FACTOR MYB3	5.8	5.7	0.1	0.5	100.0%	-5.0
12853	AT4G11080.1   high mobility group (HMG1/2) family protein, similar to SP:P40618 High mobility group protein HMG2A {Gallus gallus}; contains Pfam profile PF00505: HMG (high mobility group) box   chr4:6760863-6763268 REVERSE   Aliases: T22B4.60, T22B4_60	6.1	5.9	0.2	0.5	100.0%	-4.5
12854	AT2G33020.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr2:14020951-14023593 REVERSE   Aliases: T21L14.1	3.4	3.5	-0.1	-0.5	100.0%	-4.9
12855	AT5G02980.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr5:697991-698998 FORWARD   Aliases: F15A17.10, F15A17_10	3.8	3.7	0.1	0.5	100.0%	-4.9
12856	AT2G21200.1   auxin-responsive protein, putative, similar to small auxin-up regulated protein SAUR (GI:3043536) (Raphanus sativus)   chr2:9090987-9091456 REVERSE   Aliases: F26H11.4, F26H11_4	2.8	2.7	0.1	0.5	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12857	AT3G14730.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:4949392-4951353 REVERSE   Aliases: MIE1.23	3.7	3.8	-0.1	-0.5	100.0%	-5.1
12858	AT3G56140.1   expressed protein, At2g40400 - Arabidopsis thaliana, EMBL:AC007020   chr3:20840325-20843813 FORWARD   Aliases: F18O21.100	7.6	7.5	0.1	0.5	100.0%	-4.8
12859	AT4G32130.1   expressed protein   chr4:15520037-15522589 REVERSE   Aliases: F10N7.60, F10N7_60	5.1	4.6	0.5	0.5	100.0%	-4.2
12860	AT1G68510.1   LOB domain protein 42 / lateral organ boundaries domain protein 42 (LBD42), identical to LOB DOMAIN 42 (Arabidopsis thaliana) GI:17227174; supported by full-length cDNA gi:17227173.   chr1:25710545-25711917 FORWARD   Aliases: T26J14.8, T26J14_8	1.9	1.9	-0.0	-0.5	100.0%	-6.0
12861	AT3G60210.1   chloroplast chaperonin 10, putative, similar to chloroplast chaperonin 10 GI:14041813 from (Arabidopsis thaliana)   chr3:22262219-22263800 REVERSE   Aliases: F27H5.5	9.5	9.7	-0.3	-0.5	100.0%	-4.5
12862	AT2G27100.1   Symbol: SE   C2H2 zinc-finger protein SERRATE (SE), identical to C2H2 zinc-finger protein SERRATE GI:14486602 from (Arabidopsis thaliana)   chr2:11579628-11583736 FORWARD   Aliases: SERRATE, T20P8.15, T20P8_15	4.0	3.9	0.1	0.5	100.0%	-5.1
12863	AT5G06270.1   expressed protein   chr5:1912551-1913675 FORWARD   Aliases: MHF15.21, MHF15_21	3.6	3.5	0.1	0.5	100.0%	-4.8
12864	AT1G30370.1   lipase class 3 family protein, similar to DEFECTIVE IN ANTHOR DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile: PF01764: Lipase   chr1:10719151-10720740 REVERSE   Aliases: T4K22.3, T4K22_3	3.6	3.3	0.2	0.5	100.0%	-4.1
12865	AT2G01500.1   Symbol: PFS2   homeobox-leucine zipper transcription factor family protein, similar to wuschel protein (GI:22087128) (Arabidopsis thaliana)   chr2:224155-226191 REVERSE   Aliases: F2I9.12, F2I9_12, PRETTY FEW SEEDS 2, WOX6, WUSCHEL RELATED HOMEBOX 6	3.1	3.2	-0.1	-0.5	100.0%	-5.7
12866	AT5G55940.1   Symbol: EMB2731   expressed protein, contains Pfam PF03665: Uncharacterised protein family (UPF0172)   chr5:22672658-22675274 REVERSE   Aliases: EMB2731, EMBRYO DEFECTIVE 2731, MYN21.5, MYN21_5	6.8	7.0	-0.2	-0.5	100.0%	-4.7
12867	AT3G20510.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)   chr3:7160683-7161997 FORWARD   Aliases: K10D20.5	9.2	9.1	0.1	0.5	100.0%	-5.1
12868	AT1G26440.4   Symbol: ATUPS5	3.9	3.7	0.2	0.5	100.0%	-4.2
12869	AT5G24100.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:8149219-8151311 FORWARD   Aliases: MZF18.1, MZF18_1	2.6	2.5	0.1	0.5	100.0%	-5.1
12870	AT3G49560.1   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr3:18381554-18383060 FORWARD   Aliases: T9C5.150	8.0	8.2	-0.2	-0.5	100.0%	-5.3
12871	AT3G20760.1   expressed protein   chr3:7257193-7258897 REVERSE   Aliases: MOE17.7	3.6	3.5	0.1	0.5	100.0%	-5.4
12872	AT4G14070.1   AMP-binding protein, putative, similar to AMP-binding protein (gi:1617272) from Brassica napus; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA acyl-CoA synthetase-like protein GI:20799730   chr4:8111957-8118155 REVERSE   Aliases: DL3075C, FCAALL.81	7.0	6.8	0.2	0.5	100.0%	-4.4
12873	AT4G30720.1   expressed protein, hypothetical protein - Synechocystis sp. (strain PCC 6803),PIR2:S76076   chr4:14971859-14976174 REVERSE   Aliases: T10C21.70, T10C21_70	3.9	4.0	-0.1	-0.5	100.0%	-5.1
12874	AT2G38350.1   expressed protein   chr2:16075419-16076386 FORWARD   Aliases: T19C21.16, T19C21_16	2.2	2.3	-0.1	-0.5	100.0%	-5.3
12875	AT1G66950.1   ABC transporter family protein, similar to PDR5-like ABC transporter GI:1514643 from (Spirodela polyrhiza)   chr1:24981868-24988282 FORWARD   Aliases: T4O24.9, T4O24_9	2.1	2.2	-0.1	-0.5	100.0%	-5.1
12876	AT1G68040.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292), S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase (Clarkia breweri)(GI:6002712)   chr1:25506539-25508895 FORWARD   Aliases: T23K23.11, T23K23_11	2.4	2.5	-0.1	-0.5	100.0%	-5.3
12877	AT1G23960.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g23970.1); contains InterPro domain Arabidopsis paralogous family (InterPro:IPR006462)   chr1:8478396-8480231 REVERSE   Aliases: T23E23.14, T23E23_14	7.2	7.0	0.2	0.5	100.0%	-4.7
12878	AT1G64770.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g55370.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g55370.2); similar to putative antifreeze glycoprotein precursor [Oryza sativa] (GB:XP_469743.1)   chr1:24061102-24062237 FORWARD   Aliases: F13O11.8, F13O11_8	4.4	4.1	0.2	0.5	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12879	AT4G15140.1   expressed protein   chr4:8639422-8640292 REVERSE   Aliases: DL3615C, FCAALL.236	3.2	3.1	0.1	0.5	100.0%	-5.0
12880	AT2G41810.1   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr2:17446452-17448428 REVERSE   Aliases: T11A7.9, T11A7_9	3.0	3.1	-0.1	-0.5	100.0%	-5.0
12881	AT3G11090.1   LOB domain family protein / lateral organ boundaries domain family protein (LBD21), identical to SP:Q9SRL8 Putative LOB domain protein 21 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis thaliana	3.1	3.2	-0.1	-0.5	100.0%	-5.0
12882	AT3G32190.1   expressed protein   chr3:13166991-13168270 REVERSE   Aliases: F6H5.102	3.0	2.9	0.1	0.5	100.0%	-5.2
12883	AT1G17310.1   MADS-box protein (AGL100), similar to transcription factor GB:BAA25245 GI:2981610 from (Ceratopteris richardii); contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr1:5928007-5928660 REVERSE   Aliases: T13M22.2, T13M22_2	3.2	3.0	0.1	0.5	100.0%	-4.8
12884	AT4G01740.1   DC1 domain-containing protein, similar to T15B16.6 similar to A. thaliana CHP-rich hypothetical proteins encoded by T10M13, GenBank accession number AF001308   chr4:753422-755456 FORWARD   Aliases: T15B16.10, T15B16_10	3.1	3.4	-0.3	-0.5	100.0%	-4.5
12885	AT3G58290.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:21591549-21592838 REVERSE   Aliases: F9D24.200	3.4	3.3	0.1	0.5	100.0%	-4.8
12886	AT5G23610.2   similar to meiosis protein-related (DYAD) (SWI1) [Arabidopsis thaliana] (TAIR:At5g51330.1); similar to expressed protein (with alternative splicing) [Oryza sativa (japonica cultivar-group)] (GB:XP_469018.1)   chr5:7957343-7959354 REVERSE   Aliases: MQM1.12, MQM1_12	9.1	9.2	-0.1	-0.5	100.0%	-4.9
12887	AT1G72830.3   Symbol: HAP2C   similar to CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis thaliana] (TAIR:At1g17590.3); similar to CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis thaliana] (TAIR:At1g17590.1); similar to CCAAT-binding transcription factor (CBF-B/NF-YA) family protein [Arabidopsis thaliana] (TAIR:At1g17590.2); similar to putative CCAAT-binding transcription factor [Oryza sativa (japonica cultivar-group)] (GB:AAW39026.1); contains InterPro domain CCAAT-binding transcription factor, subunit B (InterPro:IPR001289)   chr1:27409118-27411629 REVERSE   Aliases: ATHAP2C, F3N23.3, F3N23_3, HAP2	7.2	7.0	0.2	0.5	100.0%	-4.8
12888	AT3G18810.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr3:6480707-6483599 REVERSE   Aliases: MVE11.19	2.6	2.5	0.1	0.5	100.0%	-5.6
12889	AT5G03690.2   fructose-bisphosphate aldolase, putative, similar to PIR:S65073 fructose-bisphosphate aldolase (EC 4.1.2.13) isoenzyme C-1, cytosolic (Oryza sativa); contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I   chr5:963147-964988 REVERSE   Aliases: F17C15.110, F17C15_110	4.4	4.3	0.1	0.5	100.0%	-4.9
12890	AT4G38560.1   expressed protein   chr4:18029269-18031185 FORWARD   Aliases: F20M13.120, F20M13_120	2.9	2.8	0.1	0.5	100.0%	-5.3
12891	AT4G23280.1   protein kinase, putative, similar to receptor-like protein kinase 4 (gi:13506745), 5 (gi:13506747), and 6 (gi:13506749) from Arabidopsis thaliana; contains Pfam protein kinase domain PF00069   chr4:12174750-12177481 FORWARD   Aliases: F21P8.170, F21P8_170	2.7	2.7	-0.1	-0.5	100.0%	-5.4
12892	AT2G42060.1   CHP-rich zinc finger protein, putative   chr2:17555268-17556078 FORWARD   Aliases: T6D20.5, T6D20_5	2.2	2.4	-0.2	-0.5	100.0%	-4.5
12893	AT3G20690.1   F-box protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; contains weak hit to Pfam PF00646: F-box domain	3.3	3.2	0.1	0.5	100.0%	-5.2
12894	AT1G03710.1   expressed protein   chr1:923487-924657 FORWARD   Aliases: F21B7.31	3.0	3.2	-0.1	-0.5	100.0%	-4.9
12895	AT5G62760.2   nuclear protein ZAP-related, similar to nuclear protein ZAP, Mus musculus, EMBL:AB033168 this cDNA provides a truncated ORF likely due to a skipped exon. An alternative ORF is provided.   chr5:25221698-25226734 REVERSE   Aliases: MQB2.8, MQB2_8	2.2	2.3	-0.0	-0.5	100.0%	-5.8
12896	AT3G44460.1   Symbol: DPBF2   basic leucine zipper transcription factor (BZIP67), identical to basic leucine zipper transcription factor GI:18656053 from (Arabidopsis thaliana); identical to cDNA basic leucine zipper transcription factor (atbzip67 gene) GI:18656052. Located in the nucleus and expressed during seed maturation in the cotyledons.   chr3:16090970-16092893 REVERSE   Aliases: ATBZIP67, F14L2.10	2.6	2.5	0.1	0.5	100.0%	-5.6
12897	AT3G52550.1   expressed protein   chr3:19503354-19503890 REVERSE   Aliases: F3C22.7	3.2	3.1	0.1	0.5	100.0%	-5.5
12898	AT5G45260.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18343438-18348322 FORWARD   Aliases: K9E15.2, K9E15_2	4.3	4.5	-0.3	-0.5	100.0%	-4.7
12899	AT3G29070.1   emp24/gp25L/p24 family protein, similar to SP:Q28735 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Oryctolagus cuniculus}; contains Pfam profile: PF01105 emp24/gp25L/p24 family   chr3:11051493-11052390 FORWARD   Aliases: MRI12.8	2.5	2.5	0.1	0.5	100.0%	-5.6
12900	AT4G17980.1   Symbol: ANAC071   no apical meristem (NAM) family protein, NAM (GI:6066595) (Petunia x hybrida)	3.6	3.8	-0.1	-0.5	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12901	AT1G68140.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g77770.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g77770.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466297.1)   chr1:25542650-25545374 REVERSE   Aliases: T23K23.1	7.1	6.9	0.2	0.5	100.0%	-4.9
12902	AT3G24280.1   expressed protein   chr3:8798941-8799408 REVERSE   Aliases: K7M2.4	2.3	2.3	0.0	0.5	100.0%	-5.9
12903	AT3G23340.1   casein kinase, putative, similar to casein kinase I (Arabidopsis thaliana) gi:1197461:emb:CAA55396   chr3:8350810-8353966 FORWARD   Aliases: MLM24.21	5.6	5.5	0.1	0.5	100.0%	-4.9
12904	AT3G01890.1   SWIB complex BAF60b domain-containing protein, similar to brahma associated protein 60 kDa (Drosophila melanogaster) GI:3378134, SWI/SNF-related, matrix-associated, actin-dependent regulator of chromatin D1 (Homo sapiens) GI:4566530; contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr3:310022-311983 FORWARD   Aliases: F1C9.33, F1C9_33	3.0	3.1	-0.1	-0.5	100.0%	-5.3
12905	AT2G45630.2   oxidoreductase family protein, low similarity to SP:P36234 Glycerate dehydrogenase (EC 1.1.1.29) (NADH-dependent hydroxypyruvate reductase) {Hyphomicrobium methylovorum}; contains Pfam profile PF00389: D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain   chr2:18803074-18804163 FORWARD   Aliases: F17K2.16	2.9	2.8	0.1	0.5	100.0%	-5.4
12906	AT2G05850.1   Symbol: SCPL38	2.4	2.3	0.1	0.5	100.0%	-5.7
12907	AT3G22930.1   calmodulin, putative, strong similarity to calmodulin 8 GI:5825600 from (Arabidopsis thaliana); contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr3:8124090-8125938 REVERSE   Aliases: F5N5.10	3.6	3.4	0.2	0.5	100.0%	-5.1
12908	AT4G04190.2   expressed protein   chr4:2024576-2026415 FORWARD   Aliases: T27D20.12, T27D20_12	4.9	5.1	-0.2	-0.5	100.0%	-4.7
12909	AT1G25510.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr1:8959181-8960835 REVERSE   Aliases: F2J7.6, F2J7_6	3.3	3.5	-0.2	-0.5	100.0%	-4.6
12910	AT1G11400.3   similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG03976.1)   chr1:3838016-3840207 FORWARD   Aliases: T23J18.7, T23J18_7	6.9	7.1	-0.2	-0.5	100.0%	-4.7
12911	AT1G13580.2   similar to longevity-assurance (LAG1) family protein [Arabidopsis thaliana] (TAIR:At3g19260.1); similar to putative ASC1 [Oryza sativa (japonica cultivar-group)] (GB:BAD27639.1); contains InterPro domain TRAM, LAG1 and CLN8 homology (InterPro:IPR006634); contains InterPro domain Longevity-assurance protein (LAG1) (InterPro:IPR005547)   chr1:4644610-4646850 REVERSE   Aliases: F13B4.7, F13B4_7	4.2	4.3	-0.1	-0.5	100.0%	-5.1
12912	AT3G06870.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:2167853-2168966 REVERSE   Aliases: F17A9.2	2.5	2.5	0.1	0.5	100.0%	-5.6
12913	AT5G59310.1   Symbol: LTP4   lipid transfer protein 4 (LTP4), identical to lipid transfer protein 4 from Arabidopsis thaliana (gi:8571923); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:23942311-23943078 REVERSE   Aliases: LIPID TRANSFER PROTEIN 4, MNC17.4, MNC17_4	2.8	2.7	0.1	0.5	100.0%	-5.3
12914	AT1G10000.1   expressed protein   chr1:3263879-3264790 REVERSE   Aliases: T27I1.2, T27I1_2	3.2	3.1	0.1	0.5	100.0%	-5.1
12915	AT3G02900.1   expressed protein   chr3:645828-647622 FORWARD   Aliases: F13E7.15, F13E7_15	7.0	7.2	-0.2	-0.5	100.0%	-4.4
12916	AT2G33000.1   ubiquitin-associated (UBA)/TS-N domain-containing protein-related, contains weak hit to Pfam F00627: UBA/TS-N domain; supported by tandem duplication of ubiquitin-associated (UBA)/TS-N domain protein (GI:2924790) (TIGR_Ath1:At2g33010) (Arabidopsis thaliana)   chr2:14013212-14015612 FORWARD   Aliases: T21L14.6, T21L14_6	2.5	2.6	-0.1	-0.5	100.0%	-5.5
12917	AT5G41550.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:16634460-16638013 REVERSE   Aliases: MBK23.7, MBK23_7	3.2	3.0	0.1	0.5	100.0%	-4.9
12918	AT5G02070.1   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:405892-408217 REVERSE   Aliases: T7H20.120, T7H20_120	2.8	2.7	0.1	0.5	100.0%	-5.8
12919	AT2G21470.2   Symbol: SAE2   SUMO activating enzyme 2 (SAE2), nearly identical to SUMO activating enzyme 2 (Arabidopsis thaliana) GI:22652854; contains Pfam profiles PF00899: ThiF family, PF02134: Repeat in ubiquitin-activating (UBA) protein   chr2:9205674-9209530 FORWARD   Aliases: ATSAE2, F3K23.23, F3K23_23, SUMO ACTIVATING ENZYME 2	3.8	3.7	0.1	0.5	100.0%	-4.8
12920	AT1G54240.1   expressed protein   chr1:20256755-20258240 FORWARD   Aliases: F20D21.6, F20D21_6	2.4	2.5	-0.1	-0.5	100.0%	-5.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12921	AT3G60880.2   dihydrodipicolinate synthase 1 (DHDPS1) (DHDPS) (DHPS1), identical to SP:Q9LZX6 Dihydrodipicolinate synthase 1, chloroplast precursor (EC 4.2.1.52) (DHDPS 1) {Arabidopsis thaliana}   chr3:22505827-22507672 FORWARD   Aliases: T4C21.290	7.8	7.5	0.3	0.5	100.0%	-4.4
12922	AT4G05490.1   F-box family protein (FBL22), contains similarity to N7 protein GI:3273101 from (Medicago truncatula)   chr4:2771041-2772249 REVERSE   Aliases: C6L9.170, C6L9_170	2.7	2.6	0.1	0.5	100.0%	-5.2
12923	AT2G26080.1   glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative, strong similarity to SP:P26969 Glycine dehydrogenase (decarboxylating), mitochondrial precursor (EC 1.4.4.2) {Pisum sativum}; contains Pfam profile PF02347: Glycine cleavage system P-protein   chr2:11116098-11120906 REVERSE   Aliases: T19L18.11, T19L18_11	10.6	10.3	0.3	0.5	100.0%	-4.8
12924	AT1G16150.1   Symbol: WAKL4   wall-associated kinase, putative, contains similarity to wall-associated kinase 4 GI:3355308 from (Arabidopsis thaliana)   chr1:5532409-5534871 FORWARD   Aliases: T24D18.23, T24D18_23, WALL ASSOCIATED KINASE LIKE 4	3.5	3.7	-0.2	-0.5	100.0%	-4.5
12925	AT3G57800.2   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; supported by full-length cDNA gi:20127059   chr3:21418786-21422698 REVERSE   Aliases: AT3G57795, T10K17.10	4.6	4.7	-0.1	-0.5	100.0%	-5.0
12926	AT3G49660.1   transducin family protein / WD-40 repeat family protein, beta-transducin, Schizosaccharomyces pombe, EMBL:CAA17803   chr3:18424675-18426379 FORWARD   Aliases: T16K5.10	4.2	4.3	-0.1	-0.5	100.0%	-4.7
12927	AT1G28190.1   expressed protein   chr1:9846871-9847910 REVERSE   Aliases: F3H9.15, F3H9_15	3.1	3.2	-0.1	-0.5	100.0%	-5.1
12928	AT3G26120.1   RNA-binding protein, putative, similar to GB:AAC39463 from (Zea mays), PF00076 RNA recognition motif (2 copies)   chr3:9547635-9550423 FORWARD   Aliases: MJL14.2	2.7	2.6	0.1	0.5	100.0%	-5.2
12929	AT3G51590.1   Symbol: LTP12   lipid transfer protein, putative, similar to lipid transfer protein E2 precursor, Brassica napus, PIR:T07984 (GI:899224); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:19146644-19147654 REVERSE   Aliases: LIPID TRANSFER PROTEIN 12, T18N14.1	2.3	2.3	-0.1	-0.5	100.0%	-5.7
12930	AT5G51690.1   Symbol: ACS12   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to ACC synthases from Solanum tuberosum (GI:520958), Triticum aestivum (GI:1173638)   chr5:21014546-21018250 REVERSE   Aliases: MIO24.18, MIO24_18	3.5	3.4	0.1	0.5	100.0%	-5.3
12931	AT5G25770.2   expressed protein   chr5:8969219-8972049 REVERSE   Aliases: F18A17.20, F18A17_20	9.7	9.6	0.1	0.5	100.0%	-5.1
12932	AT1G31270.1   hypothetical protein   chr1:11178330-11178639 FORWARD   Aliases: T19E23.20	2.7	2.7	-0.1	-0.5	100.0%	-5.6
12933	AT1G09800.1   tRNA pseudouridine synthase family protein, contains Pfam profile PF01416: tRNA pseudouridine synthase   chr1:3176921-3180423 REVERSE   Aliases: F21M12.18, F21M12_18	3.7	3.8	-0.1	-0.5	100.0%	-4.9
12934	AT5G21170.2   similar to 5'-AMP-activated protein kinase beta-2 subunit, putative [Arabidopsis thaliana] (TAIR:At4g16360.1); similar to GAL83 protein [Solanum tuberosum] (GB:CAB52141.1)   chr5:7205565-7208494 FORWARD   Aliases: T10F18.200, T10F18_200	5.7	5.3	0.4	0.5	100.0%	-4.6
12935	AT5G17730.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr5:5852500-5854001 REVERSE   Aliases: MVA3.80, MVA3_80	2.3	2.3	0.1	0.5	100.0%	-5.8
12936	AT4G14350.2   protein kinase family protein, contains similarity to Swiss-Prot:O13310 serine/threonine-protein kinase orb6 (Schizosaccharomyces pombe)	5.0	4.8	0.2	0.5	100.0%	-4.7
12937	AT3G53690.1   zinc finger (C3HC4-type RING finger) family protein, contains a Zinc finger, C3HC4 type (RING finger) signature, PROSITE:PS00518 and a IBR domain, Pfam:PF01485   chr3:19909794-19911043 REVERSE   Aliases: F5K20.1	6.0	5.9	0.2	0.5	100.0%	-4.5
12938	AT2G45060.1   expressed protein   chr2:18591427-18593851 REVERSE   Aliases: T14P1.13	5.4	5.1	0.3	0.5	100.0%	-4.5
12939	AT5G51320.1   expressed protein, contains Pfam profile PF03778: Protein of unknown function (DUF321)   chr5:20873295-20874090 REVERSE   Aliases: MFG13.2, MFG13_2	2.6	2.5	0.1	0.5	100.0%	-5.8
12940	AT2G45640.1   sin3 associated polypeptide p18 family protein, similar to Sin3 associated polypeptide p18 (2HOR0202) (Swiss-Prot:O00422) (Homo sapiens)	7.6	7.5	0.1	0.5	100.0%	-4.8
12941	AT3G04110.1   Symbol: GLR1   glutamate receptor family protein (GLR1.1) (GLR1), identical to putative glutamate receptor (GLR1) GB:AF079998 (Arabidopsis thaliana); plant glutamate receptor family, PMID:11379626   chr3:1077335-1080412 FORWARD   Aliases: ATGLR1.1, GLUTAMATE RECEPTOR 1, T6K12.27, T6K12_27	2.5	2.4	0.1	0.5	100.0%	-5.2
12942	AT3G61780.1   Symbol: EMB1703   expressed protein, ; expression supported by MPSS   chr3:22878789-22882437 REVERSE   Aliases: EMB1703, EMBRYO DEFECTIVE 1703, F21F14.1	3.4	3.3	0.1	0.5	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12943	AT4G19095.1   expressed protein   chr4:10452903-10453532 REVERSE   Aliases: None	3.1	3.0	0.1	0.5	100.0%	-5.0
12944	NA	9.9	9.4	0.6	0.5	100.0%	-5.3
12945	AT5G38890.1   exoribonuclease-related, similar to SP:P53859 3'-5' exoribonuclease CSL4 (EC 3.1.13.-) {Saccharomyces cerevisiae}   chr5:15586722-15588325 FORWARD   Aliases: K15E6.10	6.0	6.2	-0.2	-0.5	100.0%	-4.4
12946	AT5G21110.1   expressed protein, predicted protein - Arabidopsis thaliana, EMBL:AL163852   chr5:7178618-7179089 FORWARD   Aliases: T10F18.140, T10F18_140	3.0	2.9	0.1	0.5	100.0%	-5.3
12947	AT4G14290.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g23540.1); similar to similar to Dictyostelium discoideum (Slime mold). Random slug cDNA-11 (Fragment) (GB:AAM33192.2); similar to random slug cDNA-11 [Dictyostelium discoideum] (GB:EAL71033.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379)   chr4:8225497-8230277 REVERSE   Aliases: DL3185C, FCAALL.155	2.8	2.9	-0.1	-0.5	100.0%	-5.5
12948	AT3G55380.1   ubiquitin-conjugating enzyme 14 (UBC14), E2; UbcAT3; identical to gi:2129757, S46656   chr3:20542396-20544150 FORWARD   Aliases: T22E16.40	7.0	7.1	-0.2	-0.5	100.0%	-4.7
12949	AT2G20770.1   lanthionine synthetase C-like family protein, contains Pfam domain, PF05147: Lanthionine synthetase C-like protein   chr2:8952399-8955361 FORWARD   Aliases: F5H14.26, F5H14_26	3.4	3.5	-0.1	-0.5	100.0%	-5.0
12950	AT3G42340.1   hypothetical protein, various predicted Helicases, Arabidopsis thaliana   chr3:14498624-14499605 FORWARD   Aliases: T14K23.50	2.5	2.6	-0.1	-0.5	100.0%	-5.7
12951	AT1G32960.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 (Oryza sativa)   chr1:11945287-11948630 FORWARD   Aliases: F9L11.13, F9L11_13	3.1	3.1	-0.1	-0.5	100.0%	-5.1
12952	AT3G63330.2   similar to Snf1-related protein kinase, putative [Arabidopsis thaliana] (TAIR:At5g39440.1); similar to protein kinase [Cryptosporidium hominis] (GB:EAL35993.1); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:23402603-23405738 REVERSE   Aliases: MAA21.2	3.8	3.7	0.1	0.5	100.0%	-4.9
12953	AT5G28310.1   oxidoreductase-related, low similarity to glyoxylate reductase from Thermococcus litoralis (gi:13515409)	3.0	2.9	0.1	0.5	100.0%	-5.2
12954	AT2G45550.1   Symbol: CYP76C4   cytochrome P450 family protein   chr2:18780615-18782728 REVERSE   Aliases: F17K2.8	3.0	2.9	0.1	0.5	100.0%	-5.2
12955	AT5G04230.1   Symbol: PAL3   similar to phenylalanine ammonia-lyase 1 (PAL1) [Arabidopsis thaliana] (TAIR:At2g37040.1); similar to phenylalanine ammonia-lyase 2 (PAL2) [Arabidopsis thaliana] (TAIR:At3g53260.1); similar to phenylalanine ammonia-lyase, putative [Arabidopsis thaliana] (TAIR:At3g10340.1); similar to phenylalanine ammonia lyase [Populus balsamifera subsp. trichocarpa x Populus deltoides] (GB:AAQ74878.1); similar to phenylalanine ammonia-lyase 1 [Manihot esculenta] (GB:AAK62030.1); similar to PAL1_DAUCA Phenylalanine ammonia-lyase 1 (GB:O23865); similar to phenylalanine ammonia-lyase 1 [Petunia x hybrida] (GB:AAV98199.1); similar to PALY_CITLI Phenylalanine ammonia-lyase (GB:Q42667); contains InterPro domain Phenylalanine ammonia-lyase (InterPro:IPR005922); contains InterPro domain Phenylalanine/histidine ammonia-lyase (InterPro:IPR001106)	2.3	2.3	-0.1	-0.5	100.0%	-5.6
12956	AT4G04910.1   Symbol: NSF   AAA-type ATPase family protein, similar to SP:P18708 Vesicular-fusion protein NSF (N-ethylmaleimide-sensitive fusion protein) (NEM-sensitive fusion protein) {Cricetulus griseus}; contains Pfam profiles PF00004: ATPase AAA family, PF02359: Cell division protein 48 (CDC48) N-terminal domain; contains non-consensus AT-AC splice sites at intron 2   chr4:2489415-2495752 REVERSE   Aliases: T1J1.4, T1J1_4	7.0	6.5	0.5	0.5	100.0%	-4.5
12957	AT2G39910.1   expressed protein   chr2:16667674-16670122 FORWARD   Aliases: T28M21.7, T28M21_7	3.1	3.2	-0.1	-0.5	100.0%	-5.6
12958	AT3G28140.2   calmodulin-binding protein   chr3:10471683-10472625 FORWARD   Aliases: MMG15.17	3.5	3.4	0.1	0.5	100.0%	-5.3
12959	AT4G16444.1   expressed protein   chr4:9274467-9276349 REVERSE   Aliases: None	7.0	6.9	0.1	0.5	100.0%	-5.0
12960	AT1G68090.1   Symbol: ANN5   annexin 5 (ANN5), identical to calcium-binding protein annexin 5 (Arabidopsis thaliana) GI:12667520   chr1:25523105-25524437 REVERSE   Aliases: T23K23.6, T23K23_6, annexin 5	2.4	2.3	0.1	0.5	100.0%	-5.6
12961	AT4G29870.1   expressed protein, predicted protein, Arabidopsis thaliana, PIR2:T01282   chr4:14606007-14606680 FORWARD   Aliases: F27B13.110, F27B13_110	6.1	6.0	0.1	0.5	100.0%	-4.7
12962	AT1G24600.1   expressed protein   chr1:8720295-8720707 FORWARD   Aliases: None	3.4	3.5	-0.1	-0.5	100.0%	-4.8
12963	AT5G06630.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:2036362-2037844 REVERSE   Aliases: F15M7.16, F15M7_16	3.2	3.8	-0.6	-0.5	100.0%	-4.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12964	AT1G50250.1   Symbol: FTSH1   encodes an FTSH protease that is localized to the chloroplast   chr1:18617877-18620731 REVERSE   Aliases: F14I3.14, F14I3_14, FTSH1	9.1	9.0	0.1	0.5	100.0%	-5.5
12965	NA	10.1	10.0	0.1	0.5	100.0%	-5.8
12966	AT2G28830.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr2:12375299-12377761 REVERSE   Aliases: F8N16.12, F8N16_12	2.7	2.7	0.1	0.5	100.0%	-5.4
12967	AT5G47450.1   Symbol: AtTIP2;3   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr5:19265476-19266731 REVERSE   Aliases: DELTA TIP3, MNJ7.4, MNJ7_4, TIP2;3	2.9	2.8	0.2	0.5	100.0%	-4.5
12968	AT1G25340.2   Symbol: MYB116	2.9	2.8	0.1	0.5	100.0%	-5.3
12969	AT2G23110.1   expressed protein   chr2:9847606-9848126 FORWARD   Aliases: F21P24.17, F21P24_17	2.7	2.7	0.1	0.5	100.0%	-5.6
12970	AT2G31660.1   importin beta-2 subunit family protein, similar to D-Importin 7/RanBP7 (Drosophila melanogaster) GI:7542336; contains Pfam profile PF03810: Importin-beta N-terminal domain   chr2:13471375-13478898 FORWARD   Aliases: T9H9.18, T9H9_18	3.5	3.4	0.1	0.5	100.0%	-5.0
12971	AT3G61600.2   Symbol: ATPOB1	7.4	7.6	-0.2	-0.5	100.0%	-5.0
12972	AT3G09860.1   expressed protein   chr3:3026125-3027213 FORWARD   Aliases: F8A24.9	10.6	10.4	0.3	0.5	100.0%	-4.4
12973	AT1G16440.1   protein kinase, putative, similar to viroid symptom modulation protein (Lycopersicon esculentum) gi:7672777:gb:AAF66637   chr1:5616259-5617666 FORWARD   Aliases: F3O9.24, F3O9_24	2.7	2.6	0.1	0.5	100.0%	-5.1
12974	AT2G25470.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591   chr2:10845498-10848959 FORWARD   Aliases: F13B15.13, F13B15_13	2.6	2.7	-0.1	-0.5	100.0%	-5.4
12975	AT3G30160.1   expressed protein, similar to hypothetical protein GB:CAB55689 GI:5881771 from (Arabidopsis thaliana)   chr3:11787469-11787856 REVERSE   Aliases: T20F20.6	4.3	4.2	0.1	0.5	100.0%	-4.9
12976	AT5G41070.1   double-stranded RNA-binding domain (DsRBD)-containing protein, contains Pfam profile PF00035: Double-stranded RNA binding motif   chr5:16455535-16457274 FORWARD   Aliases: MEE6.14, MEE6_14	2.5	2.5	-0.1	-0.5	100.0%	-5.6
12977	AT1G05310.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr1:1550614-1552433 REVERSE   Aliases: YUP8H12.7, YUP8H12_7	4.5	4.2	0.3	0.5	100.0%	-4.6
12978	AT1G73290.1   Symbol: SCPL5   serine carboxypeptidase S10 family protein, similar to serine carboxypeptidase I precursor (SP:P07519) (Hordeum vulgare); glucose acyltransferase GB:AAD01263 (Solanum berthaultii); contains Pfam profile: PF00450 Serine carboxypeptidase;   chr1:27560058-27562434 REVERSE   Aliases: SCPL5, T18K17.4, T18K17_4	2.2	2.3	-0.0	-0.5	100.0%	-5.9
12979	AT5G36120.1   YGGT family protein, contains Pfam profile PF02325: YGGT family (unknown function)   chr5:14215818-14216473 REVERSE   Aliases: MAB16.6, MAB16_6	4.3	4.2	0.1	0.5	100.0%	-4.9
12980	AT3G50870.1   Symbol: MNP   zinc finger (GATA type) family protein, Arabidopsis thaliana mRNA for GATA transcription factor 3, PID:e1254739   chr3:18921971-18923589 FORWARD   Aliases: F18B3.150, MONOPOLE	2.7	2.7	0.1	0.5	100.0%	-5.3
12981	AT5G52030.2   TraB protein-related   chr5:21145355-21147316 FORWARD   Aliases: MSG15.11, MSG15_11	5.6	5.5	0.1	0.5	100.0%	-4.9
12982	AT5G27290.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g54680.1); similar to similar to Oryza sativa chromosome 3, OSJNBa0077G22.24 [Oryza sativa (japonica cultivar-group)] (GB:NP_918819.1)   chr5:9617978-9620536 REVERSE   Aliases: F21A20.3	4.2	4.1	0.1	0.5	100.0%	-4.9
12983	AT3G05900.1   neurofilament protein-related, similar to NF-180 (GI:632549) (Petromyzon marinus) similar to Neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H) (Swiss-Prot:P12036) (Homo sapiens)	7.0	6.8	0.2	0.5	100.0%	-4.9
12984	AT3G45260.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:16607366-16609683 REVERSE   Aliases: F18N11.20	3.0	2.8	0.1	0.5	100.0%	-5.0
12985	AT1G47570.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:17481095-17485842 FORWARD   Aliases: F16N3.15, F16N3_15	6.3	6.4	-0.1	-0.5	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
12986	AT5G12210.2   geranylgeranyl transferase type II beta subunit, putative / RAB geranylgeranyltransferase beta subunit, putative, similar to rab geranylgeranyl transferase GB:CAA69383 GI:1552549 from (Homo sapiens)   chr5:3947133-3949855 FORWARD   Aliases: MXC9.17, MXC9_17	7.0	7.3	-0.3	-0.5	100.0%	-4.7
12987	AT5G61190.1   zinc finger protein-related, contains Pfam profile PF04396: Protein of unknown function DUF537, weak hit to PF00096: Zinc finger C2H2 type   chr5:24632706-24637279 FORWARD   Aliases: MAF19.19, MAF19_19	6.2	6.4	-0.2	-0.5	100.0%	-4.9
12988	AT5G59105.1   Encodes a defensin-like (DEFL) family protein.   chr5:23879685-23880279 REVERSE   Aliases: None	3.2	3.1	0.1	0.5	100.0%	-5.1
12989	AT5G10520.1   protein kinase family protein, contains protein kinase domain, INTERPRO:IPR000719   chr5:3320379-3322911 REVERSE   Aliases: F12B17.130, F12B17_130	3.2	3.5	-0.2	-0.5	100.0%	-4.3
12990	AT4G26440.1   Symbol: WRKY34	2.3	2.2	0.1	0.5	100.0%	-5.5
12991	AT5G64350.1   Symbol: FKBP12	13.2	13.1	0.1	0.5	100.0%	-5.2
12992	AT4G28190.1   Symbol: ULT1   expressed protein   chr4:13985476-13987267 FORWARD   Aliases: F26K10.70, F26K10_70, ULT, ULTRAPETALA, ULTRAPETALA1	7.2	7.4	-0.2	-0.5	100.0%	-4.8
12993	AT1G02340.1   Symbol: HFR1   long hypocotyl in far-red 1 (HFR1) / reduced phytochrome signaling (REP1) / basic helix-loop-helix FBI1 protein (FBI1) / reduced sensitivity to far-red light (RSF1) / bHLH protein 26 (BHLH026) (BHLH26), identical to SP:Q9FE22 Long hypocotyl in far-red 1 (bHLH-like protein HFR1) (Reduced phytochrome signaling) (Basic helix-loop-helix FBI1 protein) (Reduced sensitivity to far-red light) (Arabidopsis thaliana)   chr1:465718-467844 REVERSE   Aliases: FBI1, LONG HYPOCOTYL IN FAR RED, REDUCED PHYTOCHROME SIGNALING 1, REDUCED SENSITIVITY TO FAR RED LIGHT 1, REP1, RSF1, T6A9.4, T6A9_4	2.7	2.6	0.1	0.5	100.0%	-4.5
12994	AT1G71410.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:26916421-26921337 REVERSE   Aliases: F3I17.28, F3I17_28	3.8	3.6	0.3	0.5	100.0%	-4.9
12995	AT5G26230.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:9173520-9174545 REVERSE   Aliases: F9D12.20	3.7	3.6	0.1	0.5	100.0%	-4.9
12996	AT1G51550.1   F-box family protein, similar to F-box ZEITLUPE/FKF/LKP/ADAGIO proteins e.g. GI:13487068 from (Arabidopsis thaliana)   chr1:19121094-19122975 REVERSE   Aliases: F5D21.4, F5D21_4	4.6	4.5	0.1	0.5	100.0%	-5.0
12997	AT4G24960.1   Symbol: ATHVA22D   ABA-responsive protein (HVA22d), identical to AtHVA22d (Arabidopsis thaliana) GI:4884938   chr4:12827947-12829249 FORWARD   Aliases: F13M23.100, F13M23_100	4.7	5.0	-0.3	-0.5	100.0%	-4.3
12998	AT4G15550.1   Symbol: IAGLU   UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (IAGLU), identical to UDP-glucose:indole-3-acetate beta-D-glucosyltransferase (iaglu) GI:2149126 from (Arabidopsis thaliana)   chr4:8877486-8879325 REVERSE   Aliases: DL3815C, FCAALL.103, INDOLE 3 ACETATE BETA D GLUCOSYLTRANSFERASE, UDP GLUCOSE:INDOLE 3 ACETATE BETA D GLUCOSYLTRANSFERASE	8.2	8.4	-0.2	-0.5	100.0%	-4.9
12999	AT4G22760.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:11958488-11962881 FORWARD   Aliases: T12H17.150, T12H17_150	3.3	3.2	0.1	0.5	100.0%	-5.2
13000	AT1G49450.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to En/Spm-like transposon protein GI:2739374 from (Arabidopsis thaliana); no characterized homologs	3.6	3.4	0.1	0.5	100.0%	-4.6
13001	AT1G52510.2   similar to hydrolase, alpha/beta fold family protein [Arabidopsis thaliana] (TAIR:At4g12830.1); similar to alpha/beta hydrolase [Oryza sativa] (GB:CAD23147.1); contains InterPro domain Esterase/lipase/thioesterase (InterPro:IPR000379); contains InterPro domain Epoxide hydrolase (InterPro:IPR000639); contains InterPro domain Alpha/beta hydrolase (InterPro:IPR003089); contains InterPro domain Alpha/beta hydrolase fold (InterPro:IPR000073)	3.7	3.6	0.1	0.5	100.0%	-4.8
13002	AT5G27020.1   expressed protein   chr5:9508190-9508684 FORWARD   Aliases: F2P16.13, F2P16_13	3.0	3.1	-0.1	-0.5	100.0%	-5.3
13003	AT3G59460.1   hypothetical protein, putative proteins - Arabidopsis thaliana   chr3:21988490-21989300 FORWARD   Aliases: T16L24.10	4.1	3.9	0.2	0.5	100.0%	-4.8
13004	AT5G07050.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr5:2191386-2193409 REVERSE   Aliases: MOJ9.22, MOJ9_22	3.0	2.9	0.1	0.5	100.0%	-5.2
13005	AT3G25500.1   Symbol: AFH1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr3:9252335-9256239 REVERSE   Aliases: AHF1, FH1, FORMIN HOMOLOGY 1, FORMIN LIKE PROTEIN AHF1, MWL2.16	5.7	5.5	0.2	0.5	100.0%	-4.4
13006	AT1G78920.1   Symbol: AVP2   vacuolar-type H <sup>+</sup> -translocating inorganic pyrophosphatase (AVPL1), identical to vacuolar-type H <sup>+</sup> -translocating inorganic pyrophosphatase GI:6901676 from (Arabidopsis thaliana)   chr1:29676386-29681874 FORWARD   Aliases: F9K20.2, F9K20_2, VACUOLAR TYPE H <sup>+</sup> TRANSLOCATING INORGANIC PYROPHOSPHATASE	8.6	8.4	0.2	0.5	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13007	AT2G16595.1   similar to putative SSR alpha subunit [Oryza sativa (japonica cultivar-group)] (GB:BAD53577.1); contains InterPro domain Translocon-associated protein (TRAP), alpha subunit (InterPro:IPR005595)   chr2:7205209-7207379 FORWARD   Aliases: None	6.5	6.3	0.2	0.5	100.0%	-4.9
13008	AT1G03920.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr1:1001320-1004382 FORWARD   Aliases: F21M11.15, F21M11_15	8.8	8.5	0.3	0.5	100.0%	-4.9
13009	AT5G16710.1   dehydroascorbate reductase, putative, Strong similarity to dehydroascorbate reductase (Spinacia oleracea) gi:10952512 gb:AAG24945   chr5:5483291-5485069 FORWARD   Aliases: F5E19.50, F5E19_50	9.9	10.1	-0.2	-0.5	100.0%	-4.7
13010	AT1G05230.2   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to homeobox 1 (GP:12002853) {Picea abies}; Strong similarity to Phalaenopsis homeobox protein (gb:U34743)   chr1:1512900-1518804 REVERSE   Aliases: YUP8H12.16, YUP8H12_16	3.5	3.4	0.1	0.5	100.0%	-5.0
13011	AT1G59680.1   F-box family protein, similar to mDj6 GB:BAA88304 GI:6567123 from (Mus musculus); contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain and weak hit to Pfam PF00646: F-box domain   chr1:21936686-21937881 FORWARD   Aliases: T30E16.27, T30E16_27	2.4	2.5	-0.1	-0.5	100.0%	-5.4
13012	AT4G08960.1   phosphotyrosyl phosphatase activator (PTPA) family protein, similar to Protein phosphatase 2A, regulatory subunit B' (PP2A, subunit B', PR53 isoform) (Phosphotyrosyl phosphatase activator) (PTPA) (Swiss-Prot:Q28717) (Oryctolagus cuniculus)   chr4:5746286-5748282 FORWARD   Aliases: T3H13.2, T3H13_2	6.1	6.0	0.2	0.5	100.0%	-4.9
13013	AT2G37750.1   expressed protein   chr2:15838067-15838636 FORWARD   Aliases: T8P21.37	3.9	3.7	0.2	0.5	100.0%	-4.2
13014	AT1G51070.1   basic helix-loop-helix (bHLH) family protein, similar to bHLH transcription factor GI:3757520 from (Arabidopsis thaliana)   chr1:18931559-18933430 FORWARD   Aliases: F23H24.8, F23H24_8	8.7	8.4	0.3	0.5	100.0%	-4.7
13015	AT1G59800.1   cullin-related, similar to cullin 3 (Homo sapiens) GI:3639052   chr1:22008629-22009837 FORWARD   Aliases: F23H11.12, F23H11_12	2.8	2.8	0.1	0.5	100.0%	-5.4
13016	AT5G38100.1   methyltransferase-related, similar to defense-related protein cjs1 (Brassica carinata)(GI:14009292), caffeine synthase (Camellia sinensis)(GI:9967143), SAM:benzoic acid carboxyl methyltransferase (Antirrhinum majus)(GI:9789277)   chr5:15216719-15218415 REVERSE   Aliases: F16F17.100, F16F17_100	1.9	2.0	-0.1	-0.5	100.0%	-4.9
13017	AT5G52440.1   Symbol: HCF106	7.1	6.9	0.2	0.5	100.0%	-4.4
13018	AT5G25090.1   plastocyanin-like domain-containing protein   chr5:8647059-8647820 REVERSE   Aliases: T11H3.100, T11H3_100	2.7	2.7	0.1	0.5	100.0%	-5.2
13019	AT1G53700.1   protein kinase, putative, similar to cucumber protein kinase CsPK3 (Cucumis sativus) gi:7416109:dbj:BAA93704   chr1:20052254-20053783 FORWARD   Aliases: F22G10.21, F22G10_21	3.5	3.4	0.1	0.5	100.0%	-4.7
13020	AT5G04210.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:1155056-1155725 REVERSE   Aliases: F21E1.130, F21E1_130	3.1	3.2	-0.1	-0.5	100.0%	-5.2
13021	AT1G78100.1   F-box family protein, contains F-box domain Pfam:PF00646	7.2	7.0	0.2	0.5	100.0%	-4.9
13022	AT3G61730.1   expressed protein   chr3:22859402-22861450 REVERSE   Aliases: F21F14.11	2.4	2.5	-0.1	-0.5	100.0%	-5.3
13023	AT5G36000.1   expressed protein, strong similarity to unknown protein (emb:CAB71103.1)	2.4	2.5	-0.1	-0.5	100.0%	-5.3
13024	AT2G33160.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Salix gilgiana) GI:6714524; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr2:14060481-14063323 FORWARD   Aliases: F25I18.10, F25I18_10	2.6	2.7	-0.1	-0.5	100.0%	-5.7
13025	AT5G03090.1   expressed protein   chr5:725280-725961 FORWARD   Aliases: F15A17.120, F15A17_120	3.8	3.7	0.1	0.5	100.0%	-5.4
13026	AT1G52670.1   biotin/lipoyl attachment domain-containing protein, similar to SP:Q06881 Biotin carboxyl carrier protein of acetyl-CoA carboxylase (BCCP) {Anabaena sp.}; contains Pfam profile PF00364: Biotin-requiring enzyme	6.1	6.4	-0.3	-0.5	100.0%	-4.4
13027	AT3G06610.1   DNA-binding enhancer protein-related, similar to huntingtin interacting protein HYPK (GI:3329429) (Homo sapiens); identical to Egd2p (GI:172043) (Saccharomyces cerevisiae) similar to EGD2 protein (GAL4 DNA-binding enhancer protein 2) (Swiss-Prot:P38879) (Saccharomyces cerevisiae)	10.4	10.3	0.1	0.5	100.0%	-4.9
13028	AT3G60700.1   expressed protein   chr3:22449377-22450180 FORWARD   Aliases: T4C21.110	3.1	3.0	0.1	0.5	100.0%	-5.2
13029	AT5G50470.1   CCAAT-box binding transcription factor Hap5a, putative, contains similarity to GI:14577940 CCAAT-binding protein subunit HAP5 {Hypocrea jecorina}   chr5:20572346-20572984 REVERSE   Aliases: MBA10.2, MBA10_2	3.2	3.4	-0.1	-0.5	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13030	AT1G23220.1   dynein light chain type 1 family protein, similar to SP:O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassispina}; contains Pfam profile PF01221: Dynein light chain type 1   chr1:8242499-8244307 FORWARD   Aliases: F26F24.7, F26F24_7	9.9	10.1	-0.2	-0.5	100.0%	-4.9
13031	AT2G36170.1   ubiquitin extension protein 2 (UBQ2) / 60S ribosomal protein L40 (RPL40A), identical to GI:166930, GI:166931   chr2:15179196-15180358 FORWARD   Aliases: F9C22.10, F9C22_10	12.1	12.2	-0.1	-0.5	100.0%	-4.8
13032	AT4G14600.1   expressed protein   chr4:8376396-8378331 FORWARD   Aliases: DL3340W, FCAALL.126	5.5	5.3	0.2	0.5	100.0%	-4.7
13033	AT4G01220.2   expressed protein   chr4:513773-515853 REVERSE   Aliases: F2N1.35, F2N1_35	4.3	4.4	-0.1	-0.5	100.0%	-4.8
13034	AT3G14710.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr3:4941552-4943062 FORWARD   Aliases: MIE1.21	2.6	2.7	-0.1	-0.5	100.0%	-5.5
13035	AT5G11040.1   expressed protein, weak similarity to hypercellular protein (Aspergillus nidulans) GI:9309269   chr5:3495288-3500923 FORWARD   Aliases: T5K6.30, T5K6_30	5.6	5.8	-0.2	-0.5	100.0%	-4.8
13036	AT1G75840.1   Symbol: ATROP4	6.1	6.3	-0.1	-0.5	100.0%	-4.7
13037	AT3G07670.1   SET domain-containing protein, similar to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I (Spinacia oleracea) GI:3403236; contains Pfam profile PF00856: SET domain   chr3:2451614-2454866 FORWARD   Aliases: MLP3.12	5.7	5.9	-0.2	-0.5	100.0%	-4.6
13038	AT3G08870.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr3:2700361-2702587 REVERSE   Aliases: T16O11.20	2.8	2.9	-0.1	-0.5	100.0%	-5.3
13039	AT1G08920.3   similar to early-responsive to dehydration stress protein (ERD6) / sugar transporter family protein [Arabidopsis thaliana] (TAIR:At1g08930.1); similar to integral membrane protein [Beta vulgaris] (GB:AAB53155.1); contains InterPro domain Sugar transporter superfamily (InterPro:IPR005829); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sugar transporter (InterPro:IPR003663)   chr1:2867274-2870233 FORWARD   Aliases: F7G19.20, F7G19_20	6.2	5.9	0.3	0.5	100.0%	-4.7
13040	AT2G20610.2   Symbol: SUR1   aminotransferase, putative, similar to nicotianamine aminotransferase from Hordeum vulgare (GI:6498122, GI:6469087); contains Pfam profile PF00155 aminotransferase, classes I and II   chr2:8885042-8887466 REVERSE   Aliases: ABERRANT LATERAL ROOT FORMATION 1, ALF1, F23N11.7, F23N11_7, HLS3, HOOKLESS 3, RTY, SUPERROOT 1, SUR1	6.7	7.1	-0.4	-0.5	100.0%	-4.4
13041	AT5G44680.1   methyladenine glycosylase family protein, similar to SP:P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) {Escherichia coli}; contains Pfam profile PF03352: Methyladenine glycosylase   chr5:18041442-18043172 REVERSE   Aliases: K23L20.1, K23L20_1	3.6	3.7	-0.1	-0.5	100.0%	-4.8
13042	AT4G14480.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:8330077-8331540 REVERSE   Aliases: DL3280C, FCAALL.219	2.6	2.7	-0.1	-0.5	100.0%	-5.3
13043	AT2G47690.1   NADH-ubiquinone oxidoreductase-related, contains weak similarity to NADH-ubiquinone oxidoreductase 15 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-15 kDa) (CI-15 kDa) (Swiss-Prot:O43920) (Homo sapiens   chr2:19558333-19559354 FORWARD   Aliases: F17A22.8	7.3	7.4	-0.1	-0.5	100.0%	-4.9
13044	AT4G27910.1   PHD finger protein-related / SET domain-containing protein (TX4), nearly identical over 285 amino acids to trithorax 4 (Arabidopsis thaliana) GI:16118405; contains Pfam profiles PF00856: SET domain, PF00855: PWWP domain; identical to cDNA trithorax 4 (TX4) partial cds GI:16118404	4.3	4.0	0.2	0.5	100.0%	-4.5
13045	AT1G21250.1   Symbol: WAK1   wall-associated kinase 1 (WAK1), identical to wall-associated kinase 1 (Arabidopsis thaliana) GI:3549626; expressed in leaves and stems & induced by pathogen infection (PMID:10380805)   chr1:7439255-7442082 FORWARD   Aliases: CELL WALL ASSOCIATED KINASE, F16F4.6, F16F4_6, PRO25, SERINE THREONINE KINASE	2.5	2.4	0.1	0.5	100.0%	-5.9
13046	AT4G13990.1   exostosin family protein, contains Pfam profile: PF03016	4.0	4.2	-0.1	-0.5	100.0%	-4.8
13047	AT5G41730.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr5:16702142-16704373 REVERSE   Aliases: MUF8.1, MUF8_1	2.5	2.6	-0.1	-0.5	100.0%	-5.1
13048	AT1G43670.1   fructose-1,6-bisphosphatase, putative / D-fructose-1,6-bisphosphate 1-phosphohydrolase, putative / FBPase, putative, very strong similarity to SP:P46267 Fructose-1,6-bisphosphatase, cytosolic (EC 3.1.3.11) (D-fructose-1,6- bisphosphate 1-phosphohydrolase) (FBPase) {Brassica napus}; contains Pfam profile PF00316: fructose-1,6-bisphosphatase   chr1:16470547-16472937 FORWARD   Aliases: F2J6.2, F2J6_2	7.0	7.3	-0.3	-0.5	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13049	AT1G69410.1   eukaryotic translation initiation factor 5A, putative / eIF-5A, putative, strong similarity to eukaryotic initiation factor 5A (2) (Nicotiana plumbaginifolia) GI:19702, SP:Q9AXQ6: Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) {Lycopersicon esculentum}   chr1:26092868-26094047 FORWARD   Aliases: F10D13.8, F10D13_8	9.6	9.3	0.2	0.5	100.0%	-5.0
13050	AT5G37080.1   hypothetical protein, includes At5g37080, At5g37170, At2g05090   chr5:14676363-14679638 FORWARD   Aliases: MJG14.6, MJG14_6	2.9	3.0	-0.1	-0.5	100.0%	-5.4
13051	AT3G42940.1   expressed protein   chr3:15017601-15018182 FORWARD   Aliases: F18P9.100	2.6	2.5	0.1	0.5	100.0%	-5.3
13052	AT1G01950.1   armadillo/beta-catenin repeat family protein / kinesin motor family protein, similar to kinesin-like protein GB:CAB41097 GI:5541717 from (Arabidopsis thaliana); contains Pfam profiles PF00225: Kinesin motor domain, PF00514: Armadillo/beta-catenin-like repeat   chr1:325473-330511 FORWARD   Aliases: F22M8.8, F22M8_8	5.2	5.1	0.1	0.5	100.0%	-5.0
13053	AT4G08800.1   protein kinase, putative, similar to dual specificity kinase 1 gi:1216484:gb:AAB47968; contains protein kinase domain, Pfam:PF00069   chr4:5614131-5615916 FORWARD   Aliases: T32A17.110, T32A17_110	2.0	2.0	0.0	0.5	100.0%	-5.9
13054	AT3G14760.1   expressed protein   chr3:4956356-4957262 FORWARD   Aliases: T21E2.1	2.5	2.5	0.0	0.5	100.0%	-5.8
13055	AT1G69550.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:26154443-26157218 REVERSE   Aliases: F10D13.24, F10D13_24	2.6	2.5	0.1	0.5	100.0%	-5.6
13056	AT5G58830.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo)   chr5:23773199-23775910 FORWARD   Aliases: K19M22.4, K19M22_4	2.4	2.5	-0.1	-0.5	100.0%	-5.4
13057	AT4G36160.1   Symbol: ANAC076   no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.8	2.9	-0.1	-0.5	100.0%	-5.6
13058	AT5G24480.1   expressed protein, similar to unknown protein (gb:AAD32930.1)   chr5:8363834-8365039 REVERSE   Aliases: T31K7.6, T31K7_6	3.7	3.8	-0.1	-0.5	100.0%	-5.0
13059	AT1G29020.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:10120483-10127054 REVERSE   Aliases: F28N24.34	3.1	3.3	-0.2	-0.5	100.0%	-4.3
13060	AT2G33010.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627: UBA/TS-N domain   chr2:14017969-14020323 FORWARD   Aliases: T21L14.2	2.8	2.9	-0.1	-0.5	100.0%	-5.2
13061	AT3G05180.1   GDSL-motif lipase/hydrolase family protein, similar to early nodulin ENOD8 (Medicago sativa) GI:304037, elicitor-induced glycoprotein iEP4 (Daucus carota) GI:1911765, lanatoside 15'-O-acetyesterase (Digitalis lanata) GI:3688284; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family	3.0	3.0	0.1	0.5	100.0%	-5.3
13062	AT5G39390.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:15780943-15782697 REVERSE   Aliases: MUL8.7, MUL8_7	3.4	3.2	0.1	0.5	100.0%	-4.7
13063	AT1G47540.2   trypsin inhibitor, putative, similar to SP:P26780 Trypsin inhibitor 2 precursor (MTI-2) {Sinapis alba}   chr1:17457974-17458596 REVERSE   Aliases: F16N3.19, F16N3_19	2.8	2.9	-0.1	-0.5	100.0%	-5.4
13064	AT3G57620.1   glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594   chr3:21348541-21350278 FORWARD   Aliases: F15B8.190	2.4	2.4	0.1	0.5	100.0%	-5.5
13065	AT1G21380.1   VHS domain-containing protein / GAT domain-containing protein, weak similarity to Hrs (Rattus norvegicus) GI:8547026; contains Pfam profiles PF00790: VHS domain, PF03127: GAT domain   chr1:7485206-7488675 REVERSE   Aliases: F24J8.3, F24J8_3	6.8	6.5	0.2	0.5	100.0%	-5.0
13066	AT3G24060.1   self-incompatibility protein-related, low similarity to S3 self-incompatibility protein (Papaver rhoeas) GI:1107841   chr3:8689596-8690039 REVERSE   Aliases: F14O13.25	3.9	3.8	0.1	0.5	100.0%	-5.3
13067	AT4G15810.1   chloroplast outer membrane protein, putative, similar to chloroplast protein import component Toc159 (Pisum sativum) GI:8489806, chloroplast outer envelope protein 86 (Pisum sativum) GI:599958, GTP-binding protein (Pisum sativum) GI:576509   chr4:8989175-8992604 REVERSE   Aliases: DL3945C, FCAALL.392	4.1	4.2	-0.1	-0.5	100.0%	-4.9
13068	AT1G23060.2   expressed protein, Location of EST gb:T22158 and gb:AA395675   chr1:8170796-8172473 REVERSE   Aliases: T26J12.16, T26J12_16	3.8	3.7	0.1	0.5	100.0%	-5.3
13069	AT3G22090.1   expressed protein   chr3:7782965-7783564 FORWARD   Aliases: MZN24.30	3.5	3.6	-0.1	-0.5	100.0%	-4.9
13070	AT2G13900.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr2:5840126-5842291 FORWARD   Aliases: F17L24.4, F17L24_4	2.6	2.7	-0.1	-0.5	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13071	AT5G35790.1   Symbol: G6PD1   Encodes a plastidic glucose-6-phosphate dehydrogenase that is sensitive to reduction by DTT and whose mRNA is more prevalent in developing organs but absent in the root.   chr5:13973929-13976975 REVERSE   Aliases: G6PD1, GLUCOSE 6 PHOSPHATE DEHYDROGENASE 1, MWP19.3	6.1	6.3	-0.2	-0.5	100.0%	-4.3
13072	AT2G28880.1   Symbol: EMB1997   para-aminobenzoate (PABA) synthase family protein, similar to PABA synthase from Streptomyces griseus (SP:P32483), Streptomyces pristinaespiralis (gi:1575336); contains Pfam profiles PF00425: chorismate binding enzyme, PF00117: glutamine amidotransferase class-I, PF04715: Anthranilate synthase component I, N terminal region   chr2:12405822-12410605 REVERSE   Aliases: EMB1997, EMBRYO DEFECTIVE 1997, F8N16.17, F8N16_17	4.1	4.0	0.1	0.5	100.0%	-5.1
13073	AT2G34340.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr2:14495865-14496681 REVERSE   Aliases: F13P17.18, F13P17_18	3.9	3.7	0.1	0.5	100.0%	-4.8
13074	AT5G28050.2   similar to cytidine/deoxycytidylate deaminase family protein [Arabidopsis thaliana] (TAIR:At3g05300.1); similar to putative cytidine deaminase; putative deoxycytidylate deaminase [Cicer arietinum] (GB:CAA07230.1); contains InterPro domain Cytidine/deoxycytidylate deaminase, zinc-binding region (InterPro:IPR002125)   chr5:10043918-10045886 REVERSE   Aliases: F15F15.120, F15F15_120	9.5	9.7	-0.2	-0.5	100.0%	-5.0
13075	AT1G32160.1   expressed protein   chr1:11568647-11570367 FORWARD   Aliases: F3C3.6, F3C3_6	7.1	7.2	-0.1	-0.5	100.0%	-4.7
13076	AT3G47010.1   glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1   chr3:17327645-17330450 REVERSE   Aliases: F13I12.60	7.1	7.3	-0.2	-0.5	100.0%	-4.5
13077	AT5G07990.1   Symbol: TT7   flavonoid 3'-monooxygenase / flavonoid 3'-hydroxylase (F3'H) / cytochrome P450 75B1 (CYP75B1) / transparent testa 7 protein (TT7), identical to SP:Q9SD85 Flavonoid 3'-monooxygenase (EC 1.14.13.21) (Flavonoid 3'-hydroxylase) (AtF3'H) (Cytochrome P450 75B1) (TRANSPARENT TESTA 7 protein) {Arabidopsis thaliana}; similar to gi:10334806, gi:10334808	3.4	3.3	0.1	0.5	100.0%	-5.0
13078	AT3G42990.1   hypothetical protein   chr3:15041342-15042140 FORWARD   Aliases: F18P9.150	2.1	2.1	0.1	0.5	100.0%	-5.5
13079	AT3G09870.1   auxin-responsive family protein, similar to auxin-induced proteins (SP:P33083), (SP:P33082) (Glycine max) and indole-3-acetic acid induced protein ARG7 (SP:P32295) from soybean (Vigna radiata)	2.7	2.7	-0.0	-0.5	100.0%	-5.8
13080	AT1G13420.1   sulfotransferase family protein, similar to steroid sulfotransferase 1 GI:3420004 from (Brassica napus); contains Pfam profile PF00685: Sulfotransferase domain   chr1:4604838-4606050 FORWARD   Aliases: T6J4.16, T6J4_16	2.8	2.9	-0.2	-0.5	100.0%	-4.5
13081	AT4G20780.1   calcium-binding protein, putative, similar to SP:Q09011 Calcium-binding protein CAST {Solanum tuberosum}; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:11133197-11133981 REVERSE   Aliases: F21C20.130, F21C20_130	3.3	3.2	0.1	0.5	100.0%	-4.9
13082	AT5G56460.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr5:22882336-22885222 FORWARD   Aliases: MCD7.23, MCD7_23	4.4	4.2	0.2	0.5	100.0%	-4.6
13083	AT5G45690.1   expressed protein   chr5:18552226-18553542 REVERSE   Aliases: MRA19.8, MRA19_8	2.6	2.7	-0.1	-0.5	100.0%	-5.3
13084	AT3G10250.2   expressed protein   chr3:3167956-3170908 REVERSE   Aliases: F14P13.15	3.5	3.3	0.2	0.5	100.0%	-4.6
13085	AT4G28650.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase 5, Arabidopsis thaliana, PIR1:S27756   chr4:14143990-14147543 REVERSE   Aliases: T5F17.100, T5F17_100	2.8	2.9	-0.1	-0.5	100.0%	-5.1
13086	AT5G58960.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g45260.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54541.1); contains InterPro domain Plant protein of unknown function DUF641 (InterPro:IPR006943)   chr5:23823882-23825704 FORWARD   Aliases: K19M22.15, K19M22_15	4.3	4.4	-0.1	-0.5	100.0%	-5.2
13087	AT4G27400.1   late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (Picea glauca) GI:1350543   chr4:13705347-13706674 FORWARD   Aliases: F27G19.5	2.9	2.8	0.1	0.5	100.0%	-4.9
13088	AT5G56880.1   expressed protein   chr5:23026324-23026935 REVERSE   Aliases: MPI10.4, MPI10_4	4.2	4.0	0.1	0.5	100.0%	-4.9
13089	AT2G13550.1   expressed protein   chr2:5655624-5656879 REVERSE   Aliases: T10F5.9, T10F5_9	3.1	3.0	0.1	0.5	100.0%	-5.3
13090	AT1G22335.1   expressed protein, ; expression supported by MPSS   chr1:7888300-7889230 FORWARD   Aliases: None	2.6	2.8	-0.1	-0.5	100.0%	-4.7
13091	AT3G21200.1   expressed protein   chr3:7436078-7438419 FORWARD   Aliases: MXL8.5	8.2	8.4	-0.2	-0.5	100.0%	-4.7
13092	AT5G25990.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266; expression supported by MPSS   chr5:9076110-9077382 REVERSE   Aliases: T1N24.6, T1N24_6	2.1	2.1	0.0	0.5	100.0%	-6.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13093	AT5G59700.1   protein kinase, putative, similar to receptor-like protein kinase (Catharanthus roseus) gi:1644291:emb:CAA97692   chr5:24069611-24072651 REVERSE   Aliases: MTH12.1, MTH12_1	4.2	4.3	-0.1	-0.5	100.0%	-4.8
13094	AT1G54820.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:20451032-20454528 FORWARD   Aliases: T22H22.21, T22H22_21	2.3	2.2	0.0	0.5	100.0%	-5.8
13095	AT3G46060.1   Symbol: ARA3   Ras-related protein (ARA-3) / small GTP-binding protein, putative, identical to SP:P28186 Ras-related protein ARA-3 {Arabidopsis thaliana}; contains Pfam profile: PF00071 Ras family   chr3:16928576-16930978 FORWARD   Aliases: ARA 3, F12M12.30, SMALL GTP BINDING PROTEIN	8.1	7.8	0.2	0.5	100.0%	-4.7
13096	AT3G50210.3   similar to 2-oxoacid-dependent oxidase, putative (DIN11) [Arabidopsis thaliana] (TAIR:At3g49620.1); similar to putative 2-oxoacid-dependent oxidase [Oryza sativa (japonica cultivar-group)] (GB:XP_450237.1); contains InterPro domain Isopenicillin N synthase (InterPro:IPR002283); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)   chr3:18625154-18627417 REVERSE   Aliases: F11C1.50	8.7	8.9	-0.1	-0.5	100.0%	-5.0
13097	AT3G09270.1   Symbol: ATGSTU8   glutathione S-transferase, putative, similar to glutathione transferase GB:CAA71784 (Glycine max)   chr3:2848295-2849293 REVERSE   Aliases: F3L24.14	5.2	5.5	-0.2	-0.5	100.0%	-4.4
13098	AT2G18360.1   hydrolase, alpha/beta fold family protein, low similarity to SP:P24640:LIP3_MORSP Lipase 3 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Moraxella sp}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:7983794-7986459 REVERSE   Aliases: T30D6.13, T30D6_13	3.4	3.2	0.1	0.5	100.0%	-4.7
13099	AT4G32105.1   expressed protein   chr4:15513226-15514093 REVERSE   Aliases: None	2.9	2.8	0.1	0.5	100.0%	-5.1
13100	AT2G28170.1   Symbol: ATCHX7	2.6	2.6	0.1	0.5	100.0%	-5.7
13101	AT1G62780.1   expressed protein   chr1:23252844-23254770 REVERSE   Aliases: F23N19.15, F23N19_15	4.2	4.0	0.2	0.5	100.0%	-4.7
13102	AT5G42590.1   Symbol: CYP71A16   cytochrome P450 71A16, putative (CYP71A16), Identical to Cytochrome P450 71A16 (SP:Q9FH66) (Arabidopsis thaliana)   chr5:17048375-17050924 REVERSE   Aliases: K16E1.6, K16E1_6	3.1	2.9	0.2	0.5	100.0%	-4.3
13103	AT5G20050.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:6774304-6775847 FORWARD   Aliases: F28I16.200, F28I16_200	7.7	7.5	0.2	0.5	100.0%	-4.9
13104	AT4G26220.1   caffeoyl-CoA 3-O-methyltransferase, putative, similar to caffeoyl-CoA O-methyltransferase (GI:1622926)(Nicotiana tabacum), GI:2960356 (Populus balsamifera subsp. trichocarpa), AF036095 (Pinus taeda)   chr4:13283667-13285332 FORWARD   Aliases: T25K17.30, T25K17_30	3.5	3.2	0.3	0.5	100.0%	-4.0
13105	AT3G50670.2   Symbol: U1 70K	7.5	7.8	-0.3	-0.5	100.0%	-4.7
13106	AT5G45850.1   expressed protein, contains Pfam profile: PF05097 protein of unknown function (DUF688)   chr5:18617328-18618797 REVERSE   Aliases: K15I22.5, K15I22_5	2.0	1.9	0.0	0.5	100.0%	-6.1
13107	AT1G02730.1   Symbol: ATCSLD5   cellulose synthase family protein, similar to cellulose synthase catalytic subunit (gi:13925881) from Nicotiana alata, cellulose synthase-4 (gi:9622880) from Zea mays   chr1:594590-598657 REVERSE   Aliases: CSLD5, T14P4.29	4.5	4.6	-0.1	-0.5	100.0%	-4.8
13108	AT1G31190.1   inositol monophosphatase family protein, similar to SP:P29218 Myo-inositol-1(or 4)-monophosphatase (EC 3.1.3.25) (Inositol monophosphatase) {Homo sapiens}; contains Pfam profile PF00459: Inositol monophosphatase family; EST gb:AA597395 comes from this gene	6.3	6.2	0.2	0.5	100.0%	-4.6
13109	AT1G79450.2   LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein, similar to GI:4966357; GI:4585976; GI:11994416; GI:9757735 from (Arabidopsis thaliana)   chr1:29892582-29895072 FORWARD   Aliases: T8K14.13, T8K14_13	3.8	3.5	0.3	0.5	100.0%	-4.6
13110	AT4G10380.1   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr4:6431235-6434818 REVERSE   Aliases: F7L13.6	5.5	5.4	0.1	0.5	100.0%	-4.8
13111	AT1G09080.1   luminal binding protein 3 (BiP-3) (BP3), Similar to Arabidopsis luminal binding protein (gb:D89342); contains Pfam domain PF00012: dnaK protein   chr1:2929220-2931843 REVERSE   Aliases: F7G19.5, F7G19_5	2.9	2.8	0.1	0.5	100.0%	-5.4
13112	AT2G40120.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:16762086-16764535 REVERSE   Aliases: T7M7.1, T7M7_1	4.4	4.6	-0.2	-0.5	100.0%	-4.4
13113	AT4G14280.1   expressed protein   chr4:8222513-8225069 FORWARD   Aliases: DL3180W, FCAALL.154	2.3	2.4	-0.1	-0.5	100.0%	-5.0
13114	AT3G45680.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:16781922-16784015 FORWARD   Aliases: T6D9.10	3.1	3.3	-0.1	-0.5	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13115	AT1G69540.1   similar to MADS-box protein (AGL65) [Arabidopsis thaliana] (TAIR:At1g18750.1); similar to putative MADS-domain transcription factor [Physcomitrella patens] (GB:CAD11675.1); similar to putative MADS-domain transcription factor [Physcomitrella patens] (GB:CAD18830.1); contains InterPro domain Transcription factor, MADS-box (InterPro:IPR002100)   chr1:26148707-26150822 REVERSE   Aliases: F10D13.25, F10D13_25	3.3	3.2	0.2	0.5	100.0%	-4.7
13116	AT4G15700.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	2.1	2.0	0.0	0.5	100.0%	-5.9
13117	AT2G29510.1   expressed protein   chr2:12641601-12645095 FORWARD   Aliases: F16P2.11, F16P2_11	5.8	5.6	0.2	0.5	100.0%	-4.6
13118	AT5G28170.1   expressed protein, similar to At1g35110, At1g44880, At3g42530, At4g19320, At5g36020, At4g03970, At3g43010, At2g10350   chr5:10152151-10154738 FORWARD   Aliases: F26C17.3	2.8	2.9	-0.1	-0.5	100.0%	-5.1
13119	AT1G32540.2   Symbol: LOL1   zinc finger protein, putative, similar to zinc-finger protein Lsd1 (Arabidopsis thaliana) gi:1872521:gb:AAC49660	2.3	2.4	-0.1	-0.5	100.0%	-5.4
13120	AT5G54630.1   zinc finger protein-related, contains Prosite:PS00028 Zinc finger, C2H2 type, domain   chr5:22209725-22211534 REVERSE   Aliases: MRB17.13, MRB17_13	4.3	4.1	0.1	0.5	100.0%	-5.2
13121	AT4G15010.3   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr4:8572901-8575179 REVERSE   Aliases: DL3547C, FCAALL.86	5.5	5.4	0.1	0.5	100.0%	-5.2
13122	AT1G50180.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	4.4	4.5	-0.1	-0.5	100.0%	-5.5
13123	AT1G51320.1   F-box family protein (FBX11), contains F-box domain PF:00646   chr1:19029310-19030437 FORWARD   Aliases: F11M15.18, F11M15_18	2.6	2.7	-0.1	-0.5	100.0%	-5.4
13124	AT1G50060.1   pathogenesis-related protein, putative, similar to prb-1b (Nicotiana tabacum) GI:19970; contains Pfam profile PF00188: SCP-like extracellular protein   chr1:18554854-18556246 FORWARD   Aliases: F2J10.6, F2J10_6	2.2	2.2	0.1	0.5	100.0%	-5.8
13125	AT4G33230.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:16026595-16028758 REVERSE   Aliases: F4I10.160, F4I10_160	3.2	3.1	0.1	0.5	100.0%	-5.3
13126	AT1G04010.1   lecithin:cholesterol acyltransferase family protein / LACT family protein, weak similarity to SP:P40345 Phospholipid:diacylglycerol acyltransferase (EC 2.3.1.158) (PDAT) {Saccharomyces cerevisiae}; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)   chr1:1031295-1036236 REVERSE   Aliases: F21M11.5, F21M11_5	3.6	3.7	-0.1	-0.5	100.0%	-4.8
13127	AT5G27460.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr5:9693265-9694818 REVERSE   Aliases: F21A20.170, F21A20_170	7.7	7.5	0.2	0.5	100.0%	-4.9
13128	AT2G24020.1   expressed protein, contains Pfam domain PF02575: Uncharacterized BCR, YbaB family COG0718   chr2:10224781-10226361 REVERSE   Aliases: T29E15.22, T29E15_22	7.7	7.9	-0.2	-0.5	100.0%	-4.5
13129	AT1G73410.1   Symbol: MYB54   myb family transcription factor (MYB54), identical to putative transcription factor (MYB54) GI:3941471 from (Arabidopsis thaliana)   chr1:27605293-27606978 FORWARD   Aliases: ATMYB54, BW54, MYB54, T9L24.38, T9L24_38	2.4	2.5	-0.1	-0.4	100.0%	-5.5
13130	AT5G35890.1   expressed protein   chr5:14043093-14043956 REVERSE   Aliases: MIK22.20, MIK22_20	2.0	2.0	0.0	0.4	100.0%	-5.8
13131	AT2G21080.1   expressed protein   chr2:9050780-9052421 FORWARD   Aliases: F26H11.16, F26H11_16	4.2	4.3	-0.1	-0.4	100.0%	-5.1
13132	AT3G27430.2   Symbol: PBB1   20S proteasome beta subunit B (PBB1), identical to 20S proteasome beta subunit PBB1 (PBB1) GB:AAC32066 (Arabidopsis thaliana) (Genetics 149 (2), 677-692 (1998)); contains Pfam profile: PF00227 proteasome A-type and B-type;   chr3:10153754-10156579 FORWARD   Aliases: 20S PROTEASOME BETA SUBUNIT PBB1, K1G2.26	9.0	9.5	-0.5	-0.4	100.0%	-4.4
13133	AT1G12630.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr1:4298907-4299473 FORWARD   Aliases: T12C24.16, T12C24_16	4.8	4.7	0.1	0.4	100.0%	-4.8
13134	AT4G37990.1   Symbol: ELI3 2	3.2	3.3	-0.1	-0.4	100.0%	-5.0
13135	AT4G20160.1   expressed protein, ; expression supported by MPSS   chr4:10890993-10894981 FORWARD   Aliases: F1C12.80, F1C12_80	3.0	2.9	0.1	0.4	100.0%	-5.3
13136	AT5G17070.1   expressed protein   chr5:5613371-5616141 REVERSE   Aliases: F2K13.220, F2K13_220	5.9	6.2	-0.3	-0.4	100.0%	-4.7
13137	AT4G28260.1   expressed protein   chr4:14004491-14006976 FORWARD   Aliases: F26K10.140, F26K10_140	8.5	8.3	0.2	0.4	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13138	AT4G03060.1   Symbol: AOP2   2-oxoglutarate-dependent dioxygenase, putative (AOP2), nearly identical to GI:16118891; contains Pfam profile PF03171: 2OG-Fe(II) oxygenase superfamily domain. The gene sequence is frameshifted, this could be a pseudogene or a sequencing error may exist; identical to cDNA AOP2 GI:16118890   chr4:1351687-1354023 REVERSE   Aliases: ALKENYL HYDROXALKYL PRODUCING 2, T4I9.6, T4I9_6	2.9	3.0	-0.1	-0.4	100.0%	-5.3
13139	AT5G10490.1   similar to mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana] (TAIR:At1g58200.2); similar to mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein [Arabidopsis thaliana] (TAIR:At1g58200.1); similar to unknown [Lycopersicon esculentum] (GB:AAK84478.1); contains InterPro domain Mechanosensitive (MS) ion channel (InterPro:IPR006685)   chr5:3300226-3304762 REVERSE   Aliases: F12B17.160, F12B17_160	4.7	4.9	-0.2	-0.4	100.0%	-4.8
13140	AT5G27700.1   40S ribosomal protein S21 (RPS21C), ribosomal protein S21, Zea mays, PIR:T03945   chr5:9807323-9808480 REVERSE   Aliases: T1G16.30, T1G16_30	11.1	11.3	-0.2	-0.4	100.0%	-5.0
13141	AT1G49400.1   Symbol: EMB1129   ribosomal protein S17 family protein, similar to 40S ribosomal protein S17 GI:1620985 from (Nicotiana glauca)   chr1:18286708-18287870 FORWARD   Aliases: EMB1129, EMBRYO DEFECTIVE 1129, F13F21.17, F13F21_17	5.4	5.7	-0.4	-0.4	100.0%	-4.7
13142	AT1G11060.1   expressed protein   chr1:3684568-3689844 FORWARD   Aliases: T19D16.5, T19D16_5	3.3	3.4	-0.1	-0.4	100.0%	-5.4
13143	AT1G12260.1   Symbol: ANAC007/EMB2749   no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.7	2.6	0.1	0.4	100.0%	-5.4
13144	AT1G12900.1   glyceraldehyde 3-phosphate dehydrogenase, chloroplast, putative / NADP-dependent glyceraldehydephosphate dehydrogenase, putative, similar to SP:P25856 Glyceraldehyde 3-phosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) {Arabidopsis thaliana}; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain	7.6	7.3	0.3	0.4	100.0%	-4.2
13145	AT3G13450.1   Symbol: DIN4   2-oxoisovalerate dehydrogenase / 3-methyl-2-oxobutanoate dehydrogenase / branched-chain alpha-keto acid dehydrogenase E1 beta subunit (DIN4), identical to branched chain alpha-keto acid dehydrogenase E1 beta subunit (Arabidopsis thaliana) GI:7021286   chr3:4382205-4384441 REVERSE   Aliases: DARK INDUCIBLE 4, MRP15.9	6.0	5.8	0.2	0.4	100.0%	-5.0
13146	AT1G16260.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:5559702-5562012 REVERSE   Aliases: F3O9.6, F3O9_6	2.6	2.7	-0.1	-0.4	100.0%	-5.3
13147	AT4G27220.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr4:13633959-13636718 REVERSE   Aliases: M4I22.30, M4I22_30	2.6	2.5	0.1	0.4	100.0%	-5.5
13148	AT3G15850.1   Symbol: FAD5   fatty acid desaturase family protein, similar to delta 9 acyl-lipid desaturase (ADS1) GI:2970034 from (Arabidopsis thaliana)   chr3:5359016-5361192 FORWARD   Aliases: ADS3, FADB, FATTY ACID DESATURASE 5, FATTY ACID DESATURASE B, JB67, MSJ11.25	8.7	8.9	-0.2	-0.4	100.0%	-4.4
13149	AT5G13950.1   expressed protein   chr5:4495973-4500683 REVERSE   Aliases: MAC12.8, MAC12_8	4.1	4.2	-0.1	-0.4	100.0%	-4.8
13150	AT3G16380.1   Symbol: PAB6   polyadenylate-binding protein, putative / PABP, putative, similar to polyadenylate-binding protein (poly(A)-binding protein) from {Arabidopsis thaliana} SP:P42731, (Cucumis sativus) GI:7528270, {Homo sapiens} SP:Q13310, {Arabidopsis thaliana} SP:Q05196; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM). Member of the class III family of PABP proteins.   chr3:5558682-5560999 REVERSE   Aliases: PAB6, POLY(A) BINDING PROTEIN 6, T2O4.4	3.3	3.4	-0.1	-0.4	100.0%	-5.2
13151	AT1G08370.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; contains some similarity to transcription factor (Danio rerio) gi:15617376, emb:CAC69871; similar to yeast dcp1   chr1:2638190-2640551 FORWARD   Aliases: T27G7.7, T27G7_7	5.0	4.7	0.2	0.4	100.0%	-4.8
13152	AT1G14320.1   60S ribosomal protein L10 (RPL10A) / Wilm's tumor suppressor protein-related, similar to tumor suppressor GI:575354 from (Oryza sativa)   chr1:4888209-4889656 FORWARD   Aliases: F14L17.9, F14L17_9	13.0	13.1	-0.1	-0.4	100.0%	-5.7
13153	AT3G19010.2   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains similarity to flavonol synthase (FLS) from (Solanum tuberosum) SP:Q41452, {Petunia hybrida} SP:Q07512; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr3:6556203-6557944 REVERSE   Aliases: K13E13.17	5.4	5.6	-0.2	-0.4	100.0%	-4.8
13154	AT5G56480.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:22887552-22888043 REVERSE   Aliases: MCD7.25, MCD7_25	3.0	3.0	-0.1	-0.4	100.0%	-5.3
13155	AT1G70490.3   ADP-ribosylation factor, putative, nearly identical to ADP-ribosylation factor 1 GB:P36397 (Arabidopsis thaliana), ADP-ribosylation factor GI:166586 (Arabidopsis thaliana)   chr1:26567590-26569453 REVERSE   Aliases: F24J13.6, F24J13_6	9.7	9.5	0.2	0.4	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13156	AT1G08470.1   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324)   chr1:2682130-2684103 REVERSE   Aliases: T27G7.16, T27G7_16	7.3	7.4	-0.1	-0.4	100.0%	-4.9
13157	AT1G15110.1   phosphatidyl serine synthase family protein, contains Pfam profile: PF03034 phosphatidyl serine synthase	4.6	4.5	0.2	0.4	100.0%	-4.7
13158	AT2G21770.1   Symbol: CESA9   cellulose synthase, catalytic subunit, putative, similar to gi:2827141 cellulose synthase catalytic subunit, Arabidopsis thaliana (Ath-A)   chr2:9291917-9296616 FORWARD   Aliases: CELLULASE SYNTHASE 9, CESA09, F7D8.9, F7D8_9	3.9	3.7	0.2	0.4	100.0%	-4.8
13159	AT5G32610.1   hypothetical protein, predicted proteins, Arabidopsis thaliana and Borrelia burgdorferi   chr5:12273907-12276326 REVERSE   Aliases: F15I15.20, F15I15_20	2.3	2.3	0.1	0.4	100.0%	-5.7
13160	AT3G48080.1   lipase class 3 family protein / disease resistance protein-related, similar to disease resistance protein/lipase homolog EDS1 GI:4454567; contains Pfam profile PF01764: Lipase   chr3:17763923-17766175 REVERSE   Aliases: T17F15.50	2.5	2.6	-0.1	-0.4	100.0%	-4.8
13161	NA	2.4	2.4	-0.0	-0.4	100.0%	-6.0
13162	AT1G41750.1   expressed protein   chr1:15524452-15524877 REVERSE   Aliases: F9M8.6	3.3	3.2	0.1	0.4	100.0%	-4.9
13163	AT1G72860.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:27419889-27424439 REVERSE   Aliases: F3N23.6, F3N23_6	2.7	2.6	0.1	0.4	100.0%	-5.1
13164	AT3G52560.2   ubiquitin-conjugating enzyme family protein, similar to DNA-binding protein CROC-1B (Homo sapiens) GI:1066082; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr3:19505362-19507058 REVERSE   Aliases: F3C22.2	9.7	9.4	0.3	0.4	100.0%	-4.6
13165	AT1G64560.1   expressed protein   chr1:23977487-23977840 FORWARD   Aliases: F1N19.29, F1N19_29	5.5	5.2	0.3	0.4	100.0%	-5.0
13166	AT2G40720.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:16994347-16996929 FORWARD   Aliases: T7D17.10, T7D17_10	3.4	3.5	-0.1	-0.4	100.0%	-5.1
13167	AT5G54300.1   expressed protein, contains similarity to cotton fiber expressed protein 1 (Gossypium hirsutum) gi:3264828:gb:AAC33276   chr5:22071195-22072656 REVERSE   Aliases: MDK4.12, MDK4_12	3.0	3.2	-0.2	-0.4	100.0%	-4.8
13168	AT5G35290.1   hypothetical protein   chr5:13535117-13535536 REVERSE   Aliases: T26D22.20, T26D22_20	3.8	3.7	0.1	0.4	100.0%	-5.3
13169	AT5G58920.1   expressed protein   chr5:23810355-23811471 FORWARD   Aliases: K19M22.6, K19M22_6	6.9	7.0	-0.2	-0.4	100.0%	-4.7
13170	AT5G08570.1   pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Glycine max) SWISS-PROT:Q42806	9.3	9.5	-0.2	-0.4	100.0%	-4.8
13171	AT5G04620.2   aminotransferase class I and II family protein, similar to 8-amino-7-oxononanoate synthase, Bacillus sphaericus, PIR:JQ0512 (SP:P22806), Bacillus subtilis (SP:P53556); contains Pfam profile PF00155 aminotransferase, classes I and II	8.3	8.5	-0.2	-0.4	100.0%	-4.3
13172	AT5G35740.1   glycosyl hydrolase family protein 17, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum); C-terminal homology only   chr5:13927648-13928390 REVERSE   Aliases: MXH1.15, MXH1_15	3.3	3.4	-0.1	-0.4	100.0%	-5.3
13173	AT1G73610.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL6 (GI:15054390), EXL4 (GI:15054388) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr1:27682038-27683468 FORWARD   Aliases: F25P22.2, F25P22_2	2.7	2.6	0.1	0.4	100.0%	-5.3
13174	AT2G37580.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr2:15771806-15772631 FORWARD   Aliases: F13M22.1	4.4	4.5	-0.1	-0.4	100.0%	-4.7
13175	AT4G09550.1   expressed protein   chr4:6039132-6040171 FORWARD   Aliases: T15G18.30, T15G18_30	9.8	9.6	0.2	0.4	100.0%	-4.9
13176	AT3G02340.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)   chr3:477010-478449 FORWARD   Aliases: F11A12.3, F11A12_3	6.6	6.5	0.1	0.4	100.0%	-5.3
13177	AT1G45160.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr1:17086006-17092717 REVERSE   Aliases: F27F5.23, F27F5_23	5.9	6.1	-0.2	-0.4	100.0%	-4.8
13178	AT2G28720.1   histone H2B, putative, strong similarity to histone H2B Arabidopsis thaliana GI:2407802, Gossypium hirsutum SP:O22582; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr2:12334055-12334755 FORWARD   Aliases: T11P11.3, T11P11_3	6.4	6.2	0.2	0.4	100.0%	-4.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13179	AT2G39850.1   subtilase family protein, contains similarity to subtilisin-like protease C1 GI:13325079 from (Glycine max)   chr2:16637704-16641331 FORWARD   Aliases: T5I7.15, T5I7_15	3.0	3.0	0.1	0.4	100.0%	-5.3
13180	AT5G35190.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:13451411-13452397 FORWARD   Aliases: T25C13.70, T25C13_70	3.5	3.7	-0.2	-0.4	100.0%	-4.4
13181	AT2G44060.2   late embryogenesis abundant family protein / LEA family protein, similar to ethylene-responsive late embryogenesis-like protein (Lycopersicon esculentum) GI:1684830; contains Pfam profile PF03168: Late embryogenesis abundant protein	10.5	10.2	0.3	0.4	100.0%	-4.6
13182	AT4G28540.1   casein kinase, putative, similar to casein kinase I (Arabidopsis thaliana) gi:1103318:emb:CAA55395; contains protein kinase domain, Pfam:PF00069	7.1	6.9	0.2	0.4	100.0%	-4.5
13183	AT3G09570.1   expressed protein   chr3:2940451-2942114 FORWARD   Aliases: F11F8.41	7.4	7.6	-0.2	-0.4	100.0%	-4.8
13184	AT5G50300.1   xanthine/uracil/vitamin C permease family protein, contains Pfam profile PF00860: Permease family   chr5:20483294-20485350 REVERSE   Aliases: K6A12.16, K6A12_16	3.8	3.6	0.1	0.4	100.0%	-5.1
13185	AT2G37050.3   similar to leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] (TAIR:At1g67720.1); similar to putative light repressible receptor protein kinase [Oryza sativa (japonica cultivar-group)] (GB:BAD87040.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr2:15576065-15580805 FORWARD   Aliases: T2N18.19, T2N18_19	5.8	5.5	0.2	0.4	100.0%	-4.7
13186	AT4G18040.1   Symbol: EIF4E   eukaryotic translation initiation factor 4E 1 / eIF-4E1 / mRNA cap-binding protein 1 (EIF4E1), identical to SP:O23252 Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (mRNA cap-binding protein) (eIF-4F 25 kDa subunit) (eIF-4F P26 subunit) {Arabidopsis thaliana}   chr4:10016583-10018198 REVERSE   Aliases: AT.EIF4E1, CUCUMOVIRUS MULTIPLICATION 1, CUM1, EUKARYOTIC TRANSLATION INITIATION FACTOR 4E, F15J5.10, F15J5_10, LSP1	10.2	10.5	-0.3	-0.4	100.0%	-4.7
13187	AT5G48520.1   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_476910.1)   chr5:19678439-19683662 FORWARD   Aliases: MJE7.16, MJE7_16	3.5	3.4	0.1	0.4	100.0%	-5.3
13188	AT5G47500.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:19288186-19290101 REVERSE   Aliases: MNJ7.9, MNJ7_9	3.1	3.2	-0.1	-0.4	100.0%	-5.3
13189	AT5G57880.1   expressed protein, ; expression supported by MPSS   chr5:23461203-23463665 FORWARD   Aliases: MTI20.12	3.3	3.2	0.1	0.4	100.0%	-4.9
13190	AT3G04770.2   Symbol: RPSAB   40S ribosomal protein SA (RPSaB), identical to p40 protein homolog GB:AAB67866 (Arabidopsis thaliana); similar to 40S ribosomal protein SA (P40) GB:O65751 (Cicer arietinum)   chr3:1309300-1310883 REVERSE   Aliases: F7O18.26, F7O18_26, P40 HOMOLOGUE, RPSAB	6.8	6.6	0.2	0.4	100.0%	-4.7
13191	AT5G60200.1   Dof-type zinc finger domain-containing protein, similar to dof6 zinc finger protein GI:5689615 from (Arabidopsis thaliana)   chr5:24258201-24259749 FORWARD   Aliases: F15L12.10, F15L12_10	2.9	3.0	-0.1	-0.4	100.0%	-5.0
13192	AT3G61180.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RNF6 protein (Mus musculus) GI:20530241; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:22656541-22658642 FORWARD   Aliases: T20K12.80	5.5	5.3	0.2	0.4	100.0%	-4.6
13193	AT5G57370.1   expressed protein, low similarity to nucleic acid binding protein (Homo sapiens) GI:431953   chr5:23261960-23263639 FORWARD   Aliases: MSF19.3, MSF19_3	4.3	4.4	-0.1	-0.4	100.0%	-4.7
13194	AT3G43770.1   expressed protein   chr3:15661574-15661987 REVERSE   Aliases: T28A8.60	2.7	2.8	-0.1	-0.4	100.0%	-5.5
13195	AT2G03740.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, similar to cold-regulated gene cor15b (Arabidopsis thaliana) GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr2:1142722-1143982 REVERSE   Aliases: F19B11.19, F19B11_19	3.6	3.5	0.2	0.4	100.0%	-4.7
13196	AT1G02220.1   Symbol: ANAC003   no apical meristem (NAM) family protein, similar to NAC domain protein NAC2 (GI:15148914) {Phaseolus vulgaris}; similar to NAC domain protein NAC2 (GI:21554255) {Arabidopsis thaliana}; contains Pfam PF02365 : No apical meristem (NAM) protein   chr1:428902-430567 REVERSE   Aliases: ANAC003, T6A9.17	3.0	3.2	-0.3	-0.4	100.0%	-4.4
13197	AT5G24510.1   60s acidic ribosomal protein P1, putative   chr5:8369298-8369869 REVERSE   Aliases: K18P6.3, K18P6_3	2.6	2.5	0.1	0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13198	AT2G30860.1   Symbol: ATGSTF9   glutathione S-transferase, putative, identical to GB:Y12295   chr2:13146074-13147322 FORWARD   Aliases: ATGSTF7, F7F1.7, F7F1_7, GLUTTR	8.2	8.5	-0.3	-0.4	100.0%	-4.5
13199	AT2G41760.1   expressed protein   chr2:17429848-17432066 FORWARD   Aliases: T11A7.14, T11A7_14	6.1	6.3	-0.2	-0.4	100.0%	-4.9
13200	AT1G63530.1   expressed protein   chr1:23567317-23568899 FORWARD   Aliases: F2K11.11, F2K11_11	2.6	2.6	0.1	0.4	100.0%	-5.4
13201	AT1G65170.1   ubiquitin carboxyl-terminal hydrolase family protein, contains Pfam profile PF00443: Ubiquitin carboxyl-terminal hydrolase   chr1:24213276-24214779 FORWARD   Aliases: T23K8.8, T23K8_8	2.6	2.5	0.1	0.4	100.0%	-5.3
13202	AT2G18880.1   fibronectin type III domain-containing protein, contains Pfam profile PF00041: Fibronectin type III domain   chr2:8184078-8185870 FORWARD   Aliases: F19F24.8, F19F24_8	3.0	2.9	0.1	0.4	100.0%	-5.5
13203	AT5G02120.1   Symbol: OHP   thylakoid membrane one helix protein (OHP), identical to one helix protein GI:3283057 from (Arabidopsis thaliana)	7.7	7.5	0.3	0.4	100.0%	-4.2
13204	AT1G65230.1   expressed protein   chr1:24232813-24234565 FORWARD   Aliases: T23K8.14, T23K8_14	3.6	3.7	-0.1	-0.4	100.0%	-4.8
13205	AT4G13240.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr4:7680149-7682410 FORWARD   Aliases: F17N18.130, F17N18_130, KINASE PARTNER PROTEIN LIKE, KPP LIKE	2.8	2.9	-0.1	-0.4	100.0%	-5.2
13206	AT1G69490.1   Symbol: NAP   no apical meristem (NAM) family protein, similar to N-term half of NAC domain protein NAM (Arabidopsis thaliana) GI:4325282   chr1:26125803-26127078 FORWARD   Aliases: ANAC029, F10D13.14, F10D13_14, NAC LIKE, ACTIVATED BY AP3/PI	4.6	4.4	0.1	0.4	100.0%	-5.1
13207	AT1G02190.2   CER1 protein, putative, similar to CER1 GI:1199467 and maize gl1 homolog (glossy1 locus) GI:1209703 from (Arabidopsis thaliana)   chr1:415079-418010 FORWARD   Aliases: T6A9.15	3.9	3.7	0.1	0.4	100.0%	-4.9
13208	AT3G05950.1   germin-like protein, putative, similar to germin-like protein GLP6 (SP:P92997); contains Pfam profile: PF01072 germin family   chr3:1781073-1782013 REVERSE   Aliases: F2O10.9, F2O10_9	3.0	3.1	-0.2	-0.4	100.0%	-4.6
13209	AT2G31040.1   ATP synthase protein I -related, contains weak similarity to Swiss-Prot:P08443 ATP synthase protein I (Synechococcus sp.)   chr2:13215983-13218162 REVERSE   Aliases: T16B12.15, T16B12_15	8.8	8.7	0.2	0.4	100.0%	-4.7
13210	AT3G25170.1   Symbol: RALFL26   rapid alkalization factor (RALF) family protein   chr3:9165758-9166260 REVERSE   Aliases: MJL12.13, RALF LIKE 26	3.9	3.9	0.1	0.4	100.0%	-5.4
13211	AT5G18780.1   F-box family protein, contains F-box domain Pfam:PF00646	6.7	6.5	0.2	0.4	100.0%	-4.6
13212	AT4G18800.1   Ras-related GTP-binding family protein, similar to ras-related GTP binding protein RIC2 SP:P40393 from (Oryza sativa); contains Pfam profile: PF00071 Ras family	4.8	5.0	-0.2	-0.4	100.0%	-4.9
13213	AT1G65020.1   expressed protein   chr1:24158033-24160239 REVERSE   Aliases: F13O11.31	5.8	5.4	0.4	0.4	100.0%	-4.6
13214	AT1G02950.3   Symbol: ATGSTF4   similar to glutathione S-transferase, putative [Arabidopsis thaliana] (TAIR:At1g02940.1); similar to glutathione S-transferase 1 [Brassica juncea] (GB:AAP58391.1); contains InterPro domain Glutathione S-transferase, N-terminal (InterPro:IPR004045); contains InterPro domain Glutathione S-transferase, C-terminal (InterPro:IPR004046)   chr1:665152-666451 REVERSE   Aliases: F22D16.5, F22D16_5, GLUTATHIONE S TRANSFERASE 31, GST31	2.6	2.5	0.1	0.4	100.0%	-5.0
13215	AT3G52830.1   expressed protein, MobA, Pseudomonas alcaligenes, EMBL:PAU88088   chr3:19588983-19589243 FORWARD   Aliases: F8J2.1	2.7	2.6	0.1	0.4	100.0%	-5.8
13216	AT4G28890.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:14256339-14257726 REVERSE   Aliases: F25O24.10, F25O24_10	3.4	3.2	0.2	0.4	100.0%	-4.6
13217	AT5G16820.2   Symbol: HSF3   heat shock factor protein 3 (HSF3) / heat shock transcription factor 3 (HSTF3), identical to heat shock transcription factor 3 (HSF3) SP:O81821 from (Arabidopsis thaliana)   chr5:5530333-5532813 FORWARD   Aliases: ATHSFA1B, F5E19.160, F5E19_160, HEAT SHOCK FACTOR 3, HSFA1B	4.8	4.7	0.1	0.4	100.0%	-5.0
13218	AT3G03230.1   esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379   chr3:744396-746016 REVERSE   Aliases: T17B22.8, T17B22_8	3.4	3.5	-0.1	-0.4	100.0%	-5.3
13219	AT2G37010.1   Symbol: ATNAP12   ABC transporter family protein, contains ABC transporter domain, Pfam:PF00005	2.5	2.6	-0.1	-0.4	100.0%	-5.3
13220	AT3G56380.1   Symbol: ARR17   two-component responsive regulator / response regulator 17 (ARR17), identical to response regulator 17 GI:11870070 from (Arabidopsis thaliana)   chr3:20916459-20917347 FORWARD   Aliases: RESPONSE REGULATOR 17, RR17, T5P19.30	2.5	2.4	0.0	0.4	100.0%	-6.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13221	AT1G16040.1   expressed protein, similar To Phosphatidylinositol-glycan biosynthesis, class F protein (PIG-F). (Mouse) (SP:O09101) (Mus musculus); contains six transmembrane domains;	5.2	5.1	0.1	0.4	100.0%	-5.3
13222	AT3G61230.1   LIM domain-containing protein, similar to SP:P29675 Pollen specific protein SF3 {Helianthus annuus}; contains Pfam profile PF00412: LIM domain   chr3:22674961-22676572 REVERSE   Aliases: T20K12.130	2.5	2.5	0.1	0.4	100.0%	-5.3
13223	AT3G46350.1   leucine-rich repeat protein kinase, putative, contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr3:17047412-17052665 FORWARD   Aliases: F18L15.70	2.8	2.8	-0.1	-0.4	100.0%	-5.2
13224	AT3G11350.1   expressed protein   chr3:3558501-3560084 FORWARD   Aliases: F11B9.27	3.8	3.7	0.2	0.4	100.0%	-4.8
13225	AT1G04960.1   expressed protein   chr1:1407800-1410867 REVERSE   Aliases: F13M7.5, F13M7_5	7.9	7.8	0.1	0.4	100.0%	-4.9
13226	AT1G31400.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, low similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr1:11245206-11246462 REVERSE   Aliases: T8E3.21	2.3	2.3	0.0	0.4	100.0%	-5.6
13227	AT3G03630.1   Symbol: CS26   cysteine synthase, chloroplast, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, identical to SP:O22682 Probable cysteine synthase, chloroplast precursor {Arabidopsis thaliana}, similar to SP:P31300 Cysteine synthase, chloroplast precursor {Capsicum annum}   chr3:877951-880453 REVERSE   Aliases: O ACETYL SERINE (THIOL) LYASE, T12J13.9, T12J13_9	4.5	4.6	-0.1	-0.4	100.0%	-4.8
13228	AT1G43940.1   hypothetical protein   chr1:16668858-16670257 FORWARD   Aliases: F9C16.10, F9C16_10	2.3	2.3	0.0	0.4	100.0%	-5.6
13229	AT1G07840.3   similar to Sas10/U3 ribonucleoprotein (Utp) family protein [Arabidopsis thaliana] (TAIR:At2g43650.1); similar to P0456E05.27 [Oryza sativa (japonica cultivar-group)] (GB:XP_463608.1)   chr1:2424051-2426673 FORWARD   Aliases: F24B9.6, F24B9_6	5.1	5.3	-0.1	-0.4	100.0%	-4.8
13230	AT2G29150.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12542792-12544041 REVERSE   Aliases: F16P2.47, F16P2_47	3.1	3.0	0.1	0.4	100.0%	-5.3
13231	AT1G53490.1   bZIP protein   chr1:19969496-19970382 FORWARD   Aliases: F22G10.16	3.6	3.7	-0.1	-0.4	100.0%	-5.0
13232	AT3G07840.1   polygalacturonase, putative / pectinase, putative, strong similarity to polygalacturonase PGA3 (Arabidopsis thaliana) GI:3152948; contains non-consensus AA acceptor splice site at exon 3   chr3:2501899-2503571 REVERSE   Aliases: F17A17.18	2.5	2.4	0.1	0.4	100.0%	-5.6
13233	AT4G11020.1   expressed protein   chr4:6734685-6736071 REVERSE   Aliases: T22B4.3	2.6	2.5	0.1	0.4	100.0%	-5.5
13234	AT4G28300.2   hydroxyproline-rich glycoprotein family protein   chr4:14014679-14017074 FORWARD   Aliases: F26K10.180, F26K10_180	3.9	3.7	0.2	0.4	100.0%	-4.3
13235	AT2G36040.1   expressed protein, ; expression supported by MPSS   chr2:15137725-15137907 REVERSE   Aliases: F11F19.5, F11F19_5	2.8	2.7	0.1	0.4	100.0%	-5.4
13236	AT1G70060.1   paired amphipathic helix repeat-containing protein, similar to transcription co-repressor Sin3 (Xenopus laevis) GI:4960210; contains Pfam profile PF02671: Paired amphipathic helix repeat   chr1:26387452-26393960 FORWARD   Aliases: F20P5.21, F20P5_21	3.5	3.6	-0.1	-0.4	100.0%	-4.9
13237	AT3G46930.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:17296628-17299017 FORWARD   Aliases: F13I12.1	4.4	4.2	0.2	0.4	100.0%	-4.8
13238	AT1G11320.1   expressed protein, identical to hypothetical protein GB:AAD49990 GI:5734725 from (Arabidopsis thaliana)   chr1:3807136-3808875 FORWARD   Aliases: T28P6.3, T28P6_3	3.8	3.9	-0.1	-0.4	100.0%	-5.1
13239	AT5G26910.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g05750.1); similar to hypothetical protein PpenA01001008 [Pediococcus pentosaceus ATCC 25745] (GB:ZP_00323079.1)	5.4	5.3	0.1	0.4	100.0%	-4.6
13240	AT4G26040.1   hypothetical protein   chr4:13206844-13207212 FORWARD   Aliases: F20B18.150, F20B18_150	2.9	2.8	0.1	0.4	100.0%	-5.4
13241	AT3G61070.1   peroxisomal biogenesis factor 11 family protein / PEX11 family protein, contains Pfam PF05648: Peroxisomal biogenesis factor 11 (PEX11)   chr3:22615577-22617741 REVERSE   Aliases: T27I15.160	8.4	8.7	-0.2	-0.4	100.0%	-4.9
13242	AT3G20230.1   50S ribosomal protein L18 family, similar to ribosomal protein L18 (GI:29342325) (Enterococcus faecalis V583); similar to 50S ribosomal protein L18 (Swiss-Prot:O24704) (Synechococcus sp.)   chr3:7054834-7056764 REVERSE   Aliases: MAL21.25	5.4	5.2	0.2	0.4	100.0%	-4.4
13243	AT5G09690.3   magnesium transporter CorA-like family protein (MRS2-7), weak similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg2+ transporter protein   chr5:3000810-3003501 REVERSE   Aliases: F17I14.120, F17I14_120	4.0	3.8	0.1	0.4	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13244	AT1G10980.1   expressed protein, ; expression supported by MPSS   chr1:3667531-3669821 REVERSE   Aliases: T19D16.10, T19D16_10	3.5	3.4	0.1	0.4	100.0%	-5.3
13245	AT1G48030.2   dihydrolipoamide dehydrogenase 1, mitochondrial / lipoamide dehydrogenase 1 (MTPD1), identical to GB:AAF34795 (gi:12704696) from (Arabidopsis thaliana)	10.5	10.7	-0.2	-0.4	100.0%	-4.9
13246	AT3G43790.3   transporter-related, low similarity to SP:P39843 Multidrug resistance protein 2 (Multidrug-efflux transporter 2) {Bacillus subtilis}; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:15666371-15671073 FORWARD   Aliases: T28A8.80	6.1	5.9	0.1	0.4	100.0%	-4.6
13247	AT3G28560.1   expressed protein, similar to mitochondrial protein-like protein (GI:11559424) (Cucumis sativus)	2.4	2.4	-0.0	-0.4	100.0%	-5.9
13248	AT1G66540.1   cytochrome P450, putative, Similar to cytochrome P450 91A1 (SP:Q9FG65)(Arabidopsis thaliana); contains Pfam profile: PF00067: Cytochrome P450   chr1:24828122-24830249 FORWARD   Aliases: F28G11.4, F28G11_4	4.1	4.2	-0.1	-0.4	100.0%	-5.0
13249	AT3G51830.1   Symbol: ATG5   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248:gb:AAG29810; contains Pfam domain, PF02383: Sac1 homology domain ; Contains nonconsensus AT/AA splice site at intron 7   chr3:19231126-19236257 FORWARD   Aliases: ATEM1.8, TRANSMEMBRANE PROTEIN G5P	5.3	5.5	-0.2	-0.4	100.0%	-4.7
13250	AT4G10955.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr4:6713553-6718551 REVERSE   Aliases: None	4.7	4.6	0.1	0.4	100.0%	-5.1
13251	AT4G10960.1   UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative, similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SP:Q42605, Cyamopsis tetragonoloba GI:3021357 (AJ005082)   chr4:6713553-6718546 REVERSE   Aliases: F25I24.170, F25I24_170	4.7	4.6	0.1	0.4	100.0%	-5.1
13252	AT1G09230.1   RNA recognition motif (RRM)-containing protein, contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) domain   chr1:2979522-2982626 REVERSE   Aliases: T12M4.6, T12M4_6	4.7	4.9	-0.2	-0.4	100.0%	-4.9
13253	AT3G04410.1   hypothetical protein   chr3:1168843-1169211 FORWARD   Aliases: T27C4.5, T27C4_5	2.2	2.2	-0.0	-0.4	100.0%	-6.1
13254	AT5G26640.1   expressed protein   chr5:9347844-9348177 REVERSE   Aliases: None	3.2	3.1	0.1	0.4	100.0%	-5.3
13255	AT3G12290.1   tetrahydrofolate dehydrogenase/cyclohydrolase, putative, similar to SP:P07245 C-1-tetrahydrofolate synthase, cytoplasmic (C1-THF synthase) (Includes: Methylenetetrahydrofolate dehydrogenase (EC 1.5.1.5); Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9); Formyltetrahydrofolate synthetase (EC 6.3.4.3)) {Saccharomyces cerevisiae}; contains Pfam profiles PF02882: Tetrahydrofolate dehydrogenase/cyclohydrolase, NAD(P)-binding domain, PF00763: Tetrahydrofolate dehydrogenase/cyclohydrolase, catalytic domain   chr3:3919509-3921526 FORWARD   Aliases: F28J15.8	10.7	10.5	0.2	0.4	100.0%	-5.0
13256	AT3G05930.1   Symbol: GLP8   germin-like protein (GLP8), identical to germin-like protein subfamily 2 member 3 SP:P93000 (PMID:9869400); contains Pfam profile: PF01072 germin family	2.5	2.6	-0.1	-0.4	100.0%	-5.0
13257	AT5G40740.1   expressed protein   chr5:16319142-16323641 REVERSE   Aliases: MNF13.29, MNF13_29	2.8	2.9	-0.1	-0.4	100.0%	-5.6
13258	AT1G55915.1   expressed protein, similar to Hypothetical 30.6 kDa protein in ACT5-YCK1 intergenic region (Swiss-Prot:P38838) (Saccharomyces cerevisiae); similar to Yhr134wp (GI:500671) (Saccharomyces cerevisiae)   chr1:20911212-20913303 FORWARD   Aliases: None	4.2	4.2	0.1	0.4	100.0%	-5.4
13259	AT2G46140.1   late embryogenesis abundant protein, putative / LEA protein, putative, similar to SP:P46518 Late embryogenesis abundant protein Lea14-A {Gossypium hirsutum}; contains Pfam profile PF03168: Late embryogenesis abundant protein	9.3	9.6	-0.3	-0.4	100.0%	-4.5
13260	AT5G64690.1   neurofilament triplet H protein-related, contains weak similarity to neurofilament triplet H protein (200 kDa neurofilament protein) (Neurofilament heavy polypeptide) (NF-H) (Swiss-Prot:P12036) (Homo sapiens)	3.0	2.9	0.1	0.4	100.0%	-5.4
13261	ATMG00160.1   Symbol: COX2   cytochrome c oxidase subunit 2   chrM:40502-42628 REVERSE   Aliases: COX2	3.6	3.8	-0.2	-0.4	100.0%	-4.8
13262	AT1G14060.1   expressed protein   chr1:4817141-4818017 REVERSE   Aliases: None	5.7	5.9	-0.1	-0.4	100.0%	-4.6
13263	AT5G44550.1   integral membrane family protein, similar to unknown protein (pir::T10581) This family of plant proteins contains a domain that may have a catalytic activity. It has a conserved arginine and aspartate that could form an active site. These proteins are predicted to contain 3 or 4 transmembrane helices; contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr5:17959102-17960435 REVERSE   Aliases: MFC16.23, MFC16_23	2.2	2.4	-0.2	-0.4	100.0%	-4.7
13264	AT5G06860.1   Symbol: PGIP1   polygalacturonase inhibiting protein 1 (PGIP1), identical to polygalacturonase inhibiting protein 1 (PGIP1) (Arabidopsis thaliana) gi:7800199:gb:AAF69827; contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr5:2132351-2133588 FORWARD   Aliases: MOJ9.3, MOJ9_3, POLYGALACTURONASE INHIBITING PROTEIN 1	7.4	7.6	-0.2	-0.4	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13265	AT4G13050.1   acyl-(acyl carrier protein) thioesterase, putative / acyl-ACP thioesterase, putative / oleoyl-(acyl-carrier protein) hydrolase, putative / S-acyl fatty acid synthase thioesterase, putative, strong similarity to acyl-ACP thioesterase; oleoyl-(acyl-carrier protein) hydrolase (Brassica napus) GI:435011; contains Pfam profile PF01643: Acyl-ACP thioesterase   chr4:7617558-7619611 FORWARD   Aliases: F25G13.140, F25G13_140	6.6	6.7	-0.1	-0.4	100.0%	-5.0
13266	AT3G16680.1   expressed protein, ; expression supported by MPSS   chr3:5683342-5684251 FORWARD   Aliases: MGL6.11	2.8	2.9	-0.1	-0.4	100.0%	-5.7
13267	AT3G49480.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr3:18353529-18354458 REVERSE   Aliases: T9C5.80	3.5	3.4	0.1	0.4	100.0%	-5.3
13268	AT2G47390.1   expressed protein   chr2:19448742-19453435 REVERSE   Aliases: T8I13.23	8.2	8.4	-0.3	-0.4	100.0%	-4.7
13269	AT1G32530.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger); weak similarity to interaptin (GI:3549261) (Dictyostelium discoideum) weak similarity to Axoneme-associated protein mst101(2) (Swiss-Prot:Q08696) (Drosophila hydei)   chr1:11759439-11762587 REVERSE   Aliases: F5D14.34	5.8	5.7	0.1	0.4	100.0%	-5.1
13270	AT5G53280.1   expressed protein   chr5:21624733-21626560 FORWARD   Aliases: K19E1.8, K19E1_8	3.4	3.3	0.1	0.4	100.0%	-4.9
13271	AT5G27520.1   mitochondrial substrate carrier family protein   chr5:9714385-9716308 REVERSE   Aliases: F21A20.230, F21A20_230	6.5	6.6	-0.1	-0.4	100.0%	-4.8
13272	AT1G08040.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g28310.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g28310.1); similar to lysine ketoglutarate reductase trans-splicing related 1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87361.1); contains InterPro domain Protein of unknown function DUF707 (InterPro:IPR007877)   chr1:2495339-2498638 REVERSE   Aliases: T6D22.12, T6D22_12	6.7	6.9	-0.1	-0.4	100.0%	-4.7
13273	AT1G60530.1   dynamin family protein, similar to mx2 protein GI:5578742 from (Mus musculus musculus); contains Pfam profile PF00350: Dynamin family   chr1:22303462-22304832 FORWARD   Aliases: F8A5.7, F8A5_7	2.7	2.8	-0.1	-0.4	100.0%	-5.5
13274	AT2G23450.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:9995834-9998739 REVERSE   Aliases: F26B6.10, F26B6_10	5.0	4.8	0.2	0.4	100.0%	-4.4
13275	AT4G15160.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to SP:Q00451:PRF1_LYCES 36.4 kDa proline-rich protein Lycopersicon esculentum, proline-rich cell wall protein (Medicago sativa) GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family   chr4:8646193-8650082 FORWARD   Aliases: DL3625W, FCAALL.211	3.5	3.6	-0.2	-0.4	100.0%	-4.5
13276	AT1G08680.3   Symbol: ZIGA4   similar to human Rev interacting-like protein-related / hRIP protein-related [Arabidopsis thaliana] (TAIR:At4g13350.2); similar to human Rev interacting-like protein-related / hRIP protein-related [Arabidopsis thaliana] (TAIR:At4g13350.1); similar to human Rev interacting-like protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_464581.1); similar to ZIGA2 protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_464580.1); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164)   chr1:2762646-2768955 FORWARD   Aliases: AT1G08690, F22O13.16, F22O13_16, ZIGA4	3.9	3.9	-0.1	-0.4	100.0%	-5.0
13277	AT1G56700.1   pyrrolidone-carboxylate peptidase family protein, similar to Pyrrolidone-carboxylate peptidase (5-oxopropyl- peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase). (Swiss-Prot:O73944) (Pyrococcus furiosus); similar to Pyrrolidone-carboxylate peptidase (5-oxopropyl- peptidase) (Pyroglutamyl-peptidase I) (PGP-I). (Swiss-Prot:O07883) (Thermococcus litoralis); contains Pfam PF01470: pyrrolidone-carboxylate peptidase	11.8	11.6	0.1	0.4	100.0%	-5.1
13278	AT4G20800.1   FAD-binding domain-containing protein, similar to SP:P93479 Reticuline oxidase precursor (EC 1.5.3.9) (Berberine-bridge-forming enzyme) {Papaver somniferum}; contains Pfam profile PF01565: FAD binding domain   chr4:11139620-11141322 FORWARD   Aliases: F21C20.150, F21C20_150	3.0	3.0	-0.1	-0.4	100.0%	-5.4
13279	AT4G14820.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:8507789-8510033 REVERSE   Aliases: DL3450C, FCAALL.330	4.7	4.6	0.1	0.4	100.0%	-5.0
13280	AT3G29190.1   terpene synthase/cyclase family protein, contains Pfam profile: PF01397 terpene synthase family   chr3:11160610-11163800 REVERSE   Aliases: MXO21.3	3.9	3.8	0.2	0.4	100.0%	-5.0
13281	AT1G04440.1   casein kinase, putative, similar to casein kinase I (Arabidopsis thaliana) gi:1103318:emb:CAA55395; contains protein kinase domain, Pfam:PF00069	5.5	5.7	-0.2	-0.4	100.0%	-4.5
13282	AT2G29400.1   Symbol: TOPP1   serine/threonine protein phosphatase PP1 isozyme 1 (TOPP1) / phosphoprotein phosphatase 1, identical to SP:P30366: Serine/threonine protein phosphatase PP1 isozyme 1 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GI:166572 (Arabidopsis thaliana)   chr2:12620158-12622475 REVERSE   Aliases: PP1 AT, PROTEIN PHOSPHATASE 1, TYPE ONE PROTEIN PHOSPHATASE 1	8.6	8.3	0.3	0.4	100.0%	-4.8
13283	AT2G26580.2   plant-specific transcription factor YABBY family protein, contains Pfam profile: PF04690 YABBY protein   chr2:11310670-11314031 REVERSE   Aliases: T9J22.25, T9J22_25	2.5	2.6	-0.1	-0.4	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13284	AT4G39480.1   Symbol: CYP96A9   similar to cytochrome P450, putative [Arabidopsis thaliana] (TAIR:At4g32170.1); similar to cytochrome P450, putative [Arabidopsis thaliana] (TAIR:At1g65340.1); similar to cytochrome P450, putative [Arabidopsis thaliana] (TAIR:At2g23180.1); similar to putative phytochrome P450 [Oryza sativa (japonica cultivar-group)] (GB:NP_914475.1); contains InterPro domain E-class P450, group I (InterPro:IPR002401); contains InterPro domain Cytochrome P450 (InterPro:IPR001128)   chr4:18362252-18364202 FORWARD   Aliases: AT4G39490, F23K16.110, F23K16_110	2.5	2.4	0.1	0.4	100.0%	-5.5
13285	AT2G46070.1   Symbol: ATMPK12   mitogen-activated protein kinase, putative / MAPK, putative (MPK12), mitogen-activated protein kinase (MAPK)(AtMPK12), PMID:12119167   chr2:18953054-18954896 REVERSE   Aliases: T3F17.28	2.8	2.7	0.1	0.4	100.0%	-5.4
13286	AT1G19870.1   calmodulin-binding family protein, contains Pfam profile: PF00612 IQ calmodulin-binding motif   chr1:6895017-6898600 REVERSE   Aliases: F6F9.8, F6F9_8	4.1	4.6	-0.5	-0.4	100.0%	-4.6
13287	AT2G20330.1   transducin family protein / WD-40 repeat family protein, similar to Transcriptional repressor rco-1 (SP:P78706) (Neurospora crassa); similar to TUP1(GB:AF079369); contains 6 WD-40 repeats (PF00400)   chr2:8779856-8782695 REVERSE   Aliases: F11A3.12, F11A3_12	5.4	5.6	-0.2	-0.4	100.0%	-4.6
13288	AT1G72080.1   expressed protein   chr1:27124069-27126423 REVERSE   Aliases: F28P5.14, F28P5_14	3.6	3.6	0.1	0.4	100.0%	-5.3
13289	AT1G17665.1   expressed protein   chr1:6072591-6074477 REVERSE   Aliases: None	3.3	3.2	0.1	0.4	100.0%	-5.3
13290	AT5G48250.1   zinc finger (B-box type) family protein, contains similarity to CONSTANS homologs   chr5:19578545-19580948 REVERSE   Aliases: MIF21.14, MIF21_14	3.8	3.7	0.1	0.4	100.0%	-5.0
13291	AT2G37070.1   expressed protein   chr2:15586065-15588387 FORWARD   Aliases: T2N18.17, T2N18_17	3.5	3.6	-0.1	-0.4	100.0%	-5.1
13292	AT4G35980.1   expressed protein   chr4:17030575-17031695 REVERSE   Aliases: T19K4.110	8.3	8.4	-0.1	-0.4	100.0%	-4.7
13293	AT1G31640.1   MADS-box protein-related, contains INTERPRO:IPR02100 MADS-box domain ;similar to MADS box transcription factor Gl:3688589 from (Triticum aestivum)   chr1:11322673-11324157 REVERSE   Aliases: F27M3.16, F27M3_16	2.6	2.7	-0.1	-0.4	100.0%	-5.6
13294	AT5G44460.1   calcium-binding protein, putative, similar to SP:Q09011 Calcium-binding protein CAST {Solanum tuberosum}; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:17934513-17935140 FORWARD   Aliases: MFC16.12, MFC16_12	3.9	3.8	0.1	0.4	100.0%	-4.8
13295	AT2G26590.3   similar to Adrm1 protein [Mus musculus] (GB:AAH19746.1); contains InterPro domain Adhesion regulating molecule (InterPro:IPR006773)   chr2:11318082-11322173 REVERSE   Aliases: T9J22.26, T9J22_26	8.4	8.2	0.1	0.4	100.0%	-5.1
13296	AT5G05130.1   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to transcription factor RUSH-1alpha (Oryctolagus cuniculus) Gl:1655930; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:1512121-1515080 FORWARD   Aliases: MUG13.1, MUG13_1	3.9	3.8	0.1	0.4	100.0%	-5.1
13297	AT3G07110.2   similar to 60S ribosomal protein L13A (RPL13aD) [Arabidopsis thaliana] (TAIR:At5g48760.1); similar to ribosomal protein L13a [Lupinus luteus] (GB:CAA11283.1); contains InterPro domain Ribosomal protein L13, bacterial and organelle form (InterPro:IPR005823); contains InterPro domain Ribosomal protein L13, archea and eukaryotic form (InterPro:IPR005755); contains InterPro domain Ribosomal protein L13 (InterPro:IPR005822)   chr3:2252025-2253534 FORWARD   Aliases: T1B9.24, T1B9_24	11.4	11.5	-0.1	-0.4	100.0%	-5.0
13298	AT4G07530.1   expressed protein   chr4:4365347-4368612 REVERSE   Aliases: T3E15.23, T3E15_23	3.5	3.7	-0.2	-0.4	100.0%	-4.8
13299	AT2G21420.1   zinc finger protein-related, contains low similarity to zinc finger proteins and Pfam PF01485: IBR domain   chr2:9176793-9178826 FORWARD   Aliases: F3K23.18, F3K23_18	2.7	2.8	-0.1	-0.4	100.0%	-5.1
13300	AT2G47920.1   kinase interacting family protein, similar to kinase interacting protein 1 (Gl:13936326) (Petunia integrifolia)   chr2:19622847-19623974 FORWARD   Aliases: F17A22.31, F17A22_31	2.2	2.2	-0.0	-0.4	100.0%	-5.8
13301	AT1G16680.1   DNAJ heat shock N-terminal domain-containing protein / S-locus protein, putative, similar to S-locus protein 5 Gl:6069485 from (Brassica rapa); contains Pfam profile PF00226 DnaJ domain   chr1:5702806-5705831 FORWARD   Aliases: F19K19.3, F19K19_3	5.8	5.6	0.1	0.4	100.0%	-4.7
13302	AT3G52720.2   carbonic anhydrase family protein, low similarity to storage protein (dioscorin) (Dioscorea cayenensis) Gl:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase   chr3:19550256-19552262 REVERSE   Aliases: F3C22.120	2.9	3.0	-0.1	-0.4	100.0%	-5.1
13303	AT5G11910.1   esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase CinI (Butyrivibrio fibrisolvens) Gl:1622732; contains Interpro entry IPR000379   chr5:3836338-3838214 REVERSE   Aliases: F14F18.80, F14F18_80	8.3	8.2	0.1	0.4	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13304	AT3G12340.1   similar to immunophilin-related / FKBP-type peptidyl-prolyl cis-trans isomerase-related [Arabidopsis thaliana] (TAIR:At4g25340.1); similar to putative immunophilin/FKBP-type peptidyl-prolyl cis-trans isomerase [Helianthus annuus] (GB:AAR23804.1); contains InterPro domain Peptidylprolyl isomerase, FKBP-type (InterPro:IPR001179)	5.5	5.7	-0.2	-0.4	100.0%	-4.7
13305	AT5G39090.1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family   chr5:15660831-15662344 FORWARD   Aliases: MXF12.100, MXF12_100	4.9	4.8	0.1	0.4	100.0%	-5.1
13306	AT2G28700.1   MADS-box protein-related, contains INTERPRO: IPR002100 MADS-box domain   chr2:12324243-12325823 REVERSE   Aliases: T11P11.1, T11P11_1	2.8	2.8	-0.0	-0.4	100.0%	-5.6
13307	AT1G75600.1   histone H3.2, putative, strong similarity to histone H3.2 SP:P11105 GI:417103 from Lolium temulentum, histone H3.2 from Mus pahari GI:515005; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:28394414-28395122 FORWARD   Aliases: F10A5.32, F10A5_32	2.8	2.8	0.1	0.4	100.0%	-5.6
13308	AT1G11890.1   Symbol: SEC22   vesicle transport protein SEC22, putative, identified as SEC22 by Raikhel, NV, et al. in Plant Physiol. 124: 1558-69 (2000); similar to vesicle trafficking protein gb:U91538 from Mus musculus; ESTs gb:F15494 and gb:F14097 come from this gene   chr1:4010778-4013122 FORWARD   Aliases: ATSEC22, F12F1.27, F12F1_27	7.5	7.7	-0.2	-0.4	100.0%	-4.7
13309	AT2G41850.1   endo-polygalacturonase, putative, similar to endo-polygalacturonase (Arabidopsis thaliana) GI:2597824; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr2:17468983-17471239 REVERSE   Aliases: T11A7.5, T11A7_5	3.3	3.2	0.1	0.4	100.0%	-5.1
13310	AT2G17240.1   expressed protein   chr2:7505214-7506288 FORWARD   Aliases: T23A1.10, T23A1_10	6.9	6.6	0.3	0.4	100.0%	-4.4
13311	AT1G53940.1   GDSL-motif lipase/hydrolase family protein, similar to lipase GI:1145627 from (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr1:20146947-20149448 FORWARD   Aliases: T18A20.17	3.0	2.7	0.3	0.4	100.0%	-4.1
13312	AT5G49960.1   expressed protein, ; expression supported by MPSS   chr5:20341399-20344913 REVERSE   Aliases: K9P8.10, K9P8_10	5.3	5.5	-0.2	-0.4	100.0%	-4.7
13313	AT5G39430.1   expressed protein   chr5:15792530-15794827 REVERSE   Aliases: MUL8.11, MUL8_11	2.7	2.7	0.1	0.4	100.0%	-5.6
13314	AT5G02440.1   expressed protein   chr5:531064-532723 FORWARD   Aliases: T22P11.30, T22P11_30	3.3	3.4	-0.1	-0.4	100.0%	-5.1
13315	AT1G67460.1   expressed protein, contains Pfam domain PF03193: Protein of unknown function, DUF258   chr1:25273289-25275280 REVERSE   Aliases: T1F15.7, T1F15_7	4.6	4.4	0.1	0.4	100.0%	-4.9
13316	AT2G15420.1   myosin heavy chain-related   chr2:6731030-6735265 REVERSE   Aliases: F26H6.6, F26H6_6	3.0	2.9	0.1	0.4	100.0%	-5.3
13317	AT1G09060.3   similar to transcription factor jumonji (jmc) domain-containing protein [Arabidopsis thaliana] (TAIR:At4g00990.1); similar to putative DNA-binding protein PD3, chloroplast [Oryza sativa (japonica cultivar-group)] (GB:XP_468520.1); contains InterPro domain Transcription factor jumonji, jmc (InterPro:IPR003347)	6.7	6.9	-0.2	-0.4	100.0%	-4.8
13318	AT3G06230.1   Symbol: ATMKK8	2.3	2.3	-0.0	-0.4	100.0%	-5.6
13319	AT5G54950.1   aconitate hydratase-related / citrate hydro-lyase-related / aconitase-related, similar to SP:Q42560 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Arabidopsis thaliana}   chr5:22327058-22327468 REVERSE   Aliases: MBG8.22, MBG8_22	3.3	3.3	0.1	0.4	100.0%	-5.3
13320	AT2G10370.1   hypothetical protein, includes At2g10370, At5g36050, At1g35090, At1g44860, At4g19300, At1g42400, At3g43040, At3g42500   chr2:4003719-4004733 FORWARD   Aliases: F12P23.12, F12P23_12	2.3	2.3	-0.0	-0.4	100.0%	-5.9
13321	AT2G45420.1   LOB domain protein 18 / lateral organ boundaries domain protein 18 (LBD18), identical to LOB DOMAIN 18 (Arabidopsis thaliana) GI:17227164; supported by full-length cDNA gi:17227163   chr2:18725422-18727803 FORWARD   Aliases: F4L23.7	2.1	2.1	0.1	0.4	100.0%	-5.5
13322	AT1G52770.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr1:19659507-19661402 FORWARD   Aliases: F14G24.4, F14G24_4	2.8	2.9	-0.1	-0.4	100.0%	-5.4
13323	AT4G10360.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g31300.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475446.1); contains InterPro domain TRAM, LAG1 and CLN8 homology (InterPro:IPR006634)   chr4:6420465-6422376 FORWARD   Aliases: F24G24.160, F24G24_160	5.3	5.5	-0.2	-0.4	100.0%	-4.5
13324	AT3G22990.1   expressed protein   chr3:8163965-8166352 FORWARD   Aliases: MXC7.2	6.8	6.5	0.3	0.4	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13325	AT5G51340.1   expressed protein   chr5:20880169-20884596 FORWARD   Aliases: MFG13.4, MFG13_4	4.9	5.1	-0.2	-0.4	100.0%	-4.7
13326	AT2G25610.1   H <sup>+</sup> -transporting two-sector ATPase, C subunit family protein, similar to SP:P23968 Vacuolar ATP synthase 22 kDa proteolipid subunit (EC 3.6.3.14) {Saccharomyces cerevisiae}; contains Pfam profile PF00137: ATP synthase subunit C   chr2:10908369-10909609 REVERSE   Aliases: F3N11.6, F3N11_6	7.8	7.5	0.3	0.4	100.0%	-4.6
13327	AT4G37840.1   hexokinase, putative, similar to hexokinase 1 (Spinacia oleracea) Swiss-Prot:Q9SEK3   chr4:17790141-17792192 REVERSE   Aliases: T28I19.120, T28I19_120	2.7	2.6	0.1	0.4	100.0%	-5.3
13328	AT2G03840.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr2:1173167-1174112 FORWARD   Aliases: T18C20.4, T18C20_4	3.1	3.0	0.1	0.4	100.0%	-5.0
13329	AT2G47490.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr2:19494316-19496689 FORWARD   Aliases: T30B22.21	5.8	5.6	0.2	0.4	100.0%	-4.7
13330	AT4G03670.1   expressed protein   chr4:1626627-1627735 FORWARD   Aliases: T5L23.17, T5L23_17	2.6	2.6	0.1	0.4	100.0%	-5.6
13331	AT4G08590.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profiles PF00097: Zinc finger C3HC4 type (RING finger), PF02182: YDG/SRA domain   chr4:5463892-5466653 REVERSE   Aliases: T3F12.10	5.3	5.1	0.1	0.4	100.0%	-4.5
13332	AT5G18270.2   Symbol: ANAC087   no apical meristem (NAM) family protein, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (GI:1944132) (Arabidopsis thaliana)   chr5:6040921-6042940 REVERSE   Aliases: ANAC087, MRG7.23, MRG7_23	3.6	3.4	0.2	0.4	100.0%	-4.3
13333	AT1G72260.1   Symbol: THI2.1	3.6	3.6	-0.1	-0.4	100.0%	-5.3
13334	AT5G51120.1   polyadenylate-binding protein, putative / PABP, putative, contains similarity to poly(A)-binding protein II (Mus musculus) GI:2351846; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	5.2	5.3	-0.1	-0.4	100.0%	-5.1
13335	AT1G18650.1   glycosyl hydrolase family protein 17, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis); C-terminal homology only   chr1:6418852-6420521 REVERSE   Aliases: F25I16.1, F25I16_1	4.2	4.1	0.1	0.4	100.0%	-4.8
13336	AT2G26710.1   Symbol: BAS1   Encodes a member of the cytochrome p450 family. Involved in brassinolide metabolism. Mediates response to a variety of light signals including hypocotyl elongation and cotyledon expansion.   chr2:11387584-11390690 FORWARD   Aliases: BAS1, CYP72B1, CYP734A1, F18A8.8, F18A8_8, PHYB ACTIVATION TAGGED SUPPRESSOR 1	2.4	2.5	-0.1	-0.4	100.0%	-5.1
13337	AT1G51730.1   RWD domain-containing protein, contains Pfam profile PF05773: RWD domain; similar to GCN2 eIF2alpha kinase (GI:6066585) (Mus musculus); similar to GCN2beta (GI:10764163) (Mus musculus); similar to RING finger protein 25 (RING finger protein AO7) (Swiss-Prot:Q9QZR0) (Mus musculus); similar to RING finger protein 25 (Swiss-Prot:Q96BH1) (Homo sapiens)   chr1:19190171-19192441 REVERSE   Aliases: F19C24.6, F19C24_6	8.4	8.2	0.2	0.4	100.0%	-4.6
13338	AT1G25570.1   leucine-rich repeat protein-related, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains some similarity to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376   chr1:8991813-8995469 REVERSE   Aliases: F2J7.2	5.2	5.3	-0.1	-0.4	100.0%	-4.6
13339	AT2G39340.1   SAC3/GANP family protein, contains Pfam profile: PF03399 SAC3/GANP family   chr2:16430719-16437679 FORWARD   Aliases: T16B24.2, T16B24_2	5.0	4.9	0.1	0.4	100.0%	-5.0
13340	AT4G03000.2   expressed protein, contains similarity to hypothetical proteins   chr4:1324136-1327520 FORWARD   Aliases: T4I9.12, T4I9_12	6.8	6.9	-0.2	-0.4	100.0%	-5.0
13341	AT5G47680.1   expressed protein, contains Pfam profile PF04243: Protein of unknown function (DUF425)   chr5:19332309-19334748 REVERSE   Aliases: MNJ7.27, MNJ7_27	9.4	9.5	-0.2	-0.4	100.0%	-4.5
13342	AT5G27890.1   expressed protein   chr5:9903644-9905918 FORWARD   Aliases: F14I23.50, F14I23_50	4.0	4.1	-0.1	-0.4	100.0%	-4.8
13343	AT3G49680.1   branched-chain amino acid aminotransferase 3 / branched-chain amino acid transaminase 3 (BCAT3), identical to SP:Q9M401 Branched-chain amino acid aminotransferase 3, chloroplast precursor (EC 2.6.1.42) (Atbcat-3){Arabidopsis thaliana}   chr3:18433644-18436674 FORWARD   Aliases: T16K5.30	8.9	9.2	-0.3	-0.4	100.0%	-4.6
13344	AT5G20860.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:7076892-7079079 REVERSE   Aliases: F22D1.30, F22D1_30	2.8	2.8	0.1	0.4	100.0%	-5.5
13345	AT2G19390.1   expressed protein   chr2:8396882-8404944 REVERSE   Aliases: F27F23.19, F27F23_19	3.7	4.1	-0.4	-0.4	100.0%	-4.6
13346	AT1G80510.1   amino acid transporter family protein, similar to amino acid transporter system N2 (Rattus norvegicus) GI:14578932; contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:30277741-30279685 FORWARD   Aliases: T21F11.16, T21F11_16	3.8	3.7	0.1	0.4	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13347	AT3G24530.1   AAA-type ATPase family protein / ankyrin repeat family protein, contains Pfam profiles: PF00023 ankyrin repeat, PF00004 ATPase family associated with various cellular activities (AAA)   chr3:8945432-8947933 REVERSE   Aliases: MOB24.10	4.2	4.1	0.2	0.4	100.0%	-5.0
13348	AT1G68380.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr1:25639501-25641125 REVERSE   Aliases: T2E12.7	2.1	2.0	0.0	0.4	100.0%	-5.8
13349	AT3G21260.2   glycolipid transfer protein-related, contains weak similarity to Glycolipid transfer protein (GLTP) (Swiss-Prot:P17403) (Sus scrofa)   chr3:7464026-7465100 REVERSE   Aliases: MXL8.12	3.4	3.2	0.2	0.4	100.0%	-4.7
13350	AT2G40090.1   Symbol: ATATH9	5.3	5.4	-0.1	-0.4	100.0%	-4.9
13351	AT4G33630.2   expressed protein   chr4:16155506-16159938 FORWARD   Aliases: T16L1.120, T16L1_120	4.0	4.0	-0.1	-0.4	100.0%	-5.1
13352	AT1G01960.1   guanine nucleotide exchange family protein, similar to guanine nucleotide exchange factor (Homo sapiens) GI:5456754; contains Pfam profile PF01369: Sec7 domain   chr1:330588-337582 REVERSE   Aliases: F22M8.9, F22M8_9	5.0	5.2	-0.1	-0.4	100.0%	-5.0
13353	AT4G15415.2   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'gamma), identical to B' regulatory subunit of PP2A (Arabidopsis thaliana) GI:2160694; similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)	3.1	3.2	-0.1	-0.4	100.0%	-4.9
13354	AT1G05440.1   expressed protein, contains domain THR_RICH (PS50325)   chr1:1596006-1597847 REVERSE   Aliases: T25N20.9, T25N20_9	2.7	2.8	-0.1	-0.4	100.0%	-5.5
13355	AT5G13420.1   transaldolase, putative, similar to transaldolase (Solanum tuberosum) gi:2078350:gb:AAB54016   chr5:4301795-4304315 REVERSE   Aliases: T22N19.70, T22N19_70	10.8	11.0	-0.2	-0.4	100.0%	-5.4
13356	AT5G62250.1   microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr5:25022982-25025322 FORWARD   Aliases: MMI9.8, MMI9_8	2.4	2.3	0.0	0.4	100.0%	-5.9
13357	AT2G28290.2   Symbol: SYD   chromatin remodeling protein, putative (SYD), similar to transcriptional activator HBRM (Homo sapiens) GI:414117; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain; identical to cDNA putative chromatin remodeling protein SYD (SPLAYED) GI:13603720	7.0	7.2	-0.2	-0.4	100.0%	-4.8
13358	AT2G02150.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:547260-552228 REVERSE   Aliases: F5O4.8, F5O4_8	4.8	4.7	0.2	0.4	100.0%	-4.7
13359	AT3G20940.1   Symbol: CYP705A30   cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) (Glycine max); similar to cytochrome P450 (SP:H71417) (Arabidopsis thaliana)   chr3:7339723-7341656 FORWARD   Aliases: MFD22.8	3.0	3.0	0.1	0.4	100.0%	-4.9
13360	AT1G03457.2   RNA-binding protein, putative, similar to Etr-1 (Danio rerio) GI:7670536, BRUNO-like 6 RNA-binding protein (Homo sapiens) GI:15341327; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	3.2	3.3	-0.1	-0.4	100.0%	-5.1
13361	AT1G74720.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr1:28078834-28082417 FORWARD   Aliases: F25A4.35, F25A4_35	7.0	7.2	-0.2	-0.4	100.0%	-4.3
13362	AT5G49080.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:19908010-19910035 REVERSE   Aliases: K20J1.5, K20J1_5	3.8	4.3	-0.5	-0.4	100.0%	-4.1
13363	AT2G35470.1   expressed protein   chr2:14916005-14916881 REVERSE   Aliases: T32F12.15, T32F12_15	4.6	4.7	-0.1	-0.4	100.0%	-4.9
13364	AT2G24430.2   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;	2.6	2.6	-0.1	-0.4	100.0%	-5.2
13365	AT5G42740.1   glucose-6-phosphate isomerase, cytosolic (PGIC), identical to SP:P34795 Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI) (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI) {Arabidopsis thaliana}; contains Pfam profile PF00342: glucose-6-phosphate isomerase   chr5:17153028-17158120 FORWARD   Aliases: MJB21.12, MJB21_12	6.5	7.0	-0.4	-0.4	100.0%	-4.4
13366	AT1G69080.2   universal stress protein (USP) family protein, contains Pfam profile PF00582: universal stress protein family   chr1:25975580-25976920 REVERSE   Aliases: F4N2.5, F4N2_5	3.5	3.7	-0.2	-0.4	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13367	AT4G23510.1   disease resistance protein (TIR class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr4:12267526-12270553 REVERSE   Aliases: F16G20.210, F16G20_210	2.5	2.7	-0.2	-0.4	100.0%	-4.3
13368	AT1G51260.1   Symbol: LPAT3   acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, putative, similar to acyl-CoA:1-acylglycerol-3-phosphate acyltransferase Gl:4583544 from (Brassica napus)   chr1:19007044-19009309 REVERSE   Aliases: F11M15.12, F11M15_12	3.4	3.2	0.1	0.4	100.0%	-5.0
13369	AT1G52050.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) Gl:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	2.7	2.8	-0.1	-0.4	100.0%	-5.3
13370	AT1G48780.1   expressed protein   chr1:18045657-18046412 FORWARD   Aliases: F11I4.5, F11I4_5	2.5	2.5	-0.1	-0.4	100.0%	-5.0
13371	AT1G22010.1   hypothetical protein   chr1:7749560-7750051 FORWARD   Aliases: F2E2.5, F2E2_5	2.9	2.8	0.1	0.4	100.0%	-5.4
13372	AT2G36390.1   Symbol: SBE2.1	7.8	8.0	-0.2	-0.4	100.0%	-4.9
13373	AT2G04675.1   expressed protein   chr2:1637481-1638644 REVERSE   Aliases: None	2.8	2.7	0.1	0.4	100.0%	-4.8
13374	AT5G63900.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr5:25585924-25587597 FORWARD   Aliases: MGI19.10, MGI19_10	3.3	3.3	0.1	0.4	100.0%	-5.5
13375	AT3G25280.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:9207420-9209273 FORWARD   Aliases: MJL12.24	3.6	3.5	0.1	0.4	100.0%	-5.2
13376	AT3G15605.1   expressed protein   chr3:5287970-5290948 FORWARD   Aliases: MQD17.8	3.2	3.3	-0.1	-0.4	100.0%	-5.0
13377	AT1G14550.1   anionic peroxidase, putative, similar to anionic peroxidase Gl:170202 from (Nicotiana glauca)   chr1:4979023-4980319 FORWARD   Aliases: F14L17.33, F14L17_33	2.8	2.7	0.1	0.4	100.0%	-4.7
13378	AT5G59130.1   subtilase family protein, contains similarity to prepro-cucumisin Gl:807698 from (Cucumis melo)   chr5:23887418-23890917 REVERSE   Aliases: MNC17.3, MNC17_3	2.3	2.3	-0.0	-0.4	100.0%	-5.8
13379	AT5G06510.3   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr5:1985003-1986922 FORWARD   Aliases: F15M7.4, F15M7_4	3.3	3.1	0.1	0.4	100.0%	-5.1
13380	AT2G29960.1   Symbol: CYP5   peptidyl-prolyl cis-trans isomerase / cyclophilin (CYP5) / rotamase, identical to cyclophilin (Arabidopsis thaliana) gi:2443755:gb:AAB71401   chr2:12776134-12777656 REVERSE   Aliases: ATCYP5, F23F1.12, F23F1_12	9.3	9.4	-0.1	-0.4	100.0%	-4.9
13381	AT2G15325.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:6676736-6677463 REVERSE   Aliases: F27O10.2, F27O10_2	2.7	2.7	-0.1	-0.4	100.0%	-5.5
13382	AT4G21710.1   Symbol: NRPB2   DNA-directed RNA polymerase II 135 kDa polypeptide / RNA polymerase II subunit 2 (RPB135) (RPB2) (RP140), identical to SP:P38420 DNA-directed RNA polymerase II 135 kDa polypeptide (EC 2.7.7.6) (RNA polymerase II subunit 2) {Arabidopsis thaliana}   chr4:11535537-11542212 REVERSE   Aliases: EMB1989, EMBRYO DEFECTIVE 1989, F17L22.170, F17L22_170, RPB2	7.6	7.4	0.2	0.4	100.0%	-5.1
13383	AT3G57600.1   encodes a member of the DREB subfamily A-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are eight members in this subfamily including DREB2A AND DREB2B that are involved in response to drought.   chr3:21343760-21344840 FORWARD   Aliases: F15B8.210	2.7	2.7	-0.1	-0.4	100.0%	-5.2
13384	AT3G23830.2   glycine-rich RNA-binding protein, putative, similar to Glycine-rich RNA-binding protein 2, mitochondrial precursor (AtGRP2) (Swiss-Prot:Q9SVM8) (Arabidopsis thaliana); contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:8606484-8608041 REVERSE   Aliases: F14O13.2	6.5	6.6	-0.2	-0.4	100.0%	-4.8
13385	AT3G53670.1   expressed protein   chr3:19901399-19903380 FORWARD   Aliases: AT3G53660, F4P12.370	4.8	4.9	-0.1	-0.4	100.0%	-5.1
13386	AT1G78650.1   expressed protein, weak similarity to DNA polymerase delta subunit 3 (DNA polymerase delta subunit p66) (Swiss-Prot:Q15054) (Homo sapiens)   chr1:29587822-29590534 FORWARD   Aliases: T30F21.2, T30F21_2	4.6	4.8	-0.1	-0.4	100.0%	-4.9
13387	AT5G59590.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:24026209-24027875 REVERSE   Aliases: F2O15.19, F2O15_19	3.7	3.4	0.2	0.4	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13388	AT3G54610.1   Symbol: GCN5   histone acetyltransferase (GCN5), nearly identical to histone acetyltransferase GCN5 (Arabidopsis thaliana) GI:13591696; contains Pfam profiles PF00583: acetyltransferase, GNAT family, PF00439: Bromodomain   chr3:20224538-20228631 FORWARD   Aliases: ATGCN5, HAT1, HISTONE ACETYLTRANSFERASE 1	5.1	5.2	-0.1	-0.4	100.0%	-4.8
13389	AT5G22790.1   expressed protein   chr5:7599149-7601693 REVERSE   Aliases: K8E10.2, K8E10_2	7.4	7.5	-0.2	-0.4	100.0%	-4.6
13390	AT3G29220.1   hypothetical protein   chr3:11186915-11187508 FORWARD   Aliases: MXO21.7	2.5	2.5	-0.1	-0.4	100.0%	-5.7
13391	AT2G06200.1   Symbol: AtGRF6	2.3	2.2	0.0	0.4	100.0%	-5.8
13392	AT2G26930.1   Symbol: ATCDPMEK   4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (CMK) (CDPMEK), identical to 4-diphosphocytidyl-2-C-methyl-D-erythritol kinase, chloroplast precursor (CMK) (4-(cytidine-5'-diphospho)-2-C-methyl- D-erythritol kinase)(CDPMEK) (Arabidopsis thaliana) SWISS-PROT:O81014   chr2:11498299-11501324 REVERSE   Aliases: 4 (CYTIDINE 5' PHOSPHO) 2 C METHYL D ERITHRITOL KINASE, 4 DIPHOSPHOCYTIDYL 2C METHYL D ERYTHRITOL KINASE, F12C20.3, F12C20_3, ISPE, PDE277, PIGMENT DEFECTIVE 277	5.1	5.2	-0.2	-0.4	100.0%	-4.7
13393	AT3G42300.1   expressed protein   chr3:14465318-14466582 FORWARD   Aliases: T14K23.10	3.2	3.3	-0.1	-0.4	100.0%	-5.2
13394	AT5G62050.1   Symbol: OXA1   OXA1 protein (OXA1), identical to AtOXA1 (Arabidopsis thaliana) GI:6624207   chr5:24941000-24944538 REVERSE   Aliases: ATOXA1, MTG10.19, MTG10_19, OXA1AT	7.3	7.5	-0.2	-0.4	100.0%	-4.6
13395	AT3G14270.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to SP:Q9Z1T6 FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) {Mus musculus}; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF01363: FYVE zinc finger, PF00118: TCP-1/cpn60 chaperonin family   chr3:4753932-4761460 FORWARD   Aliases: MLN21.6	6.3	6.5	-0.2	-0.4	100.0%	-4.8
13396	AT1G49530.1   Symbol: GGPS6   geranylgeranyl pyrophosphate synthase (GGPS6) / GGPP synthetase / farnesyltranstransferase, identical to gi:2578821; similar to geranyl geranyl pyrophosphate synthase GI:2578822 from (Arabidopsis thaliana)   chr1:18336197-18337258 FORWARD   Aliases: F14J22.23, GERANYLGERANYL PYROPHOSPHATE SYNTHASE 6	4.1	4.0	0.2	0.4	100.0%	-5.0
13397	AT5G57170.1   macrophage migration inhibitory factor family protein / MIF family protein, contains Pfam profile: PF01187 Macrophage migration inhibitory factor(MIF)   chr5:23179300-23180506 REVERSE   Aliases: MUL3.12, MUL3_12	4.1	4.2	-0.1	-0.4	100.0%	-4.7
13398	AT4G28110.1   myb family transcription factor (MYB41), contains PFAM profile: myb DNA binding protein PF00249   chr4:13968035-13969390 REVERSE   Aliases: T13J8.220, T13J8_220	3.8	4.0	-0.1	-0.4	100.0%	-4.8
13399	AT5G21120.1   Symbol: EIL2   ethylene-insensitive3-like2 (EIL2), identical to ethylene-insensitive3-like2 (EIL2) GI:2224929 from (Arabidopsis thaliana)   chr5:7182624-7184345 FORWARD   Aliases: ETHYLENE INSENSITIVE3 LIKE 2, T10F18.150, T10F18_150	2.5	2.6	-0.1	-0.4	100.0%	-5.4
13400	AT1G05470.1   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr1:1608557-1611166 REVERSE   Aliases: T25N20.12, T25N20_12	2.4	2.3	0.1	0.4	100.0%	-5.7
13401	AT2G20010.1   expressed protein   chr2:8644828-8648555 REVERSE   Aliases: T2G17.19, T2G17_19	4.8	5.1	-0.2	-0.4	100.0%	-4.8
13402	AT3G22160.1   VQ motif-containing protein, contains PF05678: VQ motif   chr3:7817864-7818992 REVERSE   Aliases: MKA23.7	3.6	3.6	-0.1	-0.4	100.0%	-5.4
13403	AT2G25500.1   similar to Maf family protein [Arabidopsis thaliana] (TAIR:At5g66550.1); similar to hypothetical protein DDB0218334 [Dictyostelium discoideum] (GB:EAL66528.1)   chr2:10861730-10862023 REVERSE   Aliases: F13B15.16, F13B15_16	2.7	2.6	0.1	0.4	100.0%	-5.7
13404	AT1G34120.3   Symbol: IP5PI   inositol polyphosphate 5-phosphatase I (IP5PI), nearly identical to inositol polyphosphate 5-phosphatase I (Arabidopsis thaliana) GI:10444261   chr1:12426756-12429688 FORWARD   Aliases: F12G12.6, F12G12_6, INOSITOL POLYPHOSPHATE 5 PHOSPHATASE AT5P1, INOSITOL POLYPHOSPHATE 5 PHOSPHATASE I	5.0	4.7	0.2	0.4	100.0%	-4.4
13405	AT5G66160.2   Symbol: JR700   protease-associated zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); similar to ReMemBR-H2 protein JR702 (Arabidopsis thaliana) gi:6942149;gb:AAF32326; identical to cDNA ReMemBR-H2 protein JR700 mRNA, complete cds GI:6942146   chr5:26462343-26464659 FORWARD   Aliases: K2A18.24, K2A18_24, REMEMBR H2 PROTEIN JR700	3.7	3.6	0.1	0.4	100.0%	-4.8
13406	AT4G20250.1   expressed protein   chr4:10938000-10940538 REVERSE   Aliases: F1C12.170, F1C12_170	2.8	2.9	-0.1	-0.4	100.0%	-5.7
13407	AT4G35170.1   hypothetical protein, predicted protein, Arabidopsis thaliana   chr4:16736844-16737335 FORWARD   Aliases: T12J5.40, T12J5_40	2.3	2.3	0.1	0.4	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13408	AT1G05710.4   ethylene-responsive protein, putative, similar to ethylene-inducible ER33 protein ( <i>Lycopersicon esculentum</i> ) gi:5669656:gb:AAD46413; identical to bHLH transcription factor (bHLH-alpha gene)   chr1:1715779-1717243 FORWARD   Aliases: F3F20.16, F3F20_16	6.1	6.3	-0.1	-0.4	100.0%	-4.8
13409	AT3G51180.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr3:19024369-19027164 FORWARD   Aliases: F24M12.220	3.3	3.4	-0.1	-0.4	100.0%	-4.9
13410	AT5G07230.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, identical to tapetum-specific protein A9 (Precursor) SP: Q00762; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:2270966-2271565 FORWARD   Aliases: T28J14.170, T28J14_170	2.4	2.4	0.1	0.4	100.0%	-5.5
13411	AT1G04220.1   beta-ketoacyl-CoA synthase, putative, Strong similarity to beta-keto-Coa synthase gb:U37088 from <i>Simmondsia chinensis</i> , GI:4091810   chr1:1119359-1122525 REVERSE   Aliases: F20D22.1, F20D22_1	2.5	2.9	-0.3	-0.4	100.0%	-4.0
13412	AT2G02400.1   cinnamoyl-CoA reductase family, similar to cinnamoyl-CoA reductase from <i>Pinus taeda</i> (GI:17978649), <i>Eucalyptus gunnii</i> (GI:2058311)   chr2:631266-632574 REVERSE   Aliases: T16F16.19, T16F16_19	7.7	7.5	0.2	0.4	100.0%	-4.6
13413	AT5G51420.1   long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase wax synthase - <i>Simmondsia chinensis</i> , PID:g5020219 similar to wax synthase (gi:5020219) from <i>Simmondsia chinensis</i>   chr5:20902645-20903952 REVERSE   Aliases: MFG13.13, MFG13_13	3.3	3.2	0.1	0.4	100.0%	-5.0
13414	AT1G31817.1   chloroplast 30S ribosomal protein S11, putative, contains Pfam profile: PF00411: Ribosomal protein S11   chr1:11414730-11416418 REVERSE   Aliases: F5M6.25, F5M6_25	5.8	6.0	-0.2	-0.4	100.0%	-4.5
13415	AT2G42440.1   LOB domain protein 17 / lateral organ boundaries domain protein 17 (LBD17), nearly identical to SP:Q9SLB6 LOB domain protein 17 ( <i>Arabidopsis thaliana</i> ); identical to ASYMMETRIC LEAVES2-like protein 15 ( <i>Arabidopsis thaliana</i> ) GI:19919001   chr2:17675920-17676794 REVERSE   Aliases: MHK10.16, MHK10_16	4.2	4.3	-0.1	-0.4	100.0%	-5.1
13416	AT5G06780.1   emsy N terminus domain-containing protein / ENT domain-containing protein, contains Pfam profile PF03735: ENT domain   chr5:2093928-2097124 REVERSE   Aliases: MPH15.14, MPH15_14	6.7	7.0	-0.2	-0.4	100.0%	-4.5
13417	AT3G52210.3   similar to mRNA capping enzyme family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g20650.1); similar to hypothetical protein DDB0188046 [ <i>Dictyostelium discoideum</i> ] (GB:EAL63113.1); contains InterPro domain mRNA capping enzyme, large subunit (InterPro:IPR004971)	3.1	3.0	0.1	0.4	100.0%	-4.8
13418	AT2G14450.1   expressed protein, includes At5g34960, At2g14450, At1g35920   chr2:6156679-6159199 FORWARD   Aliases: T13P21.17, T13P21_17	2.5	2.5	-0.1	-0.4	100.0%	-5.7
13419	AT3G56950.1   small basic membrane integral family protein, contains similarity to small basic membrane integral protein ZmSIP2-1 (GI:13447817) ( <i>Zea mays</i> )   chr3:21088985-21090810 REVERSE   Aliases: T8M16.9	9.1	8.9	0.2	0.4	100.0%	-4.8
13420	AT1G08100.1   Symbol: ATNRT2.2   high-affinity nitrate transporter (ACH2), identical to high-affinity nitrate transporter ACH2 ( <i>Arabidopsis thaliana</i> ) GI:3608364   chr1:2527167-2529117 REVERSE   Aliases: ACH2, NITRATE TRANSPORTER 2, NRT2;2AT, T6D22.18, T6D22_18	3.1	3.2	-0.1	-0.4	100.0%	-4.5
13421	AT1G03210.1   phenazine biosynthesis PhzC/PhzF family protein, contains Pfam profile: PF02567 phenazine biosynthesis-like protein   chr1:782948-784240 FORWARD   Aliases: F15K9.19, F15K9_19	7.7	7.6	0.1	0.4	100.0%	-4.6
13422	AT5G34450.1   replication protein-related, weak similarity to Replication Protein A 70	2.8	2.9	-0.1	-0.4	100.0%	-5.4
13423	AT3G12210.2   expressed protein   chr3:3894800-3896073 FORWARD   Aliases: F28J15.5	6.8	7.0	-0.2	-0.4	100.0%	-4.4
13424	AT5G06040.1   self-incompatibility protein-related   chr5:1815129-1816038 FORWARD   Aliases: K18J17.24, K18J17_24	2.7	2.8	-0.0	-0.4	100.0%	-5.8
13425	AT1G60550.1   naphthoate synthase, putative / dihydroxynaphthoic acid synthetase, putative / DHNA synthetase, putative, contains similarity to MENB from <i>Escherichia coli</i> (SP:P27290), <i>Bacillus subtilis</i> (SP:P23966); contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr1:22309496-22311838 REVERSE   Aliases: F8A5.9, F8A5_9	6.2	6.0	0.3	0.4	100.0%	-4.5
13426	AT5G35480.1   expressed protein   chr5:13706434-13706788 REVERSE   Aliases: MOK9.7, MOK9_7	3.2	3.3	-0.1	-0.4	100.0%	-5.4
13427	AT4G17460.1   Symbol: HAT1   homeobox-leucine zipper protein 1 (HAT1) / HD-ZIP protein 1, identical to Homeobox-leucine zipper protein HAT1 (SP:P46600) ( <i>Arabidopsis thaliana</i> )   chr4:9739692-9741158 FORWARD   Aliases: DL4765W, FCAALL.65	5.7	5.5	0.2	0.4	100.0%	-4.7
13428	AT3G61990.1   O-methyltransferase family 3 protein, several O-methyltransferases - different species; contains Pfam 01596 O-methyltransferase domain   chr3:22968048-22969970 REVERSE   Aliases: F21F14.160	8.8	8.4	0.4	0.4	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13429	AT3G56440.1   WD-40 repeat protein family, contains 4 WD-40 repeats (PF00400) (2 weak); PS00778 Histidine acid phosphatases active site signature; similar to Gsa12p (GI:18307769) {Pichia pastoris}-similar to uncharacterized protein JM5 (GP:3114828) (Homo sapiens)   chr3:20936980-20939954 FORWARD   Aliases: T5P19.90	3.9	4.0	-0.1	-0.4	100.0%	-4.7
13430	AT5G49130.1   MATE efflux family protein, contains Pfam profile PF01554: MatE Uncharacterized membrane protein family   chr5:19933130-19934751 FORWARD   Aliases: K20J1.11, K20J1_11	3.0	2.9	0.1	0.4	100.0%	-5.3
13431	AT2G16920.1   ubiquitin-conjugating enzyme family protein, low similarity to ubiquitin-conjugating BIR-domain enzyme APOLLON (Homo sapiens) GI:8489831, ubiquitin-conjugating enzyme (Mus musculus) GI:3319990; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr2:7341308-7346249 REVERSE   Aliases: F12A24.10, F12A24_10	3.9	4.0	-0.2	-0.4	100.0%	-4.9
13432	AT2G30410.1   Symbol: KIS   tubulin folding cofactor A (KIESEL), identical to cDNA tubulin folding cofactor A, GI:20514256, SP:O04350 Tubulin-specific chaperone A (Tubulin-folding cofactor A) (CFA) (TCP1-chaperonin cofactor A homolog) {Arabidopsis thaliana}   chr2:12966403-12967845 FORWARD   Aliases: KIESEL, T9D9.22, T9D9_22	10.7	10.6	0.1	0.4	100.0%	-4.9
13433	AT3G06960.2   Symbol: PDE320	6.4	6.2	0.1	0.4	100.0%	-4.8
13434	AT4G39070.1   zinc finger (B-box type) family protein, salt-tolerance protein - Arabidopsis thaliana, PID:e224078   chr4:18204864-18206768 REVERSE   Aliases: F19H22.170, F19H22_170	3.2	3.3	-0.1	-0.4	100.0%	-4.6
13435	AT2G13650.2   Symbol: GONST1	5.8	5.6	0.3	0.4	100.0%	-4.6
13436	AT2G38910.1   Symbol: CPK20   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase, isoform AK1 (CDPK) (Arabidopsis thaliana) SWISS-PROT:Q06850; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr2:16252292-16254561 REVERSE   Aliases: T7F6.8, T7F6_8	3.5	3.4	0.1	0.4	100.0%	-5.4
13437	AT2G27570.1   sulfotransferase family protein, similar to steroid sulfotransferase from (Brassica napus) GI:3420008, GI:3420006; contains Pfam profile PF00685: Sulfotransferase domain   chr2:11782406-11783382 FORWARD   Aliases: F10A12.24, F10A12_24	2.4	2.4	-0.1	-0.4	100.0%	-5.8
13438	AT5G66130.1   Symbol: ATRAD17   cell cycle checkpoint protein-related, weak similarity to cell cycle checkpoint protein RAD17 (Homo sapiens) GI:4102916   chr5:26451290-26454448 FORWARD   Aliases: K2A18.21, K2A18_21, RAD17, RADIATION SENSITIVE	6.3	6.1	0.1	0.4	100.0%	-4.8
13439	AT5G04030.1   expressed protein   chr5:1088461-1088691 REVERSE   Aliases: F8F6.240, F8F6_240	2.8	2.7	0.1	0.4	100.0%	-5.4
13440	AT2G07180.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr2:2980896-2983448 REVERSE   Aliases: T25N22.14, T25N22_14	6.2	6.1	0.1	0.4	100.0%	-4.9
13441	AT1G31340.1   Symbol: RUB1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr1:11217865-11219437 REVERSE   Aliases: ATRUB1, NEDD8, RELATED TO UBIQUITIN 1, T19E23.13, T19E23_13	9.6	9.3	0.3	0.4	100.0%	-4.4
13442	AT5G08060.1   expressed protein, sigma factor F inhibitor spollAB, Bacillus megaterium, PIR:B48402   chr5:2580538-2582565 FORWARD   Aliases: T22D6.4	6.2	6.6	-0.4	-0.4	100.0%	-4.6
13443	AT1G10340.2   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr1:3390324-3392526 REVERSE   Aliases: F14N23.22, F14N23_22	3.3	3.4	-0.1	-0.4	100.0%	-4.8
13444	AT1G70230.1   expressed protein   chr1:26453983-26455608 FORWARD   Aliases: F20P5.5, F20P5_5	4.1	4.3	-0.2	-0.4	100.0%	-4.4
13445	AT4G26310.1   elongation factor P (EF-P) family protein, similar to SP:Q45288 Elongation factor P (EF-P) {Corynebacterium glutamicum}; contains Pfam profile PF01132: Elongation factor P (EF-P)   chr4:13313780-13316114 REVERSE   Aliases: T25K17.120, T25K17_120	6.9	6.7	0.2	0.4	100.0%	-4.6
13446	AT2G20875.1   expressed protein   chr2:8990260-8990660 REVERSE   Aliases: None	3.7	3.6	0.1	0.4	100.0%	-5.1
13447	AT5G12480.1   Symbol: CPK7   calmodulin-domain protein kinase isoform 7 (CPK7), identical to calmodulin-domain protein kinase CDPK isoform 7 (Arabidopsis thaliana) gi:1399277:gb:AAB03247   chr5:4047519-4050536 REVERSE   Aliases: CALMODULIN DOMAIN PROTEIN KINASE 7	5.4	5.6	-0.2	-0.4	100.0%	-4.9
13448	AT4G38080.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; Common family member: At2g22510 (Arabidopsis thaliana)   chr4:17882958-17883606 FORWARD   Aliases: F20D10.200, F20D10_200	2.6	2.9	-0.3	-0.4	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13449	AT4G03400.1   Symbol: DFL2   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr4:1497535-1499864 REVERSE   Aliases: DWARF IN LIGHT 2, F9H3.1, GH3_10	4.0	3.9	0.2	0.4	100.0%	-4.8
13450	AT2G43400.1   electron transfer flavoprotein-ubiquinone oxidoreductase family protein, contains Pfam profile: PF05187 Electron transfer flavoprotein-ubiquinone oxidoreductase   chr2:18028329-18032272 FORWARD   Aliases: T1O24.14	5.6	5.4	0.2	0.4	100.0%	-4.8
13451	AT3G02080.1   40S ribosomal protein S19 (RPS19A), similar to 40S ribosomal protein S19 GB:P40978 (Oryza sativa)   chr3:363918-365255 REVERSE   Aliases: F1C9.13, F1C9_13	10.6	10.8	-0.2	-0.4	100.0%	-4.9
13452	AT4G23220.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:12153967-12156948 REVERSE   Aliases: F21P8.110, F21P8_110	2.4	2.5	-0.1	-0.4	100.0%	-5.7
13453	AT4G37320.1   Symbol: CYP81D5   cytochrome P450 family protein   chr4:17559574-17561690 REVERSE   Aliases: F6G17.8	7.7	7.6	0.1	0.4	100.0%	-5.1
13454	AT4G37160.1   Symbol: SKS15   multi-copper oxidase type I family protein, contains Pfam profile: PF00394 Multicopper oxidase   chr4:17494699-17497118 REVERSE   Aliases: AP22.55, AP22_55, SKS15	2.1	2.2	-0.1	-0.4	100.0%	-5.9
13455	AT4G19140.1   expressed protein   chr4:10469675-10472152 FORWARD   Aliases: T18B16.110, T18B16_110	7.2	7.2	-0.1	-0.4	100.0%	-5.0
13456	AT4G36580.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family ('A'TPases 'A'ssociated with diverse cellular 'A'ctivities)   chr4:17257963-17260666 FORWARD   Aliases: AP22.32, AP22_32	6.2	6.4	-0.2	-0.4	100.0%	-4.3
13457	AT3G53800.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr3:19941839-19943868 FORWARD   Aliases: F5K20.100	2.8	2.8	0.1	0.4	100.0%	-5.2
13458	AT2G42320.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g57780.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483236.1)   chr2:17635041-17637870 FORWARD   Aliases: MHK10.4, MHK10_4	3.8	3.9	-0.1	-0.4	100.0%	-4.5
13459	AT1G09350.1   galactinol synthase, putative, contains Pfam profile: PF01501 glycosyl transferase family 8   chr1:3019821-3021443 FORWARD   Aliases: F14J9.1, F14J9_1	2.7	2.8	-0.1	-0.4	100.0%	-5.1
13460	AT3G42960.1   Symbol: ATA1   alcohol dehydrogenase (ATA1), identical to alcohol dehydrogenase (ATA1) GI:2501781 from (Arabidopsis thaliana)   chr3:15029683-15030673 REVERSE   Aliases: ALCOHOL DEHYDROGENASE, ARABIDOPSIS TAPETUM 1, ASD, F18P9.120	2.5	2.4	0.1	0.4	100.0%	-5.3
13461	AT4G12500.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:7414147-7414924 REVERSE   Aliases: T1P17.90, T1P17_90	2.5	2.5	-0.0	-0.4	100.0%	-5.6
13462	AT1G28170.1   sulfotransferase family protein, similar to steroid sulfotransferase 3 GI:3420008 from (Brassica napus); contains Pfam profile PF00685: Sulfotransferase domain   chr1:9841319-9842299 FORWARD   Aliases: F3H9.17, F3H9_17	2.5	2.6	-0.1	-0.4	100.0%	-5.3
13463	AT2G34990.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:14757339-14758247 REVERSE   Aliases: F19I3.22, F19I3_22	3.9	3.8	0.1	0.4	100.0%	-5.0
13464	AT3G27950.1   early nodule-specific protein, putative, similar to nodulin (GI:1009720) and early nodulin(GI:304037 ) Medicago truncatula);   chr3:10379285-10381133 FORWARD   Aliases: K24A2.4	2.3	2.4	-0.1	-0.4	100.0%	-5.9
13465	AT2G43650.1   Sas10/U3 ribonucleoprotein (Utp) family protein, contains Pfam profile PF04000: Sas10/Utp3 family; contains Prosite PS00761: Signal peptidases I signature 3; weak similarity to PEBP2 beta-binding protein / charged amino acid rich leucine zipper factor-1 (GI:12061569) (Mus musculus)   chr2:18106329-18110422 FORWARD   Aliases: F18O19.24	3.8	3.7	0.1	0.4	100.0%	-5.1
13466	AT2G36700.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:15391785-15393500 REVERSE   Aliases: F13K3.10, F13K3_10	3.2	3.1	0.1	0.4	100.0%	-5.0
13467	AT4G14510.1   expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578)   chr4:8337272-8341155 REVERSE   Aliases: DL3295C, FCAALL.243	4.4	4.3	0.1	0.4	100.0%	-5.1
13468	AT5G12290.1   expressed protein, similarity to NCA2 protein, yeast, PIR:S54389~Contains 'Homeobox' domain signature and profile AA305-328   chr5:3974137-3978151 REVERSE   Aliases: None	5.1	5.3	-0.2	-0.4	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13469	AT1G74120.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr1:27875584-27876921 REVERSE   Aliases: F9E11.3, F9E11_3	3.7	3.8	-0.1	-0.4	100.0%	-5.0
13470	AT1G07530.1   scarecrow-like transcription factor 14 (SCL14), identical to GB:AAD24412 from (Arabidopsis thaliana) (Plant J. 18 (1), 111-119 (1999))   chr1:2313579-2316425 REVERSE   Aliases: F22G5.9, F22G5_9	4.4	4.3	0.1	0.4	100.0%	-4.8
13471	AT5G13180.1   Symbol: ANAC083   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; hypothetical protein SENU5, senescence up-regulated - Lycopersicon esculentum, EMBL:Z75524   chr5:4196579-4197851 FORWARD   Aliases: ANAC083, T19L5.140, T19L5_140	4.3	4.0	0.3	0.4	100.0%	-4.4
13472	AT2G34660.1   Symbol: ATMRP2	7.5	7.7	-0.3	-0.4	100.0%	-4.6
13473	AT5G59560.2   Symbol: SRR1   sensitivity to red light reduced protein (SRR1), identical to sensitivity to red light reduced protein (Arabidopsis thaliana) GI:25527089; supporting cDNA gi:25527088:gb:AY127047.1:   chr5:24017782-24019183 REVERSE   Aliases: F2O15.23, F2O15_23, SENSITIVITY TO RED LIGHT REDUCED 1	6.4	6.5	-0.1	-0.4	100.0%	-5.1
13474	AT3G13790.1   beta-fructosidase (BFRUCT1) / beta-fructofuranosidase / cell wall invertase, identical to beta-fructofuranosidase GI:402740 from (Arabidopsis thaliana)   chr3:4532918-4535865 REVERSE   Aliases: MMM17.26	3.0	3.5	-0.4	-0.4	100.0%	-4.7
13475	AT4G26550.1   expressed protein, probable membrane protein YBL102w, yeast, PIR2:S45393	4.6	4.5	0.2	0.4	100.0%	-4.9
13476	AT1G52180.1   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr1:19428613-19429597 REVERSE   Aliases: F9I5.3, F9I5_3	3.1	3.0	0.1	0.4	100.0%	-4.7
13477	AT5G26930.1   zinc finger (GATA type) family protein, various predicted proteins, Arabidopsis thaliana	3.9	3.8	0.1	0.4	100.0%	-5.0
13478	AT2G37030.1   auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana)   chr2:15560811-15561185 FORWARD   Aliases: T1J8.21, T1J8_21	2.6	2.6	0.1	0.4	100.0%	-5.6
13479	AT5G13620.1   expressed protein, ; expression supported by MPSS   chr5:4385388-4386376 REVERSE   Aliases: T6I14.11	2.3	2.4	-0.1	-0.4	100.0%	-5.4
13480	AT5G48540.1   33 kDa secretory protein-related, contains Pfam PF01657: Domain of unknown function, duplicated in 33 KDa secretory proteins   chr5:19686190-19687146 REVERSE   Aliases: MJE7.18, MJE7_18	7.2	7.4	-0.1	-0.4	100.0%	-5.0
13481	AT3G17810.1   dihydroorotate dehydrogenase family protein / dihydroorotate oxidase family protein, low similarity to SP:Q12882 Dihydropyrimidine dehydrogenase (NADP+) precursor (EC 1.3.1.2) (DPD) (DHPDHase) (Dihydrouracil dehydrogenase) (Dihydrothymine dehydrogenase) {Homo sapiens}; contains Pfam profile PF01180: Dihydroorotate dehydrogenase   chr3:6094157-6096572 FORWARD   Aliases: MEB5.3	10.2	9.8	0.4	0.4	100.0%	-4.6
13482	AT5G28030.2   cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, similar to O-acetylserine(thiol) lyase (Brassica juncea) GI:2245144; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme   chr5:10030410-10032455 REVERSE   Aliases: F15F15.100, F15F15_100	2.6	2.7	-0.1	-0.4	100.0%	-5.4
13483	AT4G31940.1   Symbol: CYP82C4   cytochrome P450, putative, cytochrome P450 monooxygenase, Pisum sativum, PATCHX:G894153   chr4:15451994-15454166 FORWARD   Aliases: F11C18.7	2.9	2.9	-0.1	-0.4	100.0%	-5.7
13484	AT5G18680.1   F-box family protein / tubby family protein, similar to phosphodiesterase (GI:467578) (Mus musculus); similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein (GI:6730158) (Mus musculus); contains Pfam PF00646: F-box domain and Pfam PF01167: Tub family   chr5:6228167-6230539 REVERSE   Aliases: T1A4.60, T1A4_60	7.6	7.4	0.2	0.4	100.0%	-4.7
13485	AT2G10440.1   expressed protein   chr2:4020835-4025129 REVERSE   Aliases: F12P23.5, F12P23_5	2.2	2.2	0.0	0.4	100.0%	-5.9
13486	AT4G17200.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.7	-0.1	-0.4	100.0%	-5.4
13487	AT5G59460.1   scarecrow-like transcription factor 11 (SCL11), identical to cDNA scarecrow-like 11 (SCL11) mRNA, partial cds gi:4580526	5.0	5.2	-0.2	-0.4	100.0%	-4.9
13488	AT5G23270.1   sugar transporter, putative, similar to sugar transport protein (Arabidopsis thaliana) GI:16524, sugar transporter (Medicago truncatula) GI:1353516; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:7838937-7841024 FORWARD   Aliases: MKD15.13, MKD15_13	3.3	3.4	-0.1	-0.4	100.0%	-5.3
13489	AT4G11730.1   ATPase, plasma membrane-type, putative / proton pump, putative, similar to plasma membrane-type ATPase SP:P20431 and SP:P19456 {Arabidopsis thaliana}; contains InterPro accession IPR001757: ATPase, E1-E2 type	2.6	2.7	-0.1	-0.4	100.0%	-5.3
13490	AT1G31630.1   MADS-box family protein, similar to MADS-box protein NMH 7 GI:2827300 from (Medicago sativa)   chr1:11318509-11319528 REVERSE   Aliases: F27M3.17, F27M3_17	2.7	2.6	0.1	0.4	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13491	AT2G42940.1   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr2:17869331-17870533 REVERSE   Aliases: F23E6.8, F23E6_8	3.0	3.0	0.1	0.4	100.0%	-5.3
13492	AT4G24140.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoate hydrolase (Pseudomonas putida) GI:2822275, hydroxymuconic semialdehyde hydrolase, Pseudomonas stutzeri, AF039534; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:12529885-12533803 REVERSE   Aliases: T19F6.130, T19F6_130	2.4	2.6	-0.2	-0.4	100.0%	-4.4
13493	AT4G17505.1   expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function; expression supported by MPSS   chr4:9764389-9766328 REVERSE   Aliases: FCAALL.20	3.2	3.1	0.1	0.4	100.0%	-5.5
13494	AT5G19490.1   repressor protein-related, similar to repressor protein (Oryza sativa) GI:18481624   chr5:6576771-6577843 REVERSE   Aliases: T20D1.10, T20D1_10	3.9	4.1	-0.1	-0.4	100.0%	-5.0
13495	AT3G20240.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier proteins   chr3:7057023-7058897 FORWARD   Aliases: MAL21.26	6.1	5.9	0.2	0.4	100.0%	-4.5
13496	AT5G42960.1   expressed protein   chr5:17252320-17253886 FORWARD   Aliases: MBD2.16, MBD2_16	6.0	6.1	-0.1	-0.4	100.0%	-4.6
13497	AT5G27170.1   expressed protein   chr5:9566010-9566415 FORWARD   Aliases: T21B4.80, T21B4_80	2.1	2.1	0.0	0.4	100.0%	-6.1
13498	AT4G28820.2   similar to PREDICTED: similar to thyroid hormone receptor interactor 3 [Canis familiaris] (GB:XP_537712.1); similar to ENSANGP00000021276 [Anopheles gambiae str. PEST] (GB:XP_320662.2); contains InterPro domain HIT Zn-finger (InterPro:IPR007529)   chr4:14230704-14232348 REVERSE   Aliases: F16A16.70, F16A16_70	4.7	4.5	0.2	0.4	100.0%	-4.4
13499	AT2G17120.1   peptidoglycan-binding LysM domain-containing protein, contains Pfam profile PF01476: LysM domain; supporting cDNA gi:16226688:gb:AF428464.1:AF428464   chr2:7466129-7468388 FORWARD   Aliases: F6P23.25, F6P23_25	8.5	8.7	-0.2	-0.4	100.0%	-4.7
13500	AT2G24560.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 GI:15054386 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr2:10438616-10439968 FORWARD   Aliases: F25P17.14, F25P17_14	2.5	2.4	0.1	0.4	100.0%	-5.5
13501	AT5G25480.1   C-5 cytosine-specific DNA methylase family protein, contains Pfam profile PF00145: C-5 cytosine-specific DNA methylase   chr5:8869876-8872265 REVERSE   Aliases: T14C9.10, T14C9_10	3.7	3.7	-0.1	-0.4	100.0%	-5.4
13502	AT4G29120.1   6-phosphogluconate dehydrogenase NAD-binding domain-containing protein, similar to SP:P23523 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) {Escherichia coli}; contains Pfam profile PF03446: NAD binding domain of 6-phosphogluconate dehydrogenase   chr4:14350864-14352018 FORWARD   Aliases: F19B15.150, F19B15_150	8.6	8.4	0.2	0.4	100.0%	-4.7
13503	AT3G20270.2   lipid-binding serum glycoprotein family protein, similar to SP:P17213 Bactericidal permeability-increasing protein precursor (BPI) {Homo sapiens}; contains Pfam profile PF02886: LBP / BPI / CETP family, C-terminal domain   chr3:7067065-7070952 FORWARD   Aliases: MQC12.2	3.9	3.8	0.1	0.4	100.0%	-4.8
13504	AT5G52170.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to Anthocyaninless2 (ANL2) (GP:5702094) (Arabidopsis thaliana); contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain   chr5:21214200-21217185 FORWARD   Aliases: F17P19.7, F17P19_7	3.2	3.1	0.1	0.4	100.0%	-5.5
13505	AT4G08310.1   expressed protein, glutamic acid-rich protein precursor - Plasmodium falciparum, PIR2:A54514   chr4:5248861-5252145 REVERSE   Aliases: T12G13.150, T12G13_150	8.0	7.8	0.2	0.4	100.0%	-4.7
13506	AT3G50690.1   leucine-rich repeat family protein   chr3:18845948-18848078 REVERSE   Aliases: T3A5.70	7.8	7.6	0.2	0.4	100.0%	-4.8
13507	AT5G52480.1   similar to F-box family protein (FBL20) [Arabidopsis thaliana] (TAIR:At4g05460.1); similar to putative N7 protein [Oryza sativa (japonica cultivar-group)] (GB:XP_480503.1); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr5:21314059-21315084 REVERSE   Aliases: K24M7.23, K24M7_23	2.5	2.6	-0.1	-0.4	100.0%	-5.4
13508	AT5G38970.3   Symbol: BR6OX   cytochrome P450, putative, similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum};	2.2	2.3	-0.1	-0.4	100.0%	-5.6
13509	AT5G08270.1   expressed protein   chr5:2661748-2663483 FORWARD   Aliases: F8L15.1, F8L15_1	4.5	4.6	-0.1	-0.4	100.0%	-5.1
13510	AT2G31050.1   plastocyanin-like domain-containing protein, contains plastocyanin-like domain Pfam:PF02298   chr2:13219227-13219829 FORWARD   Aliases: T16B12.14	2.7	2.6	0.1	0.4	100.0%	-5.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13511	AT1G51080.1   expressed protein   chr1:18933551-18934408 REVERSE   Aliases: F23H24.7, F23H24_7	4.0	3.9	0.1	0.4	100.0%	-5.1
13512	AT2G38760.1   Symbol: ANNAT3	4.0	3.9	0.1	0.4	100.0%	-4.9
13513	AT3G32260.1   hypothetical protein   chr3:13222881-13225169 FORWARD   Aliases: F6H5.17	2.9	3.0	-0.1	-0.4	100.0%	-5.3
13514	AT1G30690.2   similar to SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] (TAIR:At1g72150.1); similar to putative cellular retinaldehyde-binding/triple function [Oryza sativa (japonica cultivar-group)] (GB:AAV59419.1); similar to P0698A10.6 [Oryza sativa (japonica cultivar-group)] (GB:XP_463507.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251); contains InterPro domain Cellular retinaldehyde binding/alpha-tocopherol transport (InterPro:IPR001071); contains InterPro domain Cellular retinaldehyde-binding/triple function, N-terminal (InterPro:IPR008273)   chr1:10887677-10890314 FORWARD   Aliases: T5I8.14, T5I8_14	4.4	4.2	0.2	0.4	100.0%	-4.7
13515	AT1G70830.2   similar to Bet v I allergen family protein [Arabidopsis thaliana] (TAIR:At1g70850.2); similar to Csf-2 [Cucumis sativus] (GB:BAA83470.1); contains InterPro domain Bet v I allergen (InterPro:IPR000916)	2.9	3.0	-0.1	-0.4	100.0%	-5.2
13516	AT4G28170.1   expressed protein   chr4:13981641-13982048 FORWARD   Aliases: F26K10.50, F26K10_50	3.1	3.0	0.0	0.4	100.0%	-5.7
13517	AT5G05090.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:1503233-1504495 FORWARD   Aliases: MUG13.5, MUG13_5	2.5	2.5	0.0	0.4	100.0%	-5.8
13518	AT5G19520.1   mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, contains Pfam profile PF00924: Mechanosensitive ion channel   chr5:6585423-6588937 FORWARD   Aliases: T20D1.40, T20D1_40	2.8	3.0	-0.1	-0.4	100.0%	-5.1
13519	AT3G27550.1   group II intron splicing factor CRS1-related, contains weak similarity to CRS1 (Zea mays) gi:9837550:gb:AAG00595	3.2	3.2	-0.1	-0.4	100.0%	-5.3
13520	AT3G23730.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endotransglycosylase-related protein GI:1244760 from (Arabidopsis thaliana)   chr3:8550117-8551341 FORWARD   Aliases: MYM9.11	2.7	2.6	0.1	0.4	100.0%	-5.6
13521	AT1G53990.1   GDSL-motif lipase/hydrolase family protein, similar to myrosinase-associated proteins from (Brassica napus) GI:1769968 GI:1769970, SP:P40603 Anther-specific proline-rich protein APG {Brassica napus}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr1:20154684-20156420 FORWARD   Aliases: F15I1.7, F15I1_7	2.8	2.6	0.2	0.4	100.0%	-4.8
13522	AT5G45790.1   expressed protein, ; expression supported by MPSS   chr5:18589620-18590891 FORWARD   Aliases: MRA19.23, MRA19_23	3.1	3.1	0.1	0.4	100.0%	-5.1
13523	AT3G13190.2   myosin heavy chain-related, contains weak similarity to Myosin II heavy chain, non muscle (Swiss-Prot:P05659) (Acanthamoeba castellanii)	5.9	6.0	-0.2	-0.4	100.0%	-4.6
13524	AT4G01390.1   meprip and TRAF homology domain-containing protein / MATH domain-containing protein, weak similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr4:570242-571483 REVERSE   Aliases: F2N1.33, F2N1_33	3.7	3.6	0.1	0.4	100.0%	-5.0
13525	AT2G31290.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g63090.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD86888.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_908517.1); contains InterPro domain Plant specific of unknown function DUF860 (InterPro:IPR008578)   chr2:13350924-13352506 FORWARD   Aliases: F16D14.13, F16D14_13	3.6	3.5	0.1	0.4	100.0%	-4.9
13526	AT5G56750.1   Ndr family protein, similar to SP:O23969 Pollen specific protein SF21 {Helianthus annuus}; contains Pfam profile PF03096: Ndr family   chr5:22975103-22978142 FORWARD   Aliases: MIK19.22, MIK19_22	3.5	3.6	-0.1	-0.4	100.0%	-4.8
13527	AT3G15230.1   expressed protein   chr3:5133761-5134028 FORWARD   Aliases: K7L4.3	2.6	2.5	0.1	0.4	100.0%	-5.4
13528	AT3G22590.1   RNA pol II accessory factor Cdc73 family protein, contains Pfam PF05179: RNA pol II accessory factor, Cdc73 family   chr3:8003941-8005586 FORWARD   Aliases: F16J14.15	7.1	7.2	-0.1	-0.4	100.0%	-4.9
13529	AT5G46080.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:18706769-18708084 REVERSE   Aliases: MCL19.13, MCL19_13	2.9	2.8	0.1	0.4	100.0%	-5.0
13530	AT1G68910.1   expressed protein, similar to Myosin heavy chain, nonmuscle type B (Cellular myosin heavy chain, type B) (Nonmuscle myosin heavy chain-B) (NMMHC-B) (Swiss-Prot:Q27991) (Bos taurus); contains 1 transmembrane domain   chr1:25911794-25914148 REVERSE   Aliases: T6L1.9, T6L1_9	3.0	2.9	0.1	0.4	100.0%	-5.3
13531	AT2G42110.1   expressed protein   chr2:17569312-17569811 REVERSE   Aliases: T24P15.2	3.3	3.4	-0.1	-0.4	100.0%	-5.3
13532	AT5G16030.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g02500.1); similar to conserved protein [Cryptosporidium parvum] (GB:EAK89575.1)   chr5:5238183-5240750 FORWARD   Aliases: F1N13.170, F1N13_170	2.7	2.8	-0.1	-0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13533	AT2G26870.1   phosphoesterase family protein, low similarity to SP:Q9RGS8 Non-hemolytic phospholipase C precursor (EC 3.1.4.3) (Phosphatidylcholine cholinephosphohydrolase) {Burkholderia pseudomallei}; contains Pfam profile PF04185: Phosphoesterase family   chr2:11464086-11466443 REVERSE   Aliases: F12C20.9, F12C20_9	3.6	3.8	-0.1	-0.4	100.0%	-4.8
13534	AT3G59840.1   expressed protein   chr3:22116499-22117175 REVERSE   Aliases: F24G16.110	8.3	8.0	0.3	0.4	100.0%	-4.4
13535	AT4G13550.1   lipase class 3 family protein, very low similarity to diacylglycerol lipase (Aspergillus oryzae) GI:1772352; contains Pfam profiles PF01764: Lipase (class 3), PF00168: C2 domain   chr4:7871247-7876873 REVERSE   Aliases: T6G15.100, T6G15_100	4.6	4.5	0.1	0.4	100.0%	-4.8
13536	AT5G33200.1   hypothetical protein, predicted replication A1 proteins - Arabidopsis thaliana   chr5:12468882-12471971 REVERSE   Aliases: T29A4.10, T29A4_10	2.5	2.6	-0.1	-0.4	100.0%	-5.6
13537	AT5G60190.1   Ulp1 protease family protein, low similarity to sentrin/SUMO-specific protease (Homo sapiens) GI:6906859; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr5:24251780-24253381 FORWARD   Aliases: F15L12.8, F15L12_8	3.6	3.5	0.1	0.4	100.0%	-4.9
13538	AT5G43410.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr5:17452238-17452633 REVERSE   Aliases: MWF20.11, MWF20_11	3.9	3.9	0.1	0.4	100.0%	-5.4
13539	AT5G66380.1   Encodes a folate transporter that is located in the chloroplast envelope and is able to mediate exogenous folate uptake when expressed in E. coli. However, this is not the sole folate transporter for chloroplasts as null mutants of this gene have no discernable phenotype when grown under folate-sufficient conditions and contained wild-type levels of folates in leaves.   chr5:26530750-26532891 REVERSE   Aliases: K1F13.3, K1F13_3	7.4	7.3	0.1	0.4	100.0%	-4.7
13540	AT1G03130.1   photosystem I reaction center subunit II, chloroplast, putative / photosystem I 20 kDa subunit, putative / PSI-D, putative (PSAD2), similar to SP:P12353 Photosystem I reaction center subunit II, chloroplast precursor (Photosystem I 20 kDa subunit) (PSI-D) {Spinacia oleracea}; contains Pfam profile PF02531: PsaD	6.1	6.3	-0.2	-0.4	100.0%	-4.2
13541	AT3G54360.1   expressed protein, DNA-binding Mel-18 protein, Homo sapiens, PIR:JN0717   chr3:20139283-20142832 REVERSE   Aliases: T12E18.50	8.0	7.8	0.2	0.4	100.0%	-4.8
13542	AT4G39180.1   Symbol: SEC14   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, phosphatidylinositol-phosphatidylcholine transfer protein SEC14, Yarrowia lipolytica, PIR2:S43745; contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus   chr4:18243768-18248799 REVERSE   Aliases: ATSEC14, T22F8.80, T22F8_80	3.5	3.6	-0.1	-0.4	100.0%	-5.1
13543	AT4G16447.1   expressed protein   chr4:9278809-9279411 FORWARD   Aliases: None	3.2	3.6	-0.4	-0.4	100.0%	-4.6
13544	AT2G19980.1   allergen V5/Tpx-1-related family protein, low similarity to SP:P33154 Pathogenesis-related protein 1 precursor (PR-1) {Arabidopsis thaliana}; contains Pfam profile PF00188: SCP-like extracellular protein   chr2:8634780-8635301 REVERSE   Aliases: T2G17.22, T2G17_22	2.7	2.6	0.1	0.4	100.0%	-5.5
13545	AT2G39900.1   LIM domain-containing protein, similar to pollen specific LIM domain protein 1b (Nicotiana tabacum) GI:6467905, PGPS/D1 (Petunia x hybrida) GI:4105772; contains Pfam profile PF00412: LIM domain   chr2:16665789-16667515 FORWARD   Aliases: T28M21.6, T28M21_6	8.0	7.6	0.4	0.4	100.0%	-4.6
13546	AT5G04070.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr5:1102091-1104447 FORWARD   Aliases: F21E1.2	3.4	3.4	-0.1	-0.4	100.0%	-5.4
13547	AT5G10950.1   cylicin-related, low similarity to SP:Q28092 Cylicin II (Multiple-band polypeptide II) {Bos taurus}   chr5:3459274-3461705 REVERSE   Aliases: T30N20.220, T30N20_220	4.7	5.0	-0.3	-0.4	100.0%	-4.9
13548	AT2G44610.1   Symbol: RAB6   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:623586 from (Nicotiana tabacum) ; contains an ADP-ribosylation factors family signature for proteins involved in protein trafficking   chr2:18418507-18421149 REVERSE   Aliases: F16B22.10	7.2	7.4	-0.2	-0.4	100.0%	-4.5
13549	AT5G63460.2   SAP domain-containing protein, contains Pfam domain PF02037: SAP domain   chr5:25430599-25432716 REVERSE   Aliases: MLE2.9, MLE2_9	4.3	4.5	-0.1	-0.4	100.0%	-4.5
13550	AT5G05890.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:1772544-1774088 FORWARD   Aliases: K18J17.4, K18J17_4	4.9	4.8	0.1	0.4	100.0%	-4.9
13551	AT5G56450.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:22875735-22877288 REVERSE   Aliases: MCD7.21, MCD7_21	4.5	4.6	-0.1	-0.4	100.0%	-4.9
13552	AT5G53470.1   Symbol: ACBP1   acyl-CoA binding protein, putative / ACBP, putative, similar to acyl-CoA binding protein 2 (Arabidopsis thaliana) gi:12039034:gb:AAG46057   chr5:21727577-21729836 FORWARD   Aliases: ACBP, ACYL COA BINDING PROTEIN, MYN8.8, MYN8_8	5.1	5.3	-0.2	-0.4	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13553	AT4G39790.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g27090.1); similar to leucine zipper protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_450675.1); contains InterPro domain Protein of unknown function DUF632 (InterPro:IPR006867); contains InterPro domain Protein of unknown function DUF630 (InterPro:IPR006868)   chr4:18462184-18464818 REVERSE   Aliases: T19P19.180, T19P19_180	3.2	3.3	-0.1	-0.4	100.0%	-5.1
13554	AT5G15930.1   Symbol: PAM1   plant adhesion molecule 1 (PAM1), identical to plant adhesion molecule 1 (Arabidopsis thaliana) GI:3511223; contains Pfam profile PF00566: TBC domain   chr5:5199749-5202452 FORWARD   Aliases: F1N13.70, F1N13_70, PLANT ADHESION MOLECULE 1	7.6	7.4	0.1	0.4	100.0%	-4.6
13555	AT2G16520.1   expressed protein   chr2:7169004-7169466 REVERSE   Aliases: F1P15.10, F1P15_10	2.6	2.7	-0.1	-0.4	100.0%	-5.8
13556	AT1G42630.1   zinc knuckle (CCHC-type) family protein,	2.7	2.8	-0.1	-0.4	100.0%	-4.6
13557	AT2G17033.2   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:7408275-7410728 FORWARD   Aliases: None	4.1	4.2	-0.1	-0.4	100.0%	-4.7
13558	AT5G13380.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr5:4289842-4292444 FORWARD   Aliases: T22N19.30, T22N19_30	2.6	2.5	0.1	0.4	100.0%	-5.4
13559	AT2G34850.1   NAD-dependent epimerase/dehydratase family protein, similar to UDP-galactose 4-epimerase from Cyamopsis tetragonoloba GI:3021357, Lactococcus lactis GI:3703056; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family   chr2:14711711-14713262 REVERSE   Aliases: F19I3.8, F19I3_8	4.3	4.4	-0.1	-0.4	100.0%	-4.8
13560	ATCG00730.1   Symbol: PETD   A chloroplast gene encoding subunit IV of the cytochrome b6/f complex   chrC:76481-77672 FORWARD   Aliases: PETD	3.4	3.1	0.3	0.4	100.0%	-4.6
13561	AT1G17260.1   Symbol: AHA10   ATPase 10, plasma membrane-type, putative / proton pump 10, putative / proton-exporting ATPase, putative, strong similarity to SP:Q43128 ATPase 10, plasma membrane-type (EC 3.6.3.6) (Proton pump 10) {Arabidopsis thaliana}; contains InterPro accession IPR001757: ATPase, E1-E2 type; contains Pfam profile PF00690: Cation transporter/ATPase, N-terminus   chr1:5904051-5908891 FORWARD   Aliases: F20D23.4, F20D23_4	2.6	2.5	0.1	0.4	100.0%	-5.5
13562	AT2G35370.1   Symbol: GDCH   glycine cleavage system H protein 1, mitochondrial (GDCSH) (GCDH), identical to SP:P25855 Glycine cleavage system H protein 1, mitochondrial precursor {Arabidopsis thaliana}   chr2:14898181-14899297 FORWARD   Aliases: GLYCINE DECARBOXYLASE COMPLEX H PROTEIN, T32F12.25, T32F12_25	7.6	7.8	-0.3	-0.4	100.0%	-4.0
13563	AT5G45040.1   cytochrome c6 (ATC6), identical to c6 type cytochrome (Arabidopsis thaliana) gi:19571824:emb:CAD27418   chr5:18192200-18194110 REVERSE   Aliases: K21C13.23, K21C13_23	4.8	4.6	0.2	0.4	100.0%	-4.2
13564	AT2G41040.1   methyltransferase-related, eak similarity to C5-O-methyltransferase (GI:5921167) (Streptomyces avermitilis); weak similarity to Probable menaquinone biosynthesis methyltransferase (EC 2.1.1.-) (gerC2 protein homolog) (Swiss-Prot:P49016) (Lactococcus lactis)   chr2:17128454-17130260 FORWARD   Aliases: T3K9.19, T3K9_19	4.8	4.6	0.2	0.4	100.0%	-4.2
13565	AT4G05260.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:2693678-2694457 FORWARD   Aliases: C17L7.180, C17L7_180	2.8	2.9	-0.1	-0.4	100.0%	-5.2
13566	AT5G53080.1   kinesin light chain-related, low similarity to kinesin light chain from (Plectonema boryanum) GI:2645229, (Loligo pealei) GI:403179; contains Pfam profile PF00515: TPR Domain   chr5:21537739-21540492 FORWARD   Aliases: MNB8.14, MNB8_14	3.7	3.7	-0.1	-0.4	100.0%	-5.1
13567	AT1G35210.1   expressed protein   chr1:12896630-12897380 REVERSE   Aliases: T32G9.25, T32G9_25	3.5	3.6	-0.1	-0.4	100.0%	-5.3
13568	AT5G63710.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:25516640-25520024 FORWARD   Aliases: MBK5.19, MBK5_19	4.8	4.9	-0.1	-0.4	100.0%	-5.1
13569	AT3G22110.1   Symbol: PAC1   20S proteasome alpha subunit C (PAC1) (PRC9), identical to GB:AAC32057 from (Arabidopsis thaliana) (Genetics (1998) 149 (2), 677-692); identical to cDNA proteasome subunit prc9 GI:2511583   chr3:7792645-7794161 REVERSE   Aliases: 20S PROTEASOME SUBUNIT PAC1, MKA23.2	11.3	11.5	-0.2	-0.4	100.0%	-5.2
13570	AT2G28190.1   Symbol: CSD2   superoxide dismutase (Cu-Zn), chloroplast (SODCP) / copper/zinc superoxide dismutase (CSD2), identical to GP:3273753:AF061519   chr2:12021579-12023620 FORWARD   Aliases: COPPER/ZINC SUPEROXIDE DISMUTASE, COPPER/ZINC SUPEROXIDE DISMUTASE 2, CZSOD2, F24D13.2, F24D13_2	11.0	11.3	-0.3	-0.4	100.0%	-5.0
13571	AT5G53480.1   importin beta-2, putative, similar to importin-beta2 (Oryza sativa (japonica cultivar-group)) GI:3983665; contains Pfam profile PF03810: Importin-beta N-terminal domain	5.4	5.3	0.1	0.4	100.0%	-4.8
13572	AT1G32850.1   ubiquitin carboxyl-terminal hydrolase family protein, similar to ubiquitin-specific protease UBP5 (Arabidopsis thaliana) GI:6648604; contains Pfam profile PF00443: Ubiquitin carboxyl-terminal hydrolase   chr1:11902609-11906880 FORWARD   Aliases: F9L11.5, F9L11_5	3.1	3.0	0.0	0.4	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13573	AT2G42030.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:17545986-17548044 REVERSE   Aliases: T6D20.8, T6D20_8	6.5	6.6	-0.1	-0.4	100.0%	-5.0
13574	AT5G66510.1   bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)   chr5:26566930-26568856 REVERSE   Aliases: K1F13.17, K1F13_17	8.8	8.4	0.4	0.4	100.0%	-4.5
13575	AT3G56460.1   oxidoreductase, zinc-binding dehydrogenase family protein, low similarity to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), zeta-crystallin / quinone reductase (NADPH) - Mus musculus, PIR:A54932; contains Pfam profile PF00107: oxidoreductase, zinc-binding dehydrogenase family   chr3:20943674-20945466 REVERSE   Aliases: T5P19.110	10.4	10.3	0.2	0.4	100.0%	-5.1
13576	AT3G54070.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr3:20032308-20034581 REVERSE   Aliases: F24B22.30	2.2	2.2	0.0	0.4	100.0%	-6.0
13577	AT3G15930.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:5387450-5389696 FORWARD   Aliases: MVC8.5	2.8	2.8	0.1	0.4	100.0%	-5.4
13578	AT1G21610.2   wound-responsive family protein, similar to wound-responsive protein 14.05 (GI:16506638) (Castanea sativa); ESTs gb T42839 and gb:AA395192 come from this gene   chr1:7573940-7578945 FORWARD   Aliases: F24J8.24	3.9	4.0	-0.1	-0.4	100.0%	-5.0
13579	AT5G53310.1   myosin heavy chain-related, contains weak similarity to Myosin IB heavy chain (Swiss-Prot:P34092) (Dictyostelium discoideum)   chr5:21651833-21653873 FORWARD   Aliases: K19E1.11, K19E1_11	7.6	7.2	0.4	0.4	100.0%	-4.6
13580	AT3G28980.1   expressed protein   chr3:10994427-10996239 REVERSE   Aliases: K5K13.11	3.4	3.3	0.1	0.4	100.0%	-5.5
13581	AT3G22710.1   F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	-0.1	-0.4	100.0%	-5.5
13582	AT1G56145.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam profiles: PF00069: Eukaryotic protein kinase domain, multiple PF00560: Leucine Rich Repeat   chr1:21011758-21017648 REVERSE   Aliases: None	3.6	3.9	-0.2	-0.4	100.0%	-4.3
13583	AT1G43580.1   expressed protein   chr1:16412974-16415168 REVERSE   Aliases: T10P12.6, T10P12_6	7.6	7.8	-0.1	-0.4	100.0%	-4.8
13584	AT5G52830.1   Symbol: WRKY27	4.2	4.4	-0.2	-0.4	100.0%	-4.8
13585	AT1G54650.1   expressed protein, similar to Actin-binding protein ABP140 (Swiss-Prot:Q08641) (Saccharomyces cerevisiae)   chr1:20409265-20411353 REVERSE   Aliases: T22H22.9, T22H22_9	5.3	5.1	0.1	0.4	100.0%	-5.0
13586	AT2G23580.1   hydrolase, alpha/beta fold family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr2:10040123-10041390 REVERSE   Aliases: F26B6.23, F26B6_23	3.3	3.2	0.1	0.4	100.0%	-5.4
13587	AT3G55250.1   expressed protein, predicted pectate-lyase, Arabidopsis thaliana, PIR:T06728   chr3:20490266-20491611 FORWARD   Aliases: T26I12.130	8.5	8.3	0.2	0.4	100.0%	-4.5
13588	AT4G10780.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.4	2.3	0.1	0.4	100.0%	-5.4
13589	AT3G07070.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:2237964-2240080 FORWARD   Aliases: F17A9.25	2.5	2.3	0.1	0.4	100.0%	-4.5
13590	AT2G02710.3   PAC motif-containing protein, similar to nonphototropic hypocotyl 1 (Zea mays) GI:2687358; contains Pfam profile PF00785: PAC motif   chr2:758696-760815 REVERSE   Aliases: T20F6.15, T20F6_15	8.6	8.4	0.2	0.4	100.0%	-4.5
13591	AT4G10550.1   subtilase family protein, contains similarity to subtilisin-like protease AIR3 GI:4218991 from (Arabidopsis thaliana)   chr4:6516578-6519763 REVERSE   Aliases: T4F9.10, T4F9_10	3.5	3.4	0.1	0.4	100.0%	-4.8
13592	AT3G03260.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to L1 specific homeobox gene ATML1/ovule-specific homeobox protein A20, GB:CAB36819   chr3:755166-759289 REVERSE   Aliases: T17B22.5, T17B22_5	2.8	2.7	0.1	0.4	100.0%	-5.2
13593	AT1G73750.1   expressed protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold   chr1:27740291-27742740 FORWARD   Aliases: F25P22.17, F25P22_17	4.6	4.4	0.2	0.4	100.0%	-4.5
13594	AT5G50780.1   ATP-binding region, ATPase-like domain-containing protein, low similarity to microrchidia (Homo sapiens) GI:5410257; contains Pfam profile PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein   chr5:20667495-20672106 FORWARD   Aliases: MFB16.18, MFB16_18	4.1	4.5	-0.3	-0.4	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13595	AT4G27050.3   similar to F-box family protein [Arabidopsis thaliana] (TAIR:At2g29930.3); similar to F-box family protein [Arabidopsis thaliana] (TAIR:At2g29930.1); similar to putative copia-type polyprotein [Oryza sativa (japonica cultivar-group)] (GB:AAP51971.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP51974.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain FBD (InterPro:IPR006566)   chr4:13575806-13578057 REVERSE   Aliases: F10M23.390, F10M23_390	5.7	5.8	-0.1	-0.4	100.0%	-4.8
13596	AT1G56020.1   expressed protein   chr1:20955811-20957077 FORWARD   Aliases: F14J16.33	3.5	3.7	-0.1	-0.4	100.0%	-4.7
13597	AT2G21870.2   expressed protein   chr2:9327278-9329814 REVERSE   Aliases: F7D8.19, F7D8_19	10.3	10.6	-0.3	-0.4	100.0%	-4.5
13598	AT1G50230.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:18610731-18612759 FORWARD   Aliases: F14I3.15, F14I3_15	3.4	3.3	0.1	0.4	100.0%	-5.1
13599	AT1G66800.1   similar to Eucalyptus gunnii alcohol dehydrogenase of unknown physiological function (GI:1143445), apple tree, PIR:T16995; NOT a cinnamyl-alcohol dehydrogenase   chr1:24928476-24930028 FORWARD   Aliases: F4N21.7, F4N21_7	3.0	3.2	-0.1	-0.4	100.0%	-4.8
13600	AT4G12130.1   similar to GA20785-PA [Drosophila pseudoobscura] (GB:EAL28126.1); contains InterPro domain Glycine cleavage T protein (aminomethyl transferase) (InterPro:IPR006222)   chr4:7263593-7265806 FORWARD   Aliases: F16J13.200, F16J13_200	6.3	6.4	-0.2	-0.4	100.0%	-4.3
13601	AT4G01400.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:573098-577243 REVERSE   Aliases: F3D13.1, F3D13_1	6.4	6.6	-0.2	-0.4	100.0%	-4.7
13602	AT1G64330.1   myosin heavy chain-related, similar to myosin heavy chain (GI:1850913) (Entamoeba histolytica); similar to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae)   chr1:23874589-23877839 FORWARD   Aliases: F15H21.4, F15H21_4	5.2	5.6	-0.4	-0.4	100.0%	-4.4
13603	AT3G02875.1   Symbol: ILR1   IAA-amino acid hydrolase 1 (ILR1), identical to IAA-amino acid hydrolase 1 (ILR1) (Arabidopsis thaliana) SWISS-PROT:P54968   chr3:631920-634081 FORWARD   Aliases: F13E7.18, F13E7_18, IAA AMINO ACID HYDROLASE, IAA LEUCINE RESISTANT 1	5.6	5.5	0.2	0.4	100.0%	-4.6
13604	AT3G25960.1   pyruvate kinase, putative, similar to pyruvate kinase, cytosolic isozyme (Nicotiana tabacum) SWISS-PROT:Q42954   chr3:9499676-9501169 FORWARD   Aliases: MPE11.9	3.2	3.1	0.1	0.4	100.0%	-5.0
13605	AT5G43890.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenases YUCCA (gi:16555352), YUCCA2 (gi:16555354), and YUCCA3 (gi:16555356) from Arabidopsis thaliana; contains Pfam profile PF00743   chr5:17666084-17667358 REVERSE   Aliases: F6B6.3, F6B6_3	3.6	3.5	0.1	0.4	100.0%	-4.8
13606	AT3G25930.1   universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family   chr3:9494082-9495154 REVERSE   Aliases: MPE11.10	3.0	3.1	-0.1	-0.4	100.0%	-5.0
13607	AT5G43745.1   phosphotransferase-related, similar to streptomycin-3'-phosphotransferase (Streptomyces griseus) GI:153164   chr5:17586374-17592198 REVERSE   Aliases: None	3.6	3.7	-0.1	-0.4	100.0%	-5.1
13608	AT4G35790.3   Symbol: ATPLDDELTA   phospholipase D delta / PLD delta (PLDDELTA), identical to phospholipase D delta SP: Q9C5Y0 from (Arabidopsis thaliana); supporting cDNA gi:11761141:dbj:AB031047.1:   chr4:16955538-16960174 REVERSE   Aliases: F4B14.60, F4B14_60, PHOSPHOLIPASE D, PLDDELTA	5.9	6.1	-0.2	-0.4	100.0%	-4.8
13609	AT4G02570.3   Symbol: ATCUL1	7.0	7.2	-0.2	-0.4	100.0%	-4.8
13610	AT4G31670.1   ubiquitin carboxyl-terminal hydrolase family protein / zinc finger (MYND type) family protein, similar to ubiquitin-specific protease 15 (UBP15) (Arabidopsis thaliana) GI:11993475; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF01753: MYND finger	5.5	5.4	0.1	0.4	100.0%	-4.8
13611	AT2G42090.1   Symbol: ACT9   actin, putative, similar to SP:P53496 Actin 11 {Arabidopsis thaliana}; contains Pfam profile PF00022: Actin   chr2:17563822-17565447 FORWARD   Aliases: ACTIN 9, T6D20.2, T6D20_2	2.3	2.3	0.1	0.4	100.0%	-5.4
13612	AT2G34640.1   expressed protein   chr2:14588969-14591736 REVERSE   Aliases: T31E10.2, T31E10_2	5.8	6.0	-0.2	-0.4	100.0%	-4.8
13613	AT5G02990.1   kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	5.0	4.8	0.1	0.4	100.0%	-5.0
13614	AT4G31010.2   expressed protein   chr4:15106650-15108967 FORWARD   Aliases: F6I18.80, F6I18_80	3.7	3.6	0.1	0.4	100.0%	-4.9
13615	AT1G43130.1   Symbol: LCV2   expressed protein, contains Pfam domain, PF04367: Protein of unknown function (DUF502)   chr1:16230648-16233663 REVERSE   Aliases: F1I21.3, F1I21_3, LCV2, LIKE COV 2	7.7	7.9	-0.2	-0.4	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13616	AT3G05480.2   similar to PCNA-like DNA checkpoint protein Rad9 [Xenopus laevis] (GB:AAP13339.1); contains InterPro domain Rad9 (InterPro:IPR007268)   chr3:1585308-1588338 FORWARD   Aliases: F22F7.7, F22F7_7	3.0	3.0	-0.1	-0.4	100.0%	-5.4
13617	AT3G22940.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:8131475-8132713 FORWARD   Aliases: F5N5.12	3.8	3.7	0.1	0.4	100.0%	-5.2
13618	AT3G42400.1   hypothetical protein, various predicted proteins, Arabidopsis thaliana   chr3:14531604-14533752 FORWARD   Aliases: T14K23.110	2.6	2.7	-0.1	-0.4	100.0%	-5.5
13619	AT4G33200.1   Symbol: XI I   myosin, putative, similar to myosin (GI:433663) (Arabidopsis thaliana)   chr4:16002535-16014971 REVERSE   Aliases: ATXI I, F4I10.130, F4I10_130	3.1	3.2	-0.1	-0.4	100.0%	-4.6
13620	AT4G33410.1   signal peptide peptidase family protein, contains Pfam domain PF04258: Membrane protein of unknown function (DUF435)   chr4:16080879-16083240 FORWARD   Aliases: F17M5.170, F17M5_170	8.3	8.4	-0.1	-0.4	100.0%	-4.6
13621	AT1G76700.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein, Saccharomyces cerevisiae; contains Pfam profile PF00226 DnaJ domain   chr1:28784670-28788142 REVERSE   Aliases: F28O16.7, F28O16_7	3.9	3.7	0.1	0.4	100.0%	-4.8
13622	AT3G61530.2   ketopantoate hydroxymethyltransferase family protein, similar to SP:Q9Y7B6 3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11) (Ketopantoate hydroxymethyltransferase) {Emericella nidulans}; contains Pfam profile PF02548: Ketopantoate hydroxymethyltransferase   chr3:22782444-22784765 REVERSE   Aliases: F2A19.130	7.3	7.0	0.3	0.4	100.0%	-4.2
13623	AT2G23630.1   Symbol: SKS16   multi-copper oxidase type I family protein, contains Pfam profile: PF00394 Multicopper oxidase   chr2:10059646-10062397 REVERSE   Aliases: F26B6.30, SKS16	2.8	2.7	0.1	0.4	100.0%	-5.2
13624	AT2G24820.1   Rieske (2Fe-2S) domain-containing protein, similar to Rieske iron-sulfur protein Tic55 from Pisum sativum (gi:2764524); contains Pfam PF00355 Rieske (2Fe-2S) domain   chr2:10582058-10584553 FORWARD   Aliases: F27C12.26, F27C12_26	6.8	7.1	-0.2	-0.4	100.0%	-4.5
13625	AT3G61010.1   glycosyl hydrolase family protein 85, hypothetical protein F9F8.14 - Arabidopsis thaliana, EMBL:AC009991	4.2	4.0	0.1	0.4	100.0%	-4.9
13626	AT3G28450.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor kinase GB:AAD02501 from (Arabidopsis thaliana)   chr3:10668499-10670614 FORWARD   Aliases: MFJ20.14	6.2	6.0	0.2	0.4	100.0%	-4.7
13627	AT1G61130.1   serine carboxypeptidase S10 family protein, similar to Serine carboxypeptidase II-3 precursor (SP:P52711) (CP-MII.3. (Hordeum vulgare)   chr1:22532689-22535449 REVERSE   Aliases: F11P17.14, F11P17_14, SCPL32	2.9	3.0	-0.1	-0.4	100.0%	-4.9
13628	AT3G53740.3   similar to 60S ribosomal protein L36 (RPL36A) [Arabidopsis thaliana] (TAIR:At2g37600.1); similar to putative 60S ribosomal protein L36 [Oryza sativa (japonica cultivar-group)] (GB:XP_475364.1); contains InterPro domain Ribosomal protein L36E (InterPro:IPR000509)   chr3:19924705-19925969 REVERSE   Aliases: F5K20.40	11.5	11.6	-0.1	-0.4	100.0%	-4.8
13629	AT3G15130.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:5097160-5099229 REVERSE   Aliases: F4B12.1	2.7	2.8	-0.1	-0.4	100.0%	-5.5
13630	AT2G17640.1   Symbol: AtSerat3;1   serine O-acetyltransferase, putative (SAT-106), similar to Arabidopsis thaliana serine acetyltransferase GI:905391	9.0	8.9	0.1	0.4	100.0%	-5.1
13631	AT1G66810.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:24931276-24932282 REVERSE   Aliases: F4N21.6, F4N21_6	2.8	2.7	0.1	0.4	100.0%	-5.2
13632	AT1G28120.1   expressed protein   chr1:9812952-9815528 REVERSE   Aliases: F13K9.21, F13K9_21	8.3	8.1	0.1	0.4	100.0%	-5.1
13633	AT1G21720.1   Symbol: PBC1   20S proteasome beta subunit C1 (PBC1) (PRCT), almost identical to GB:AAC32069 from (Arabidopsis thaliana), EST gb:T76747 comes from this gene; identical to cDNA proteasome subunit prct GI:2511567   chr1:7626272-7628251 FORWARD   Aliases: 20S PROTEASOME BETA SUBUNIT PBC1, F8K7.15, F8K7_15	10.2	9.7	0.5	0.4	100.0%	-4.4
13634	AT5G46040.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:18688624-18690778 REVERSE   Aliases: MCL19.9, MCL19_9	2.6	2.7	-0.1	-0.4	100.0%	-4.9
13635	AT2G04270.4   glycoside hydrolase starch-binding domain-containing protein, contains Pfam profile: PF00686 starch binding domain   chr2:1476107-1480583 FORWARD   Aliases: T23O15.10, T23O15_10	2.9	2.8	0.1	0.4	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13636	AT1G77300.1   similar to SET domain-containing protein (ASHH1) [Arabidopsis thaliana] (TAIR:At1g76710.2); similar to SET domain-containing protein (ASHH1) [Arabidopsis thaliana] (TAIR:At1g76710.1); similar to hypothetical protein [Nannochloris bacillaris] (GB:BAD42330.1); contains InterPro domain Nuclear protein SET (InterPro:IPR001214); contains InterPro domain AWS (InterPro:IPR006560); contains InterPro domain SET-related region (InterPro:IPR003616)   chr1:29044816-29053704 REVERSE   Aliases: T14N5.15, T14N5_15	3.3	3.5	-0.1	-0.4	100.0%	-4.8
13637	AT1G10620.1   protein kinase family protein, contains serine/threonine protein kinases active-site signature, PROSITE:PS00108   chr1:3509002-3511976 REVERSE   Aliases: F20B24.6, F20B24_6	2.0	2.1	-0.0	-0.4	100.0%	-5.8
13638	AT1G58340.1   Symbol: ZF14   MATE efflux protein-related, contains Pfam profile: PF01554 uncharacterized membrane protein family UPF0013   chr1:21656689-21659102 FORWARD   Aliases: F19C14.5, F19C14_5, ZF14	5.0	4.9	0.1	0.4	100.0%	-5.0
13639	AT5G52790.1   CBS domain-containing protein-related, contains Pfam profile PF01595: Domain of unknown function, weak hit to PF00571: CBS domain   chr5:21408943-21411585 REVERSE   Aliases: F6N7.28, F6N7_28	3.1	2.9	0.2	0.4	100.0%	-4.3
13640	AT1G09020.1   Symbol: SNF4   protein kinase, putative, similar to protein kinase AKINbetagamma-2 (Zea mays) GI:11139548, AKINbetagamma-1 (Zea mays) GI:11139546; contains Pfam profile PF00571: CBS domain   chr1:2899918-2904818 REVERSE   Aliases: ATSNF4, F7G19.11, F7G19_11, PUTATIVE ACTIVATOR SUBUNIT OF SNF1 RELATED PROTEIN KINASE SNF4	2.6	2.6	0.1	0.4	100.0%	-5.4
13641	AT2G23480.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr2:10008973-10011768 FORWARD   Aliases: F26B6.13, F26B6_13	3.0	3.1	-0.1	-0.4	100.0%	-4.8
13642	AT2G01780.1   S-locus glycoprotein, putative, similar to S-locus glycoprotein from (Brassica oleracea) GI:2351138, (Brassica napus) GI:17868; contains Pfam profile PF01453: Lectin (probable mannose binding)	2.7	2.8	-0.0	-0.4	100.0%	-5.9
13643	AT3G51430.1   Symbol: YLS2   strictosidine synthase, putative (YLS2), similar to hemomucin (Drosophila melanogaster)(GI:1280434), strictosidine synthase (Rauvolfia serpentina)(SP:P15324); contains strictosidine synthase domain PF03088; identical to cDNA YLS2 mRNA for strictosidine synthase-like protein GI:13122281   chr3:19097444-19099089 FORWARD   Aliases: F26O13.70	8.3	8.1	0.2	0.4	100.0%	-4.7
13644	AT5G04590.1   Symbol: SIR   sulfite reductase / ferredoxin (SIR), identical to sulfite reductase (Arabidopsis thaliana) GI:804953, GI:2584721	8.8	9.1	-0.3	-0.4	100.0%	-4.5
13645	AT1G18100.1   Symbol: E12A11	2.3	2.4	-0.1	-0.4	100.0%	-4.6
13646	AT2G32070.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q60809 CCR4-NOT transcription complex, subunit 7 (CCR4-associated factor 1, (CAF1) (Mus musculus)   chr2:13647745-13649013 REVERSE   Aliases: F22D22.18, F22D22_18	6.5	6.2	0.3	0.4	100.0%	-4.8
13647	AT1G26270.1   phosphatidylinositol 3- and 4-kinase family protein, similar to phosphatidylinositol 4-kinase type-II beta (Homo sapiens) GI:20159767; contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase   chr1:9089511-9092444 REVERSE   Aliases: F28B23.7, F28B23_7	10.7	11.0	-0.3	-0.4	100.0%	-4.6
13648	AT5G39880.1   expressed protein   chr5:15988115-15989465 FORWARD   Aliases: MYH19.7, MYH19_7	2.4	2.5	-0.0	-0.4	100.0%	-5.6
13649	AT5G19855.1   expressed protein   chr5:6711974-6713582 REVERSE   Aliases: None	3.4	3.3	0.1	0.4	100.0%	-5.6
13650	AT1G73370.1   sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative, similar to sucrose synthase GI:6682841 from (Citrus unshiu)   chr1:27588140-27591987 REVERSE   Aliases: T9L24.42, T9L24_42	4.6	4.8	-0.2	-0.4	100.0%	-4.4
13651	AT3G60400.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr3:22340067-22342078 FORWARD   Aliases: T8B10.60	2.7	2.8	-0.1	-0.4	100.0%	-5.3
13652	AT3G26940.1   Symbol: CDG1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:9937819-9940506 REVERSE   Aliases: CONSTITUTIVE DIFFERENTIAL GROWTH 1, MOJ10.2	3.3	3.2	0.1	0.4	100.0%	-5.1
13653	AT3G52540.1   ovate family protein, 52% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	2.9	3.0	-0.1	-0.4	100.0%	-5.3
13654	AT3G01840.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:296589-298641 REVERSE   Aliases: F28J7.37, F28J7_37	2.9	2.8	0.1	0.4	100.0%	-5.1
13655	AT1G75220.1   integral membrane protein, putative, strong similarity to integral membrane protein GI:1209756 from (Beta vulgaris); contains Pfam profile PF00083: major facilitator superfamily protein   chr1:28232851-28236492 REVERSE   Aliases: F22H5.6, F22H5_6	6.7	6.4	0.3	0.4	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13656	AT2G16690.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:7243960-7244682 REVERSE   Aliases: T24I21.10, T24I21_10	4.5	4.4	0.1	0.4	100.0%	-5.1
13657	AT1G75860.1   expressed protein   chr1:28487916-28489039 REVERSE   Aliases: T4O12.10, T4O12_10	7.4	7.2	0.3	0.4	100.0%	-4.8
13658	AT4G28500.1   Symbol: ANAC073   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr4:14083020-14084272 FORWARD   Aliases: ANAC073, F2009.190, F2009_190	3.6	3.8	-0.1	-0.4	100.0%	-4.6
13659	AT2G15560.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537   chr2:6794951-6797183 REVERSE   Aliases: F9O13.11	2.7	2.8	-0.1	-0.4	100.0%	-4.6
13660	AT3G52620.1   expressed protein, phosphate acetyltransferase, Staphylococcus aureus, EMBL:SAU271496   chr3:19524091-19524534 FORWARD   Aliases: F3C22.20	3.1	3.2	-0.1	-0.4	100.0%	-5.1
13661	AT5G40600.1   Symbol: EMB1875   expressed protein   chr5:16272272-16273993 REVERSE   Aliases: EMB1875, EMBRYO DEFECTIVE 1875, MNF13.13, MNF13_13	3.7	3.6	0.1	0.4	100.0%	-5.0
13662	AT4G31260.1   expressed protein   chr4:15182599-15182790 REVERSE   Aliases: F8F16.80, F8F16_80	2.9	2.9	-0.0	-0.4	100.0%	-5.9
13663	AT4G20830.2   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr4:11155471-11157333 FORWARD   Aliases: F21C20.180, F21C20_180	7.9	8.2	-0.3	-0.4	100.0%	-4.7
13664	AT4G07510.1   hypothetical protein   chr4:4312209-4313619 FORWARD   Aliases: T3E15.7, T3E15_7	2.9	2.9	-0.1	-0.4	100.0%	-5.4
13665	AT4G26950.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr4:13533570-13534101 REVERSE   Aliases: F10M23.290, F10M23_290	2.8	2.8	0.1	0.4	100.0%	-5.5
13666	AT2G03750.1   sulfotransferase family protein, similar to similar to steroid sulfotransferase 3 (Brassica napus) GI:3420008, steroid sulfotransferase 1 (Brassica napus) GI:3420004; contains Pfam profile PF00685: Sulfotransferase domain   chr2:1147804-1149058 REVERSE   Aliases: F19B11.20, F19B11_20	2.7	2.7	0.1	0.4	100.0%	-5.5
13667	AT4G17160.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:1208537 from (Glycine max)   chr4:9641991-9643552 REVERSE   Aliases: DL4615C, FCAALL.364	3.2	3.1	0.1	0.4	100.0%	-4.9
13668	AT5G03080.1   phosphatidic acid phosphatase-related / PAP2-related, contains Pfam profile PF01569: PAP2 superfamily   chr5:721866-723399 FORWARD   Aliases: F15A17.110, F15A17_110	5.3	5.1	0.1	0.4	100.0%	-4.9
13669	AT1G79970.2   expressed protein   chr1:30087004-30088642 FORWARD   Aliases: F18B13.5, F18B13_5	4.3	4.5	-0.2	-0.4	100.0%	-4.8
13670	AT3G23020.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to leaf protein (Ipomoea nil) GI:3107905; contains Pfam profile PF01535: PPR repeat   chr3:8177222-8179750 REVERSE   Aliases: MXC7.5	3.2	3.3	-0.1	-0.4	100.0%	-5.2
13671	AT1G73480.1   hydrolase, alpha/beta fold family protein, low similarity to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:27632600-27636467 FORWARD   Aliases: T9L24.33, T9L24_33	4.3	4.2	0.1	0.4	100.0%	-4.9
13672	AT5G35430.1   expressed protein   chr5:13679171-13683245 FORWARD   Aliases: AT5G35440, MOK9.1, MOK9_1	3.3	3.4	-0.1	-0.4	100.0%	-5.4
13673	AT3G18040.2   Symbol: ATMPK9	4.5	4.6	-0.1	-0.4	100.0%	-5.1
13674	AT5G13780.1   GCN5-related N-acetyltransferase, putative, similar to SP:P07347 N-terminal acetyltransferase complex ARD1 subunit (Arrest-defective protein 1) {Saccharomyces cerevisiae}; contains Pfam profile PF00583: acetyltransferase, GNAT family   chr5:4446945-4448643 REVERSE   Aliases: MXE10.7, MXE10_7	6.2	6.5	-0.3	-0.4	100.0%	-4.8
13675	AT2G41840.1   40S ribosomal protein S2 (RPS2C)	10.4	10.6	-0.2	-0.4	100.0%	-4.9
13676	AT4G18975.2   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At4g21190.1); contains InterPro domain PPR repeat (InterPro:IPR002885)	4.9	4.7	0.1	0.4	100.0%	-4.8
13677	AT3G10410.1   Symbol: SCPL49	10.6	10.3	0.3	0.4	100.0%	-4.8
13678	AT5G45370.3   nodulin-related / integral membrane family protein, contains Pfam profile:PF00892 integral membrane protein DUF6	4.3	4.4	-0.1	-0.4	100.0%	-4.6
13679	AT2G18040.1   Symbol: PIN1AT	9.7	9.9	-0.2	-0.4	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13680	AT3G50000.1   Symbol: CKA2   casein kinase II alpha chain 2, identical to casein kinase II, alpha chain 2 (CK II) (Arabidopsis thaliana) SWISS-PROT:Q08466   chr3:18545470-18547878 FORWARD   Aliases: ATCKA2, ATPK15D, CASEIN KINASE II, ALPHA CHAIN 2, F3A4.80	10.3	10.5	-0.2	-0.4	100.0%	-5.0
13681	AT2G11090.1   expressed protein   chr2:4406516-4407042 REVERSE   Aliases: F15K19.16, F15K19_16	2.0	2.0	0.0	0.4	100.0%	-6.3
13682	AT3G56500.1   serine-rich protein-related, contains some similarity to serine-rich proteins   chr3:20954617-20954949 FORWARD   Aliases: T5P19.150	2.7	2.6	0.1	0.4	100.0%	-5.0
13683	NA	3.0	3.0	-0.0	-0.4	100.0%	-5.7
13684	AT1G76210.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr1:28599844-28600776 REVERSE   Aliases: T23E18.14, T23E18_14	3.0	2.9	0.1	0.4	100.0%	-5.0
13685	AT2G46480.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8;   chr2:19083477-19085458 REVERSE   Aliases: F13A10.1	2.4	2.4	-0.1	-0.4	100.0%	-5.6
13686	AT4G33390.1   hypothetical protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827)   chr4:16075285-16077709 FORWARD   Aliases: F17M5.150, F17M5_150	2.4	2.3	0.1	0.4	100.0%	-5.6
13687	AT4G37950.1   expressed protein   chr4:17844424-17849266 FORWARD   Aliases: F20D10.70, F20D10_70	2.5	2.4	0.1	0.4	100.0%	-5.9
13688	AT5G53710.1   expressed protein   chr5:21822485-21823020 REVERSE   Aliases: MGN6.6, MGN6_6	3.9	4.0	-0.2	-0.4	100.0%	-4.7
13689	AT4G26180.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr4:13260272-13262044 REVERSE   Aliases: T25K17.6	4.4	4.5	-0.1	-0.4	100.0%	-5.2
13690	AT5G59080.1   expressed protein   chr5:23864634-23865721 REVERSE   Aliases: K18B18.8, K18B18_8	3.3	3.2	0.1	0.4	100.0%	-5.5
13691	AT3G07830.1   polygalacturonase, putative / pectinase, putative, strong similarity to polygalacturonase (PGA3) GI:3152948 from (Arabidopsis thaliana)   chr3:2499249-2501027 REVERSE   Aliases: F17A17.17	3.2	3.2	-0.1	-0.4	100.0%	-5.5
13692	AT1G30630.1   coatomer protein epsilon subunit family protein / COPE family protein, similar to SP:O14579 Coatomer epsilon subunit (Epsilon-coat protein) (Epsilon-COP) from Homo sapiens, SP:Q60445 from Cricetulus griseus; ESTs gb:Z17908, gb:AA728673, gb:N96555, gb:H76335, gb:AA712463, gb:W43247, gb:T45611, gb:T21160, gb:T14119 and AI100483 come from this gene   chr1:10858296-10860243 REVERSE   Aliases: T5I8.8, T5I8_8	10.7	10.9	-0.2	-0.4	100.0%	-5.1
13693	AT2G13840.1   PHP domain-containing protein, contains Pfam PF02231: PHP domain N-terminal region and Pfam PF02811: PHP domain C-terminal region; identical to Protein trpH. (Swiss-Prot:O54453) (Salmonella typhimurium)   chr2:5795634-5798198 REVERSE   Aliases: F17L24.11, F17L24_11	5.6	5.7	-0.1	-0.4	100.0%	-5.1
13694	AT1G19250.1   flavin-containing monooxygenase family protein / FMO family protein, low similarity to SP:P97501 Dimethylaniline monooxygenase (N-oxide forming) 3 (EC 1.14.13.8) (Hepatic flavin-containing monooxygenase 3) (FMO 3) {Mus musculus}; contains Pfam profile PF00743: Flavin-binding monooxygenase-like   chr1:6650520-6653069 REVERSE   Aliases: T29M8.12, T29M8_12	2.4	2.5	-0.1	-0.4	100.0%	-5.1
13695	AT5G52870.1   expressed protein, similar to unknown protein (gb:AAF24565.1)   chr5:21445190-21446671 REVERSE   Aliases: MXC20.9, MXC20_9	2.7	2.6	0.1	0.4	100.0%	-5.4
13696	AT1G55130.1   endomembrane protein 70, putative, similar to multispreading membrane protein GI:2276460 from (Homo sapiens)   chr1:20573321-20576060 FORWARD   Aliases: T7N22.7, T7N22_7	5.7	5.8	-0.2	-0.4	100.0%	-4.6
13697	AT4G28480.1   DNAJ heat shock family protein, contains Pfam profile PF00226: DnaJ domain; ; similar to DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) (Heat shock protein 40) (HSP40) (DnaJ protein homolog 1) (HDJ-1) (Swiss-Prot:P25685) (Homo sapiens) and	7.9	7.6	0.3	0.4	100.0%	-4.8
13698	AT2G36680.3   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g53120.1); similar to autophagy protein AGP6 [Hyacinthus orientalis] (GB:AAS21018.1)   chr2:15375885-15377908 REVERSE   Aliases: F13K3.8, F13K3_8	4.2	4.0	0.2	0.4	100.0%	-4.7
13699	AT4G21280.2   similar to oxygen-evolving enhancer protein 3, chloroplast, putative (PSBQ2) [Arabidopsis thaliana] (TAIR:At4g05180.1); similar to chloroplast oxygen-evolving enhancer protein [Manihot esculenta] (GB:AAV74404.1); contains InterPro domain Twin-arginine translocation pathway signal (InterPro:IPR006311); contains InterPro domain Oxygen evolving enhancer 3 (InterPro:IPR008797)   chr4:11334412-11335783 FORWARD   Aliases: T6K22.20	8.7	8.9	-0.2	-0.4	100.0%	-4.3
13700	AT1G01490.2   similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:At5g23760.1); similar to unknown [Populus tremuloides] (GB:AAO63778.1); contains InterPro domain Heavy metal transport/detoxification protein (InterPro:IPR006121)   chr1:180059-182293 REVERSE   Aliases: F22L4.5, F22L4_5	9.5	9.3	0.2	0.4	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13701	AT3G04250.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:1121957-1122835 FORWARD   Aliases: T6K12.13, T6K12_13	2.5	2.5	-0.1	-0.4	100.0%	-5.4
13702	AT3G52690.1   hypothetical protein, predicted proteins, Arabidopsis thaliana   chr3:19541714-19542789 FORWARD   Aliases: F3C22.90	3.6	3.6	0.1	0.4	100.0%	-5.4
13703	AT4G28400.1   protein phosphatase 2C, putative / PP2C, putative, protein phosphatase 2C-fission yeast, PIR2:S54297   chr4:14048360-14050341 FORWARD   Aliases: F2009.80, F2009_80	7.8	7.6	0.2	0.4	100.0%	-4.6
13704	AT5G27800.1   expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	2.4	2.5	-0.1	-0.4	100.0%	-5.4
13705	AT1G63180.1   UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative, strong similarity to SP:Q42605 (GI:1143392) from (Arabidopsis thaliana) (Arch. Biochem. Biophys. 327 (1), 27-34 (1996))   chr1:23431076-23433238 REVERSE   Aliases: F16M19.8, F16M19_8	4.5	4.7	-0.2	-0.4	100.0%	-4.6
13706	AT3G20000.1   Symbol: TOM40   porin family protein, low similarity to haymaker protein (Mus musculus) GI:17834089, mitochondrial outer membrane protein MOM35 (Mus musculus) GI:6650562; contains Pfam profile PF01459: Eukaryotic porin   chr3:6967596-6970571 FORWARD   Aliases: MZE19.5	8.5	8.7	-0.2	-0.4	100.0%	-4.8
13707	AT5G51980.2   similar to WD-40 repeat family protein / zfw1 protein (ZFWD1) [Arabidopsis thaliana] (TAIR:At4g25440.1); similar to Putative zfw1 protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470206.1); contains InterPro domain Zn-finger, C-x8-C-x5-C-x3-H type (InterPro:IPR000571); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)	5.8	5.9	-0.2	-0.4	100.0%	-4.8
13708	AT1G66940.3   similar to serine/threonine protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g66920.1); similar to P0034C09.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_917027.1); similar to receptor serine/threonine kinase PR5K-like [Oryza sativa (japonica cultivar-group)] (GB:BAD82485.1)	3.3	3.2	0.1	0.4	100.0%	-5.4
13709	AT1G34750.1   protein phosphatase 2C, putative / PP2C, putative, similar to GB:AAD17805 from (Lotus japonicus) (Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1738-1743 (1999))   chr1:12736073-12737705 REVERSE   Aliases: F11O6.14	4.5	4.4	0.1	0.4	100.0%	-4.7
13710	AT4G37300.1   expressed protein   chr4:17554749-17555855 FORWARD   Aliases: F6G17.14	6.6	7.0	-0.4	-0.4	100.0%	-4.7
13711	AT2G15490.2   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:6768717-6770556 FORWARD   Aliases: F9O13.4	4.7	4.8	-0.2	-0.4	100.0%	-4.7
13712	AT5G63070.1   40S ribosomal protein S15, putative   chr5:25316404-25316886 REVERSE   Aliases: MDC12.3, MDC12_3	3.7	3.6	0.1	0.4	100.0%	-5.0
13713	AT5G19410.1   ABC transporter family protein, white membrane transporter, Bactrocera tryoni, EMBL:U97104   chr5:6545239-6547113 REVERSE   Aliases: F7K24.160, F7K24_160	2.6	2.8	-0.2	-0.4	100.0%	-4.4
13714	AT5G10300.1   hydrolase, alpha/beta fold family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, alpha-hydroxynitrile lyase (Manihot esculenta) GI:2780225; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:3239624-3240871 FORWARD   Aliases: F18D22.70, F18D22_70	8.0	7.9	0.1	0.4	100.0%	-4.6
13715	AT3G07940.1   zinc finger and C2 domain protein, putative, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana); contains Pfam profile: PF01412 Putative GTP-ase activating protein for Arf   chr3:2529245-2531539 FORWARD   Aliases: F17A17.28	4.9	4.7	0.2	0.4	100.0%	-4.5
13716	AT5G65270.1   Ras-related GTP-binding family protein, similar to GTP-binding protein RAB11A GI:1370142 from (Lotus japonicus); contains Pfam profile: PF00071 Ras family   chr5:26100602-26101940 FORWARD   Aliases: MQN23.22, MQN23_22	9.4	9.1	0.3	0.4	100.0%	-4.8
13717	AT4G24620.1   Symbol: PGI1   glucose-6-phosphate isomerase, putative, similar to glucose-6-phosphate isomerase (Spinacia oleracea) GI:3413511; contains Pfam profile PF00342: glucose-6-phosphate isomerase   chr4:12708767-12712835 REVERSE   Aliases: CHLOROPLASTIC PHOSPHOGLUCOSE ISOMERASE, F22K18.180, F22K18_180, PGI, PHOSPHO GLC ISOMERASE, PHOSPHOGLUCOSE ISOMERASE PRECURSOR	11.7	11.9	-0.2	-0.4	100.0%	-5.0
13718	AT4G25530.1   Symbol: FWA   homeodomain protein (FWA), identical to Homeobox protein FWA (SP:Q9FVI6) (Arabidopsis thaliana); contains Pfam profiles PF01852: START domain and PF00046: Homeobox domain; identical to cDNA homeobox-containing transcription factor FWA (FWA)GI:13506819   chr4:13038369-13042452 FORWARD   Aliases: FWA, M7J2.100, M7J2_100	2.5	2.5	0.1	0.4	100.0%	-5.5
13719	AT4G25230.2   zinc finger (C3HC4-type RING finger) family protein, similar to autocrine motility factor receptor (Mus musculus) GI:5931953; contains Pfam profiles PF00097: Zinc finger, C3HC4 type (RING finger), PF02845: CUE domain	3.8	3.7	0.1	0.4	100.0%	-5.0
13720	AT2G23410.1   Symbol: ACPT   dehydrololichyl diphosphate synthase / DEDOL-PP synthase (DPS), identical to dehydrololichyl diphosphate synthase (Arabidopsis thaliana) GI:7960765   chr2:9973210-9974850 REVERSE   Aliases: None	2.3	2.4	-0.1	-0.4	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13721	AT5G65990.1   amino acid transporter family protein, similar to proton/amino acid transporter 1 (Mus musculus) GI:21908024; contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr5:26412108-26414108 FORWARD   Aliases: K2A18.5, K2A18_5	7.0	6.8	0.2	0.4	100.0%	-4.4
13722	AT3G20030.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.5	-0.1	-0.4	100.0%	-5.5
13723	AT3G14400.1   Symbol: UBP25   ubiquitin-specific protease 25 (UBP25), similar to GI:11993490   chr3:4811539-4815504 REVERSE   Aliases: MLN21.18, UBIQUITIN SPECIFIC PROTEASE 25	4.8	4.5	0.3	0.4	100.0%	-4.7
13724	AT1G05740.1   expressed protein, contains Pfam PF05811: Eukaryotic protein of unknown function (DUF842)   chr1:1720673-1721308 FORWARD   Aliases: F3F20.19, F3F20_19	3.0	2.9	0.1	0.4	100.0%	-5.0
13725	AT5G03180.1   zinc finger (C3HC4-type RING finger) family protein, various predicted proteins, Arabidopsis thaliana ; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:753950-756645 REVERSE   Aliases: F15A17.210, F15A17_210	3.0	2.9	0.1	0.4	100.0%	-4.8
13726	AT3G60770.1   40S ribosomal protein S13 (RPS13A), AtRPS13A mRNA for cytoplasmic ribosomal protein S13, Arabidopsis thaliana,AB031739   chr3:22471265-22472718 REVERSE   Aliases: T4C21.180	11.7	11.8	-0.1	-0.4	100.0%	-5.0
13727	AT5G28500.1   expressed protein, predicted proteins, Arabidopsis thaliana and Synechocystis sp.   chr5:10477775-10479388 FORWARD   Aliases: T26D3.4, T26D3_4	7.9	8.1	-0.2	-0.4	100.0%	-4.3
13728	AT2G42050.1   expressed protein, similar to SP:Q07981 FMRFamide-related peptides precursor HF-4 (HeptaFaRP) {Helix aspersa}; contains Pfam profile PF03778: Protein of unknown function (DUF321)   chr2:17553218-17553637 REVERSE   Aliases: T6D20.6, T6D20_6	3.3	3.2	0.1	0.4	100.0%	-5.4
13729	AT1G01190.1   Symbol: CYP78A8   cytochrome P450, putative, similar to cytochrome P450 SP:O48927 from (Glycine max)   chr1:83045-84864 REVERSE   Aliases: F6F3.25	3.5	3.7	-0.2	-0.4	100.0%	-4.5
13730	AT5G06100.2   Symbol: MYB33   Encodes a member of the myb family of transcription factors (MYB33), contains Pfam profile: PF00249 myb DNA-binding domain. Double mutants with MYB65 are male sterile- anthers are small, pollen development is defective. Spatial expression appears to be under the control of miR159, contains a target site for this micro RNA. When the target site is mutated , expression is detected in leaves, roots, anther filament, pistil. The expression of a translational fusion is specific to anther locules in contrast to constructs lacking the miR159 target site. Phenotype is conditional and can be restored by lower temperature or higher light intensity.   chr5:1837915-1840728 FORWARD   Aliases: K16F4.6, K16F4_6, MYB33	2.8	2.8	-0.1	-0.4	100.0%	-5.5
13731	AT1G71960.1   ABC transporter family protein, similar to breast cancer resistance protein GB:AAC97367 from (Homo sapiens)   chr1:27086056-27091910 REVERSE   Aliases: F17M19.11, F17M19_11	3.4	3.3	0.1	0.4	100.0%	-5.1
13732	AT1G07550.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:2322652-2326558 REVERSE   Aliases: F22G5.7, F22G5_7	2.8	2.8	0.1	0.4	100.0%	-5.3
13733	AT5G07180.1   Symbol: ERL2   similar to leucine-rich repeat protein kinase, putative (ERECTA) [Arabidopsis thaliana] (TAIR:At2g26330.1); similar to leucine-rich repeat family protein / protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g62230.1); similar to receptor-like protein kinase [Elaeis guineensis] (GB:AAO26312.1); similar to putative receptor protein kinase [Oryza sativa (japonica cultivar-group)] (GB:BAD35990.1); similar to transmembrane protein kinase [Oryza sativa (japonica cultivar-group)] (GB:AAQ01160.1); similar to putative receptor protein kinase [Sorghum bicolor] (GB:AAL68842.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr5:2227572-2233418 REVERSE   Aliases: ERECTA LIKE 2, T28J14.120, T28J14_120	2.8	2.9	-0.1	-0.4	100.0%	-5.4
13734	AT3G62450.1   expressed protein   chr3:23109120-23109606 FORWARD   Aliases: T12C14.150	9.2	9.1	0.1	0.4	100.0%	-5.0
13735	AT4G23000.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.7	2.7	0.1	0.4	100.0%	-5.4
13736	AT2G43330.1   sugar transporter family protein, similar to SP:Q96QE2 Proton myo-inositol co-transporter (Hmit) (Homo sapiens), SP:Q01440 Membrane transporter D1 {Leishmania donovani}; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:18007931-18011160 FORWARD   Aliases: T1O24.7	5.5	5.6	-0.1	-0.4	100.0%	-4.9
13737	AT2G29220.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr2:12569858-12571741 REVERSE   Aliases: F16P2.40, F16P2_40	2.9	2.9	-0.1	-0.4	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13738	AT5G23790.1   galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 GI:5608497 from (Ajuga reptans); contains Pfam profile: PF01501 glycosyl transferase family 8   chr5:8020107-8021600 REVERSE   Aliases: MRO11.17, MRO11_17	2.8	2.8	-0.1	-0.4	100.0%	-5.5
13739	AT4G03950.1   glucose-6-phosphate/phosphate translocator, putative, similar to glucose-6-phosphate/phosphate-translocator precursor (Pisum sativum) gi:2997591:gb:AAC08525   chr4:1879516-1881109 FORWARD   Aliases: T24M8.5, T24M8_5	2.6	2.7	-0.1	-0.4	100.0%	-5.0
13740	AT2G40475.1   expressed protein   chr2:16913989-16915206 REVERSE   Aliases: None	3.7	3.9	-0.1	-0.4	100.0%	-5.0
13741	ATMG00630.1   Symbol: ORF110B   hypothetical protein   chrM:183111-183443 FORWARD   Aliases: ORF110B	4.1	4.6	-0.5	-0.4	100.0%	-4.6
13742	AT1G09750.1   chloroplast nucleoid DNA-binding protein-related, contains Pfam profile PF00026: Eukaryotic aspartyl protease;b similar to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) (Nicotiana tabacum)   chr1:3157503-3159147 FORWARD   Aliases: F21M12.13, F21M12_13	2.4	2.3	0.0	0.4	100.0%	-5.7
13743	AT4G37760.1   squalene monooxygenase, putative / squalene epoxidase, putative, similar to SP:O65404 (SE 1,1), SP:O65402 (SE 1,2), SP:O65403 (SE 2)   chr4:17743881-17746672 FORWARD   Aliases: T28I19.40, T28I19_40	4.3	4.1	0.3	0.4	100.0%	-4.9
13744	NA	3.4	3.3	0.1	0.4	100.0%	-5.0
13745	AT1G07560.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:2327317-2331093 FORWARD   Aliases: F22G5.6, F22G5_6	3.3	3.5	-0.2	-0.4	100.0%	-4.3
13746	AT5G50750.1   Symbol: RGP4   reversibly glycosylated polypeptide, putative, strong similarity to reversibly glycosylated polypeptide-1 (AtRGP) (Arabidopsis thaliana) GI:2317729; contains Pfam profile PF03214: Reversibly glycosylated polypeptide   chr5:20658218-20659886 FORWARD   Aliases: MFB16.25, MFB16_25, reversibly glycosylated polypeptide 4	3.8	4.0	-0.2	-0.4	100.0%	-4.7
13747	AT1G17630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:6064518-6066713 FORWARD   Aliases: F11A6.24	3.6	3.5	0.1	0.4	100.0%	-5.1
13748	AT5G06540.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:1999182-2001050 REVERSE   Aliases: F15M7.7, F15M7_7	3.3	3.2	0.1	0.4	100.0%	-5.3
13749	NA	2.3	2.3	0.0	0.4	100.0%	-6.4
13750	AT2G30820.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g06660.1); similar to dentin sialophosphoprotein precursor-like [Oryza sativa (japonica cultivar-group)] (GB:XP_464257.1)   chr2:13136811-13139541 FORWARD   Aliases: F7F1.3, F7F1_3	2.9	3.0	-0.1	-0.4	100.0%	-5.2
13751	AT5G39380.1   calmodulin-binding protein-related, has weak similarity to calmodulin-binding proteins   chr5:15775945-15777914 REVERSE   Aliases: MUL8.6, MUL8_6	4.0	3.9	0.1	0.4	100.0%	-5.2
13752	AT2G31960.1   Symbol: ATGSL03   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase; contains non-consensus splice aite AC at exon 33   chr2:13596622-13607143 FORWARD   Aliases: ATGSL3, F22D22.29, F22D22_29, GLUCAN SYNTHASE LIKE 3, GSL03	5.7	5.8	-0.2	-0.4	100.0%	-4.7
13753	AT4G40020.1   expressed protein   chr4:18553447-18555294 REVERSE   Aliases: T5J17.190, T5J17_190	2.5	2.5	0.1	0.4	100.0%	-5.5
13754	AT2G03540.1   expressed protein, ; expression supported by MPSS   chr2:1073756-1074512 FORWARD   Aliases: T4M8.2, T4M8_2	3.5	3.4	0.1	0.4	100.0%	-4.8
13755	AT1G51640.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr1:19153429-19155520 REVERSE   Aliases: F19C24.13, F19C24_13	2.6	2.5	0.1	0.4	100.0%	-5.0
13756	AT3G43680.1   hypothetical protein   chr3:15587444-15589257 FORWARD   Aliases: F23N14.60	3.3	3.4	-0.1	-0.4	100.0%	-4.9
13757	AT1G59725.1   DNAJ heat shock protein, putative, similar to SP:Q9QYJ3 DnaJ homolog subfamily B member 1 (Heat shock 40 kDa protein 1) {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr1:21954403-21955875 FORWARD   Aliases: F23H11.4, F23H11_4	2.9	2.8	0.1	0.4	100.0%	-5.0
13758	AT5G37130.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr5:14698608-14703914 FORWARD   Aliases: MJG14.18, MJG14_18	4.1	4.3	-0.2	-0.4	100.0%	-4.5
13759	AT5G48730.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:19780378-19782362 FORWARD   Aliases: K24G6.6, K24G6_6	4.7	4.8	-0.1	-0.4	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13760	AT4G34560.1   expressed protein   chr4:16507640-16508759 FORWARD   Aliases: T4L20.140, T4L20_140	2.5	2.4	0.1	0.4	100.0%	-5.3
13761	AT5G45910.1   GDSL-motif lipase/hydrolase family protein, similar to lipase (Arabidopsis thaliana) GI:1145627; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr5:18637526-18639528 REVERSE   Aliases: K15I22.11, K15I22_11	2.1	2.1	0.0	0.4	100.0%	-5.6
13762	AT2G01490.1   phytanoyl-CoA dioxygenase (PhyH) family protein, contains Pfam profile PF05721: Phytanoyl-CoA dioxygenase (PhyH); weak similarity to Phytanoyl-CoA dioxygenase, peroxisomal precursor (EC 1.14.11.18) (Phytanoyl-CoA alpha-hydroxylase) (PhyH) (Phytanic acid oxidase) (Swiss-Prot:O14832) (Homo sapiens)   chr2:221251-223406 FORWARD   Aliases: F2I9.11, F2I9_11	8.3	8.6	-0.3	-0.4	100.0%	-4.8
13763	AT4G39240.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr4:18269151-18270781 REVERSE   Aliases: T22F8.140, T22F8_140	8.7	8.8	-0.1	-0.4	100.0%	-4.9
13764	AT2G33735.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P30725 Chaperone protein dnaJ Clostridium acetobutylicum; contains Pfam profile PF00226 DnaJ domain   chr2:14275345-14276517 REVERSE   Aliases: None	4.8	4.9	-0.1	-0.4	100.0%	-4.6
13765	AT4G03500.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr4:1553090-1556569 FORWARD   Aliases: F9H3.13, F9H3_13	3.5	3.3	0.2	0.4	100.0%	-4.2
13766	AT4G27550.1   Symbol: ATTPS4	3.4	3.3	0.1	0.4	100.0%	-4.9
13767	AT2G23920.1   hypothetical protein   chr2:10188078-10188291 FORWARD   Aliases: T29E15.12, T29E15_12	2.7	2.8	-0.1	-0.4	100.0%	-5.7
13768	AT2G22160.1   cysteine endopeptidase-related, similar to cysteine endopeptidase precursor GI:2944446 from (Ricinus communis)   chr2:9432223-9432540 REVERSE   Aliases: T26C19.18, T26C19_18	2.4	2.4	-0.0	-0.4	100.0%	-5.6
13769	AT1G79540.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:29925227-29927569 REVERSE   Aliases: T8K14.4, T8K14_4	3.7	3.8	-0.1	-0.4	100.0%	-5.0
13770	AT1G20220.1   expressed protein   chr1:7004889-7007640 REVERSE   Aliases: T20H2.2, T20H2_2	6.1	6.2	-0.1	-0.4	100.0%	-4.8
13771	AT1G22990.1   heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID:9701579); strong similarity to farnesylated protein ATPF7 (GI:4097555); contains heavy-metal-associated domain PF00403   chr1:8139154-8140191 FORWARD   Aliases: F19G10.25	5.6	5.3	0.3	0.4	100.0%	-4.7
13772	AT4G32470.2   ubiquinol-cytochrome C reductase complex 14 kDa protein, putative, similar to SP:P48502 Ubiquinol-cytochrome C reductase complex 14 kDa protein (EC 1.10.2.2) (CR14) {Solanum tuberosum}; contains Pfam profile PF02271: Ubiquinol-cytochrome C reductase complex 14kD subunit   chr4:15669225-15671200 REVERSE   Aliases: F8B4.170, F8B4_170	12.0	12.1	-0.1	-0.4	100.0%	-5.3
13773	AT2G03360.1   expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)   chr2:1022284-1023465 REVERSE   Aliases: T4M8.21, T4M8_21	3.4	3.5	-0.1	-0.4	100.0%	-5.3
13774	AT2G15620.1   Symbol: NIR1   ferredoxin--nitrite reductase, putative, strong similarity to ferredoxin--nitrite reductase (Nicotiana tabacum) GI:19893; contains Pfam profiles PF03460: Nitrite/Sulfite reductase ferredoxin-like half domain, PF01077: Nitrite and sulphite reductase 4Fe-4S domain   chr2:6817558-6820021 FORWARD   Aliases: ATHNIR, F9O13.17, F9O13_17, NIR, NITRITE REDUCTASE	8.2	8.4	-0.2	-0.4	100.0%	-4.8
13775	AT5G44860.1   expressed protein, strong similarity to unknown protein (gb AAC79135.1)   chr5:18127685-18129014 REVERSE   Aliases: K21C13.3, K21C13_3	6.5	6.3	0.1	0.4	100.0%	-5.0
13776	AT3G19650.1   cyclin-related, contains weak similarity to Cyclin I (Multiple-band polypeptide I) (Swiss-Prot:P35662) (Bos taurus)   chr3:6823526-6825267 FORWARD   Aliases: MMB12.12	6.4	6.2	0.2	0.4	100.0%	-4.8
13777	AT1G57906.1   expressed protein   chr1:21439092-21440475 FORWARD   Aliases: F13D13.1, F13D13_1	3.5	3.6	-0.1	-0.4	100.0%	-5.0
13778	AT3G56050.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr3:20808934-20811869 REVERSE   Aliases: F18O21.10	5.3	5.2	0.2	0.4	100.0%	-4.9
13779	AT5G48150.2   Symbol: PAT1   phytochrome A signal transduction 1 (PAT1)   chr5:19539485-19541834 REVERSE   Aliases: MIF21.4, MIF21_4, PHYTOCHROME A SIGNAL TRANSDUCTION 1	6.6	6.4	0.2	0.4	100.0%	-4.6
13780	AT1G65480.1   Symbol: FT   flowering locus T protein (FT), identical to SP:Q9SXZ2 FLOWERING LOCUS T protein {Arabidopsis thaliana}; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein   chr1:24335091-24337597 FORWARD   Aliases: F5I14.3, F5I14_3, FLOWERING LOCUS T	2.3	2.4	-0.1	-0.4	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13781	AT5G10680.1   calmodulin-binding protein-related, contains weak similarity to calmodulin-binding proteins   chr5:3373585-3374310 FORWARD   Aliases: MAJ23.40, MAJ23_40	2.8	2.8	-0.1	-0.4	100.0%	-5.5
13782	AT5G16150.3   hexose transporter, putative, strong similarity to hexose transporter (Arabidopsis thaliana) GI:8347250; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:5272690-5275818 FORWARD   Aliases: T21H19.70, T21H19_70	9.9	9.8	0.1	0.4	100.0%	-4.8
13783	AT5G12450.1   expressed protein, similarity to predicted proteins, Arabidopsis thaliana   chr5:4040940-4041131 FORWARD   Aliases: None	3.3	3.4	-0.1	-0.4	100.0%	-5.5
13784	AT4G07990.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:Q9QYI5 DnaJ homolog subfamily B member 10 Mus musculus ; contains Pfam profile PF00226 DnaJ domain   chr4:4825409-4829605 REVERSE   Aliases: None	4.2	4.0	0.1	0.4	100.0%	-4.7
13785	AT5G50860.1   protein kinase family protein, contains PF00069: Protein kinase domain   chr5:20710689-20714265 REVERSE   Aliases: K16E14.1	4.1	4.2	-0.1	-0.4	100.0%	-5.1
13786	AT4G39030.1   Symbol: EDS5   enhanced disease susceptibility 5 (EDS5) / salicylic acid induction deficient 1 (SID1), identical to SP:Q945F0; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr4:18185734-18189015 FORWARD   Aliases: ENHANCED DISEASE SUSCEPTIBILITY 5, F19H22.130, F19H22_130, SALICYLIC ACID INDUCTION DEFICIENT 1, SID1	2.6	2.7	-0.1	-0.4	100.0%	-5.3
13787	AT3G48580.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endoxyloglucan transferase EXGT-A4 GI:5139002 from (Arabidopsis thaliana)   chr3:18018166-18019472 FORWARD   Aliases: T8P19.90	3.1	3.0	0.1	0.4	100.0%	-5.0
13788	AT1G10330.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3388749-3390152 FORWARD   Aliases: F14N23.21, F14N23_21	4.1	4.3	-0.1	-0.4	100.0%	-4.6
13789	AT1G32130.1   similar to IWS1 C-terminus family protein [Arabidopsis thaliana] (TAIR:At4g19000.1); similar to P0416D03.25 [Oryza sativa (japonica cultivar-group)] (GB:XP_462790.1); contains InterPro domain IWS1, C-terminal (InterPro:IPR008654)   chr1:11558861-11561845 REVERSE   Aliases: F3C3.8, F3C3_8	7.7	7.9	-0.1	-0.4	100.0%	-4.9
13790	AT4G15920.1   nodulin MtN3 family protein, similar to MtN3 GI:1619602 (root nodule development) from (Medicago truncatula)   chr4:9030531-9033409 REVERSE   Aliases: DL4000C, FCAALL.237	6.2	6.3	-0.1	-0.4	100.0%	-4.7
13791	AT4G31320.1   auxin-responsive protein, putative / small auxin up RNA (SAUR_C), similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana); similar to auxin-induced protein 15A (SP:P33081) from (Glycine max)   chr4:15193999-15194568 REVERSE   Aliases: F8F16.140, F8F16_140	2.7	2.9	-0.1	-0.4	100.0%	-5.0
13792	AT5G26900.1   WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to fizzy1 (GI:3298595) {Xenopus laevis}; WD-repeat protein, carrot, PIR:T14352   chr5:9463755-9465089 FORWARD   Aliases: F2P16.8, F2P16_8	3.3	3.2	0.1	0.4	100.0%	-5.7
13793	AT5G14920.2   similar to proline-rich family protein [Arabidopsis thaliana] (TAIR:At2g27380.1); similar to cell wall-plasma membrane linker protein [Brassica napus] (GB:CAA64425.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr5:4826546-4827983 FORWARD   Aliases: F2G14.40, F2G14_40	7.7	7.9	-0.2	-0.4	100.0%	-4.3
13794	AT1G80860.2   expressed protein   chr1:30393156-30394194 REVERSE   Aliases: F23A5.21, F23A5_21	7.2	7.1	0.1	0.4	100.0%	-4.9
13795	AT3G52380.1   Symbol: CP33   33 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp33, putative, similar to chloroplast RNA-binding protein (cp33) GB:BAA06523 (Arabidopsis thaliana) (Plant Mol. Biol. 27 (3), 529-539 (1995)); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:19432375-19434072 FORWARD   Aliases: PDE322, PIGMENT DEFECTIVE 322, T25B15.18	8.3	8.1	0.2	0.4	100.0%	-4.4
13796	AT5G41560.1   expressed protein   chr5:16638481-16639884 REVERSE   Aliases: MBK23.8, MBK23_8	7.1	7.0	0.2	0.4	100.0%	-5.1
13797	AT5G38120.1   4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein, similar to 4CL2, Arabidopsis thaliana (gi:12229665), 4CL1, Nicotiana tabacum (gi:12229631); contains Pfam AMP-binding enzyme domain PF00501   chr5:15230995-15233433 FORWARD   Aliases: MXA21.2, MXA21_2	3.7	3.8	-0.1	-0.4	100.0%	-4.9
13798	AT1G02790.1   Symbol: PGA4   exopolysaccharide / galacturan 1,4-alpha-galacturonidase (PGA3) / pectinase, identical to SP:P49062 Exopolysaccharide clone GBGE184 precursor (EC 3.2.1.67) (ExoPG) (Galacturan 1,4-alpha-galacturonidase) {Arabidopsis thaliana}   chr1:610448-612294 REVERSE   Aliases: POLYGALACTURONASE, POLYGALACTURONASE 4, T14P4.31	3.0	2.9	0.1	0.4	100.0%	-5.2
13799	AT3G13920.2   Symbol: EIF4A1	9.2	8.9	0.3	0.4	100.0%	-4.6
13800	NA	2.6	2.6	0.0	0.4	100.0%	-5.9
13801	AT5G37290.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr5:14779618-14781574 FORWARD   Aliases: MNJ8.8, MNJ8_8	5.8	5.7	0.1	0.4	100.0%	-4.6
13802	AT5G18510.1   expressed protein   chr5:6141780-6143888 REVERSE   Aliases: T28N17.4	3.3	3.2	0.1	0.4	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13803	AT2G25780.1   hypothetical protein   chr2:11002247-11003001 FORWARD   Aliases: F17H15.19, F17H15_19	3.1	3.1	-0.1	-0.4	100.0%	-5.7
13804	AT4G13160.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr4:7653651-7654921 FORWARD   Aliases: F17N18.50, F17N18_50	4.9	4.7	0.1	0.4	100.0%	-5.0
13805	AT2G34900.2   Symbol: IMB1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr2:14730221-14732708 REVERSE   Aliases: F19I3.13, F19I3_13, IMBIBITION INDUCIBLE 1	8.2	8.4	-0.2	-0.4	100.0%	-4.6
13806	AT2G33310.2   Symbol: IAA13   auxin-responsive protein / indoleacetic acid-induced protein 13 (IAA13), identical to SP:Q38831 Auxin-responsive protein IAA13 (Indoleacetic acid-induced protein 13) {Arabidopsis thaliana}   chr2:14121358-14123046 REVERSE   Aliases: F4P9.8, F4P9_8, IAA13	8.3	8.5	-0.2	-0.4	100.0%	-4.7
13807	AT1G12220.1   Symbol: RPS5   disease resistance protein RPS5 (CC-NBS-LRR class) / resistance to Pseudomonas syringae protein 5 (CC-NBS-LRR class), domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPS5 (resistance to Pseudomonas syringae protein 5)(gi:3309620)   chr1:4145009-4147678 FORWARD   Aliases: DISEASE RESISTANCE PROTEIN RPS5, RESISTANT TO P. SYRINGAE 5, T28K15.5, T28K15_5	2.3	2.4	-0.1	-0.4	100.0%	-5.6
13808	AT2G28080.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	5.8	5.9	-0.1	-0.4	100.0%	-5.2
13809	AT1G60950.1   Symbol: FED A   ferredoxin, chloroplast (PETF), identical to FERREDOXIN PRECURSOR GB:P16972 (SP:P16972) from (Arabidopsis thaliana)   chr1:22448185-22448826 FORWARD   Aliases: FERRODOXIN A	10.3	10.6	-0.3	-0.4	100.0%	-4.4
13810	AT1G43690.1   ubiquitin interaction motif-containing protein, contains Pfam profile PF02809: Ubiquitin interaction motif   chr1:16480687-16485277 FORWARD   Aliases: F2J6.5, F2J6_5	7.4	7.5	-0.1	-0.4	100.0%	-4.7
13811	AT5G19020.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:6352773-6357085 REVERSE   Aliases: T16G12.60, T16G12_60	3.7	3.7	-0.1	-0.4	100.0%	-5.2
13812	AT2G46190.1   hypothetical protein   chr2:18978872-18979877 FORWARD   Aliases: T3F17.16	2.4	2.4	0.0	0.4	100.0%	-6.0
13813	AT4G00440.1   expressed protein   chr4:193879-198579 FORWARD   Aliases: A_IG005I10.23, A_IG005I10_23, F5I10.23, F5I10_23	4.2	4.1	0.1	0.4	100.0%	-5.1
13814	AT4G32180.2   similar to eukaryotic pantothenate kinase family protein [Arabidopsis thaliana] (TAIR:At1g60440.1); similar to pantothenate kinase 4 [Homo sapiens] (GB:CAI20410.1); similar to pantothenate kinase 4 variant [Homo sapiens] (GB:BAD97266.1); similar to hypothetical protein [Homo sapiens] (GB:CAC09438.1); contains InterPro domain Eukaryotic pantothenate kinase (InterPro:IPR004567)   chr4:15537565-15543910 REVERSE   Aliases: F10M6.180, F10M6_180	7.4	7.2	0.1	0.4	100.0%	-4.8
13815	AT3G55270.1   Symbol: MKP1   MAP kinase phosphatase (MKP1), identical to MAP kinase phosphatase (MKP1) GI:13540262 from (Arabidopsis thaliana)   chr3:20507136-20510993 FORWARD   Aliases: MAP kinase phosphatase 1, T26I12.150	2.8	2.9	-0.1	-0.4	100.0%	-5.2
13816	AT3G52100.1   PHD finger family protein, contains Pfam profile PF00628: PHD-finger   chr3:19330321-19333751 FORWARD   Aliases: F4F15.210	5.8	6.2	-0.3	-0.4	100.0%	-4.0
13817	AT4G00090.1   transducin family protein / WD-40 repeat family protein, similar to Transducin beta-like 2 protein (WS beta-transducin repeats protein) (WS-betaTRP) (Williams-Beuren syndrome chromosome region 13 protein) (SP:Q9Y4P3) {Homo sapiens}   chr4:34128-36880 FORWARD   Aliases: F6N15.8, F6N15_8	6.8	6.6	0.2	0.4	100.0%	-5.0
13818	AT5G25560.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	7.3	7.1	0.1	0.4	100.0%	-4.9
13819	AT3G50890.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, hypothetical protein T8K22.16 - Arabidopsis thaliana, chromosome II BAC T8K22, PIR2:T00609   chr3:18927147-18928309 FORWARD   Aliases: F18B3.170	3.1	3.2	-0.1	-0.4	100.0%	-5.4
13820	AT4G39550.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr4:18380520-18381899 REVERSE   Aliases: F23K16.180, F23K16_180	5.5	5.6	-0.1	-0.4	100.0%	-5.1
13821	AT5G15240.2   similar to amino acid transporter family protein [Arabidopsis thaliana] (TAIR:At3g28960.1); similar to putative amino acid transport protein [Oryza sativa (japonica cultivar-group)] (GB:BAD37472.1); contains InterPro domain Amino acid/polyamine transporter, family II (InterPro:IPR002422)	3.3	3.4	-0.1	-0.4	100.0%	-5.2
13822	AT5G65620.1   peptidase M3 family protein / thimet oligopeptidase family protein, similar to SP:P27237 Oligopeptidase A (EC 3.4.24.70) {Salmonella typhimurium}; contains Pfam profile PF01432: Peptidase family M3   chr5:26239174-26243549 FORWARD   Aliases: K21L13.14, K21L13_14	10.0	10.2	-0.2	-0.4	100.0%	-4.8
13823	AT1G49320.1   BURP domain-containing protein, similarity to SP:Q08298 Dehydration-responsive protein RD22 precursor {Arabidopsis thaliana}; contains Pfam profile PF03181: BURP domain	3.9	4.0	-0.2	-0.4	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13824	AT4G12730.1   Symbol: FLA2   fasciclin-like arabinogalactan-protein (FLA2), identical to gi_13377778_gb_AAK20858   chr4:7491380-7492873 REVERSE   Aliases: T20K18.80, T20K18_80, fasciclin like arabinogalactan protein 2	6.5	6.2	0.2	0.4	100.0%	-4.4
13825	AT2G23160.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.1	3.0	0.1	0.4	100.0%	-5.3
13826	AT3G46660.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:17200249-17202152 REVERSE   Aliases: F12A12.180	2.6	2.6	0.1	0.4	100.0%	-5.4
13827	AT3G18100.2   Symbol: MYB4R1	3.3	3.5	-0.2	-0.4	100.0%	-5.2
13828	AT1G33870.1   avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}; contains Pfam profile PF04548: AIG1 family   chr1:12301305-12302447 REVERSE   Aliases: T3M13.11, T3M13_11	3.0	2.9	0.1	0.4	100.0%	-5.0
13829	AT1G60450.1   galactinol synthase, putative, similar to galactinol synthase GI:5608497 from (Ajuga reptans); contains Pfam profile: PF01501 glycosyl transferase family 8   chr1:22274891-22276879 REVERSE   Aliases: T13D8.32, T13D8_32	3.0	3.0	0.1	0.4	100.0%	-5.4
13830	AT1G61170.1   expressed protein   chr1:22553303-22554340 FORWARD   Aliases: F11P17.11, F11P17_11	3.8	4.0	-0.1	-0.4	100.0%	-5.0
13831	AT1G31460.1   expressed protein   chr1:11261522-11263345 REVERSE   Aliases: T8E3.13, T8E3_13	5.6	5.5	0.1	0.4	100.0%	-5.0
13832	AT1G55430.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.7	0.1	0.4	100.0%	-5.3
13833	AT3G17780.1   expressed protein   chr3:6086954-6088342 FORWARD   Aliases: MIG5.8	9.3	9.1	0.2	0.4	100.0%	-5.2
13834	AT2G19420.1   expressed protein   chr2:8418783-8420965 FORWARD   Aliases: F27F23.26	2.6	2.6	-0.0	-0.4	100.0%	-5.8
13835	AT5G03620.1   subtilase family protein, contains similarity to subtilisin-type serine endopeptidase XSP1 GI:6708179 from (Arabidopsis thaliana)   chr5:918737-921873 FORWARD   Aliases: F17C15.40, F17C15_40	3.2	3.1	0.1	0.4	100.0%	-5.5
13836	AT4G11440.1   mitochondrial substrate carrier family protein   chr4:6955845-6958548 FORWARD   Aliases: F25E4.60, F25E4_60	3.0	2.9	0.0	0.4	100.0%	-5.6
13837	AT4G33010.1   glycine dehydrogenase (decarboxylating), putative / glycine decarboxylase, putative / glycine cleavage system P-protein, putative, strong similarity to SP:P49361 Glycine dehydrogenase (decarboxylating) A, mitochondrial precursor (EC 1.4.4.2) {Flaveria pringlei}; contains Pfam profile PF02347: Glycine cleavage system P-protein   chr4:15926673-15931335 REVERSE   Aliases: F4I10.7	11.7	11.4	0.3	0.4	100.0%	-5.0
13838	AT1G01420.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:154566-156011 REVERSE   Aliases: F6F3.22, F6F3_22	3.4	3.3	0.1	0.4	100.0%	-5.1
13839	AT1G58370.1   Symbol: RXF12   glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein, similar to (1,4)-beta-xylan endohydrolase GI:5306060 from (Triticum aestivum) ; contains Pfam profiles PF00331: Glycosyl hydrolase family 10, PF02018: Carbohydrate binding domain   chr1:21688399-21691986 FORWARD   Aliases: F9K23.10, RXF12	4.0	4.2	-0.2	-0.4	100.0%	-4.4
13840	AT3G14320.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:4777738-4778352 REVERSE   Aliases: MLN21.11	2.3	2.2	0.0	0.4	100.0%	-5.6
13841	AT1G57790.1   F-box family protein, contains Pfam PF00646: F-box domain   chr1:21408073-21409621 REVERSE   Aliases: F12K22.16, F12K22_16	3.0	2.9	0.1	0.4	100.0%	-5.5
13842	AT2G36250.2   Symbol: FTSZ2 1   chloroplast division protein FtsZ (FtsZ2-1), identical to chloroplast division protein AtFtsZ2-1 (Arabidopsis thaliana) GI:15636809, plastid division protein FtsZ (Arabidopsis thaliana) GI:14195704	7.7	7.9	-0.2	-0.4	100.0%	-4.4
13843	AT3G10400.1   RNA recognition motif (RRM)-containing protein, low similarity to splicing factor SC35 (Arabidopsis thaliana) GI:9843653; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:3232613-3233690 FORWARD   Aliases: F13M14.33	4.0	3.9	0.1	0.4	100.0%	-5.0
13844	AT4G17130.1   expressed protein   chr4:9624275-9627621 REVERSE   Aliases: DL4600C, FCAALL.361	3.8	4.1	-0.3	-0.4	100.0%	-4.6
13845	AT2G21270.2   similar to ubiquitin fusion degradation UFD1 family protein [Arabidopsis thaliana] (TAIR:At4g38930.2); similar to putative ubiquitin fusion degradation protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464339.1); contains InterPro domain Ubiquitin fusion degradation protein UFD1 (InterPro:IPR004854)   chr2:9114700-9117342 FORWARD   Aliases: F3K23.3, F3K23_3	7.9	8.1	-0.2	-0.4	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13846	AT3G57660.1   Symbol: NRPA1   DNA-directed RNA polymerase family protein, similar to SP:O35134 DNA-directed RNA polymerase I largest subunit (EC 2.7.7.6) (RNA polymerase I 194 kDa subunit) (RPA194) {Mus musculus}; contains InterPro accession IPR000722: RNA polymerase, alpha subunit   chr3:21364723-21373791 FORWARD   Aliases: F15B8.150	3.4	3.5	-0.1	-0.4	100.0%	-5.3
13847	AT2G31880.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:13561973-13564054 FORWARD   Aliases: F20M17.8, F20M17_8	5.1	4.9	0.2	0.4	100.0%	-4.6
13848	AT3G46380.1   expressed protein   chr3:17070203-17070881 REVERSE   Aliases: F18L15.100	5.2	4.9	0.3	0.4	100.0%	-4.5
13849	ATMG00580.1   Symbol: NAD4   NADH dehydrogenase subunit 4   chrM:161693-169674 FORWARD   Aliases: NAD4	6.6	6.9	-0.3	-0.4	100.0%	-4.2
13850	AT2G21610.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:9252241-9254105 REVERSE   Aliases: F2G1.12, F2G1_12	2.8	2.9	-0.1	-0.4	100.0%	-5.4
13851	AT1G28460.1   MADS-box family protein, contains similarity to MADS-box transcription factor Gl:6580947 from (Picea abies)   chr1:10006216-10006764 FORWARD   Aliases: F3M18.10, F3M18_10	2.9	3.0	-0.1	-0.4	100.0%	-4.9
13852	AT5G28550.1   hypothetical protein   chr5:10557726-10559783 REVERSE   Aliases: T10I18.10, T10I18_10	2.8	2.9	-0.1	-0.4	100.0%	-5.1
13853	AT1G33040.1   nascent polypeptide-associated complex (NAC) domain-containing protein, similar to alpha-NAC, non-muscle form (Mus musculus) Gl:1666690; contains Pfam profile PF01849: NAC domain   chr1:11966479-11967823 FORWARD   Aliases: F9L11.19, F9L11_19	10.5	10.8	-0.3	-0.4	100.0%	-4.7
13854	AT2G37000.1   TCP family transcription factor, putative, similar to TFPD (Gl:6681577) (Arabidopsis thaliana)   chr2:15547469-15548227 FORWARD   Aliases: T1J8.18, T1J8_18	2.4	2.3	0.0	0.4	100.0%	-5.6
13855	NA	2.5	2.5	0.1	0.4	100.0%	-5.7
13856	AT5G10720.1   Symbol: AHK5   sensory transduction histidine kinase-related, similar to Sensor protein rcsC (Capsular synthesis regulator component C) (SP:Q56128) {Salmonella typhi}; sensory transduction histidine kinase slr1759, Synechocystis sp., PIR:S75142   chr5:3386848-3390542 FORWARD   Aliases: CKI2, MAJ23.80, MAJ23_80	4.5	4.5	-0.1	-0.4	100.0%	-5.4
13857	AT1G66470.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.8	2.7	0.1	0.4	100.0%	-5.3
13858	AT4G25680.1   expressed protein   chr4:13088249-13090170 FORWARD   Aliases: L73G19.60, L73G19_60	6.9	6.6	0.3	0.4	100.0%	-4.7
13859	AT4G28700.1   ammonium transporter, putative, similar to SP:O04161 Ammonium transporter 1, member 2 (LeAMT1;2) {Lycopersicon esculentum}; contains Pfam profile PF00909: Ammonium Transporter Family   chr4:14161687-14163201 FORWARD   Aliases: F16A16.190, F16A16_190	5.1	5.0	0.1	0.4	100.0%	-5.0
13860	AT5G20840.1   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248;gb:AAG29810; contains Pfam domain, PF02383: SacI homology domain; identical to cDNA SAC domain protein 4 (SAC4) Gl:31415724   chr5:7061105-7069221 REVERSE   Aliases: F22D1.10, F22D1_10	4.6	4.5	0.1	0.4	100.0%	-4.9
13861	AT1G72870.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27424739-27426761 FORWARD   Aliases: F3N23.7, F3N23_7	3.0	2.9	0.1	0.4	100.0%	-5.0
13862	AT3G27580.2   Symbol: ATPK7   similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At5g47750.1); similar to protein kinase C (EC 2.7.1.-) homolog - kidney bean (GB:A30311); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:10218664-10221213 REVERSE   Aliases: MMJ24.13	2.8	2.7	0.2	0.4	100.0%	-4.4
13863	AT1G79600.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr1:29954839-29957583 REVERSE   Aliases: F20B17.3, F20B17_3	6.0	6.1	-0.1	-0.4	100.0%	-4.8
13864	AT5G47650.1   MutT/nudix family protein, similar to Nucleoside diphosphate-linked moiety X motif 6 (Protein GFG) from {Xenopus laevis} SP:P13420, {Homo sapiens} SP:P53370; contains Pfam profile PF00293: NUDIX domain   chr5:19326453-19329653 REVERSE   Aliases: MNJ7.24, MNJ7_24	6.0	6.2	-0.2	-0.4	100.0%	-4.5
13865	AT1G22830.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat. Gene continues on the 3' end of BAC F19G10 gb:AF000657 gene F19G10.21   chr1:8076910-8079021 FORWARD   Aliases: T2J18.1	3.2	3.3	-0.1	-0.4	100.0%	-5.0
13866	AT3G02060.1   DEAD/DEAH box helicase, putative, similar to C-terminal half of transcription-repair coupling factor (TRCF) GB:Q55750 (Synechocystis PCC6803); contains Pfam profile: helicases conserved C-terminal domain   chr3:354367-358812 FORWARD   Aliases: F1C9.16, F1C9_16	3.7	3.6	0.1	0.4	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13867	AT3G22950.1   Symbol: ATARFC1   Gene encoding ADP-ribosylation factor and similar to ADP-ribosylation factor GB:P91924 ( <i>Dugesia japonica</i> ), other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding.	8.6	8.4	0.2	0.4	100.0%	-4.8
13868	AT1G69370.1   Symbol: CM3   chorismate mutase, putative, similar to gi:5732016 and SP:P42738; contains Pfam profile: PF01817: Chorismate mutase   chr1:26083619-26085390 FORWARD   Aliases: CHORISMATE MUTASE 3, CM 3, CM3, F10D13.6, F10D13_6	7.4	7.6	-0.2	-0.4	100.0%	-4.4
13869	AT4G19570.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QYI4 DnaJ homolog subfamily B member 12 { <i>Mus musculus</i> }; contains Pfam profile PF00226: DnaJ domain   chr4:10665304-10667328 FORWARD   Aliases: F24J7.130, F24J7_130	3.3	3.4	-0.1	-0.4	100.0%	-5.3
13870	AT5G58770.1   dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076   chr5:23751602-23752860 FORWARD   Aliases: MZN1.21, MZN1_21	2.5	2.7	-0.2	-0.4	100.0%	-4.1
13871	AT3G46740.1   Symbol: TOC75   chloroplast outer envelope protein, putative, similar to chloroplastic outer envelope membrane protein (OEP75) ( <i>Pisum sativum</i> ) GI:633607; contains Pfam profile PF01103: outer membrane protein, OMP85 family   chr3:17226798-17230328 REVERSE   Aliases: T6H20.230, TOC75 III	6.8	6.6	0.2	0.4	100.0%	-4.8
13872	AT4G16750.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr4:9421143-9421682 REVERSE   Aliases: DL4400C, FCAALL.19	2.9	2.8	0.1	0.4	100.0%	-5.1
13873	AT3G12420.1   expressed protein   chr3:3947927-3948889 REVERSE   Aliases: T2E22.26	2.1	2.2	-0.1	-0.4	100.0%	-5.6
13874	AT1G65910.1   Symbol: ANAC028   no apical meristem (NAM) family protein, similar to jasmonic acid 2 GI:6175246 from ( <i>Lycopersicon esculentum</i> ); similar to NAC2 (GI:6456751) { <i>Arabidopsis thaliana</i> }   chr1:24524454-24527827 REVERSE   Aliases: ANAC028, F12P19.8, F12P19_8	2.7	2.6	0.1	0.4	100.0%	-5.5
13875	AT2G19480.1   nucleosome assembly protein (NAP), putative, similar to nucleosome assembly protein 1 ( <i>Glycine max</i> ) GI:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP)	8.0	8.2	-0.2	-0.4	100.0%	-5.1
13876	AT2G26940.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:11503596-11504456 REVERSE   Aliases: F12C20.2, F12C20_2	2.4	2.5	-0.1	-0.4	100.0%	-5.4
13877	AT5G49510.2   similar to unnamed protein product [ <i>Mus musculus</i> ] (GB:BAC37066.1); similar to PREDICTED: similar to von Hippel-Lindau binding protein 1 [ <i>Canis familiaris</i> ] (GB:XP_538210.1); similar to PFD3_MOUSE Prefoldin subunit 3 (Von Hippel-Lindau binding protein 1) (VHL binding protein-1) (VBP-1) (GB:P61759); similar to von Hippel-Lindau binding protein 1 [ <i>Homo sapiens</i> ] (GB:AAV38411.1); similar to von Hippel-Lindau binding protein 1 [synthetic construct] (GB:AAV38448.1); contains InterPro domain Putative prefoldin chaperone (InterPro:IPR004127)   chr5:20097841-20100147 FORWARD   Aliases: K6M13.5, K6M13_5	8.9	8.7	0.1	0.4	100.0%	-4.7
13878	AT1G66390.1   Symbol: PAP2   myb family transcription factor, putative / production of anthocyanin pigment 2 protein (PAP2), contains Pfam profile: PF00249 myb-like DNA-binding domain; similar to GB:AAF66727 from ( <i>Petunia x hybrida</i> ) (Plant Cell 11 (8), 1433-1444 (1999)); identical to cDNA production of anthocyanin pigment 2 protein (PAP2) GI:11935172   chr1:24767620-24769203 FORWARD   Aliases: MYB90, PRODUCTION OF ANTHOCYANIN PIGMENT 2, T27F4.14, T27F4_14	3.0	2.9	0.1	0.4	100.0%	-4.9
13879	AT4G25370.1   Clp amino terminal domain-containing protein, contains Pfam profile: PF02861 Clp amino terminal domain   chr4:12972718-12974880 FORWARD   Aliases: T30C3.40, T30C3_40	7.0	7.1	-0.1	-0.4	100.0%	-5.1
13880	AT1G48870.1   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP:Q9UGP9) ( <i>Homo sapiens</i> ); similar to rab11 binding protein GI:4512103 from ( <i>Bos taurus</i> )   chr1:18075993-18078125 REVERSE   Aliases: T24P22.7	3.8	3.7	0.1	0.4	100.0%	-4.9
13881	AT1G23310.2   Symbol: GGT1   similar to glutamate:glyoxylate aminotransferase 2 (GGT2) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g70580.1); similar to glutamate:glyoxylate aminotransferase 2 (GGT2) [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g70580.2); similar to alanine aminotransferase [ <i>Oryza sativa</i> (indica cultivar-group)] (GB:AAO84040.1); contains InterPro domain 1-aminocyclopropane-1-carboxylate synthase (InterPro:IPR001176)   chr1:8268393-8271922 REVERSE   Aliases: ALANINE 2 OXOGLUTARATE AMINOTRANSFERASE 1, AOAT1, F26F24.16, F26F24_16, GLUTAMATE:GLYOXYLATE AMINOTRANSFERASE	10.3	10.4	-0.1	-0.4	100.0%	-4.9
13882	AT2G14250.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:6044056-6045463 FORWARD   Aliases: T1016.16, T1016_16	3.2	3.1	0.1	0.4	100.0%	-4.6
13883	AT2G33670.1   Symbol: MLO5   seven transmembrane MLO family protein / MLO-like protein 5 (MLO5), identical to MLO-like protein 5 (AtMlo5) ( <i>Arabidopsis thaliana</i> ) SWISS-PROT:O22815; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 ( <i>Hordeum vulgare</i> )(Barley)   chr2:14252106-14255007 FORWARD   Aliases: F4P9.44, F4P9_44	2.7	2.8	-0.1	-0.4	100.0%	-5.4
13884	AT3G62780.1   C2 domain-containing protein, contains similarity to shock protein SRC2 ( <i>Glycine max</i> ) gi:2055230:dbj:BAA19769 ; contains Pfam profile PF00168:C2 domain   chr3:23233004-23233916 REVERSE   Aliases: F26K9.210	2.6	2.5	0.1	0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13885	AT2G27480.1   similar to calcium-binding EF hand family protein [Arabidopsis thaliana] (TAIR:At5g04170.1); similar to fiber protein Fb1 [Gossypium barbadense] (GB:AAN77144.1); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048)   chr2:11753798-11755551 FORWARD   Aliases: F10A12.16, F10A12_16	3.9	4.1	-0.1	-0.4	100.0%	-4.6
13886	AT4G34215.2   expressed protein   chr4:16379607-16381230 REVERSE   Aliases: None	5.2	5.3	-0.1	-0.4	100.0%	-4.8
13887	AT2G39800.2   Symbol: P5CS1   delta 1-pyrroline-5-carboxylate synthetase A / P5CS A (P5CS1), identical to SP:P54887:P5C1_ARATH   chr2:16605245-16610137 REVERSE   Aliases: DELTA1 PYRROLINE 5 CARBOXYLATE SYNTHASE 1, T5I7.10, T5I7_10	3.7	3.9	-0.2	-0.4	100.0%	-4.6
13888	AT3G55610.1   delta 1-pyrroline-5-carboxylate synthetase B / P5CS B (P5CS2), identical to SP:P54888   chr3:20635001-20640072 REVERSE   Aliases: F1I16.20	3.7	3.9	-0.2	-0.4	100.0%	-4.6
13889	AT1G65580.1   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase II isoform (GI:15418718) (Mus musculus); contains 6 (5 weak) Pfam: Pf00400 WD domain, G-beta repeats and Pfam PF03372: Endonuclease/Exonuclease/phosphatase family   chr1:24380977-24387742 REVERSE   Aliases: F5I14.11, F5I14_11	8.7	8.6	0.1	0.4	100.0%	-5.1
13890	AT2G14095.1   expressed protein   chr2:5939477-5940873 REVERSE   Aliases: None	3.6	3.5	0.2	0.4	100.0%	-4.5
13891	AT2G02520.1   expressed protein   chr2:676770-678144 REVERSE   Aliases: T8K22.18, T8K22_18	2.2	2.2	-0.0	-0.4	100.0%	-5.7
13892	AT5G63490.1   CBS domain-containing protein / octicosapeptide/Phox/Bemp1 (PB1) domain-containing protein, contains Pfam profiles: PF00571 CBS domain, PF00564: PB1 domain   chr5:25435820-25439410 REVERSE   Aliases: MLE2.12, MLE2_12	6.6	6.5	0.1	0.4	100.0%	-4.9
13893	AT3G57450.1   expressed protein   chr3:21272911-21273599 FORWARD   Aliases: T8H10.50	11.0	10.8	0.2	0.4	100.0%	-5.1
13894	AT1G49200.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:18201895-18202836 FORWARD   Aliases: F27J15.33	3.3	3.4	-0.1	-0.4	100.0%	-5.0
13895	AT1G44930.1   expressed protein   chr1:16987550-16988109 FORWARD   Aliases: T12C22.25, T12C22_25	5.0	4.7	0.2	0.4	100.0%	-4.7
13896	AT5G13640.1   Symbol: ATPDAT	6.8	6.9	-0.1	-0.4	100.0%	-5.1
13897	AT1G17750.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor-like protein kinase INRPK1 GI:1684913 from (Ipomoea nil)	3.6	3.7	-0.1	-0.4	100.0%	-5.2
13898	AT1G34260.1   phosphatidylinositol-4-phosphate 5-kinase family protein, low similarity to SP:Q9Z1T6 FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) {Mus musculus}; contains Pfam profile PF01504: Phosphatidylinositol-4-phosphate 5-Kinase   chr1:12485945-12492126 FORWARD   Aliases: F23M19.8, F23M19_8	4.8	4.9	-0.1	-0.4	100.0%	-4.6
13899	AT1G24560.1   expressed protein   chr1:8702372-8705835 FORWARD   Aliases: F21J9.22	7.9	8.1	-0.1	-0.4	100.0%	-4.5
13900	AT1G07320.4   Symbol: RPL4   similar to ribosomal protein L4 family protein [Arabidopsis thaliana] (TAIR:At2g20060.1); similar to ribosomal protein L4 [Spinacia oleracea] (GB:CAA63651.1); contains InterPro domain Ribosomal protein L4/L1e (InterPro:IPR002136)   chr1:2249133-2250490 FORWARD   Aliases: F22G5.34, F22G5_34, RIBOSOMAL PROTEIN L4	7.1	7.2	-0.1	-0.4	100.0%	-4.4
13901	AT4G17050.1   expressed protein   chr4:9589601-9592606 FORWARD   Aliases: DL4555W, FCAALL.343	5.5	5.2	0.4	0.4	100.0%	-4.3
13902	AT4G22400.1   expressed protein   chr4:11816841-11817824 FORWARD   Aliases: F7K2.5, F7K2_5	2.7	2.8	-0.1	-0.4	100.0%	-5.3
13903	AT5G37710.1   lipase class 3 family protein / calmodulin-binding heat-shock protein, putative, similar to almodulin-binding heat-shock protein, common tobacco, PIR:T04107; contains Pfam profiles PF03893: Lipase 3 N-terminal region, PF01764: Lipase	4.4	4.2	0.3	0.4	100.0%	-4.4
13904	AT1G19950.1   abscisic acid-responsive HVA22 family protein, weak similarity to SP:Q00765 Polyposis locus protein 1 (TB2 protein) {Homo sapiens}; contains Pfam profile PF03134: TB2/DP1, HVA22 family	3.0	3.1	-0.1	-0.4	100.0%	-5.2
13905	AT3G32140.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr3:13141934-13142722 REVERSE   Aliases: F1M23.25	2.8	2.9	-0.0	-0.4	100.0%	-5.4
13906	AT5G14730.1   expressed protein   chr5:4756221-4757660 FORWARD   Aliases: T9L3.30, T9L3_30	3.7	3.5	0.1	0.4	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13907	AT1G55390.1   DC1 domain-containing protein, similar to hypothetical protein GI:4204272 from (Arabidopsis thaliana) contains weak PHD zinc finger motifs contains weak PHD zinc finger motifs DC1 domain, a divergent protein kinase C domain of unknown function.   chr1:20684542-20686709 REVERSE   Aliases: T18I3.3, T18I3_3	3.1	3.0	0.1	0.4	100.0%	-5.0
13908	AT1G10050.1   glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein, similar to GB:AAD27896 to endoxylanases gi:1255238 (Thermoanaerobacterium thermosulfurigenes), gi:1813595 (Hordeum vulgare) and others ; contains Pfam profiles PF00331: Glycosyl hydrolase family 10, PF02018: Carbohydrate binding domain   chr1:3279272-3283484 FORWARD   Aliases: T27I1.7, T27I1_7	4.5	4.4	0.1	0.4	100.0%	-5.0
13909	AT1G29780.1   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr1:10426935-10427600 FORWARD   Aliases: F1N18.16, F1N18_16	2.3	2.3	-0.0	-0.4	100.0%	-5.8
13910	AT1G67310.1   similar to calmodulin-binding protein [Arabidopsis thaliana] (TAIR:At5g64220.1); similar to calmodulin-binding transcription activator [Brassica napus] (GB:AAM10969.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048); contains InterPro domain CG-1 domain (InterPro:IPR005559); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr1:25201845-25206789 REVERSE   Aliases: F1N21.13	4.8	5.0	-0.2	-0.4	100.0%	-4.8
13911	AT4G02300.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:1009366-1013034 REVERSE   Aliases: T2H3.6, T2H3_6	2.8	2.8	0.1	0.4	100.0%	-5.4
13912	AT3G28670.1   expressed protein   chr3:10745060-10748400 FORWARD   Aliases: MZN14.14	7.1	7.2	-0.1	-0.4	100.0%	-4.8
13913	AT3G45630.1   RNA recognition motif (RRM)-containing protein, similar to SP:P34909 General negative regulator of transcription subunit 4 {Saccharomyces cerevisiae}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	4.3	4.2	0.1	0.4	100.0%	-5.2
13914	AT5G42680.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr5:17131824-17132640 FORWARD   Aliases: MJB21.5, MJB21_5	6.4	6.3	0.2	0.4	100.0%	-4.4
13915	AT5G49070.1   beta-ketoacyl-CoA synthase family protein, similar to very-long-chain fatty acid condensing enzyme CUT1 (GI:5001734), beta-ketoacyl-CoA synthase (Simmondsia chinensis)(GI:1045614)   chr5:19905977-19907371 REVERSE   Aliases: K20J1.4, K20J1_4	2.4	2.3	0.0	0.4	100.0%	-5.8
13916	AT5G65500.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr5:26198319-26201223 REVERSE   Aliases: K19O4.3, K19O4_3	3.2	3.3	-0.1	-0.4	100.0%	-5.4
13917	AT3G32120.1   hypothetical protein   chr3:13128179-13129029 FORWARD   Aliases: F1M23.21	3.0	2.8	0.1	0.4	100.0%	-5.0
13918	AT2G37270.2   Symbol: ATRPS5B   similar to 40S ribosomal protein S5 (RPS5B) [Arabidopsis thaliana] (TAIR:At3g11940.1); similar to 40S ribosomal protein S5 (RPS5B) [Arabidopsis thaliana] (TAIR:At3g11940.2); similar to putative 40S ribosomal protein S5 [Oryza sativa (japonica cultivar-group)] (GB:NP_908322.1); contains InterPro domain Ribosomal protein S7, eukaryotic and archaeal form (InterPro:IPR005716); contains InterPro domain Ribosomal protein S7 (InterPro:IPR000235)   chr2:15654756-15656282 REVERSE   Aliases: F3G5.6, F3G5_6, RIBOSOMAL PROTEIN 5B	13.3	13.4	-0.1	-0.4	100.0%	-5.3
13919	AT3G11940.2   Symbol: ATRPS5A   40S ribosomal protein S5 (RPS5B), similar to 40S ribosomal protein S5 GB:AAC98068 GI:4056502 from (Arabidopsis thaliana)   chr3:3777901-3779509 REVERSE   Aliases: AML1, ARABIDOPSIS MINUTE LIKE 1, MEC18.11, RIBOSOMAL PROTEIN 5A	13.3	13.4	-0.1	-0.4	100.0%	-5.3
13920	AT5G42230.1   Symbol: SCPL41	2.9	2.9	-0.1	-0.4	100.0%	-5.4
13921	AT4G23600.3   Symbol: CORI3   similar to aminotransferase class I and II family protein [Arabidopsis thaliana] (TAIR:At4g23590.1); similar to putative nicotianamine aminotransferase A [Oryza sativa (japonica cultivar-group)] (GB:XP_465128.1); contains InterPro domain Tyrosine/nicotianamine aminotransferases (InterPro:IPR005958); contains InterPro domain 1-aminocyclopropane-1-carboxylate synthase (InterPro:IPR001176)   chr4:12311265-12313222 FORWARD   Aliases: CORONATINE INDUCED 1, F9D16.70, F9D16_70, JASMONIC ACID RESPONSIVE 2	1.9	1.9	0.0	0.4	100.0%	-6.3
13922	AT2G35670.1   Symbol: FIS2   transcription factor, putative / fertilization-independent seed 2 protein (FIS2), identical to GB:AF096095   chr2:15000348-15004466 FORWARD   Aliases: FERTILIZATION INDEPENDENT SEED 2, FERTILIZATION INDEPENDENT SEED 2 PROTEIN, FIE2, T20F21.14, T20F21_14	2.4	2.3	0.1	0.4	100.0%	-5.5
13923	AT5G55210.1   expressed protein, similar to unknown protein (pir::T04913)   chr5:22413756-22414614 REVERSE   Aliases: MCO15.16, MCO15_16	4.4	4.5	-0.1	-0.4	100.0%	-4.7
13924	AT1G61440.1   S-locus protein kinase, putative, contains similarity to receptor protein kinase (Ipomoea trifida) gi:836954:gb:AAC23542; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22672910-22675988 REVERSE   Aliases: T1F9.7, T1F9_7	3.1	3.2	-0.1	-0.4	100.0%	-5.2
13925	AT1G29460.1   auxin-responsive protein, putative, similar to auxin-induced protein 6B (SP:P33083) (Glycine max)   chr1:10307493-10308129 REVERSE   Aliases: F15D2.35, F15D2_35	2.8	2.8	0.0	0.4	100.0%	-5.8
13926	AT1G10430.1   Symbol: PP2A 2	5.6	5.5	0.1	0.4	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13927	AT5G02650.1   expressed protein   chr5:598774-599784 FORWARD   Aliases: T22P11.240, T22P11_240	4.4	4.3	0.1	0.4	100.0%	-4.8
13928	AT2G42960.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:17875674-17877707 REVERSE   Aliases: F7D19.4, F7D19_4	3.1	3.2	-0.1	-0.4	100.0%	-5.2
13929	AT1G73740.1   glycosyl transferase family 28 protein, similar to UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)-pyrophosphoryl-undecaprenol N-acetylglucosamine transferase GB:O07670 (SP:O07670) from Enterococcus hirae, )SP:O07109) from Enterococcus faecalis; contains Pfam profile PF04101: Glycosyltransferase family 28 C-terminal domain   chr1:27737940-27739844 FORWARD   Aliases: F25P22.16, F25P22_16	5.7	5.8	-0.1	-0.4	100.0%	-4.9
13930	AT2G18100.1   expressed protein   chr2:7874910-7878724 FORWARD   Aliases: T27K22.3, T27K22_3	4.6	4.5	0.1	0.4	100.0%	-4.8
13931	AT3G61350.1   Symbol: SKIP4   SKP1 interacting partner 4 (SKIP4), almost identical to SKP1 interacting partner 4 GI:10716953 from (Arabidopsis thaliana), 42 aa extension at N-terminal; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr3:22713661-22717114 FORWARD   Aliases: SKP1 INTERACTING PARTNER 4, T20K12.250	5.7	5.5	0.2	0.4	100.0%	-4.9
13932	AT2G36060.2   ubiquitin-conjugating enzyme family protein, similar to DNA-binding protein CROC-1B (Homo sapiens) GI:1066082; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr2:15149876-15151261 REVERSE   Aliases: F11F19.3, F11F19_3	11.4	11.3	0.1	0.4	100.0%	-5.3
13933	AT1G02816.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr1:621461-622469 FORWARD   Aliases: None	6.4	6.6	-0.2	-0.4	100.0%	-4.6
13934	AT5G56290.1   Symbol: PEX5   peroxisomal targeting signal type 1 receptor (PEX5), identical to GI:3603353; contains Pfam profile PF00515 TPR Domain   chr5:22803755-22809345 FORWARD   Aliases: MXK23.3, MXK23_3	9.0	8.8	0.2	0.4	100.0%	-4.7
13935	AT1G03530.1   expressed protein, similar to hypothetical protein GB:O14360   chr1:880497-883391 REVERSE   Aliases: F21B7.15	4.7	4.6	0.2	0.4	100.0%	-4.6
13936	AT1G68220.1   expressed protein   chr1:25573894-25575375 FORWARD   Aliases: T22E19.15, T22E19_15	9.3	9.2	0.1	0.4	100.0%	-5.2
13937	AT2G20380.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr2:8801899-8803061 REVERSE   Aliases: F11A3.7, F11A3_7	3.3	3.3	0.1	0.4	100.0%	-5.2
13938	AT2G38120.1   Symbol: AUX1   amino acid permease, putative (AUX1), identical to AUX1 GI:1531758 from (Arabidopsis thaliana)   chr2:15980071-15984258 FORWARD   Aliases: AUX1, AUXIN RESISTANT 1, AUXIN HERBICIDE RESISTANT, F16M14.5, F16M14_5, MAP1, MODIFIER OF ARF7/NPH4 PHENOTYPES 1, PIR1, WAV5, WAVY ROOTS 5	5.9	6.0	-0.2	-0.4	100.0%	-4.9
13939	AT2G22260.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr2:9468205-9470264 FORWARD   Aliases: T26C19.8, T26C19_8	4.7	4.6	0.1	0.4	100.0%	-4.5
13940	AT3G48910.1   expressed protein   chr3:18146073-18147324 FORWARD   Aliases: T2J13.250	3.0	2.9	0.1	0.4	100.0%	-5.2
13941	AT4G24760.1   expressed protein   chr4:12761293-12763791 REVERSE   Aliases: F22K18.40, F22K18_40	5.4	5.5	-0.2	-0.4	100.0%	-4.7
13942	AT5G62830.1   F-box family protein-related, similar to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana); contains TIGRFAM TIGR01640 : F-box protein interaction domain   chr5:25243394-25244008 REVERSE   Aliases: MQB2.15, MQB2_15	3.1	3.0	0.1	0.4	100.0%	-5.2
13943	AT5G01075.1   expressed protein   chr5:26881-27448 REVERSE   Aliases: None	2.2	2.2	-0.0	-0.4	100.0%	-5.9
13944	AT1G09000.1   Symbol: ANP1   NPK1-related protein kinase, putative (ANP1), similar to protein kinase (Nicotiana tabacum) gi:456309:dbj:BAA05648; identical to cDNA NPK1-related protein kinase 1S GI:2342422   chr1:2891040-2895777 FORWARD   Aliases: F7G19.13, F7G19_13, MAPKKK1, NPK1 RELATED PROTEIN KINASE 1S	3.3	3.4	-0.1	-0.4	100.0%	-5.3
13945	AT2G39240.1   RNA polymerase I specific transcription initiation factor RRN3 family protein, contains Pfam profile PF05327: RNA polymerase I specific transcription initiation factor RRN3   chr2:16391864-16394905 REVERSE   Aliases: T16B24.12, T16B24_12	2.3	2.3	0.0	0.4	100.0%	-5.6
13946	AT1G47260.1   Symbol: APFI   bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)   chr1:17323048-17325924 REVERSE   Aliases: F8G22.2, F8G22_2	10.2	10.3	-0.1	-0.4	100.0%	-4.8
13947	AT5G38300.1   expressed protein, predicted protein, rice   chr5:15323162-15324238 FORWARD   Aliases: MSI17.3, MSI17_3	5.8	5.7	0.1	0.4	100.0%	-4.9
13948	AT3G05720.1   importin alpha-1 subunit, putative, similar to importin alpha subunit (Karyopherin alpha subunit) (KAP alpha) SP:O22478 from (Lycopersicon esculentum)   chr3:1687998-1691742 REVERSE   Aliases: F18C1.1, F18C1_1	2.4	2.4	-0.1	-0.4	100.0%	-5.7
13949	AT5G41600.1   reticulon family protein (RTNLB4), weak similarity to Nogo-C protein (Rattus norvegicus) GI:6822251, SP:O95197 Reticulon protein 3 (Neuroendocrine-specific protein-like) {Homo sapiens}; contains Pfam profile PF02453: Reticulon   chr5:16653358-16654921 FORWARD   Aliases: MBK23.13, MBK23_13	9.0	8.6	0.4	0.4	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13950	AT5G14330.1   expressed protein   chr5:4619800-4620554 REVERSE   Aliases: F18O22.120, F18O22_120	3.0	3.3	-0.3	-0.4	100.0%	-3.8
13951	AT3G10090.1   40S ribosomal protein S28 (RPS28A), similar to ribosomal protein S28 GB:P34789 (Arabidopsis thaliana)   chr3:3108815-3110022 REVERSE   Aliases: T22K18.8	10.6	10.9	-0.2	-0.4	100.0%	-5.1
13952	AT5G61550.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain; protein kinase 1, PnPK1, Populus nigra, EMBL:AB041503   chr5:24765328-24768980 FORWARD   Aliases: K11J9.12, K11J9_12	2.6	2.5	0.1	0.4	100.0%	-5.1
13953	AT2G32720.1   Symbol: B5 #4   cytochrome b5, putative, similar to Cytochrome B5 SP:P49098 from (Nicotiana tabacum)   chr2:13883887-13885566 REVERSE   Aliases: F24L7.14, F24L7_14	8.0	8.2	-0.2	-0.4	100.0%	-4.9
13954	AT3G61970.1   DNA-binding protein, putative, similar to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857 and RAV2 GI:3868859, AP2 domain containing protein RAP2.8 (Arabidopsis thaliana) GI:2281641; contains Pfam profile PF02362: B3 DNA binding domain   chr3:22962438-22963826 FORWARD   Aliases: F21F14.140	4.3	4.4	-0.1	-0.4	100.0%	-5.2
13955	AT3G12000.1   S-locus related protein SLR1, putative (S1), identical to S-locus related protein SLR1 homolog (AtS1) GI:246209 Arabidopsis thaliana); contains Pfam profiles PF01453: Lectin (probable mannose binding), PF00954: S-locus glycoprotein family   chr3:3818268-3819626 REVERSE   Aliases: MEC18.8	3.1	3.1	0.1	0.4	100.0%	-5.4
13956	AT1G72540.1   protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821; similar to serine/threonine protein kinase gi:1066501:gb:AAA81538   chr1:27318594-27320331 REVERSE   Aliases: F28P22.27, F28P22_27	4.2	4.3	-0.1	-0.4	100.0%	-5.1
13957	AT4G08710.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr4:5567739-5570569 FORWARD   Aliases: T32A17.20, T32A17_20	3.7	3.6	0.1	0.4	100.0%	-5.2
13958	AT4G20400.2   similar to transcription factor jumonji (jmi) family protein / zinc finger (C5HC2 type) family protein [Arabidopsis thaliana] (TAIR:At2g34880.1); similar to transcription factor jumonji (jmi) family protein / zinc finger (C5HC2 type) family protein [Arabidopsis thaliana] (TAIR:At1g30810.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG03900.1); contains InterPro domain Transcription factor jumonji, JmjN (InterPro:IPR003349); contains InterPro domain Zn-finger, C5HC2 type (InterPro:IPR004198); contains InterPro domain FY-rich domain, C-terminal (InterPro:IPR003889); contains InterPro domain FY-rich domain, N-terminal (InterPro:IPR003888); contains InterPro domain Transcription factor jumonji, jmiC (InterPro:IPR003347)   chr4:11009704-11013871 FORWARD   Aliases: F9F13.50, F9F13_50	4.5	4.6	-0.1	-0.4	100.0%	-5.5
13959	AT1G51840.1   protein kinase-related, contains similarity to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376   chr1:19253118-19253819 REVERSE   Aliases: T14L22.5, T14L22_5	2.5	2.5	-0.1	-0.4	100.0%	-5.7
13960	AT1G20190.1   Symbol: ATEXPA11   expansin, putative (EXP11), similar to GB:U30460 from (Cucumis sativus); alpha-expansin gene family, PMID:11641069   chr1:6998480-6999742 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A11, ATEXP11, ATHEXP ALPHA 1.14, EXP11, T20H2.4, T20H2_4	3.9	3.7	0.1	0.4	100.0%	-4.9
13961	AT4G30360.1   Symbol: ATCNGC17   cyclic nucleotide-regulated ion channel, putative (CNGC17), similar to cyclic nucleotide and calmodulin-regulated ion channel cngc5 GI:4581205 from (Arabidopsis thaliana)   chr4:14854820-14858001 REVERSE   Aliases: CNGC17, F17I23.300, F17I23_300	4.5	4.4	0.1	0.4	100.0%	-4.9
13962	AT5G48830.1   expressed protein   chr5:19817340-19820241 REVERSE   Aliases: K24G6.16, K24G6_16	4.0	3.9	0.1	0.4	100.0%	-5.0
13963	AT3G10140.1   recA family protein, contains Pfam profile: PF00154 recA bacterial DNA recombination protein   chr3:3134910-3137422 FORWARD   Aliases: T22K18.3	4.6	4.5	0.1	0.4	100.0%	-4.9
13964	AT5G23970.1   transferase family protein, similar to acetyl CoA: benzylalcohol acetyltransferase; BEAT (Clarkia breweri)(GI:3170250)(PMID:9628024), deacetylindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034)   chr5:8096293-8097657 FORWARD   Aliases: MZF18.15, MZF18_15	2.8	2.7	0.1	0.4	100.0%	-5.5
13965	AT1G68760.1   MutT/nudix family protein, similar to SP:Q58549 ADP-ribose pyrophosphatase (EC 3.6.1.13) {Methanococcus jannaschii}; contains Pfam profile PF00293: NUDIX domain	6.0	5.9	0.1	0.4	100.0%	-4.8
13966	AT4G25330.1   expressed protein   chr4:12957844-12958719 FORWARD   Aliases: T30C3.2	2.5	2.6	-0.1	-0.4	100.0%	-5.4
13967	AT3G13772.1   endomembrane protein 70, putative, TM4 family;   chr3:4521540-4524401 REVERSE   Aliases: MMM17.22	9.1	9.0	0.1	0.4	100.0%	-5.1
13968	AT3G28310.1   expressed protein, similar to At14a (TIGR_Ath1:At3g28290, TIGR_Ath1:At3g28300) (Arabidopsis thaliana)   chr3:10578198-10578612 FORWARD   Aliases: MZF16.11	2.4	2.5	-0.1	-0.4	100.0%	-5.4
13969	AT1G32320.1   Symbol: ATMKK10   mitogen-activated protein kinase kinase (MAPKK), putative (MKK10), mitogen-activated protein kinase kinase (MAPKK) family, PMID:12119167   chr1:11655136-11656053 FORWARD   Aliases: F27G20.9	2.4	2.4	-0.0	-0.4	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13970	AT5G58030.1   transport protein particle (TRAPP) component Bet3 family protein, very strong similarity to SPP30 (Solanum pollinatum) (Solanum chacoense) GI:4959712; contains Pfam profile PF04051: Transport protein particle (TRAPP) component, Bet3   chr5:23504042-23505833 REVERSE   Aliases: K21L19.2	7.3	7.5	-0.2	-0.4	100.0%	-5.1
13971	AT3G19620.1   glycosyl hydrolase family 3 protein, similar to beta-xylosidase A GB:BAA28267 from (Aspergillus oryzae)   chr3:6815619-6818314 REVERSE   Aliases: MMB12.15	2.8	2.9	-0.0	-0.4	100.0%	-5.6
13972	AT5G24550.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to anther-specific protein ATA27 (GI:2746341) (Arabidopsis thaliana)   chr5:8392062-8395305 REVERSE   Aliases: K18P6.8, K18P6_8	2.4	2.5	-0.1	-0.4	100.0%	-5.5
13973	AT1G19485.1   AT hook motif-containing protein, contains Pfam profile: PF00730 HhH-GPD superfamily base excision DNA repair protein; contains Pfam PF02178: AT hook motif; contains Pfam PF00400: WD domain, G-beta repeat (5 copies); contains Prosite PS00354: HMG-I and HMG-Y DNA-binding domain (A+T-hook)	4.5	4.7	-0.2	-0.4	100.0%	-4.7
13974	AT4G34760.1   auxin-responsive family protein, auxin-induced protein X15, Glycine max, PIR2:JQ1097   chr4:16582188-16582884 REVERSE   Aliases: F11I11.11	4.3	4.5	-0.2	-0.4	100.0%	-4.9
13975	AT1G75490.1   encodes a member of the DREB subfamily A-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are eight members in this subfamily including DREB2A AND DREB2B that are involved in response to drought.   chr1:28339163-28340367 FORWARD   Aliases: F1B16.21	2.7	2.6	0.1	0.4	100.0%	-5.2
13976	AT1G69820.1   gamma-glutamyltranspeptidase family protein, similar to SP:P19440 Gamma-glutamyltranspeptidase 1 precursor (EC 2.3.2.2) (Gamma-glutamyltransferase 1) (CD224 antigen) {Homo sapiens}; contains Pfam profile PF01019: Gamma-glutamyltranspeptidase	2.8	2.7	0.1	0.4	100.0%	-5.4
13977	AT5G54400.1   expressed protein   chr5:22107906-22109352 FORWARD   Aliases: F24B18.2, F24B18_2	4.2	4.3	-0.1	-0.4	100.0%	-4.9
13978	AT1G08860.1   Symbol: BON3   similar to copine BONZAI1 (BON1) [Arabidopsis thaliana] (TAIR:At5g61900.1); similar to copine BONZAI1 (BON1) [Arabidopsis thaliana] (TAIR:At5g61900.3); similar to copine, putative [Arabidopsis thaliana] (TAIR:At5g07300.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475150.1); contains InterPro domain von Willebrand factor, type A (InterPro:IPR002035); contains InterPro domain C2 domain (InterPro:IPR000008)   chr1:2842156-2846141 FORWARD   Aliases: BONZAI 3, F7G19.25, F7G19_25	3.4	3.3	0.1	0.4	100.0%	-5.3
13979	AT1G19410.1   expressed protein   chr1:6714483-6716430 REVERSE   Aliases: F18O14.17, F18O14_17	3.1	3.0	0.1	0.4	100.0%	-5.3
13980	AT4G31720.2   Symbol: TAFII15   transcription initiation factor IID (TFIID) 23-30kDa subunit (TAF2H) family protein, contains Pfam profile: PF03540 transcription initiation factor TFIID 23-30kDa   chr4:15353958-15356352 REVERSE   Aliases: F28M20.90, F28M20_90	9.6	9.4	0.2	0.4	100.0%	-4.6
13981	AT2G13760.1   hypothetical protein   chr2:5742037-5742726 REVERSE   Aliases: F13J11.11, F13J11_11	2.3	2.4	-0.1	-0.4	100.0%	-5.5
13982	AT5G13500.3   expressed protein, predicted protein At2g25260 - Arabidopsis thaliana, EMBL:AC007070   chr5:4338234-4340998 FORWARD   Aliases: T6I14.30, T6I14_30	5.7	5.8	-0.1	-0.4	100.0%	-5.0
13983	AT1G22900.1   similar to disease resistance-responsive family protein [Arabidopsis thaliana] (TAIR:At5g42500.1); similar to At5g42500 [Oryza sativa (japonica cultivar-group)] (GB:AAX96290.1); contains InterPro domain Plant disease resistance response protein (InterPro:IPR004265)   chr1:8103648-8104494 REVERSE   Aliases: F19G10.14, F19G10_14	2.6	2.5	0.1	0.4	100.0%	-5.3
13984	AT3G02170.1   expressed protein   chr3:396019-399786 REVERSE   Aliases: F1C9.4	2.2	2.2	-0.0	-0.4	100.0%	-6.0
13985	AT5G03130.1   hypothetical protein   chr5:736149-736559 FORWARD   Aliases: F15A17.160, F15A17_160	2.8	2.8	0.1	0.4	100.0%	-5.4
13986	AT1G72710.1   casein kinase, putative, similar to casein kinase I, delta isoform (Arabidopsis thaliana) SWISS-PROT:P42158   chr1:27375933-27380246 FORWARD   Aliases: F28P22.10, F28P22_10	7.2	7.4	-0.2	-0.4	100.0%	-4.9
13987	AT1G64920.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	2.6	2.6	-0.1	-0.4	100.0%	-5.5
13988	AT5G56240.1   expressed protein   chr5:22777029-22781728 REVERSE   Aliases: K24C1.5, K24C1_5	5.0	5.2	-0.2	-0.4	100.0%	-4.8
13989	AT1G11370.1   pectinesterase family protein, similar to pectin methylesterase GI:1279597 from (Nicotiana glauca); contains Pfam profile: PF01095 pectinesterase   chr1:3828098-3830945 REVERSE   Aliases: T23J18.3, T23J18_3	2.1	2.1	0.0	0.4	100.0%	-5.8
13990	AT5G50020.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr5:20368568-20371662 FORWARD   Aliases: MPF21.3, MPF21_3	4.1	4.0	0.2	0.4	100.0%	-4.7
13991	AT1G23870.1   Symbol: ATTPS9	3.4	3.2	0.2	0.4	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
13992	AT3G48100.1   Symbol: ARR5   two-component responsive regulator / response regulator 5 (ARR5) / response reactor 2 (RR2), identical to response reactor2 (AtRR2) (Arabidopsis thaliana) GI:3273198, response regulator 5 (ARR5) (Arabidopsis thaliana) GI:3953599; contains Pfam profile: PF00072 response regulator receiver domain   chr3:17769412-17771859 REVERSE   Aliases: ARABIDOPSIS RESPONSE REGULATOR 5, ATRR2, IBC6, INDUCED BY CYTOKININ 6, T17F15.30	3.9	3.8	0.1	0.4	100.0%	-4.8
13993	AT5G42130.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:16852527-16854067 REVERSE   Aliases: MJC20.24, MJC20_24	6.2	6.3	-0.1	-0.4	100.0%	-4.6
13994	AT1G70040.1   hypothetical protein   chr1:26384896-26385571 FORWARD   Aliases: F20P5.22, F20P5_22	2.6	2.6	0.1	0.4	100.0%	-5.3
13995	AT5G43310.1   COP1-interacting protein-related, contains similarity to COP1-Interacting Protein 7 (CIP7) (Arabidopsis thaliana) GI:3327868   chr5:17396819-17402615 REVERSE   Aliases: MNL12.14, MNL12_14	4.7	4.7	0.1	0.4	100.0%	-5.0
13996	AT1G11440.1   expressed protein   chr1:3849360-3850662 FORWARD   Aliases: T23J18.11, T23J18_11	4.9	5.0	-0.1	-0.4	100.0%	-4.6
13997	AT5G54510.1   Symbol: DFL1   encodes an IAA-amido synthase that conjugates Ala, Asp, Phe, and Trp to auxin. Lines overexpressing this gene accumulate IAA-ASP and are hypersensitive to several auxins.   chr5:22148319-22150904 REVERSE   Aliases: DWARF IN LIGHT 1, F24B18.13, F24B18_13, GH3.6	8.2	7.9	0.3	0.4	100.0%	-4.6
13998	AT2G45850.2   DNA-binding family protein, contains a AT hook motif (DNA binding motifs with a preference for A/T rich regions), Pfam:PF02178   chr2:18878226-18880758 REVERSE   Aliases: F4I18.17	3.5	3.5	-0.1	-0.4	100.0%	-5.0
13999	AT3G05440.1   C2 domain-containing protein, similar to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain   chr3:1572724-1573272 FORWARD   Aliases: F22F7.11, F22F7_11	2.4	2.3	0.0	0.4	100.0%	-5.6
14000	AT5G44150.1   expressed protein   chr5:17780911-17782328 REVERSE   Aliases: MLN1.7, MLN1_7	5.9	5.8	0.1	0.4	100.0%	-4.8
14001	AT3G53250.1   auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana and auxin-induced protein 6B (SP:P33083) (PIR:T10942) (Glycine max)	3.0	3.0	-0.0	-0.4	100.0%	-5.8
14002	AT5G64240.2   latex-abundant family protein (AMC3) / caspase family protein, contains similarity to latex-abundant protein (Hevea brasiliensis) gb:AAD13216; contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain   chr5:25712846-25715046 FORWARD   Aliases: MSJ1.8, MSJ1_8	3.2	3.0	0.2	0.4	100.0%	-4.2
14003	AT2G19700.1   expressed protein   chr2:8512053-8512721 REVERSE   Aliases: F6F22.27, F6F22_27	2.3	2.2	0.0	0.4	100.0%	-5.6
14004	AT1G65040.2   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At3g16090.1); similar to hypothetical protein [Homo sapiens] (GB:CAD38937.1); similar to PREDICTED: similar to synoviolin 1 isoform a [Pan troglodytes] (GB:XP_522059.1); similar to Syvn1 protein [Mus musculus] (GB:AAH46829.1); similar to Synoviolin1 [Homo sapiens] (GB:BAC57449.1); similar to Synoviolin 1, isoform b [Homo sapiens] (GB:AAH30530.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr1:24163497-24167291 REVERSE   Aliases: F16G16.3, F16G16_3	4.2	4.4	-0.2	-0.4	100.0%	-4.4
14005	AT1G10660.4   expressed protein   chr1:3532474-3535132 FORWARD   Aliases: F20B24.10, F20B24_10	6.9	6.7	0.3	0.4	100.0%	-4.6
14006	AT2G01810.1   PHD finger family protein, contains Pfam profile: PF00628: PHD-finger   chr2:347536-349951 FORWARD   Aliases: T8O11.2, T8O11_2	3.7	3.8	-0.1	-0.4	100.0%	-5.0
14007	AT4G32960.1   expressed protein   chr4:15908621-15910183 REVERSE   Aliases: F26P21.80, F26P21_80	7.9	7.7	0.2	0.4	100.0%	-4.9
14008	AT3G26960.1   expressed protein   chr3:9945905-9946816 REVERSE   Aliases: MOJ10.4	3.1	3.2	-0.1	-0.4	100.0%	-5.4
14009	AT1G68890.1   menaquinone biosynthesis protein-related, similar to menaquinone biosynthesis protein menD (SP:P17109)(E. coli) ; Pfam HMM hit: 2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylic acid synthase / 2-oxoglutarate decarboxylase   chr1:25900608-25906163 FORWARD   Aliases: T6L1.7, T6L1_7	3.2	3.1	0.1	0.4	100.0%	-5.3
14010	AT5G55620.1   expressed protein, similar to unknown protein (gb:AAF04428.1)   chr5:22547430-22548165 FORWARD   Aliases: MDF20.6, MDF20_6	2.6	2.6	-0.0	-0.4	100.0%	-5.6
14011	AT1G53180.1   expressed protein   chr1:19835109-19836510 FORWARD   Aliases: F12M16.8, F12M16_8	2.4	2.6	-0.2	-0.4	100.0%	-4.5
14012	AT3G54520.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At3g54530.1)   chr3:20194538-20196178 REVERSE   Aliases: T14E10.90	2.5	2.5	-0.1	-0.4	100.0%	-5.7
14013	AT4G30060.1   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr4:14689135-14692486 REVERSE   Aliases: F6G3.90, F6G3_90	2.5	2.5	0.1	0.4	100.0%	-5.3
14014	AT4G05310.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:2714763-2716010 FORWARD   Aliases: C17L7.230, C17L7_230	3.1	3.0	0.1	0.4	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14015	ATMG01410.1   Symbol: ORF204	2.9	2.8	0.1	0.4	100.0%	-5.4
14016	AT1G29990.1   prefoldin, putative, similar to Swiss-Prot:O15212 prefoldin subunit 6 (Protein Ke2) (Homo sapiens)   chr1:10507577-10509029 FORWARD   Aliases: T1P2.3, T1P2_3	9.0	8.8	0.2	0.4	100.0%	-4.5
14017	AT3G43660.1   nodulin, putative, similar to nodulin 21 (N-21) (Glycine max) SWISS-PROT:P16313   chr3:15576320-15576916 FORWARD   Aliases: F23N14.40	4.7	4.5	0.1	0.4	100.0%	-4.8
14018	AT3G18060.1   transducin family protein / WD-40 repeat family protein, similar to 66 kDa stress protein (SP:P90587) (Physarum polycephalum (Slime mold)); similar to WDR1 protein GB:AAD05042 (Gallus gallus) (Genomics 56 (1), 59-69 (1999)); contains 11 WD-40 repeats (PF00400)   chr3:6183779-6187049 FORWARD   Aliases: MRC8.5	4.7	4.4	0.3	0.4	100.0%	-4.5
14019	AT2G18210.1   expressed protein   chr2:7932280-7932948 REVERSE   Aliases: F8D23.2	3.0	3.0	-0.1	-0.4	100.0%	-5.0
14020	AT5G45220.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr5:18316153-18318296 REVERSE   Aliases: K18C1.10, K18C1_10	3.8	3.6	0.2	0.4	100.0%	-4.5
14021	AT3G18930.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)   chr3:6523536-6525549 REVERSE   Aliases: AT3G18920, K13E13.2	3.3	3.2	0.1	0.4	100.0%	-5.2
14022	AT3G04080.1   Symbol: ATAPY1	6.2	6.1	0.2	0.4	100.0%	-4.5
14023	AT4G31310.1   avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related, similar to SP:P54121 AIG2 protein {Arabidopsis thaliana}   chr4:15191331-15192602 FORWARD   Aliases: F8F16.130, F8F16_130	6.3	6.5	-0.2	-0.4	100.0%	-4.5
14024	AT1G13210.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) (Chromaffin granule ATPase) from {Homo sapiens} SP:Q9Y2Q0, {Mus musculus} SP:P98200, {Bos taurus} SP:Q29449; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase; ESTs gb:T45045 and gb:AA394473 come from this gene   chr1:4508960-4513935 REVERSE   Aliases: F3F19.24, F3F19_24	3.3	3.3	-0.1	-0.4	100.0%	-4.9
14025	AT5G16160.1   expressed protein   chr5:5275515-5276609 REVERSE   Aliases: T21H19.80, T21H19_80	3.0	3.0	0.1	0.4	100.0%	-5.5
14026	AT5G59940.1   DC1 domain-containing protein / UV-B light-insensitive protein, putative, similar to ULI3 (UV-B light insensitive) (Arabidopsis thaliana) GI:17225050; contains Pfam profile PF03107: DC1 domain	3.6	3.8	-0.2	-0.4	100.0%	-4.4
14027	AT1G33250.1   fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	5.2	5.3	-0.1	-0.4	100.0%	-5.0
14028	AT3G47630.2   similar to Hypothetical protein CBG04116 [Caenorhabditis briggsae] (GB:CAE60498.1)   chr3:17574031-17576414 REVERSE   Aliases: F1P2.180	4.9	4.8	0.1	0.4	100.0%	-4.8
14029	AT5G20480.1   leucine-rich repeat transmembrane protein kinase, putative, protein kinase Xa21, Oryza sativa, PIR:A57676   chr5:6922484-6925877 FORWARD   Aliases: F7C8.70, F7C8_70	2.6	2.6	0.1	0.4	100.0%	-5.4
14030	AT1G14940.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:5154538-5155556 REVERSE   Aliases: F10B6.37, F10B6_37	2.9	3.0	-0.1	-0.4	100.0%	-5.4
14031	AT3G56110.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr3:20832913-20833987 REVERSE   Aliases: F18O21.70	6.0	5.7	0.3	0.4	100.0%	-4.7
14032	AT5G15910.1   dehydrogenase-related, low similarity to SP:Q9R1J0 NAD(P)-dependent steroid dehydrogenase (EC 1.1.1.-) {Mus musculus}   chr5:5193140-5195399 FORWARD   Aliases: F1N13.50, F1N13_50	8.9	9.0	-0.1	-0.4	100.0%	-5.2
14033	AT4G40080.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to CLATHRIN COAT ASSEMBLY PROTEIN AP180 - Mus musculus, SWISSPROT:Q61548   chr4:18579308-18580711 FORWARD   Aliases: T5J17.250, T5J17_250	4.8	4.7	0.2	0.4	100.0%	-4.7
14034	AT5G16630.2   similar to PREDICTED: similar to DNA-repair protein complementing XP-C cells homolog (Xeroderma pigmentosum group C complementing protein homolog) (p125) [Rattus norvegicus] (GB:XP_232194.2); contains InterPro domain DNA repair protein Rad4 (InterPro:IPR004583)   chr5:5454806-5459620 FORWARD   Aliases: MTG13.7, MTG13_7	6.7	7.0	-0.2	-0.4	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14035	AT3G53890.1   40S ribosomal protein S21 (RPS21B), ribosomal protein S21, cytosolic - <i>Oryza sativa</i> , PIR:S38357   chr3:19966322-19967327 REVERSE   Aliases: F5K20.190	11.1	11.2	-0.1	-0.4	100.0%	-4.9
14036	AT5G19660.1   subtilase family protein, contains Pfam profile: PF00082 subtilase family   chr5:6642006-6646532 REVERSE   Aliases: T29J13.80, T29J13_80	5.6	5.4	0.2	0.4	100.0%	-4.8
14037	AT1G79580.3   Symbol: ANAC033   no apical meristem (NAM) family protein, similar to OsNAC7 protein (GI:6730944) ( <i>Oryza sativa</i> ); contains weak hit to Pfam PF02365 : No apical meristem (NAM) protein	2.1	2.0	0.0	0.4	100.0%	-5.8
14038	ATCG00790.1   Symbol: RPL16   chloroplast gene encoding a ribosomal protein L16, which is a constituent of 50S large ribosomal subunit   chrC:81189-82652 REVERSE   Aliases: RIBOSOMAL PROTEIN L16, RPL16	10.1	10.5	-0.4	-0.4	100.0%	-4.8
14039	AT5G13240.1   expressed protein, predicted proteins, <i>Schizosaccharomyces pombe</i>	6.4	6.2	0.2	0.4	100.0%	-4.9
14040	AT3G13330.1   expressed protein   chr3:4319654-4330068 REVERSE   Aliases: MDC11.16	7.9	8.1	-0.2	-0.4	100.0%	-4.7
14041	AT1G03050.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to CLATHRIN COAT ASSEMBLY PROTEIN AP180 - <i>Mus musculus</i> , SWISSPROT:Q61548   chr1:707726-709860 FORWARD   Aliases: F1003.13, F1003_13	2.6	2.7	-0.1	-0.4	100.0%	-5.5
14042	AT2G26920.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627: UBA/TS-N domain   chr2:11496083-11498829 FORWARD   Aliases: F12C20.4, F12C20_4	6.8	6.7	0.1	0.4	100.0%	-5.1
14043	AT5G16050.1   Symbol: GRF5   14-3-3 protein GF14 epsilon (GRF5), identical to 14-3-3 protein GF14 epsilon GI:2232148 from ( <i>Arabidopsis thaliana</i> )   chr5:5243748-5245814 REVERSE   Aliases: F1N13.190, F1N13_190, GF14 UPSILON, GF14 UPSILON CHAIN	9.8	9.4	0.3	0.4	100.0%	-4.8
14044	AT5G50970.1   WD-40 repeat family protein, contains Pfam profile PF00400: WD domain, G-beta repeat   chr5:20753563-20756521 FORWARD   Aliases: K3K7.13, K3K7_13	2.7	2.7	0.1	0.4	100.0%	-5.3
14045	AT5G63790.1   Symbol: ANAC102   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; contains similarity to NAC-domain protein   chr5:25543735-25545239 REVERSE   Aliases: ANAC102, MBK5.27, MBK5_27	6.7	6.8	-0.2	-0.4	100.0%	-4.6
14046	AT3G43270.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:15233113-15236448 REVERSE   Aliases: F7K15.120	4.8	4.7	0.1	0.4	100.0%	-4.9
14047	AT3G09790.1   Symbol: UBQ8   polyubiquitin (UBQ8), identical to polyubiquitin (ubq8) GI:870793, GB:L05917 ( <i>Arabidopsis thaliana</i> ) ( <i>Genetics</i> 139 (2), 921-939 (1995))   chr3:3003867-3006197 REVERSE   Aliases: F11F8.38	2.7	2.7	-0.1	-0.4	100.0%	-5.4
14048	AT1G60500.1   dynamin family protein, similar to RBTMx2 ( <i>Oncorhynchus mykiss</i> ) GI:1399452; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain   chr1:22295247-22297629 FORWARD   Aliases: F8A5.5, F8A5_5	2.7	2.7	-0.0	-0.4	100.0%	-5.7
14049	AT5G43230.1   hypothetical protein   chr5:17367665-17369975 FORWARD   Aliases: MNL12.5, MNL12_5	2.6	2.6	-0.1	-0.4	100.0%	-5.1
14050	AT4G11120.1   translation elongation factor Ts (EF-Ts), putative, similar to ethylene-responsive elongation factor EF-Ts precursor ( <i>Lycopersicon esculentum</i> ) GI:5669636; contains Pfam profile PF00889: Elongation factor TS   chr4:6777800-6780162 FORWARD   Aliases: T22B4.100, T22B4_100	6.5	6.6	-0.1	-0.4	100.0%	-4.5
14051	AT4G24540.1   Symbol: AGL24   MADS-box family protein	2.9	3.0	-0.1	-0.4	100.0%	-5.3
14052	AT1G49510.1   Symbol: EMB1273   expressed protein   chr1:18330586-18332229 FORWARD   Aliases: EMB1273, EMBRYO DEFECTIVE 1273, F13F21.5, F13F21_5	4.0	4.1	-0.1	-0.4	100.0%	-5.0
14053	AT2G31420.1   expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)   chr2:13400441-13401070 REVERSE   Aliases: T28P16.9, T28P16_9	3.5	3.4	0.1	0.4	100.0%	-5.1
14054	AT4G22120.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) ( <i>Arabidopsis thaliana</i> ) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr4:11715836-11719557 REVERSE   Aliases: F1N20.220, F1N20_220	7.6	7.8	-0.2	-0.4	100.0%	-4.9
14055	AT5G61160.1   Symbol: AACT1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from <i>Gentiana triflora</i> GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from <i>Perilla frutescens</i> GI:17980232, <i>Salvia splendens</i> GI:17980234; contains Pfam profile PF02458 transferase family   chr5:24625950-24627530 FORWARD   Aliases: AACT1, MAF19.17, MAF19_17	2.5	2.6	-0.1	-0.4	100.0%	-5.4
14056	AT5G53900.2   expressed protein, similar to unknown protein (gb:AAF34833.1)   chr5:21898368-21900478 REVERSE   Aliases: K19P17.6, K19P17_6	4.2	4.1	0.1	0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14057	AT5G63760.2   IBR domain-containing protein, contains similarity to Swiss-Prot:Q94981 ariadne-1 protein (Ari-1) (Drosophila melanogaster) and Pfam:PF01485 IBR domain   chr5:25533104-25535059 REVERSE   Aliases: MBK5.24, MBK5_24	6.0	6.2	-0.2	-0.4	100.0%	-4.5
14058	AT5G20830.2   Symbol: SUS1   similar to sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:At4g02280.1); similar to sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:At1g73370.1); similar to sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:At3g43190.1); similar to sucrose synthase / sucrose-UDP glucosyltransferase (SUS2) [Arabidopsis thaliana] (TAIR:At5g49190.1); similar to sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative [Arabidopsis thaliana] (TAIR:At5g37180.1); similar to sucrose synthase [Citrus unshiu] (GB:BAA89049.1); similar to sucrose synthase [Gossypium hirsutum] (GB:AAD28641.1); similar to sucrose synthase [Vicia faba] (GB:CAA49428.1); similar to sucrose synthase [Glycine max] (GB:AAC39323.1); similar to sucrose synthase [Citrus unshiu] (GB:BAA88905.1); contains InterPro domain Sucrose synthase (InterPro:IPR000368); contains InterPro domain Glycosyl transferase, group 1 (InterPro:IPR001296)	6.3	6.6	-0.3	-0.4	100.0%	-4.7
14059	AT4G32010.1   transcriptional factor B3 family protein, low similarity to FUSCA3 (Arabidopsis thaliana) GI:3582518, VIVIPAROUS1 protein (Triticum aestivum) GI:7801376; contains Pfam profile PF02362: B3 DNA binding domain   chr4:15479530-15485359 FORWARD   Aliases: F10N7.180, F10N7_180	5.6	5.7	-0.2	-0.4	100.0%	-4.6
14060	AT2G05380.1   Symbol: GRP3S   glycine-rich protein (GRP3S), identical to cDNA glycine-rich protein 3 short isoform (GRP3S) GI:4206766   chr2:1966817-1968033 FORWARD   Aliases: F16J10.7, F16J10_7, GLYCINE RICH PROTEIN 3 SHORT ISOFORM	5.3	5.4	-0.1	-0.4	100.0%	-4.6
14061	AT4G32750.1   expressed protein   chr4:15795990-15798245 REVERSE   Aliases: F4D11.50, F4D11_50	4.6	4.7	-0.1	-0.4	100.0%	-4.9
14062	AT1G73700.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family   chr1:27721041-27723309 REVERSE   Aliases: F25P22.12, F25P22_12	3.6	3.5	0.1	0.4	100.0%	-5.2
14063	AT1G09290.1   expressed protein, This gene is continued on the 5' end of BAC T12M14   chr1:3001519-3003764 REVERSE   Aliases: T12M4.20	4.2	4.3	-0.1	-0.4	100.0%	-4.9
14064	AT5G09940.1   expressed protein   chr5:3101193-3101834 FORWARD   Aliases: MYH9.15, MYH9_15	2.8	2.9	-0.1	-0.4	100.0%	-5.3
14065	AT1G53165.1   protein kinase, putative, similar to serine/threonine protein kinase 24 (Homo sapiens) SWISS-PROT:Q9Y6E0	4.9	4.8	0.1	0.4	100.0%	-4.9
14066	AT3G09240.1   protein kinase-related, low similarity to protein kinase GI:166809; contains Pfam profile: Eukaryotic protein kinase domain   chr3:2835674-2837962 REVERSE   Aliases: F3L24.11	2.2	2.4	-0.2	-0.4	100.0%	-4.0
14067	AT3G09040.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:2761200-2764286 REVERSE   Aliases: MZB10.7	2.7	2.6	0.0	0.4	100.0%	-5.6
14068	AT2G33845.1   DNA-binding protein-related, contains weak similarity to G-quartet DNA binding protein 3 (Tetrahymena thermophila) gi:4583503:gb:AAD25098   chr2:14324771-14326465 FORWARD   Aliases: None	6.6	6.4	0.2	0.4	100.0%	-4.7
14069	AT1G63120.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr1:23412541-23414480 REVERSE   Aliases: F16M19.4, F16M19_4	6.2	5.9	0.2	0.4	100.0%	-4.8
14070	AT2G39710.1   aspartyl protease family protein, contains profile Pfam PF00026: Eukaryotic aspartyl protease; contains Prosite PS00141: Eukaryotic and viral aspartyl proteases active site.;   chr2:16568866-16570458 REVERSE   Aliases: F17A14.9	4.0	4.1	-0.1	-0.4	100.0%	-5.2
14071	AT2G18240.2   RER1 protein, putative, similar to SP:O48671 RER1B protein (AtRER1B) {Arabidopsis thaliana}, SP:O48670 RER1A protein (AtRER1A) {Arabidopsis thaliana}; contains Pfam profile PF03248: Rer1 family   chr2:7942367-7943803 FORWARD   Aliases: T30D6.25	4.4	4.3	0.1	0.4	100.0%	-4.8
14072	AT2G42270.1   U5 small nuclear ribonucleoprotein helicase, putative   chr2:17611408-17618411 FORWARD   Aliases: T24P15.18, T24P15_18	5.6	5.7	-0.2	-0.4	100.0%	-5.0
14073	AT2G43580.1   chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus)   chr2:18085726-18087105 REVERSE   Aliases: F18O19.31	2.0	2.0	0.0	0.4	100.0%	-5.8
14074	AT3G59680.2   similar to unknown [Zea mays] (GB:AAV64233.1)   chr3:22055134-22057017 FORWARD   Aliases: T16L24.230	3.6	3.5	0.1	0.4	100.0%	-5.2
14075	AT5G36170.3   Symbol: HCF109	7.3	7.2	0.1	0.4	100.0%	-4.8
14076	AT2G15010.1   thionin, putative, similar to thionin (Arabidopsis thaliana) gi:1181533:gb:AAC41679   chr2:6491461-6492234 FORWARD   Aliases: T15J14.5, T15J14_5	2.8	2.9	-0.1	-0.4	100.0%	-5.4
14077	AT5G63080.1   transcription factor jumonji (jmjC) domain-containing protein, contains Pfam domain PF02373: jmjC domain	5.4	5.6	-0.1	-0.4	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14078	AT3G58040.1   seven in absentia (SINA) family protein, similar to siah-1A protein (Mus musculus) GI:297035; contains Pfam profile PF03145: Seven in absentia protein family   chr3:21499493-21502465 FORWARD   Aliases: T10K17.250	5.5	5.3	0.2	0.4	100.0%	-4.7
14079	AT2G46950.1   Symbol: CYP709B2   cytochrome P450 family protein, similar to cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus); contains Pfam profile: PF00067: Cytochrome P450   chr2:19296207-19298683 REVERSE   Aliases: F14M4.22	2.4	2.5	-0.1	-0.4	100.0%	-5.4
14080	AT1G48100.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:17770543-17774255 FORWARD   Aliases: F21D18.18, F21D18_18	2.3	2.3	-0.1	-0.4	100.0%	-5.4
14081	AT4G36800.1   Symbol: RCE1   RUB1-conjugating enzyme, putative (RCE1), this gene is frameshifted and may be a pseudogene; identical over first 79 amino acids to RUB1 conjugating enzyme (Arabidopsis thaliana) GI:6635457   chr4:17340955-17342736 REVERSE   Aliases: AP22.40, AP22_40, RUB1 CONJUGATING ENZYME 1	8.1	7.7	0.3	0.4	100.0%	-4.7
14082	AT2G36610.1   homeobox-leucine zipper family protein, similar to homeobox protein PpHB8 (GP:7415628) (Physcomitrella patens); contains PfamPF00046: Homeobox domain   chr2:15356406-15357167 FORWARD   Aliases: F13K3.1, F13K3_1	3.0	3.0	-0.1	-0.4	100.0%	-5.2
14083	AT5G56760.1   Symbol: AtSerat1;1   serine O-acetyltransferase (SAT-52), identical to GI:905391   chr5:22978535-22979886 REVERSE   Aliases: MIK19.23, MIK19_23, SAT 52, SERINE ACETYLTRANSFERASE 52	7.9	7.6	0.3	0.4	100.0%	-4.3
14084	AT1G77980.1   MADS-box family protein, MADS-box protein AGL66   chr1:29320106-29321961 REVERSE   Aliases: F28K19.20, F28K19_20	3.6	3.7	-0.1	-0.4	100.0%	-5.3
14085	AT2G44620.1   Symbol: mtACP 1   acyl carrier protein, mitochondrial / ACP / NADH-ubiquinone oxidoreductase 9.6 kDa subunit, identical to SP:P53665 Acyl carrier protein, mitochondrial precursor (ACP) (NADH-ubiquinone oxidoreductase 9.6 kDa subunit) (MtACP-1) {Arabidopsis thaliana}; identical to cDNA acyl carrier protein precursor GI:468265   chr2:18421359-18422310 FORWARD   Aliases: F16B22.11, F16B22.28, F16B22_28, MITOCHONDRIAL ACYL CARRIER PROTEIN 1	8.8	9.1	-0.2	-0.4	100.0%	-4.7
14086	AT3G03690.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr3:911245-913684 REVERSE   Aliases: T12J13.3, T12J13_3	3.0	3.0	0.1	0.4	100.0%	-5.2
14087	AT2G28460.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.1	3.3	-0.2	-0.4	100.0%	-4.5
14088	AT2G27320.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g38255.1); similar to P0518C01.31 [Oryza sativa (japonica cultivar-group)] (GB:NP_914365.1); contains InterPro domain Protein of unknown function DUF239 (InterPro:IPR004314)   chr2:11699968-11701760 FORWARD   Aliases: F12K2.10, F12K2_10	3.3	3.4	-0.1	-0.4	100.0%	-5.0
14089	AT3G26880.1   self-incompatibility protein-related, similar to S1 self-incompatibility protein (Papaver rhoeas) GI:452430   chr3:9907571-9907972 REVERSE   Aliases: MDJ14.22	2.9	2.8	0.1	0.4	100.0%	-5.1
14090	AT5G51480.1   multi-copper oxidase type I family protein, contains Pfam profile: PF00394 Multicopper oxidase; similar to pollen-specific protein   chr5:20927470-20930674 FORWARD   Aliases: K17N15.3, K17N15_3, SKS2	3.7	3.6	0.1	0.4	100.0%	-5.4
14091	AT3G15650.1   phospholipase/carboxylesterase family protein, low similarity to lysophospholipase I (Mus musculus) GI:1864159; contains Pfam profile PF02230: Phospholipase/Carboxylesterase family   chr3:5305985-5307771 FORWARD   Aliases: MSJ11.7	4.3	4.2	0.1	0.4	100.0%	-5.0
14092	AT2G27380.1   Symbol: ATEPR1	2.5	2.6	-0.1	-0.4	100.0%	-5.4
14093	NA	12.4	12.3	0.1	0.4	100.0%	-5.3
14094	AT4G19730.1   glycosyl hydrolase family 18 protein, similar to chitinase, class V GI:505267 from (Nicotiana tabacum)   chr4:10733874-10734985 REVERSE   Aliases: T16H5.90, T16H5_90	2.3	2.3	0.1	0.4	100.0%	-5.3
14095	AT5G41990.1   Symbol: WNK8   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:16811805-16815234 REVERSE   Aliases: MJC20.9, MJC20_9	7.4	7.6	-0.1	-0.4	100.0%	-4.7
14096	AT1G69400.2   transducin family protein / WD-40 repeat family protein, similar to mitotic checkpoint protein (GI:9294423) {Arabidopsis thaliana}; similar to mitotic checkpoint protein (BUB3) (SP:O43684) (Homo sapiens)   chr1:26090611-26092640 FORWARD   Aliases: F10D13.23, F10D13_23	3.6	3.7	-0.1	-0.4	100.0%	-5.2
14097	AT5G10650.2   similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At5g24870.1); similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:At5g24870.2); similar to putative RING-H2 finger protein RHG1a [Oryza sativa (japonica cultivar-group)] (GB:BAD38048.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841)   chr5:3365018-3367604 REVERSE   Aliases: MAJ23.10, MAJ23_10	5.3	5.1	0.1	0.4	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14098	AT2G21390.1   coatomer protein complex, subunit alpha, putative, contains Pfam PF00400: WD domain, G-beta repeat; similar to Coatomer alpha subunit (Alpha-coat protein) (Alpha-COP) (HEPCOP) (HEP-COP) (SP:P53621) (Homo sapiens)   chr2:9159086-9163957 FORWARD   Aliases: F3K23.15, F3K23_15	8.4	8.5	-0.2	-0.4	100.0%	-4.9
14099	AT4G32170.1   Symbol: CYP96A2   cytochrome P450, putative, cytochrome p450, Arabidopsis thaliana, PID:G2252844   chr4:15533778-15535339 FORWARD   Aliases: F10M6.190	3.0	2.9	0.1	0.4	100.0%	-5.4
14100	AT3G14820.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 GI:15054386 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr3:4978954-4980248 FORWARD   Aliases: T21E2.10	2.9	2.9	0.0	0.4	100.0%	-5.6
14101	AT4G16180.1   expressed protein   chr4:9168338-9170449 REVERSE   Aliases: DL4130C, FCAALL.295	3.0	2.9	0.1	0.4	100.0%	-5.1
14102	AT1G04240.1   Symbol: SHY2   auxin-responsive protein / indoleacetic acid-induced protein 3 (IAA3), identical to SP:Q38822 Auxin-responsive protein IAA3 (Indoleacetic acid-induced protein 3) {Arabidopsis thaliana}; EST gb:T04296 comes from this gene   chr1:1128187-1129414 REVERSE   Aliases: F19P19.32, F19P19_32, IAA3, SHORT HYPOCOTYL 2	3.7	3.5	0.2	0.4	100.0%	-4.6
14103	AT4G33180.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoate hydrolase (Pseudomonas fluorescens) GI:1871461; contains Pfam profile PF00561: alpha/beta hydrolase fold   chr4:16000244-16002272 FORWARD   Aliases: AT4G33190, F4I10.110, F4I10_110	4.4	4.6	-0.2	-0.4	100.0%	-5.0
14104	AT5G61650.1   Symbol: CYCP4;2   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr5:24795491-24796245 FORWARD   Aliases: CYCP4, K11J9.17, K11J9_17	3.1	3.0	0.2	0.4	100.0%	-4.3
14105	AT2G42220.1   rhodanese-like domain-containing protein, contains rhodanese-like domain PF:00581   chr2:17599167-17600783 FORWARD   Aliases: T24P15.13, T24P15_13	8.2	8.4	-0.2	-0.4	100.0%	-4.2
14106	AT3G62180.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pollen-specific pectin esterase from Brassica rapa subsp. pekinensis GI:1620652; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr3:23030807-23031454 REVERSE   Aliases: T17J13.140	2.7	2.6	0.1	0.4	100.0%	-5.4
14107	AT5G06070.1   Symbol: RBE   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:1828157-1829187 REVERSE   Aliases: RAB, RABBIT EARS	3.0	3.0	0.1	0.4	100.0%	-5.4
14108	AT1G01940.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr1:323027-324917 FORWARD   Aliases: F22M8.7, F22M8_7	9.2	9.5	-0.2	-0.4	100.0%	-4.4
14109	AT1G41820.1   expressed protein   chr1:15584864-15587584 REVERSE   Aliases: T4I21.4, T4I21_4	2.6	2.5	0.1	0.4	100.0%	-5.3
14110	AT5G10270.1   Symbol: CDKC;1	5.7	5.8	-0.1	-0.4	100.0%	-4.8
14111	AT4G38050.1   similar to xanthine/uracil permease family protein [Arabidopsis thaliana] (TAIR:At2g27810.1); similar to PREDICTED P0477A12.37 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_506346.1); contains InterPro domain Xanthine/uracil/vitamin C permease family (InterPro:IPR006043)   chr4:17869374-17872476 REVERSE   Aliases: F20D10.170, F20D10_170	4.3	4.2	0.1	0.4	100.0%	-4.8
14112	AT5G12940.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611   chr5:4087715-4089007 FORWARD   Aliases: T24H18.110, T24H18_110	4.3	4.5	-0.1	-0.4	100.0%	-4.6
14113	AT1G58190.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr1:21544385-21551661 FORWARD   Aliases: T18I24.10, T18I24_10	2.2	2.3	-0.1	-0.4	100.0%	-5.4
14114	AT1G62500.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to auxin down regulated GB:X69640 GI:296442 from (Glycine max); contains Pfam profile PF00234: Protease inhibitor/seed storage/LTP family   chr1:23135710-23137167 FORWARD   Aliases: T3P18.6, T3P18_6	2.9	3.0	-0.1	-0.4	100.0%	-5.5
14115	AT3G52370.1   beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein, weak similarity to osteoblast specific factor 2 (Homo sapiens) GI:393319; contains Pfam profile PF02469: Fasciclin domain; supporting cDNA gi:26450295:dbj:AK117608.1:   chr3:19428468-19430760 FORWARD   Aliases: T25B15.140	6.0	6.2	-0.2	-0.4	100.0%	-4.6
14116	AT5G50210.1   quinolinate synthetase A-related, contains weak similarity to Swiss-Prot:P11458 quinolinate synthetase A (Escherichia coli)   chr5:20459873-20463217 FORWARD   Aliases: K6A12.7, K6A12_7	8.2	8.0	0.2	0.4	100.0%	-4.4
14117	AT3G59920.1   Symbol: ATGDI2	10.6	10.8	-0.2	-0.4	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14118	AT1G14970.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr1:5162080-5164912 REVERSE   Aliases: T15D22.1	2.8	2.8	-0.1	-0.4	100.0%	-5.4
14119	AT5G05510.1   protein kinase-related, low similarity to SP:O60566 Mitotic checkpoint serine/threonine-protein kinase BUB1 beta (EC 2.7.1.-) {Homo sapiens}   chr5:1630652-1632569 REVERSE   Aliases: MOP10.5, MOP10_5	2.4	2.4	-0.1	-0.4	100.0%	-5.3
14120	AT3G54870.1   armadillo/beta-catenin repeat family protein / kinesin motor family protein, kinesin, Syncephalastrum racemosum, AJ225894   chr3:20341784-20347695 FORWARD   Aliases: F28P10.150	3.5	3.4	0.1	0.4	100.0%	-5.1
14121	AT4G21160.4   Symbol: ZAC   zinc finger and C2 domain protein (ZAC), identical to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr4:11284387-11286755 FORWARD   Aliases: None	8.4	8.7	-0.3	-0.4	100.0%	-4.7
14122	AT3G59000.2   similar to F-box family protein [Arabidopsis thaliana] (TAIR:At3g58930.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD54099.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain FBD (InterPro:IPR006566)   chr3:21810253-21812720 FORWARD   Aliases: F17J16.50	6.1	6.0	0.1	0.4	100.0%	-4.8
14123	AT3G60730.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:22455865-22458248 FORWARD   Aliases: T4C21.140	2.2	2.2	-0.0	-0.4	100.0%	-5.7
14124	AT1G61110.1   Symbol: ANAC025   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM protein GI:1279639 from (Petunia hybrida)   chr1:22520271-22521952 FORWARD   Aliases: ANAC025, F11P17.16, F11P17_16	3.6	3.4	0.2	0.4	100.0%	-4.6
14125	AT2G44870.1   expressed protein   chr2:18510213-18511755 FORWARD   Aliases: T13E15.12	6.8	6.7	0.1	0.4	100.0%	-4.9
14126	AT5G19400.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g28260.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g28260.1); similar to putative cig3 [Oryza sativa (japonica cultivar-group)] (GB:BAD30976.1); similar to putative cytokinin inducible protein [Oryza sativa (japonica cultivar-group)] (GB:AAQ56472.1)   chr5:6540005-6545017 FORWARD   Aliases: F7K24.150, F7K24_150	3.6	3.5	0.1	0.4	100.0%	-5.4
14127	AT2G06820.1   expressed protein, low similarity to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:2726653-2727481 REVERSE   Aliases: T9F8.1, T9F8_1	2.2	2.1	0.0	0.4	100.0%	-5.9
14128	AT4G39400.1   Symbol: BRI1   brassinosteroid insensitive 1 (BRI1), identical to GI:2392895   chr4:18324655-18328820 FORWARD   Aliases: BIN1, BRASSINOSTEROID INSENSITIVE 1, CABBAGE 2, CBB2, DWARF 2, DWF2, F23K16.30, F23K16_30	5.4	5.5	-0.1	-0.4	100.0%	-5.0
14129	AT3G45300.1   Symbol: IVD   isovaleryl-CoA-dehydrogenase (IVD), identical to isovaleryl-CoA-dehydrogenase precursor (Arabidopsis thaliana) GI:5596622	8.4	8.1	0.2	0.4	100.0%	-4.6
14130	AT2G01480.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'axi 1 protein from Nicotiana tabacum -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.	2.7	2.8	-0.1	-0.4	100.0%	-5.3
14131	AT4G36460.1   expressed protein   chr4:17212665-17213102 REVERSE   Aliases: AP22.6, AP22_6	3.0	2.9	0.1	0.4	100.0%	-5.3
14132	AT5G20580.2   expressed protein, predicted protein, Arabidopsis thaliana   chr5:6958619-6962768 REVERSE   Aliases: F7C8.170, F7C8_170	5.6	5.5	0.1	0.4	100.0%	-4.7
14133	AT2G36560.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr2:15336272-15339526 REVERSE   Aliases: F1O11.19, F1O11_19	2.2	2.2	-0.1	-0.4	100.0%	-5.7
14134	AT1G77950.1   similar to MADS-box family protein [Arabidopsis thaliana] (TAIR:At1g22130.1); similar to putative MADS-box protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483124.1); contains InterPro domain Transcription factor, MADS-box (InterPro:IPR002100)   chr1:29311851-29314757 FORWARD   Aliases: F28K19.16, F28K19_16	3.1	3.0	0.1	0.4	100.0%	-5.0
14135	AT3G47330.1   expressed protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	2.8	2.9	-0.0	-0.4	100.0%	-5.7
14136	AT1G71500.1   Rieske (2Fe-2S) domain-containing protein, contains Pfam profile PF00355: iron-sulfur cluster-binding protein, rieske family   chr1:26939700-26941269 FORWARD   Aliases: F26A9.12	7.3	7.1	0.2	0.4	100.0%	-4.3
14137	AT4G38590.1   Symbol: BGAL14	3.4	3.5	-0.1	-0.4	100.0%	-5.2
14138	AT1G02250.1   Symbol: ANAC005   no apical meristem (NAM) family protein, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to NAC1 (GI:21554126) (Arabidopsis thaliana)   chr1:437951-439559 REVERSE   Aliases: ANAC005, T6A9.20	2.4	2.4	-0.1	-0.4	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14139	AT1G26460.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:9151719-9154727 FORWARD   Aliases: T1K7.17, T1K7_17	7.3	7.7	-0.3	-0.4	100.0%	-4.4
14140	AT4G18160.1   Symbol: KCO6   outward rectifying potassium channel, putative (KCO6), similar to kco1 (Arabidopsis thaliana) gi:2230761:emb:CAA69158; member of the 2 pore, 4 transmembrane (2P/4TM) K+ channel family, PMID:11500563   chr4:10055707-10057747 FORWARD   Aliases: F15J5.130, F15J5_130	5.5	5.3	0.2	0.4	100.0%	-4.9
14141	AT4G25110.2   similar to latex-abundant family protein (AMC1) / caspase family protein [Arabidopsis thaliana] (TAIR:At1g02170.1); similar to putative metacaspase [Oryza sativa (japonica cultivar-group)] (GB:AAR06365.1); contains InterPro domain Zn-finger, LSD1 type (InterPro:IPR005735); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Caspase-1, p20 (InterPro:IPR001309)   chr4:12887528-12890271 REVERSE   Aliases: F24A6.7	2.8	2.8	0.1	0.4	100.0%	-5.0
14142	AT2G41260.2   Symbol: M17   glycine-rich protein / late embryogenesis abundant protein (M17), identical to late-embryogenesis abundant M17 protein GI:3342551 from (Arabidopsis thaliana)   chr2:17213592-17214776 FORWARD   Aliases: ATM17, F13H10.19, F13H10_19	2.1	2.1	0.0	0.4	100.0%	-6.1
14143	AT4G25610.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr4:13063273-13067949 FORWARD   Aliases: M7J2.20, M7J2_20	3.3	3.4	-0.1	-0.4	100.0%	-5.0
14144	AT2G46930.1   pectinacetyltransferase, putative, similar to pectinacetyltransferase precursor GI:1431629 from (Vigna radiata)   chr2:19290588-19293416 FORWARD   Aliases: F14M4.24	7.2	7.4	-0.2	-0.4	100.0%	-4.6
14145	AT1G58265.1   cytochrome P450-related   chr1:21614574-21615053 FORWARD   Aliases: None	2.2	2.3	-0.1	-0.4	100.0%	-5.1
14146	AT5G24250.1   expressed protein   chr5:8233699-8234655 REVERSE   Aliases: MOP9.6, MOP9_6	2.3	2.3	-0.1	-0.4	100.0%	-5.8
14147	AT3G04360.1   C2 domain-containing protein, low similarity to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain   chr3:1157011-1158316 REVERSE   Aliases: T6K12.2, T6K12_2	4.3	4.1	0.1	0.4	100.0%	-4.8
14148	AT3G03170.1   expressed protein   chr3:731898-732882 FORWARD   Aliases: T17B22.14, T17B22_14	5.0	5.1	-0.1	-0.4	100.0%	-4.8
14149	AT4G17620.2   similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:At4g30460.1); similar to glycine-rich protein [Haloxylon ammodendron] (GB:AAS99237.1); contains domain GLY_RICH (PS50315); contains domain SER_RICH (PS50324)   chr4:9821927-9825019 FORWARD   Aliases: DL4845W, FCAALL.74	8.7	8.6	0.1	0.4	100.0%	-5.0
14150	AT3G10525.1   expressed protein   chr3:3281367-3282037 REVERSE   Aliases: None	3.1	2.9	0.2	0.4	100.0%	-4.8
14151	AT4G38520.2   protein phosphatase 2C family protein / PP2C family protein, similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain;   chr4:18015730-18018267 REVERSE   Aliases: F20M13.80, F20M13_80	6.3	6.1	0.1	0.4	100.0%	-4.8
14152	AT3G04920.1   40S ribosomal protein S24 (RPS24A), similar to ribosomal protein S19 GB:445612 (Solanum tuberosum) and similar to ribosomal protein S24 GB:4506703 (Homo sapiens)   chr3:1360888-1362301 FORWARD   Aliases: T9J14.13, T9J14_13	9.5	9.7	-0.2	-0.4	100.0%	-4.5
14153	AT1G80560.1   3-isopropylmalate dehydrogenase, chloroplast, putative, strong similarity to 3-ISOPROPYLMALATE DEHYDROGENASE PRECURSOR GB:P29102 SP:P29102 from (Brassica napus)	10.3	10.5	-0.2	-0.4	100.0%	-4.5
14154	AT1G54170.1   Symbol: CID3   ataxin-2-related, similar to SCA2 (GI:1770390) (Homo sapiens); similar to ataxin-2 (GI:3005020) (Mus musculus). Member of a family of PAM2 motif containing proteins.   chr1:20224727-20229613 REVERSE   Aliases: CID3, F15I1.27, F15I1_27	3.8	3.7	0.1	0.4	100.0%	-5.0
14155	AT4G35670.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase PG1 (Vitis vinifera) GI:15081600; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr4:16915001-16917206 FORWARD   Aliases: F8D20.180, F8D20_180	2.7	2.7	-0.1	-0.4	100.0%	-5.7
14156	AT2G34330.1   expressed protein   chr2:14493706-14494380 FORWARD   Aliases: F13P17.17, F13P17_17	3.6	3.5	0.1	0.4	100.0%	-5.1
14157	AT1G74190.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.1 (Lycopersicon pimpinellifolium) gi:1184075:gb:AAC15779   chr1:27906251-27909819 REVERSE   Aliases: F9E11.4	3.2	3.3	-0.1	-0.4	100.0%	-5.5
14158	AT5G60350.1   expressed protein   chr5:24294956-24296340 FORWARD   Aliases: K9B18.6, K9B18_6	2.5	2.6	-0.1	-0.4	100.0%	-5.4
14159	AT5G22680.1   expressed protein   chr5:7540044-7540751 REVERSE   Aliases: MDJ22.10, MDJ22_10	2.9	3.0	-0.1	-0.4	100.0%	-5.0
14160	AT3G21865.1   expressed protein   chr3:7701139-7703328 REVERSE   Aliases: MSD21.24, MSD21_24	9.6	9.7	-0.1	-0.4	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14161	AT1G72170.1   expressed protein, contains Pfam PF04418: Domain of unknown function (DUF543)   chr1:27159997-27161338 FORWARD   Aliases: T9N14.2	9.6	9.7	-0.1	-0.4	100.0%	-4.7
14162	AT3G62660.1   glycosyl transferase family 8 protein, low similarity to glycosyl transferase lgtC - Neisseria gonorrhoeae, EMBL:AF208062; contains Pfam glycosyl transferase family 8 domain PF01501   chr3:23183782-23185737 FORWARD   Aliases: F26K9.90	5.7	5.7	0.1	0.4	100.0%	-5.0
14163	AT4G36210.2   expressed protein, contains Pfam PF05277: Protein of unknown function (DUF726)   chr4:17130249-17134305 FORWARD   Aliases: F23E13.100, F23E13_100	7.2	7.2	0.1	0.4	100.0%	-5.0
14164	AT4G15420.1   PRLI-interacting factor K, nearly identical to PRLI-interacting factor K (Arabidopsis thaliana) GI:11139266; contains Pfam profiles PF03152: Ubiquitin fusion degradation protein UFD1, PF00096: Zinc finger, C2H2 type   chr4:8823725-8826096 FORWARD   Aliases: DL3755W, FCAALL.127	7.2	7.0	0.1	0.4	100.0%	-4.9
14165	AT5G57990.1   Symbol: UBP23   ubiquitin-specific protease 23, putative (UBP23), identical to GI:11993486   chr5:23487240-23491330 REVERSE   Aliases: MTI20.25, MTI20_25, UBIQUITIN SPECIFIC PROTEASE 23	8.3	8.6	-0.2	-0.4	100.0%	-4.9
14166	AT5G60410.4   Symbol: ATSIZ1	4.4	4.5	-0.1	-0.4	100.0%	-5.1
14167	AT4G29100.1   ethylene-responsive family protein, contains similarity to ethylene-inducible ER33 protein (Lycopersicon esculentum) gi:5669656:gb:AAD46413   chr4:14341006-14344609 FORWARD   Aliases: F19B15.130, F19B15_130	6.8	6.5	0.3	0.4	100.0%	-4.5
14168	AT3G07680.1   emp24/gp25L/p24 family protein, similar to SP:Q15363 Cop-coated vesicle membrane protein p24 precursor (p24A) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family   chr3:2455308-2456885 FORWARD   Aliases: MLP3.13	10.1	10.3	-0.2	-0.4	100.0%	-4.9
14169	AT4G05570.1   expressed protein   chr4:2839609-2840634 REVERSE   Aliases: T1J24.5, T1J24_5	3.1	3.0	0.1	0.4	100.0%	-5.4
14170	AT3G04370.2   similar to 33 kDa secretory protein-related [Arabidopsis thaliana] (TAIR:At1g04520.1); similar to 33 kDa secretory protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD46165.1); contains InterPro domain Protein of unknown function DUF26 (InterPro:IPR002902)   chr3:1159429-1161132 FORWARD   Aliases: T27C4.1, T27C4_1	3.6	3.6	-0.1	-0.4	100.0%	-4.9
14171	AT2G05710.1   aconitate hydratase, cytoplasmic, putative / citrate hydro-lyase/aconitase, putative, nearly identical to SP:P49608 Aconitate hydratase, cytoplasmic (EC 4.2.1.3) (Citrate hydro-lyase) (Aconitase) {Cucurbita maxima}; contains Pfam profiles PF00330: Aconitase family (aconitate hydratase), PF00694: Aconitase C-terminal domain   chr2:2141396-2146675 FORWARD   Aliases: T3P4.5, T3P4_5	10.9	11.1	-0.2	-0.4	100.0%	-5.3
14172	AT5G45710.2   Symbol: AT HSFA4C   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr5:18558096-18560090 FORWARD   Aliases: HSFA4C, MRA19.11, MRA19_11, RHA1	4.7	4.6	0.1	0.4	100.0%	-4.5
14173	AT5G05660.1   zinc finger (NF-X1 type) family protein, contains PF01422: NF-X1 type zinc finger   chr5:1690862-1695474 REVERSE   Aliases: MJJ3.6, MJJ3_6	3.4	3.5	-0.1	-0.4	100.0%	-5.2
14174	AT4G28680.1   tyrosine decarboxylase, putative, similar to SP:P54768 Tyrosine/DOPA decarboxylase 1 (Includes: DOPA decarboxylase (EC 4.1.1.28) (DDC); Tyrosine decarboxylase (EC 4.1.1.25)) {Papaver somniferum}, SP:Q06086 Tyrosine decarboxylase 2 (EC 4.1.1.25) {Petroselinum crispum}; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain   chr4:14155254-14158676 FORWARD   Aliases: T5F17.130, T5F17_130	2.9	2.9	0.1	0.4	100.0%	-5.3
14175	AT2G44910.1   homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein 4, identical to Homeobox-leucine zipper protein ATHB-4 (HD-ZIP protein ATHB-4) (SP:P92953) (Arabidopsis thaliana)   chr2:18524962-18526600 REVERSE   Aliases: T13E15.8	2.6	2.7	-0.1	-0.4	100.0%	-5.5
14176	AT4G36480.2   Symbol: ATLCB1	4.3	4.5	-0.1	-0.4	100.0%	-4.8
14177	AT5G47190.1   ribosomal protein L19 family protein, similar to plastid ribosomal protein L19 precursor (Spinacia oleracea) gi:7582403:gb:AAF64312   chr5:19181475-19183334 REVERSE   Aliases: MQL5.4, MQL5_4	6.0	6.2	-0.1	-0.4	100.0%	-4.4
14178	AT4G26480.1   KH domain-containing protein, qkl-7, Mus musculus   chr4:13372893-13378398 REVERSE   Aliases: M3E9.90, M3E9_90	6.3	6.0	0.3	0.4	100.0%	-4.4
14179	AT1G66360.1   C2 domain-containing protein, similar to zinc finger and C2 domain protein GI:9957238 from (Arabidopsis thaliana)   chr1:24755040-24756497 FORWARD   Aliases: T27F4.11, T27F4_11	2.9	2.9	-0.1	-0.4	100.0%	-5.6
14180	AT2G42680.1   ethylene-responsive transcriptional coactivator, putative, similar to ethylene-responsive transcriptional coactivator (Lycopersicon esculentum) gi:5669634:gb:AAD46402   chr2:17781980-17783387 FORWARD   Aliases: F14N22.5, F14N22_5	12.3	12.4	-0.1	-0.4	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14181	AT5G47130.1   Bax inhibitor-1 family / BI-1 family, similar to SP:Q9LD45 Bax inhibitor-1 (BI-1) (AtBI-1) {Arabidopsis thaliana}   chr5:19158243-19159238 FORWARD   Aliases: K14A3.8, K14A3_8	4.0	3.9	0.1	0.4	100.0%	-5.0
14182	AT5G14040.1   mitochondrial phosphate transporter, identical to mitochondrial phosphate transporter GI:3318617 from (Arabidopsis thaliana)   chr5:4530645-4533072 REVERSE   Aliases: MUA22.4, MUA22_4	9.2	9.5	-0.3	-0.4	100.0%	-4.6
14183	AT4G16830.1   nuclear RNA-binding protein (RGGA), identical to nuclear RNA binding protein GI:6492264 from (Arabidopsis thaliana)   chr4:9470458-9472613 FORWARD   Aliases: DL4440W, FCAALL.13	9.2	9.0	0.1	0.4	100.0%	-4.8
14184	AT3G12800.1   short-chain dehydrogenase/reductase (SDR) family protein, contains Pfam profile PF00106:oxidoreductase, short chain dehydrogenase/reductase family   chr3:4063331-4064795 REVERSE   Aliases: AT3G12790, MBK21.23	8.6	8.4	0.2	0.4	100.0%	-4.9
14185	NA	2.4	2.3	0.0	0.4	100.0%	-6.2
14186	AT4G11610.1   Symbol: NTRB   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr4:7013723-7018043 REVERSE   Aliases: ATNTRB, T5C23.40, T5C23_40	3.4	3.5	-0.1	-0.4	100.0%	-4.9
14187	AT3G01670.1   expressed protein   chr3:247241-250477 FORWARD   Aliases: F4P13.21, F4P13_21	3.1	3.0	0.1	0.4	100.0%	-4.5
14188	AT1G34160.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:12441371-12443234 FORWARD   Aliases: F12G12.2, F12G12_2	5.2	5.3	-0.2	-0.4	100.0%	-4.7
14189	AT1G54780.1   thylakoid lumen 18.3 kDa protein, SP:Q9ZVL6   chr1:20443101-20444826 FORWARD   Aliases: T22H22.19, T22H22_19	8.5	8.6	-0.1	-0.4	100.0%	-4.6
14190	AT3G24590.1   signal peptidase I family protein, contains Pfam profile: PF00461 signal peptidase I   chr3:8970679-8972175 FORWARD   Aliases: MOB24.17	8.6	8.5	0.1	0.4	100.0%	-5.1
14191	AT5G06500.1   MADS-box family protein, contains similarity to MADS-box transcription factor   chr5:1982445-1983173 FORWARD   Aliases: F15M7.3, F15M7_3	3.2	3.1	0.1	0.4	100.0%	-5.5
14192	AT1G13750.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	5.2	5.4	-0.1	-0.4	100.0%	-4.7
14193	AT1G74550.1   Symbol: CYP98A9   cytochrome P450, putative, similar to cytochrome P450 98A3 (SP:O22203)(Arabidopsis thaliana); cytochrome P450 (GB:O48922) (Glycine max); contains Pfam profile: PF00067 cytochrome P450   chr1:28019706-28021523 FORWARD   Aliases: F1M20.23, F1M20_23	2.5	2.5	0.1	0.4	100.0%	-5.5
14194	AT3G17910.1   Symbol: SURF1   surfeit 1 (SURF1), identical to Surfeit 1 GB:AAF19609 from (Arabidopsis thaliana)   chr3:6133534-6136377 FORWARD   Aliases: MEB5.13, SURFEIT 1	5.3	5.4	-0.1	-0.4	100.0%	-4.9
14195	AT2G14080.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr2:5932307-5936682 FORWARD   Aliases: T22C12.1	3.3	3.2	0.1	0.4	100.0%	-4.9
14196	AT5G27550.1   kinesin motor protein-related, kinesin-like heavy chain - Arabidopsis thaliana, EMBL:AF080249   chr5:9728450-9730308 REVERSE   Aliases: F21A20.1	3.9	4.0	-0.1	-0.4	100.0%	-4.9
14197	AT4G21323.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr4:11342504-11345642 FORWARD   Aliases: None	2.8	2.7	0.1	0.4	100.0%	-5.5
14198	AT1G73860.1   kinesin motor protein-related, similar to kinesin-C GB:AAF04841 from (Strongylocentrotus purpuratus)   chr1:27774647-27780518 REVERSE   Aliases: F2P9.27, F2P9_27	2.9	3.0	-0.1	-0.4	100.0%	-5.0
14199	AT1G51820.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase GI:1321686 from (Arabidopsis thaliana); contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19241076-19245552 REVERSE   Aliases: T14L22.3, T14L22_3	2.8	2.8	-0.1	-0.4	100.0%	-5.4
14200	AT5G35230.1   expressed protein   chr5:13507208-13508903 REVERSE   Aliases: T25C13.110, T25C13_110	2.7	2.6	0.1	0.4	100.0%	-5.5
14201	AT3G13390.1   Symbol: SKS11   multi-copper oxidase type I family protein, nearly identical to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Multicopper oxidase domain PF00394   chr3:4351052-4353342 REVERSE   Aliases: MRP15.3, SKS11	3.0	2.9	0.1	0.4	100.0%	-5.5
14202	AT5G59050.2   expressed protein   chr5:23856383-23859903 REVERSE   Aliases: K18B18.4, K18B18_4	4.1	4.0	0.1	0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14203	AT3G44040.1   expressed protein   chr3:15823362-15824941 FORWARD   Aliases: T15B3.180	2.8	2.8	0.0	0.4	100.0%	-5.6
14204	AT2G29600.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:12662228-12664373 FORWARD   Aliases: F16P2.2, F16P2_2	3.6	3.7	-0.1	-0.4	100.0%	-5.1
14205	AT1G77020.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein (Saccharomyces cerevisiae); contains Pfam profile PF00226 DnaJ domain   chr1:28949775-28951761 REVERSE   Aliases: F22K20.12, F22K20_12	6.0	6.1	-0.1	-0.4	100.0%	-4.9
14206	AT2G32900.1   Symbol: ATZW10	3.8	3.9	-0.1	-0.4	100.0%	-4.9
14207	AT2G02220.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:584097-587123 REVERSE   Aliases: T16F16.1	3.2	3.2	0.1	0.4	100.0%	-5.3
14208	AT3G19184.1   similar to transcriptional factor B3 family protein [Arabidopsis thaliana] (TAIR:At5g58280.1); similar to Unknown protein [Oryza sativa] (GB:XP_470571.1); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340)   chr3:6637561-6638971 FORWARD   Aliases: None	2.5	2.4	0.0	0.4	100.0%	-5.9
14209	AT3G42120.1   expressed protein   chr3:14306707-14307936 FORWARD   Aliases: F4M19.80	2.4	2.5	-0.0	-0.4	100.0%	-5.9
14210	AT3G29420.1   geranylgeranyl pyrophosphate synthase-related / GGPP synthetase-related / farnesyltranstransferase-related, fragment similar to farnesyltranstransferase precursor GB:T10452 from (Sinapis alba)	2.9	2.8	0.1	0.4	100.0%	-5.1
14211	AT1G09760.1   Symbol: U2A'   U2 small nuclear ribonucleoprotein A, putative, identical to U2 small nuclear ribonucleoprotein A' (U2 snRNP-A') (Arabidopsis thaliana) SWISS-PROT:P43333; supported by cDNA:gi_16649064_gb_AY059902.1_   chr1:3158748-3161666 REVERSE   Aliases: F21M12.14, F21M12_14, U2A'	5.4	5.6	-0.2	-0.4	100.0%	-4.8
14212	AT4G39440.1   expressed protein, ; expression supported by MPSS   chr4:18345679-18347221 FORWARD   Aliases: F23K16.70, F23K16_70	3.2	3.1	0.1	0.4	100.0%	-5.3
14213	AT5G57785.1   expressed protein   chr5:23426122-23426648 REVERSE   Aliases: None	3.4	3.2	0.2	0.4	100.0%	-4.2
14214	AT5G07890.3   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g61200.1); similar to hypothetical protein DDB0217534 [Dictyostelium discoideum] (GB:EAL70339.1); similar to similar to Entamoeba histolytica. Myosin heavy chain [Dictyostelium discoideum] (GB:AAO52540.1); contains domain SER_RICH (PS50324)	4.8	4.8	0.1	0.4	100.0%	-5.2
14215	AT3G24000.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:8672781-8674682 FORWARD   Aliases: F14O13.19	3.6	3.5	0.1	0.4	100.0%	-5.0
14216	AT5G44330.1   male sterility MS5 family protein, similar to male sterility MS5 (Arabidopsis thaliana) GI:3859112; contains Pfam profile PF00515 TPR Domain   chr5:17874552-17876283 FORWARD   Aliases: K9L2.11, K9L2_11	3.0	3.0	-0.1	-0.4	100.0%	-5.4
14217	AT5G42970.1   Symbol: COP8   COP9 signalosome complex subunit 4 / CSN complex subunit 4 (CSN4) (COP8) (FUS4), FUSCA4, COP8, CSN4; identical to CSN complex subunit 4 (Arabidopsis thaliana) GI:18056659, COP8 (Arabidopsis thaliana) GI:5802627; contains Pfam profile PF01399: PCI domain; identical to cDNA CSN complex subunit 4 (CSN4) GI:18056658   chr5:17254413-17257961 REVERSE   Aliases: ATS4, CONSTITUTIVE PHOTOMORPHOGENIC 14, CONSTITUTIVE PHOTOMORPHOGENIC 8, COP14, CSN4, EMB134, EMBRYO DEFECTIVE 134, FUS4, FUS8, FUSCA 4, FUSCA 8, MBD2.17, MBD2_17	5.2	5.3	-0.1	-0.4	100.0%	-5.0
14218	AT5G24820.1   aspartyl protease family protein, low similarity to CND41, chloroplast nucleoid DNA binding protein (Nicotiana tabacum) GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease   chr5:8523409-8525300 FORWARD   Aliases: F6A4.30, F6A4_30	2.4	2.4	0.1	0.4	100.0%	-5.6
14219	AT5G04180.1   carbonic anhydrase family protein, similar to storage protein (dioscorin) (Dioscorea cayenensis) GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase   chr5:1147674-1149280 REVERSE   Aliases: F21E1.100, F21E1_100	2.8	2.9	-0.1	-0.4	100.0%	-5.1
14220	AT2G16210.2   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr2:7033882-7036136 REVERSE   Aliases: F7H1.23, F7H1_23	4.1	4.1	-0.1	-0.4	100.0%	-5.3
14221	AT5G47150.1   YDG/SRA domain-containing protein, low similarity to nuclear protein np95 (Mus musculus) GI:4220590; contains Pfam profile PF02182: YDG/SRA domain   chr5:19167272-19169020 FORWARD   Aliases: K14A3.10, K14A3_10	2.9	3.0	-0.1	-0.4	100.0%	-5.4
14222	AT3G60780.1   expressed protein   chr3:22473632-22474760 FORWARD   Aliases: T4C21.190	2.5	2.6	-0.1	-0.4	100.0%	-5.3
14223	AT1G76300.1   small nuclear ribonucleoprotein D3, putative / snRNP core protein D3, putative / Sm protein D3, putative, similar to SWISS-PROT:P43331 small nuclear ribonucleoprotein Sm D3 (snRNP core protein D3, Sm-D3) (Mouse)   chr1:28630778-28632257 FORWARD   Aliases: F15M4.20	7.3	7.2	0.1	0.4	100.0%	-4.5
14224	AT2G03580.1   F-box family protein-related, supported by tandem duplication of	3.3	3.2	0.1	0.4	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14225	AT1G53570.3   Symbol: MAP3KA	3.1	3.0	0.1	0.4	100.0%	-4.8
14226	AT2G36835.1   expressed protein   chr2:15456686-15458505 REVERSE   Aliases: None	7.9	7.6	0.2	0.4	100.0%	-4.6
14227	AT1G28340.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains some similarity to receptor-like protein kinases   chr1:9940162-9943536 FORWARD   Aliases: F3M18.23, F3M18_23	5.9	6.0	-0.1	-0.4	100.0%	-5.0
14228	AT3G44770.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr3:16327067-16330445 FORWARD   Aliases: T32N15.6	3.2	3.3	-0.1	-0.4	100.0%	-5.0
14229	AT5G39850.1   40S ribosomal protein S9 (RPS9C), 40S ribosomal protein S9 - Chlamydomonas sp.,EMBL:AU066528   chr5:15967250-15968653 FORWARD   Aliases: MYH19.10, MYH19_10	8.3	8.1	0.2	0.4	100.0%	-4.4
14230	AT3G10320.1   expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)   chr3:3195319-3197351 REVERSE   Aliases: F14P13.8	3.3	3.2	0.1	0.4	100.0%	-4.7
14231	AT5G20040.2   Symbol: ATIPT9	8.3	8.5	-0.2	-0.4	100.0%	-4.4
14232	AT3G03290.1   universal stress protein (USP) family protein, contains Pfam profile: PF00582 universal stress protein family   chr3:766752-767749 FORWARD   Aliases: T17B22.2, T17B22_2	2.8	2.7	0.1	0.4	100.0%	-5.4
14233	AT4G38700.1   disease resistance-responsive family protein, related to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669G   chr4:18076453-18077171 REVERSE   Aliases: T9A14.4	4.6	4.5	0.1	0.4	100.0%	-4.9
14234	AT4G20010.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g44785.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD87869.1); contains InterPro domain Protein of unknown function DUF731 (InterPro:IPR007993)	7.0	6.9	0.1	0.4	100.0%	-4.9
14235	AT2G22010.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:9370801-9376375 REVERSE   Aliases: AT2G22020, F7D8.33, F7D8_33	5.2	5.3	-0.1	-0.4	100.0%	-5.3
14236	AT1G16590.1   Symbol: REV7   mitotic spindle checkpoint protein, putative, similar to Mad2B protein (Homo sapiens) gi:4835900:gb:AAD30290   chr1:5673788-5674883 FORWARD   Aliases: F19K19.10, F19K19_10	3.5	3.4	0.1	0.4	100.0%	-4.9
14237	AT3G57030.1   strictosidine synthase family protein, similar to strictosidine synthase (Rauvolfia serpentina)(SP:P15324)   chr3:21112436-21114272 REVERSE   Aliases: F24I3.110	8.4	8.2	0.2	0.4	100.0%	-4.8
14238	AT3G11000.1   expressed protein   chr3:3447592-3450517 FORWARD   Aliases: F9F8.18	3.1	3.1	0.1	0.4	100.0%	-5.1
14239	AT3G20080.3   Symbol: CYP705A15   cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	3.6	3.5	0.1	0.4	100.0%	-4.7
14240	AT5G62130.1   Per1-like protein-related   chr5:24967543-24970417 REVERSE   Aliases: MTG10.16, MTG10_16	2.8	2.6	0.1	0.4	100.0%	-4.8
14241	AT1G21520.1   expressed protein   chr1:7534522-7534722 REVERSE   Aliases: F24J8.16, F24J8_16	2.2	2.3	-0.0	-0.4	100.0%	-5.5
14242	AT4G31130.1   expressed protein   chr4:15136941-15138801 REVERSE   Aliases: F6E21.50, F6E21_50	6.7	6.5	0.2	0.4	100.0%	-4.9
14243	AT5G35470.1   hypothetical protein   chr5:13699706-13699978 REVERSE   Aliases: MOK9.5, MOK9_5	2.2	2.2	-0.0	-0.4	100.0%	-5.9
14244	AT2G42180.1   expressed protein   chr2:17587995-17589034 REVERSE   Aliases: T24P15.9, T24P15_9	2.7	2.8	-0.1	-0.4	100.0%	-5.5
14245	AT5G56070.1   expressed protein   chr5:22725905-22726430 FORWARD   Aliases: MDA7.12, MDA7_12	2.2	2.1	0.0	0.4	100.0%	-5.9
14246	AT2G02310.1   Symbol: ATPP2 B6   F-box family protein / SKP1 interacting partner 3-related, contains similarity to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)	2.5	2.7	-0.2	-0.4	100.0%	-4.7
14247	AT1G06870.1   signal peptidase, putative, similar to chloroplast thylakoidal processing peptidase GB:CAA71502 GI:2769566 from (Arabidopsis thaliana); contains Pfam profile PF00461: Signal peptidase I   chr1:2108592-2110985 FORWARD   Aliases: F4H5.6, F4H5_6	7.2	7.3	-0.2	-0.4	100.0%	-4.9
14248	AT2G30440.1   chloroplast thylakoidal processing peptidase, identical to chloroplast thylakoidal processing peptidase (Arabidopsis thaliana) GI:2769566; contains Pfam profile PF00461: Signal peptidase I; non-consensus CG acceptor site at the intron:exon 8 boundary   chr2:12979954-12982574 FORWARD   Aliases: T6B20.20, T6B20_20	7.2	7.3	-0.2	-0.4	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14249	AT1G43680.1   expressed protein   chr1:16474645-16475706 FORWARD   Aliases: F2J6.3, F2J6_3	2.2	2.2	-0.0	-0.4	100.0%	-5.8
14250	AT2G05720.1   transducin family protein / WD-40 repeat family protein, Similar to U4/U6 small nuclear ribonucleoprotein hPrp4 (gi:2708305)(Homo sapiens); contains 4 WD-40 repeats   chr2:2147189-2148212 FORWARD   Aliases: T3P4.4, T3P4_4	3.8	3.7	0.1	0.4	100.0%	-5.1
14251	AT4G07350.1   hypothetical protein   chr4:4172606-4175224 REVERSE   Aliases: F28D6.10, F28D6_10	2.9	2.9	-0.1	-0.4	100.0%	-5.3
14252	AT5G13870.1   Symbol: EXGT A4   xyloglucan:xyloglucosyl transferase / xyloglucan endotransglycosylase / endo-xyloglucan transferase (EXGT-A4), identical to endoxyloglucan transferase EXGT-A4 GI:5533315 from (Arabidopsis thaliana)	3.1	3.0	0.1	0.4	100.0%	-4.9
14253	AT1G28490.2   Symbol: SYP61   similar to syntaxin 52 (SYP52) [Arabidopsis thaliana] (TAIR:At1g79590.1); similar to putative syntaxin 6 [Oryza sativa (japonica cultivar-group)] (GB:BAD87234.1); contains InterPro domain Target SNARE coiled-coil domain (InterPro:IPR000727)   chr1:10016419-10018011 FORWARD   Aliases: ATSYP61, F3M18.7, F3M18_7, OSM1, SYNTAXIN OF PLANTS 61	8.1	8.0	0.1	0.4	100.0%	-4.8
14254	AT1G49830.1   ethylene-responsive protein -related, similarity to ER33 protein (Lycopersicon esculentum) GI:5669656   chr1:18448779-18450327 REVERSE   Aliases: F10F5.7, F10F5_7	3.2	3.1	0.1	0.4	100.0%	-5.5
14255	AT4G11030.1   long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase, putative, similar to acyl-CoA synthetase (MF7P) gi:1617270 from Brassica napus   chr4:6738116-6742225 FORWARD   Aliases: T22B4.10, T22B4_10	2.5	2.5	0.0	0.4	100.0%	-5.7
14256	AT3G22680.1   expressed protein   chr3:8019736-8020515 FORWARD   Aliases: MWI23.5	7.4	7.2	0.2	0.4	100.0%	-4.6
14257	AT4G38930.2   ubiquitin fusion degradation UFD1 family protein, similar to SP:P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}; contains Pfam profile PF03152: Ubiquitin fusion degradation protein UFD1   chr4:18149548-18151770 FORWARD   Aliases: F19H22.30, F19H22_30	6.3	6.1	0.2	0.4	100.0%	-4.5
14258	AT5G48330.1   regulator of chromosome condensation (RCC1) family protein, contains Pfam PF00415:Regulator of chromosome condensation (RCC1) domain (5 copies); similar to UVB-resistance protein UVR8 (GI:5478530) {Arabidopsis thaliana}   chr5:19603162-19605067 FORWARD   Aliases: K23F3.5, K23F3_5	6.5	6.4	0.1	0.4	100.0%	-4.9
14259	AT3G51090.1   expressed protein   chr3:18988968-18990983 REVERSE   Aliases: F24M12.130	3.9	4.0	-0.1	-0.4	100.0%	-5.4
14260	AT3G59870.1   expressed protein, hypothetical protein F6E13.7 - Arabidopsis thaliana, PIR:T00674   chr3:22127138-22129218 REVERSE   Aliases: F24G16.140	3.2	3.3	-0.1	-0.4	100.0%	-5.3
14261	AT1G53020.1   ubiquitin-conjugating enzyme family protein, similar to ubiquitin-conjugating enzyme GB:3319990 from (Mus musculus); contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	3.6	3.5	0.1	0.4	100.0%	-5.2
14262	AT4G39753.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:18440106-18441439 FORWARD   Aliases: None	3.9	4.1	-0.1	-0.4	100.0%	-5.1
14263	AT1G10585.1   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At4g20970.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:NP_908393.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr1:3493958-3495136 REVERSE   Aliases: None	2.2	2.2	-0.0	-0.4	100.0%	-6.0
14264	AT5G57810.1   senescence-associated protein-related, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr5:23441501-23442873 REVERSE   Aliases: MTI20.4, MTI20_4	2.6	2.7	-0.1	-0.4	100.0%	-5.4
14265	AT4G12390.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Arabidopsis thaliana SP:Q42534, Lycopersicon esculentum SP:Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr4:7336494-7337353 FORWARD   Aliases: T1P17.4	6.4	6.3	0.1	0.4	100.0%	-5.5
14266	AT5G12140.1   Symbol: ATCYS1	11.9	12.0	-0.1	-0.4	100.0%	-5.2
14267	AT5G50890.1   expressed protein   chr5:20719910-20721461 FORWARD   Aliases: K3K7.3, K3K7_3	7.5	7.4	0.2	0.4	100.0%	-4.4
14268	AT2G04400.1   indole-3-glycerol phosphate synthase (IGPS), nearly identical to SP:P49572   chr2:1531159-1534041 FORWARD   Aliases: T1O3.19, T1O3_19	8.8	8.6	0.2	0.4	100.0%	-4.7
14269	AT3G08850.1   Encodes one of two Arabidopsis RAPTOR/KOG1 homologs. RAPTOR proteins are binding partners of the target of rapamycin kinase that is present in all eukaryotes and play a central role in the stimulation of cell growth and metabolism in response to nutrients. Mutants show embryo lethal phenotype which occurs at pre-globular stage. May interact with TOR kinase in a rapamycin like signaling pathway.	4.0	4.1	-0.1	-0.4	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14270	AT5G35630.2   Symbol: GS2   similar to glutamine synthetase, putative [Arabidopsis thaliana] (TAIR:At5g16570.1); similar to glutamine synthetase, putative [Arabidopsis thaliana] (TAIR:At5g37600.1); similar to glutamine synthetase, putative [Arabidopsis thaliana] (TAIR:At1g66200.1); similar to glutamine synthetase GS58 [Nicotiana attenuata] (GB:AAR86719.1); similar to glutamine synthetase precursor [Juglans nigra] (GB:AAD49734.1); similar to GLNA2_DAUCA Glutamine synthetase, chloroplast precursor (Glutamate--ammonia ligase) (GS2) (GB:O22506); similar to plastidic glutamine synthetase precursor [Brassica napus] (GB:CAA73062.1); similar to glutamine synthetase [Brassica napus] (GB:CAB72423.1); contains InterPro domain Glutamine synthetase, beta-Grasp domain (InterPro:IPR008147); contains InterPro domain Glutamine synthetase, catalytic domain (InterPro:IPR008146)   chr5:13848250-13850772 FORWARD   Aliases: ATGSL1, GLN2, GLUTAMINE SYNTHETASE 2, MJE4.9, MJE4_9	11.3	11.2	0.1	0.4	100.0%	-5.3
14271	AT3G02730.1   thioredoxin, putative, similar to SP:P29450 Thioredoxin F-type, chloroplast precursor (TRX-F) {Pisum sativum}; contains Pfam profile: PF00085 Thioredoxin   chr3:588415-589692 REVERSE   Aliases: F13E7.33, F13E7_33	8.4	8.1	0.2	0.4	100.0%	-4.2
14272	AT1G48820.1   terpene synthase/cyclase family protein, similar to terpene cyclase Gl:9293912 from (Arabidopsis thaliana)   chr1:18058897-18063035 FORWARD   Aliases: F11I4.2, F11I4_2	2.3	2.4	-0.1	-0.4	100.0%	-5.6
14273	AT4G09880.1   hypothetical protein, F21E10.5 Arabidopsis thaliana BAC F21E10, PID:g3047086   chr4:6214621-6215335 FORWARD   Aliases: T5L19.10, T5L19_10	3.4	3.4	0.1	0.4	100.0%	-5.4
14274	AT5G50450.1   zinc finger (MYND type) family protein, contains Pfam profile PF01753: MYND finger   chr5:20560536-20561979 REVERSE   Aliases: MXI22.17, MXI22_17	4.2	4.1	0.2	0.4	100.0%	-4.7
14275	AT3G42330.1   hypothetical protein   chr3:14495405-14496319 FORWARD   Aliases: T14K23.40	3.8	3.9	-0.1	-0.4	100.0%	-4.8
14276	AT2G34120.1   hypothetical protein   chr2:14412418-14412630 FORWARD   Aliases: T14G11.24, T14G11_24	2.8	2.8	-0.0	-0.4	100.0%	-5.7
14277	AT1G53270.1   ABC transporter family protein, contains similarity to ABC transporter Gl:10280532 from (Homo sapiens)   chr1:19866546-19868318 FORWARD   Aliases: F12M16.17, F12M16_17	2.5	2.6	-0.1	-0.4	100.0%	-4.9
14278	AT4G26500.1   Symbol: EMB1374   BolA-like family protein / Fe-S metabolism associated domain-containing protein, similar to SufE protein (Erwinia chrysanthemii) Gl:11342550; contains Pfam profiles PF02657: Fe-S metabolism associated domain, PF01722: BolA-like protein   chr4:13382206-13383649 REVERSE   Aliases: EMB1374, EMBRYO DEFECTIVE 1374, M3E9.70, M3E9_70	6.7	6.6	0.1	0.4	100.0%	-4.8
14279	AT3G48570.1   protein transport protein SEC61 gamma subunit, putative, similar to Swiss-Prot:Q19967 protein transport protein SEC61 gamma subunit (Caenorhabditis elegans)   chr3:18014898-18015959 REVERSE   Aliases: T8P19.80	9.1	8.9	0.2	0.4	100.0%	-5.1
14280	AT1G53290.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase ;contains similarity to Avr9 elicitor response protein Gl:4138265 from (Nicotiana tabacum)   chr1:19874967-19877158 FORWARD   Aliases: F12M16.19, F12M16_19	8.7	8.9	-0.2	-0.4	100.0%	-4.5
14281	AT3G02290.2   zinc finger (C3HC4-type RING finger) family protein, contains zinc finger motif, C3HC4 type (RING finger)   chr3:458399-460945 FORWARD   Aliases: F14P3.6, F14P3_6	3.3	3.2	0.1	0.4	100.0%	-5.1
14282	AT1G67960.1   expressed protein, AT-AC non-consensus splice sites at intron 6   chr1:25484315-25487925 REVERSE   Aliases: T23K23.19, T23K23_19	5.4	5.5	-0.1	-0.4	100.0%	-4.9
14283	AT2G40570.2   expressed protein, similar to hypothetical protein DDB0187104 [Dictyostelium discoideum] (GB:EAL64106.1); contains InterPro domain Initiator tRNA phosphoribosyl transferase (InterPro:IPR007306)   chr2:16947913-16950570 FORWARD   Aliases: T2P4.8, T2P4_8	4.0	4.1	-0.1	-0.4	100.0%	-4.9
14284	AT3G49600.1   Symbol: UBP26   ubiquitin-specific protease 26 (UBP26), similar to Gl:11993492; RNA binding protein - Homo sapiens, EMBL:AB016089 (N-terminus), several ubiquitin carboxyl-terminal hydrolases from aa pos. 712	3.8	3.7	0.1	0.4	100.0%	-5.0
14285	AT3G57360.1   expressed protein   chr3:21236549-21237662 FORWARD   Aliases: F28O9.210	7.4	7.5	-0.2	-0.4	100.0%	-4.5
14286	AT3G05860.2   MADS-box protein (AGL45), similar to MADS-box protein; PMID: 12837945; contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr3:1751412-1752361 REVERSE   Aliases: F10A16.16, F10A16_16	2.8	2.7	0.1	0.4	100.0%	-5.7
14287	AT3G24180.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g49900.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g10060.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g33700.1); similar to putative Bile acid beta-glucosidase [Oryza sativa (japonica cultivar-group)] (GB:XP_479737.1); similar to unknown protein [Oryza sativa] (GB:AAG16864.1); similar to At5g49900 [Oryza sativa (japonica cultivar-group)] (GB:AAX95400.1); contains InterPro domain Protein of unknown function DUF608 (InterPro:IPR006775)   chr3:8734641-8741732 REVERSE   Aliases: MUJ8.8	7.2	7.4	-0.2	-0.4	100.0%	-4.9
14288	AT5G43680.1   expressed protein   chr5:17561256-17562979 FORWARD   Aliases: MQO24.4, MQO24_4	3.9	3.8	0.1	0.4	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14289	AT1G52390.1   expressed protein   chr1:19515637-19515903 REVERSE   Aliases: F19K6.2, F19K6_2	3.1	3.1	-0.0	-0.4	100.0%	-5.7
14290	AT2G18920.1   hypothetical protein   chr2:8204835-8205242 REVERSE   Aliases: F19F24.12, F19F24_12	3.0	2.9	0.1	0.4	100.0%	-5.4
14291	AT3G23010.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr3:8174865-8176652 FORWARD   Aliases: MXC7.4	2.7	2.6	0.1	0.4	100.0%	-5.2
14292	AT2G19360.1   hypothetical protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr2:8385746-8390456 FORWARD   Aliases: F27F23.16, F27F23_16	2.6	2.7	-0.1	-0.4	100.0%	-5.5
14293	AT2G30670.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:13076390-13077981 REVERSE   Aliases: T11J7.6, T11J7_6	2.4	2.3	0.1	0.4	100.0%	-5.5
14294	AT3G57980.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr3:21477896-21480125 REVERSE   Aliases: T10K17.190	3.2	3.3	-0.1	-0.4	100.0%	-5.5
14295	AT2G02550.1   exonuclease family protein, contains similarity to exonuclease I (Homo sapiens) gi:4249655:gb:AAD13754   chr2:687383-688763 FORWARD   Aliases: T8K22.15, T8K22_15	2.1	2.1	-0.0	-0.4	100.0%	-5.8
14296	AT2G32140.1   similar to disease resistance protein (TIR class), putative [Arabidopsis thaliana] (TAIR:At1g65390.2); similar to disease resistance protein (TIR class), putative [Arabidopsis thaliana] (TAIR:At1g65390.1); similar to putative TIR-NBS type R protein 4 [Malus baccata] (GB:AAQ93076.1); contains InterPro domain TIR domain (InterPro:IPR000157)   chr2:13662707-13664242 REVERSE   Aliases: F22D22.11, F22D22_11	2.6	2.6	-0.1	-0.4	100.0%	-5.5
14297	AT3G27290.1   F-box family protein-related, contains weak similarity to PPA (Mus musculus) GP:18568225:gb:AAL75967   chr3:10080797-10082770 REVERSE   Aliases: K17E12.11	3.8	4.0	-0.1	-0.4	100.0%	-4.9
14298	AT3G05080.1   expressed protein   chr3:1417913-1418286 FORWARD   Aliases: T12H1.4, T12H1_4	3.2	3.3	-0.1	-0.4	100.0%	-4.8
14299	AT1G47270.1   F-box family protein / tubby family protein, contains Pfam profiles: PF00646 F-box domain, PF01167 Tub family; similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein Length(GI:6730158) (Mus musculus); similar to phosphodiesterase (GI:467578) (Mus musculus); similar to Tubby protein homolog (Swiss-Prot:O88808) (Rattus norvegicus)   chr1:17328996-17331168 FORWARD   Aliases: F8G22.1, F8G22_1	7.5	7.4	0.1	0.4	100.0%	-4.7
14300	AT1G60940.2   serine/threonine protein kinase, putative, similar to serine/threonine-protein kinase ASK1 from (Arabidopsis thaliana), SWISS-PROT:P43291   chr1:22442804-22445882 REVERSE   Aliases: T7P1.8, T7P1_8	9.9	9.8	0.1	0.4	100.0%	-5.1
14301	AT3G05620.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr3:1629664-1631772 REVERSE   Aliases: F18C1.11, F18C1_11	2.9	2.7	0.2	0.4	100.0%	-4.2
14302	AT3G59610.1   F-box family protein / jacalin lectin family protein, contains Pfam profile PF01419: Jacalin-like lectin domain   chr3:22030530-22032285 FORWARD   Aliases: T16L24.160	2.6	2.7	-0.1	-0.4	100.0%	-5.3
14303	AT2G43880.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase 4 (Lycopersicon esculentum) GI:2459815; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr2:18180111-18181559 FORWARD   Aliases: F6E13.1	2.4	2.4	0.1	0.4	100.0%	-5.4
14304	AT4G13460.2   Symbol: SUVH9   similar to SET domain-containing protein (SUVH2) [Arabidopsis thaliana] (TAIR:At2g33290.1); similar to putative SET1 [Oryza sativa (japonica cultivar-group)] (GB:XP_483836.1); contains InterPro domain Nuclear protein Zn2+-binding (InterPro:IPR003606); contains InterPro domain Nuclear protein SET (InterPro:IPR001214); contains InterPro domain Nuclear protein G9a (InterPro:IPR003105); contains InterPro domain Pre-SET (InterPro:IPR007728)	4.4	4.3	0.1	0.4	100.0%	-4.8
14305	AT1G74080.1   Symbol: MYB122	2.6	2.7	-0.1	-0.4	100.0%	-4.6
14306	AT1G11120.1   expressed protein   chr1:3715229-3719681 FORWARD   Aliases: T19D16.22, T19D16_22	5.2	5.4	-0.2	-0.4	100.0%	-4.5
14307	AT1G46696.1   expressed protein, slight similarity to maeb1 (GI:20087019)(Plasmodium falciparum).   chr1:17264300-17266623 REVERSE   Aliases: F2G19.33, F2G19_33	2.3	2.2	0.0	0.4	100.0%	-5.8
14308	AT3G26910.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g41100.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g41100.1); similar to hydroxyproline-rich glycoprotein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD38128.1)   chr3:9916365-9919980 REVERSE   Aliases: MDJ14.25	4.4	4.5	-0.1	-0.4	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14309	AT5G60800.1   heavy-metal-associated domain-containing protein, similar to farnesylated protein ATFP3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:24478115-24479760 REVERSE   Aliases: MAE1.5, MAE1_5	7.9	8.1	-0.3	-0.4	100.0%	-4.3
14310	AT1G73070.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to receptor-like protein kinase INRPK1 (Ipomoea nil) gi:14495542:gb:AAB36558   chr1:27482681-27487376 FORWARD   Aliases: F3N23.27, F3N23_27	3.6	3.6	0.1	0.4	100.0%	-5.4
14311	AT5G17560.1   BolA-like family protein, contains Pfam profile: PF01722 BolA-like protein   chr5:5788456-5789925 FORWARD   Aliases: K10A8.40, K10A8_40	6.7	6.6	0.1	0.4	100.0%	-4.7
14312	AT1G63700.1   Symbol: YDA   protein kinase, putative, contains protein kinase domain, Pfam:PF00069; similar to MEK kinase (MAP3Ka) (Arabidopsis thaliana) gi:4204912:gb:AAD10848   chr1:23628871-23632694 REVERSE   Aliases: F24D7.11, F24D7_11, MAPKKK4, YODA	2.7	2.8	-0.1	-0.4	100.0%	-5.2
14313	AT3G54510.1   early-responsive to dehydration protein-related / ERD protein-related, low similarity to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr3:20191270-20194487 FORWARD   Aliases: T14E10.80	3.0	3.0	0.1	0.4	100.0%	-5.3
14314	AT3G49960.1   peroxidase, putative, identical to peroxidase ATP21a (Arabidopsis thaliana) gi:1546696:emb:CAA67339   chr3:18535069-18536672 REVERSE   Aliases: F3A4.40	2.9	3.1	-0.2	-0.4	100.0%	-4.8
14315	AT3G29670.1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family   chr3:11530351-11531829 FORWARD   Aliases: MOD1.7	6.1	6.3	-0.2	-0.4	100.0%	-4.1
14316	AT5G07470.1   Symbol: PMSR3   peptide methionine sulfoxide reductase (MSR), nearly identical to peptide methionine sulfoxide reductase (msr) (Arabidopsis thaliana) GI:4884033   chr5:2362571-2364375 REVERSE   Aliases: PEPTIDEMETHIONINE SULFOXIDE REDUCTASE 3, T2I1.180, T2I1_180	9.1	8.9	0.2	0.4	100.0%	-5.1
14317	AT1G72960.1   root hair defective 3 GTP-binding (RHD3) family protein, contains Pfam profile: PF05879 root hair defective 3 GTP-binding protein (RHD3)	2.3	2.4	-0.1	-0.4	100.0%	-5.3
14318	AT1G63110.3   cell division cycle protein-related, contains 9 transmembrane domains; similar to PIG-U (GI:27372215) (Rattus norvegicus); similar to Cell division cycle protein 91-like 1 (CDC91-like 1 protein) (PIG-U) (Swiss-Prot:Q9H490) (Homo sapiens)   chr1:23408486-23411677 FORWARD   Aliases: F16M19.3, F16M19_3	4.6	4.7	-0.1	-0.4	100.0%	-5.0
14319	AT5G48740.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:19781910-19786595 REVERSE   Aliases: K24G6.7, K24G6_7	3.3	3.4	-0.1	-0.4	100.0%	-4.9
14320	AT3G06470.1   GNS1/SUR4 membrane family protein, similar to SP:P39540 Elongation of fatty acids protein 1 {Saccharomyces cerevisiae}; contains Pfam profile PF01151: GNS1/SUR4 family   chr3:1984174-1985265 FORWARD   Aliases: F24P17.3, F24P17_3	5.3	5.4	-0.1	-0.4	100.0%	-4.9
14321	AT5G26610.2   D111/G-patch domain-containing protein, contains Pfam PF01585: G-patch domain   chr5:9375256-9377128 FORWARD   Aliases: None	8.8	8.6	0.1	0.4	100.0%	-5.2
14322	AT2G39660.1   protein kinase, putative, similar to protein kinase gi:166809:gb:AAA18853   chr2:16538803-16540700 FORWARD   Aliases: F12L6.32, F12L6_32	7.0	7.2	-0.2	-0.4	100.0%	-4.8
14323	AT1G09795.1   Symbol: ATATP PRT2   ATP phosphoribosyl transferase 2 (ATP-PRT2), identical to ATP phosphoribosyl transferase (AtATP-PRT2) (Arabidopsis thaliana) GI:6683619; supporting cDNA gi:6683618:dbj:AB025250.1:   chr1:3173536-3176912 FORWARD   Aliases: ATP PHOSPHORIBOSYL TRANSFERASE 2	7.3	7.1	0.2	0.4	100.0%	-4.1
14324	AT1G55660.1   F-box family protein, contains F-box domain Pfam:PF00646	4.1	4.3	-0.1	-0.4	100.0%	-4.8
14325	AT4G38880.1   Symbol: ATASE3	3.0	3.0	-0.1	-0.4	100.0%	-5.5
14326	AT2G46050.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:18946335-18948107 FORWARD   Aliases: T3F17.30	3.3	3.3	0.0	0.4	100.0%	-5.5
14327	AT3G06990.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.4	3.3	0.1	0.4	100.0%	-5.0
14328	AT2G15280.2   reticulon family protein (RTNLB10), low similarity to neuroendocrine-specific protein C (Homo sapiens) GI:307311, SP:Q64548 Reticulon 1 (Neuroendocrine-specific protein) {Rattus norvegicus}; contains Pfam profile PF02453: Reticulon   chr2:6647236-6649432 FORWARD   Aliases: F27O10.7, F27O10_7	4.8	4.9	-0.1	-0.4	100.0%	-4.7
14329	AT1G54390.4   PHD finger protein-related, contains low similarity to PHD-finger domain proteins   chr1:20308290-20310657 REVERSE   Aliases: F20D21.22, F20D21_22	4.0	3.9	0.1	0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14330	AT4G17580.1   Bax inhibitor-1 family protein / BI-1 family protein, similar to SP:Q9LD45 Bax inhibitor-1 (BI-1) (AtBI-1) {Arabidopsis thaliana}; contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.5	3.4	0.1	0.4	100.0%	-5.1
14331	AT5G54980.1   integral membrane family protein, similar to unknown protein (gb:AAD50013.1); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr5:22332925-22333827 FORWARD   Aliases: MBG8.25, MBG8_25	5.8	5.7	0.1	0.4	100.0%	-4.6
14332	AT3G19550.1   expressed protein   chr3:6787247-6788296 REVERSE   Aliases: T31J18.5	2.7	2.7	0.1	0.4	100.0%	-5.7
14333	AT3G18640.1   zinc finger protein-related, contains similarity to zinc finger proteins (CCCH type)   chr3:6413623-6415835 REVERSE   Aliases: K24M9.13	4.1	4.3	-0.2	-0.4	100.0%	-4.7
14334	AT1G61790.1   OST3/OST6 family protein, weak similarity to SP:Q13454 N33 protein {Homo sapiens}; contains Pfam profile PF04756: OST3 / OST6 family   chr1:22818055-22819095 FORWARD   Aliases: T13M11.15, T13M11_15	7.9	7.5	0.3	0.4	100.0%	-4.5
14335	AT5G53680.1   RNA recognition motif (RRM)-containing protein, low similarity to RRM-containing protein SEB-4 (Xenopus laevis) GI:8895698; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:21815608-21816335 FORWARD   Aliases: MGN6.2, MGN6_2	2.7	2.7	-0.1	-0.4	100.0%	-5.5
14336	AT2G25820.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr2:11022152-11022878 FORWARD   Aliases: F17H15.15, F17H15_15	2.7	2.8	-0.1	-0.4	100.0%	-4.6
14337	AT4G16110.1   Symbol: ARR2   two-component responsive regulator family protein / response regulator family protein, similar to ARR2 protein GI:4210451 from (Arabidopsis thaliana); contains Pfam profile: PF00072 response regulator receiver domain	3.2	3.1	0.1	0.4	100.0%	-5.1
14338	AT4G10940.1   PHD finger family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr4:6708978-6710919 REVERSE   Aliases: F25I24.150, F25I24_150	3.8	3.7	0.1	0.4	100.0%	-4.8
14339	AT3G54800.2   similar to pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein [Arabidopsis thaliana] (TAIR:At2g28320.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_463792.1); contains InterPro domain Lipid-binding START (InterPro:IPR002913); contains InterPro domain Pleckstrin-like (InterPro:IPR001849)   chr3:20297062-20301050 FORWARD   Aliases: T5N23.160	3.3	3.3	-0.1	-0.4	100.0%	-5.7
14340	AT1G49810.1   Symbol: ATNHD2	4.1	4.3	-0.1	-0.4	100.0%	-5.1
14341	AT5G27200.1   Symbol: ACP5   acyl carrier protein, chloroplast, putative / ACP, putative, similar to Acyl carrier protein, chloroplast precursor (ACP) from {Arabidopsis thaliana} SP:P11829, {Brassica napus} SP:P17650; contains InterPro accession IPR003881: Isochorismatase   chr5:9571188-9571992 FORWARD   Aliases: A_TM021B04.6, T21B4.110, T21B4_110	2.4	2.5	-0.0	-0.4	100.0%	-5.5
14342	AT2G39590.1   40S ribosomal protein S15A (RPS15aC)   chr2:16524666-16525343 REVERSE   Aliases: F12L6.25, F12L6_25	3.1	3.2	-0.1	-0.4	100.0%	-5.5
14343	AT2G22660.2   similar to glycine-rich protein [Arabidopsis thaliana] (TAIR:At4g37900.1); similar to hypothetical protein [Sorghum bicolor] (GB:AAD27577.1)   chr2:9634488-9638161 FORWARD   Aliases: T9I22.10, T9I22_10	8.1	8.3	-0.2	-0.4	100.0%	-4.3
14344	AT1G75990.1   26S proteasome regulatory subunit S3, putative (RPN3), similar to 26S proteasome regulatory subunit S3 SP:P93768 (Nicotiana tabacum (Common tobacco))   chr1:28528160-28530437 REVERSE   Aliases: T4O12.21, T4O12_21	6.4	6.6	-0.2	-0.4	100.0%	-4.9
14345	AT3G49940.1   LOB domain protein 38 / lateral organ boundaries domain protein 38 (LBD38), identical to SP:Q9SN23 LOB domain protein 38 {Arabidopsis thaliana}   chr3:18525328-18526460 FORWARD   Aliases: F3A4.20	7.0	7.1	-0.2	-0.4	100.0%	-4.9
14346	AT1G57780.1   heavy-metal-associated domain-containing protein, low similarity to myosin-like antigen GI:159877 Onchocerca volvulus; contains Pfam profile PF00403: Heavy-metal-associated domain   chr1:21406665-21407893 FORWARD   Aliases: F12K22.17, F12K22_17	3.0	3.0	-0.0	-0.4	100.0%	-5.7
14347	AT5G51390.1   expressed protein, similar to unknown protein (gb:AAB68039.1)   chr5:20895193-20895690 REVERSE   Aliases: MFG13.10, MFG13_10	3.3	3.1	0.2	0.4	100.0%	-4.9
14348	AT1G16940.1   F-box family protein, contains F-box domain Pfam:PF00646	3.3	3.3	-0.1	-0.4	100.0%	-5.2
14349	AT1G31310.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965;   chr1:11198334-11200122 REVERSE   Aliases: T19E23.10, T19E23_10	3.4	3.3	0.1	0.4	100.0%	-5.1
14350	AT3G26070.1   plastid-lipid associated protein PAP / fibrillin family protein, contains Pfam profile PF04755: PAP_fibrillin   chr3:9527985-9529820 FORWARD   Aliases: MPE11.24	8.2	8.5	-0.3	-0.4	100.0%	-3.9
14351	AT3G26080.1   plastid-lipid associated protein PAP / fibrillin family protein, low similarity to Plastid-lipid-Associated Protein (Nicotiana tabacum) GI:2632088; contains Pfam profile PF04755: PAP_fibrillin	8.2	8.5	-0.3	-0.4	100.0%	-3.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14352	AT3G14250.1   zinc finger protein-related, contains weak similarity to zinc finger proteins and Pfam:PF01485 IBR domain   chr3:4745933-4746965 REVERSE   Aliases: MLN21.3	3.1	3.2	-0.1	-0.4	100.0%	-5.6
14353	AT3G01800.1   ribosome recycling factor family protein / ribosome releasing factor family protein, similar to SP:P82231 Ribosome recycling factor, chloroplast precursor (Ribosome releasing factor, chloroplast) (RRF) (CpFrr) (RRFHCP) {Spinacia oleracea}; contains Pfam profile PF01765: ribosome recycling factor	5.0	4.9	0.2	0.4	100.0%	-4.7
14354	AT5G45890.1   Symbol: SAG12   senescence-specific SAG12 protein (SAG12) / cysteine proteinase, putative, identical to senescence-specific protein SAG12 GI:1046373 from (Arabidopsis thaliana)   chr5:18630486-18632157 FORWARD   Aliases: CI0010, K15I22.9, K15I22_9, SENESCENCE ASSOCIATED GENE 12	3.3	3.2	0.1	0.4	100.0%	-5.2
14355	AT4G11060.1   single-strand-binding family protein, contains Pfam domain PF00436: Single-strand binding protein family	6.2	6.5	-0.3	-0.4	100.0%	-4.2
14356	AT1G47890.1   disease resistance family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr1:17647645-17650704 FORWARD   Aliases: T6B12.2, T6B12_2	2.6	2.5	0.1	0.4	100.0%	-5.4
14357	AT2G18550.1   Symbol: HB 2   homeobox-leucine zipper family protein, similar to CRHB6 (GI:3868839) (Ceratopteris richardii); contains Pfam PF00046: Homeobox domain   chr2:8056745-8058295 REVERSE   Aliases: F24H14.10, F24H14_10, HB 2	3.1	3.2	-0.1	-0.4	100.0%	-4.9
14358	AT4G26620.1   sucrase-related   chr4:13427417-13429965 REVERSE   Aliases: T15N24.70, T15N24_70	7.8	7.9	-0.1	-0.4	100.0%	-4.9
14359	AT4G35550.1   homeobox-leucine zipper protein (HB-2) / HD-ZIP protein, HB2 homeodomain protein (Populus tremula x Populus tremuloides) GI:3955021; contains Pfam PF00046: Homeobox domain   chr4:16875640-16877228 REVERSE   Aliases: F8D20.60, F8D20_60, HB 4	5.7	6.0	-0.2	-0.4	100.0%	-4.9
14360	AT2G20050.1   protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain;   chr2:8659554-8661274 REVERSE   Aliases: T2G17.15, T2G17_15	3.5	3.4	0.1	0.4	100.0%	-4.9
14361	AT4G32520.1   glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, similar to serine hydroxymethyltransferase (Chlamydomonas reinhardtii) GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase	10.3	10.1	0.2	0.4	100.0%	-4.5
14362	AT4G18180.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Salix gilgiana) GI:6714524; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr4:10065637-10067328 FORWARD   Aliases: T9A21.20, T9A21_20	3.1	3.0	0.1	0.4	100.0%	-5.2
14363	AT2G20630.2   protein phosphatase 2C, putative / PP2C, putative   chr2:8903993-8906916 REVERSE   Aliases: F23N11.5, F23N11_5	6.1	6.2	-0.1	-0.4	100.0%	-4.8
14364	AT5G43030.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.4	2.3	0.1	0.4	100.0%	-4.7
14365	NA	12.6	12.5	0.1	0.4	100.0%	-5.9
14366	AT3G60310.1   expressed protein   chr3:22298660-22301354 FORWARD   Aliases: F27H5.100	3.7	3.6	0.1	0.4	100.0%	-5.1
14367	AT1G60860.1   ARF GTPase-activating domain-containing protein   chr1:22404909-22411304 REVERSE   Aliases: F23C21.2, F23C21_2	5.6	5.4	0.2	0.4	100.0%	-4.8
14368	AT1G29280.1   Symbol: WRKY65	4.4	4.6	-0.2	-0.4	100.0%	-4.1
14369	AT5G55710.1   expressed protein   chr5:22572104-22572876 REVERSE   Aliases: MDF20.15, MDF20_15	5.3	5.1	0.1	0.4	100.0%	-4.7
14370	AT5G65370.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (GI:6492344) (Xenopus laevis)   chr5:26138934-26139975 FORWARD   Aliases: MNA5.10, MNA5_10	3.2	3.1	0.1	0.4	100.0%	-5.2
14371	AT1G26320.1   NADP-dependent oxidoreductase, putative, similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana; similar to allyl alcohol dehydrogenase GI:9758497 from (Arabidopsis thaliana)   chr1:9105195-9107176 FORWARD   Aliases: F28B23.3, F28B23_3	4.7	4.5	0.2	0.4	100.0%	-4.5
14372	AT3G55550.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr3:20610998-20613052 REVERSE   Aliases: T22E16.210	3.0	3.1	-0.1	-0.4	100.0%	-5.3
14373	AT1G64740.1   Symbol: TUA1   tubulin alpha-1 chain (TUA1), nearly identical to SP:P11139 Tubulin alpha-1 chain {Arabidopsis thaliana}	4.5	4.4	0.1	0.4	100.0%	-4.9
14374	AT3G03620.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296   chr3:873756-876803 REVERSE   Aliases: T12J13.10, T12J13_10	3.0	2.9	0.1	0.4	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14375	AT4G38160.2   Symbol: PDE191	2.7	2.8	-0.1	-0.4	100.0%	-5.3
14376	AT2G39520.1   expressed protein   chr2:16503891-16504699 FORWARD   Aliases: F12L6.18, F12L6_18	3.5	3.4	0.1	0.4	100.0%	-5.2
14377	AT4G37830.1   cytochrome c oxidase-related, contains weak similarity to cytochrome c oxidase polypeptide VIa-liver, mitochondrial precursor (EC 1.9.3.1) (Swiss-Prot:P10818) (Rattus norvegicus)   chr4:17787473-17788821 REVERSE   Aliases: None	11.3	11.4	-0.1	-0.4	100.0%	-5.1
14378	AT3G26125.1   Symbol: CYP86C2   cytochrome P450, putative   chr3:9553049-9554674 FORWARD   Aliases: MJL14.4	3.0	2.8	0.1	0.4	100.0%	-4.7
14379	AT1G16690.2   transcription factor-related, similar to enhancer of polycomb (GI:11907923)(Homo sapiens)   chr1:5706165-5709523 FORWARD   Aliases: F19K19.2, F19K19_2	3.7	3.8	-0.1	-0.4	100.0%	-5.1
14380	AT2G31210.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534	2.7	2.6	0.1	0.4	100.0%	-5.6
14381	AT3G27180.1   expressed protein   chr3:10028074-10031306 REVERSE   Aliases: MYF5.5	4.0	3.8	0.1	0.4	100.0%	-4.6
14382	AT5G12250.1   Symbol: TUB6   tubulin beta-6 chain (TUB6), nearly identical to SP:P29514 Tubulin beta-6 chain {Arabidopsis thaliana}   chr5:3961107-3963468 REVERSE   Aliases: BETA TUBULIN 6, BETA 6 TUBULIN, MXC9.21, MXC9_21	6.5	6.3	0.2	0.4	100.0%	-4.8
14383	AT5G58060.1   Symbol: YKT61   SNARE protein-related, similar to SNARE protein Ykt6 (Homo sapiens) GI:2507637   chr5:23515373-23517566 FORWARD   Aliases: ATGP1, ATYKT61, K21L19.5, K21L19_5, YKT61	8.5	8.2	0.3	0.4	100.0%	-4.6
14384	AT5G11610.2   exostosin family protein, contains Pfam domain, PF03016: Exostosin family   chr5:3735351-3738218 REVERSE   Aliases: T22P22.3	2.5	2.6	-0.1	-0.4	100.0%	-5.6
14385	AT1G56090.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain; similar to infertility-related sperm protein (Homo sapiens) GI:10863768, TPR-containing protein involved in spermatogenesis TPIS (Mus musculus) GI:6272680   chr1:20981360-20983014 REVERSE   Aliases: T6H22.6, T6H22_6	5.8	5.6	0.1	0.4	100.0%	-4.5
14386	AT3G25120.1   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, contains Pfam PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr3:9149551-9151112 REVERSE   Aliases: MJL12.6	7.2	7.4	-0.2	-0.4	100.0%	-4.3
14387	AT4G23610.1   expressed protein   chr4:12314035-12314839 FORWARD   Aliases: F9D16.80, F9D16_80	2.4	2.3	0.0	0.4	100.0%	-5.8
14388	AT5G60080.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:24210407-24212135 REVERSE   Aliases: MGO3.6, MGO3_6	3.1	3.0	0.2	0.4	100.0%	-4.9
14389	AT4G19040.1   pleckstrin homology (PH) domain-containing protein / lipid-binding START domain-containing protein, contains Pfam profiles PF01852: START domain, PF00169: PH domain   chr4:10431532-10437436 REVERSE   Aliases: F13C5.210, F13C5_210	7.3	7.2	0.1	0.4	100.0%	-5.0
14390	AT5G37960.1   oxidoreductase-related   chr5:15138668-15139066 FORWARD   Aliases: K18L3.120, K18L3_120	2.4	2.5	-0.0	-0.4	100.0%	-5.9
14391	AT3G01700.1   Symbol: AGP11   arabinogalactan-protein (AGP11), identical to gi:10880499:gb:AAG24279   chr3:258886-259638 FORWARD   Aliases: F4P13.24, F4P13_24	2.3	2.3	-0.1	-0.4	100.0%	-5.8
14392	AT1G04985.1   expressed protein   chr1:1416342-1418438 REVERSE   Aliases: F13M7.2, F13M7_2	7.9	7.7	0.1	0.4	100.0%	-4.8
14393	AT4G21410.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:11402325-11405067 REVERSE   Aliases: F18E5.30	5.4	5.6	-0.1	-0.4	100.0%	-4.5
14394	AT3G43810.1   Symbol: CAM7   calmodulin-7 (CAM7), almost identical to calmodulin GI:16227 from (Arabidopsis thaliana), SP:P59220 Calmodulin-7 {Arabidopsis thaliana}   chr3:15675358-15677445 REVERSE   Aliases: CALMODULIN 7, T28A8.100	11.8	12.0	-0.2	-0.4	100.0%	-4.5
14395	AT5G51810.1   Symbol: GA20OX2   Encodes gibberellin 20-oxidase. Involved in gibberellin biosynthesis. Up-regulated by far red light in elongating petioles. Not regulated by a circadian clock.   chr5:21072414-21074034 REVERSE   Aliases: AT2353, GA20OX2, MIO24.5, MIO24_5	2.5	2.6	-0.1	-0.4	100.0%	-5.6
14396	AT1G78460.1   SOUL heme-binding family protein, weak similarity to SOUL protein (Mus musculus) GI:4886906; contains Pfam profile PF04832: SOUL heme-binding protein   chr1:29523280-29524208 REVERSE   Aliases: F3F9.3	2.5	2.5	0.1	0.4	100.0%	-5.4
14397	AT1G77870.1   expressed protein, similar to geranylgeranylated protein ATGP4 (GI:4097567)   chr1:29289974-29290783 FORWARD   Aliases: F28K19.8, F28K19_8	2.6	2.6	-0.1	-0.4	100.0%	-5.3
14398	AT2G27950.1   expressed protein   chr2:11906340-11910248 REVERSE   Aliases: T1E2.13, T1E2_13	2.6	2.6	0.0	0.4	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14399	AT5G52710.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:21392979-21395398 FORWARD   Aliases: F6N7.20, F6N7_20	2.4	2.4	-0.1	-0.4	100.0%	-5.5
14400	AT3G02600.1   Symbol: LPP3   Encodes phosphatidic acid phosphatase. Expressed during germination.   chr3:551358-554678 FORWARD   Aliases: ATLPP3, F16B3.23, F16B3_23, LPP3	4.9	4.8	0.1	0.4	100.0%	-5.0
14401	AT5G17010.3   similar to sugar transporter family protein [Arabidopsis thaliana] (TAIR:At3g03090.1); similar to putative sugar transporter protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910048.1); contains InterPro domain Sugar transporter superfamily (InterPro:IPR005829); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sugar transporter (InterPro:IPR003663)   chr5:5587354-5592449 REVERSE   Aliases: F2K13.160, F2K13_160	7.3	7.4	-0.1	-0.4	100.0%	-4.8
14402	AT5G63000.1   expressed protein   chr5:25297238-25298759 REVERSE   Aliases: MJH22.6, MJH22_6	10.3	10.5	-0.1	-0.4	100.0%	-4.9
14403	AT3G21950.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri) and to SAM:benzoic acid carboxyl methyltransferase (BAMT)(GI:9789277)(Antirrhinum majus)   chr3:7735105-7736208 FORWARD   Aliases: MZN24.10	3.1	3.2	-0.1	-0.4	100.0%	-5.0
14404	AT1G52430.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr1:19535019-19539624 REVERSE   Aliases: F6D8.35, F6D8_35	3.1	3.2	-0.1	-0.4	100.0%	-4.9
14405	AT1G52450.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr1:19545353-19549935 REVERSE   Aliases: F6D8.33, F6D8_33	3.1	3.2	-0.1	-0.4	100.0%	-4.9
14406	AT5G25750.1   hypothetical protein   chr5:8950887-8951146 FORWARD   Aliases: T14C9.190, T14C9_190	3.5	3.5	-0.1	-0.4	100.0%	-5.3
14407	AT3G06483.1   Symbol: PDK   similar to mitochondrial pyruvate dehydrogenase kinase isoform 1 [Glycine max] (GB:AAT02655.1); contains InterPro domain Bacterial sensor protein, C-terminal (InterPro:IPR004358); contains InterPro domain ATP-binding region, ATPase-like (InterPro:IPR003594)	5.7	5.9	-0.2	-0.4	100.0%	-4.6
14408	AT2G05350.1   expressed protein   chr2:1950452-1954737 FORWARD   Aliases: F16J10.10, F16J10_10	2.3	2.2	0.1	0.4	100.0%	-5.7
14409	AT3G16550.1   DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana)   chr3:5629926-5632423 REVERSE   Aliases: MDC8.18	2.9	2.9	0.1	0.4	100.0%	-5.4
14410	AT4G24970.1   ATP-binding region, ATPase-like domain-containing protein, low similarity to microrchidia (Mus musculus) GI:5410255; contains Pfam profile PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein   chr4:12831019-12835459 FORWARD   Aliases: F13M23.110, F13M23_110	3.9	4.2	-0.2	-0.4	100.0%	-4.8
14411	AT4G24650.1   Symbol: ATIPT4	2.4	2.5	-0.1	-0.4	100.0%	-5.6
14412	AT3G28150.1   expressed protein   chr3:10473135-10474991 REVERSE   Aliases: MMG15.18	3.6	3.7	-0.1	-0.4	100.0%	-5.2
14413	AT2G32760.2   similar to similar to UV radiation resistance associated [Apis mellifera] (GB:XP_395920.1)   chr2:13899220-13901801 FORWARD   Aliases: F24L7.10, F24L7_10	4.0	3.9	0.1	0.4	100.0%	-4.9
14414	AT1G68630.1   expressed protein, similar to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr1:25772725-25773121 FORWARD   Aliases: F24J5.13, F24J5_13	2.3	2.3	-0.0	-0.4	100.0%	-5.6
14415	AT3G25180.2   Symbol: CYP82G1   cytochrome P450 family protein, similar to cytochrome P450 monooxygenase GB:AAC49188 (Pisum sativum); contains Pfam profile: PF00067 cytochrome P450   chr3:9167291-9169286 REVERSE   Aliases: MJL12.5	3.4	3.5	-0.1	-0.4	100.0%	-5.1
14416	AT2G15230.1   lipase family protein, similar to SP:P07098 Triacylglycerol lipase, gastric precursor (EC 3.1.1.3) {Homo sapiens}; contains Pfam profile PF04083: ab-hydrolase associated lipase region   chr2:6619663-6622477 FORWARD   Aliases: F15A23.3, F15A23_3	7.2	7.0	0.2	0.4	100.0%	-4.7
14417	AT5G62330.1   expressed protein   chr5:25048827-25049430 FORWARD   Aliases: MMI9.16, MMI9_16	2.7	2.6	0.1	0.4	100.0%	-5.2
14418	AT2G20170.1   hypothetical protein, and grail contains Pfam profile PF03080: Arabidopsis proteins of unknown function	3.3	3.2	0.1	0.4	100.0%	-5.3
14419	AT5G15140.1   aldose 1-epimerase family protein, similar to SP:P05149 Aldose 1-epimerase precursor (EC 5.1.3.3) (Mutarotase) from Acinetobacter calcoaceticus; contains Pfam profile PF01263 Aldose 1-epimerase   chr5:4908689-4910673 FORWARD   Aliases: F8M21.30, F8M21_30	2.3	2.2	0.1	0.4	100.0%	-5.6
14420	AT5G64870.1   expressed protein   chr5:25946764-25948610 REVERSE   Aliases: MXK3.10, MXK3_10	10.5	10.3	0.1	0.4	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14421	AT1G23250.1   caleosin-related, similar to calcium-binding RD20 protein (Arabidopsis thaliana) GI:10862968, caleosin GB:AAF13743 GI:6478218 from (Sesamum indicum)   chr1:8255222-8256258 REVERSE   Aliases: F26F24.9, F26F24_9	3.0	3.0	0.0	0.4	100.0%	-5.6
14422	AT1G51600.2   Symbol: ZML2   zinc finger (GATA type) family protein, contains similarity to zinc-finger protein ZIM (Arabidopsis thaliana) gi:8918533;dbj:BAA97679; contains Pfam PF00320: GATA zinc finger   chr1:19136123-19139093 FORWARD   Aliases: F5D21.22, F5D21_22, ZIM LIKE 2	5.2	5.4	-0.2	-0.4	100.0%	-4.7
14423	AT3G43760.1   expressed protein   chr3:15659200-15660409 REVERSE   Aliases: T28A8.50	2.8	2.8	-0.1	-0.4	100.0%	-5.4
14424	AT1G28630.1   expressed protein, ; expression supported by MPSS   chr1:10061209-10063438 REVERSE   Aliases: F1K23.14, F1K23_14	2.6	2.6	-0.1	-0.4	100.0%	-5.3
14425	AT2G39110.1   protein kinase, putative, similar to protein kinase (Lophopyrum elongatum) gi:13022177;gb:AAK11674   chr2:16326742-16328755 FORWARD   Aliases: T7F6.28, T7F6_28	4.9	5.0	-0.1	-0.4	100.0%	-4.3
14426	AT2G02750.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:771154-773539 REVERSE   Aliases: T20F6.11, T20F6_11	3.0	2.9	0.1	0.4	100.0%	-5.5
14427	AT4G00800.1   expressed protein, contains 1 WD-40 repeat (PF00400); 42% similarity to fimbriae-associated protein Fap1 (gi:3929312) (Streptococcus parasanguinis)   chr4:342147-345714 REVERSE   Aliases: A_TM018A10.23, A_TM018A10_23, T18A10.7, T18A10_7	4.3	4.1	0.2	0.4	100.0%	-4.6
14428	AT1G07740.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat; possible frameshift prevents accurate annotation of the gene product   chr1:2397439-2400505 REVERSE   Aliases: AT1G07730, F24B9.15, F24B9_15	4.2	4.3	-0.1	-0.4	100.0%	-4.7
14429	AT5G41280.1   expressed protein, contains Pfam profile: PF01657 domain of unknown function   chr5:16526760-16527957 FORWARD   Aliases: K1O13.8, K1O13_8	2.6	2.7	-0.1	-0.4	100.0%	-5.2
14430	AT4G10300.1   expressed protein   chr4:6384458-6386185 FORWARD   Aliases: T9A4.16	8.8	8.6	0.1	0.4	100.0%	-4.5
14431	AT2G23940.1   expressed protein, contains 2 transmembrane domains; contains Pfam profile PF05620: Protein of unknown function (DUF788)	6.3	6.2	0.1	0.4	100.0%	-5.1
14432	AT5G20630.1   Symbol: GLP3   germin-like protein (GER3), identical to germin-like protein subfamily 3 member 3 (SP:P94072)   chr5:6975106-6975995 REVERSE   Aliases: GERMIN 3, GERMIN LIKE PROTEIN 3, GLP3A, GLP3B, T1M15.30, T1M15_30	2.6	2.6	0.1	0.4	100.0%	-5.4
14433	AT1G62070.1   expressed protein   chr1:22947259-22947954 FORWARD   Aliases: F19K23.2, F19K23_2	3.3	3.2	0.1	0.4	100.0%	-5.2
14434	AT2G45080.1   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr2:18598740-18599530 FORWARD   Aliases: T14P1.11	3.5	3.4	0.1	0.4	100.0%	-4.9
14435	AT5G49370.1   hypothetical protein   chr5:20041228-20041756 FORWARD   Aliases: K7J8.4, K7J8_4	2.1	2.0	0.0	0.4	100.0%	-6.1
14436	AT2G29000.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr2:12467858-12472114 FORWARD   Aliases: T9I4.8, T9I4_8	2.7	2.6	0.1	0.4	100.0%	-5.4
14437	AT1G47220.1   Symbol: CYCA3;3   cyclin, putative, similar to cyclin A-like protein (Nicotiana tabacum) GI:1064931, A-type cyclin (Catharanthus roseus) GI:2190259; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:17306116-17307637 FORWARD   Aliases: CYCA3;3, Cyclin A3;3, F8G22.6, F8G22_6	2.6	2.6	-0.1	-0.4	100.0%	-5.2
14438	AT4G35700.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr4:16923324-16924325 FORWARD   Aliases: F8D20.210, F8D20_210	2.8	2.8	0.1	0.4	100.0%	-5.3
14439	AT3G56290.1   expressed protein   chr3:20889518-20890547 REVERSE   Aliases: F18O21.250	5.9	5.8	0.1	0.4	100.0%	-4.5
14440	AT3G45560.1   zinc finger (C3HC4-type RING finger) family protein, contains Zinc finger, C3HC4 type (RING finger) signature, PROSITE:PS00518   chr3:16730615-16733659 REVERSE   Aliases: F9K21.140	2.9	3.0	-0.1	-0.4	100.0%	-5.1
14441	AT1G77500.1   expressed protein, contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Protein of unknown function (DUF630)   chr1:29126383-29130085 FORWARD   Aliases: T5M16.9, T5M16_9	3.4	3.5	-0.1	-0.4	100.0%	-5.2
14442	AT3G14410.1   transporter-related, low similarity to SP:Q96A29 GDP-fucose transporter 1 {Homo sapiens}, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275; contains 10 predicted transmembrane domains;   chr3:4815833-4817987 REVERSE   Aliases: MLN21.19	7.9	8.0	-0.1	-0.4	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14443	AT4G02360.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr4:1041142-1041733 FORWARD   Aliases: T14P8.17, T14P8_17	3.0	3.0	-0.1	-0.4	100.0%	-5.3
14444	AT2G44300.1   lipid transfer protein-related, low similarity to lipid transfer protein Picea abies GI:2627141; contains Pfam profile: PF00234: Protease inhibitor/seed storage/LTP family   chr2:18314385-18315425 REVERSE   Aliases: F4I1.11	7.1	7.2	-0.2	-0.4	100.0%	-4.8
14445	AT4G28440.1   DNA-binding protein-related, contains weak similarity to G-quartet DNA binding protein 3 (Tetrahymena thermophila) gi:4583503:gb:AAD25098   chr4:14059994-14061392 FORWARD   Aliases: F2009.120, F2009_120	6.8	6.4	0.4	0.4	100.0%	-4.7
14446	AT5G62260.1   similar to DNA-binding protein-related [Arabidopsis thaliana] (TAIR:At4g25320.1); similar to putative AT-hook DNA-binding protein [Oryza sativa (japonica cultivar-group)] (GB:XP_463953.1); contains InterPro domain Protein of unknown function DUF296 (InterPro:IPR005175); contains InterPro domain HMG-I and HMG-Y DNA-binding domain (A+T-hook) (InterPro:IPR000637)   chr5:25026253-25028814 FORWARD   Aliases: MMI9.9, MMI9_9	2.8	2.9	-0.1	-0.4	100.0%	-5.0
14447	AT1G12150.1   expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827); expression supported by MPSS   chr1:4123528-4125326 REVERSE   Aliases: T28K15.11, T28K15_11	2.9	2.8	0.2	0.4	100.0%	-4.5
14448	AT5G24500.1   expressed protein   chr5:8367071-8368739 REVERSE   Aliases: K18P6.2, K18P6_2	6.5	6.7	-0.2	-0.4	100.0%	-4.7
14449	AT5G29210.1   expressed protein   chr5:11153470-11153949 REVERSE   Aliases: F23C8.80, F23C8_80	2.8	2.8	0.1	0.4	100.0%	-5.2
14450	AT5G55560.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:22523603-22525075 REVERSE   Aliases: MWC10.1, MWC10_1	6.3	6.2	0.1	0.4	100.0%	-4.6
14451	AT4G33510.1   Symbol: DHS2   2-dehydro-3-deoxyphosphoheptonate aldolase 2 / 3-deoxy-D-arabino-heptulosonate 7-phosphate synthase 2 / DAHP synthetase 2 (DHS2), nearly identical to SP:Q00218   chr4:16116450-16118800 FORWARD   Aliases: 3 DEOXY D ARABINO HEPTULOSONATE 7 PHOSPHATE SYNTHASE, F17M5.270, F17M5_270	10.2	10.1	0.1	0.4	100.0%	-4.9
14452	AT3G15380.1   choline transporter-related, contains weak similarity to CD92 protein (Homo sapiens) gi:16945323:emb:CAC82175   chr3:5193235-5196596 FORWARD   Aliases: MJK13.4	4.9	4.8	0.1	0.4	100.0%	-4.6
14453	AT1G52970.1   expressed protein   chr1:19740302-19740751 REVERSE   Aliases: F14G24.24, F14G24_24	2.7	2.7	-0.1	-0.4	100.0%	-5.4
14454	AT2G16980.2   expressed protein   chr2:7383431-7388176 FORWARD   Aliases: F12A24.16, F12A24_16	4.7	4.5	0.2	0.4	100.0%	-4.5
14455	AT2G27270.1   expressed protein   chr2:11679349-11680286 FORWARD   Aliases: F12K2.15, F12K2_15	2.8	2.7	0.1	0.4	100.0%	-5.3
14456	AT5G17800.1   myb family transcription factor (MYB56), identical to putative transcription factor (MYB56) GI:3941473 from (Arabidopsis thaliana)   chr5:5877249-5879333 FORWARD   Aliases: MVA3.150, MVA3_150	3.8	3.7	0.1	0.4	100.0%	-4.9
14457	AT1G56010.2   Symbol: NAC1   transcription activator NAC1 (NAC1), contains Pfam PF02365: No apical meristem (NAM) domain; identical to NAC1 GB:AAF21437 GI:6649236 from (Arabidopsis thaliana)   chr1:20950236-20952906 REVERSE   Aliases: ANAC021, ANAC022, F14J16.32, NAC1	2.8	3.0	-0.2	-0.4	100.0%	-4.3
14458	AT3G13175.1   expressed protein   chr3:4235133-4235731 REVERSE   Aliases: None	3.8	3.7	0.1	0.4	100.0%	-5.0
14459	AT2G21110.1   disease resistance-responsive family protein, similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669	3.0	3.1	-0.1	-0.4	100.0%	-5.4
14460	AT3G27020.1   oligopeptide transporter OPT family protein, similar to iron-phytosiderophore transporter protein yellow stripe 1 (Zea mays) GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein   chr3:9962556-9965834 REVERSE   Aliases: MOJ10.9	4.1	4.4	-0.2	-0.4	100.0%	-4.8
14461	AT1G64210.1   leucine-rich repeat transmembrane protein kinase, putative, contains 1 predicted transmembrane domain; similar to receptor-like protein kinase (GI:4008006) (Arabidopsis thaliana); similar to receptor-like kinase RHG1 (GI:21239382) (Glycine max); similar to receptor-like protein kinase 3 (GI:13506810) (Lycopersicon esculentum)   chr1:23834696-23836526 FORWARD   Aliases: F22C12.3, F22C12_3	3.2	3.1	0.1	0.4	100.0%	-5.4
14462	AT1G17140.2   tropomyosin-related, similar to Tropomyosin 1. (Baker's yeast)(SP:P17536) {Saccharomyces cerevisiae}   chr1:5856257-5858525 REVERSE   Aliases: F20D23.32	3.0	3.2	-0.2	-0.4	100.0%	-4.3
14463	AT3G30480.1   hypothetical protein   chr3:12116931-12117470 FORWARD   Aliases: MSJ3.12	2.2	2.2	-0.0	-0.4	100.0%	-5.8
14464	AT4G23580.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:12304256-12305407 REVERSE   Aliases: F9D16.50, F9D16_50	3.0	2.9	0.1	0.4	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14465	AT3G03400.1   calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced SP:P25070 from (Arabidopsis thaliana)   chr3:808752-809165 REVERSE   Aliases: T21P5.18, T21P5_18	3.1	3.0	0.1	0.4	100.0%	-5.4
14466	AT1G60460.3   expressed protein   chr1:22279149-22282450 FORWARD   Aliases: F8A5.1, F8A5_1	2.5	2.6	-0.1	-0.4	100.0%	-5.5
14467	AT2G15970.1   Symbol: COR413 PM1   cold-acclimation protein, putative (FL3-5A3), similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi:18449100:gb:AAL69988; similar to stress-regulated protein SAP1 (Xerophyta viscosa) gi:21360378:gb:AAM47505; identical to cDNA cold acclimation protein WCOR413-like protein alpha form GI:10121840, cold acclimation protein homolog (Arabidopsis thaliana) GI:11127595   chr2:6957170-6958274 FORWARD   Aliases: ATCOR413 PM1, COLD ACCLIMATION PROTEIN WCOR413 LIKE PROTEIN ALPHA FORM, F19G14.3, F19G14_3, FL3 5A3, WCOR413, WCOR413 LIKE	4.8	4.6	0.3	0.4	100.0%	-4.4
14468	AT3G60650.1   expressed protein   chr3:22430926-22431249 FORWARD   Aliases: T4C21.60	2.4	2.5	-0.0	-0.4	100.0%	-6.1
14469	AT4G35725.1   expressed protein   chr4:16929950-16930565 REVERSE   Aliases: None	2.6	2.6	0.1	0.4	100.0%	-5.4
14470	AT1G61860.1   protein kinase, putative, similar to protein kinase GI:9294282 from (Arabidopsis thaliana)   chr1:22866524-22868284 REVERSE   Aliases: F8K4.7, F8K4_7	2.6	2.6	0.1	0.4	100.0%	-5.0
14471	AT1G23160.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591, auxin-responsive GH3 homologue (Arabidopsis thaliana) GI:11041726; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr1:8209221-8211314 FORWARD   Aliases: T26J12.7, T26J12_7	2.8	2.7	0.1	0.4	100.0%	-5.5
14472	AT5G17710.2   Symbol: EMB1241   co-chaperone grpE family protein, similar to co-chaperone CGE1 precursor isoform a (Chlamydomonas reinhardtii) GI:15384277; contains Pfam profile PF01025: co-chaperone GrpE   chr5:5839345-5841707 REVERSE   Aliases: EMB1241, EMBRYO DEFECTIVE 1241, MVA3.60, MVA3_60	8.8	9.0	-0.2	-0.4	100.0%	-4.4
14473	AT4G33160.1   F-box family protein (FBX13), contains similarity to fimbriata GI:547307 from (Antirrhinum majus)   chr4:15994240-15995590 FORWARD   Aliases: F4I10.90, F4I10_90	4.8	4.8	0.1	0.4	100.0%	-5.2
14474	AT5G03590.1   GDSL-motif lipase/hydrolase protein-related   chr5:908562-910148 FORWARD   Aliases: F17C15.10, F17C15_10	2.3	2.3	-0.0	-0.4	100.0%	-5.8
14475	AT1G18700.2   similar to galactosyl transferase GMA12/MNN10 family protein [Arabidopsis thaliana] (TAIR:At1g18690.1); contains InterPro domain Heat shock protein DnaJ, N-terminal (InterPro:IPR001623)   chr1:6437523-6444068 FORWARD   Aliases: F6A14.19, F6A14_19	6.7	6.9	-0.2	-0.4	100.0%	-4.9
14476	AT1G68190.1   zinc finger (B-box type) family protein   chr1:25562911-25564875 FORWARD   Aliases: T22E19.18, T22E19_18	2.4	2.3	0.1	0.4	100.0%	-5.3
14477	AT1G36000.1   LOB domain family protein / lateral organ boundaries domain family protein (LBD5), identical to SP:Q9C8V8 Putative LOB domain protein 5 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis thaliana   chr1:13423779-13424235 FORWARD   Aliases: T22A15.8, T22A15_8	3.0	3.0	0.1	0.4	100.0%	-5.4
14478	AT4G22860.1   expressed protein   chr4:11997491-12001636 FORWARD   Aliases: F7H19.40, F7H19_40	4.0	4.1	-0.1	-0.4	100.0%	-4.9
14479	AT1G09980.1   expressed protein, contains Pfam profile PF05057: Protein of unknown function (DUF676); non-consensus GC donor splice site at exon boundary 144764   chr1:3256290-3261575 REVERSE   Aliases: T27I1.1	2.6	2.7	-0.0	-0.4	100.0%	-5.7
14480	AT1G34190.1   Symbol: ANAC017   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) protein; similar to NAM protein GI:6066595 (Petunia hybrida); nam-like protein 9 (GI:21105746) (Petunia x hybrida); NAC1 GI:7716952 (Medicago truncatula)   chr1:12451431-12454120 FORWARD   Aliases: ANAC017, F12G12.30	7.0	6.8	0.1	0.4	100.0%	-4.9
14481	AT5G07090.2   similar to 40S ribosomal protein S4 (RPS4D) [Arabidopsis thaliana] (TAIR:At5g58420.1); similar to ribosomal protein S4 [Solanum tuberosum] (GB:CAA54095.1); contains InterPro domain RNA-binding S4 (InterPro:IPR002942); contains InterPro domain KOW (Kyrpides, Ouzounis, Woese) motif (InterPro:IPR006646); contains InterPro domain Ribosomal protein S4E (InterPro:IPR000876); contains InterPro domain KOW (InterPro:IPR005824)   chr5:2202398-2204079 FORWARD   Aliases: T28J14.30	9.0	9.2	-0.2	-0.4	100.0%	-4.6
14482	AT1G79800.1   plastocyanin-like domain-containing protein   chr1:30023442-30024110 FORWARD   Aliases: F20B17.22, F20B17_22	2.8	2.7	0.1	0.4	100.0%	-5.1
14483	AT5G37110.1   hypothetical protein   chr5:14686824-14692143 FORWARD   Aliases: MJG14.16, MJG14_16	2.5	2.5	-0.0	-0.4	100.0%	-6.0
14484	AT1G09730.1   Ulp1 protease family protein, low similarity to SP:Q9GZR1 SUMO-1-specific protease 1 (EC 3.4.22.-) (Sentrin-specific protease SENP6) (Protease FKSG6) {Homo sapiens}; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr1:3147669-3154238 REVERSE   Aliases: F21M12.29, F21M12_29	3.3	3.1	0.2	0.4	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14485	AT3G17240.3   Symbol: LPD2   dihydrolipoamide dehydrogenase 2, mitochondrial / lipoamide dehydrogenase 2 (MTLPD2), nearly identical to GB:AAF34796 (gi:6984216) from (Arabidopsis thaliana); alternative splice form exists   chr3:5889883-5892255 REVERSE   Aliases: LIPOAMIDE DEHYDROGENASE 2, MGD8.7	8.7	8.9	-0.2	-0.4	100.0%	-5.2
14486	AT5G43000.1   expressed protein   chr5:17263582-17264430 REVERSE   Aliases: MBD2.20, MBD2_20	2.7	2.7	-0.1	-0.4	100.0%	-5.3
14487	AT2G31200.1   Symbol: ADF6   actin-depolymerizing factor 6 (ADF6), identical to SP:Q9ZSK2 Actin-depolymerizing factor 6 (ADF-6) (AtADF6) {Arabidopsis thaliana}   chr2:13301130-13302487 FORWARD   Aliases: ACTIN DEPOLYMERIZING FACTOR 6, F16D14.4, F16D14_4	10.7	10.9	-0.2	-0.4	100.0%	-4.9
14488	AT5G44440.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr5:17927784-17929539 REVERSE   Aliases: MFC16.10, MFC16_10	2.9	2.9	-0.1	-0.4	100.0%	-5.5
14489	AT3G29796.1   hypothetical protein   chr3:11711040-11715507 FORWARD   Aliases: K17E7.8	3.0	2.9	0.1	0.4	100.0%	-5.1
14490	AT1G21600.2   similar to putative tonoplast membrane integral protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81369.1)	3.9	4.0	-0.1	-0.4	100.0%	-5.2
14491	AT5G54420.1   expressed protein   chr5:22113030-22113305 FORWARD   Aliases: F24B18.4, F24B18_4	2.7	2.7	-0.0	-0.4	100.0%	-5.6
14492	AT4G39970.1   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:P95649 CbbY protein {Rhodobacter sphaeroides}   chr4:18536120-18538478 REVERSE   Aliases: T5J17.140, T5J17_140	5.4	5.5	-0.1	-0.4	100.0%	-4.6
14493	AT3G56430.1   expressed protein, unknown protein At2g40800 - Arabidopsis thaliana, EMBL:AC007660   chr3:20934579-20936788 REVERSE   Aliases: T5P19.80	5.1	5.2	-0.1	-0.4	100.0%	-4.9
14494	AT2G32580.1   expressed protein   chr2:13834740-13836386 FORWARD   Aliases: T26B15.14, T26B15_14	8.8	8.5	0.3	0.4	100.0%	-4.6
14495	AT1G09870.1   histidine acid phosphatase family protein, contains Pfam profile PF00328: Histidine acid phosphatase; similar to multiple inositol polyphosphate phosphatase (GI:4105496)(Mus musculus); EST gb:R64758 comes from this gene   chr1:3205743-3208600 FORWARD   Aliases: F21M12.26, F21M12_26	5.3	5.5	-0.2	-0.4	100.0%	-4.7
14496	AT5G20810.2   similar to auxin-responsive protein-related [Arabidopsis thaliana] (TAIR:At3g43120.1); similar to auxin-induced protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD36439.1); contains InterPro domain Auxin responsive SAUR protein (InterPro:IPR003676)   chr5:7043900-7045714 FORWARD   Aliases: T1M15.210, T1M15_210	3.2	3.1	0.1	0.4	100.0%	-5.3
14497	AT3G62160.1   transferase family protein, low similarity to Taxus cuspidata transferases: 10-deacetylbaicatin III-10-O-acetyl transferase GI:6746554, taxadienol acetyl transferase GI:6978038, 2-debenzoyl-7,13-diacetylbaicatin III-2-O-benzoyl transferase GI:11559716; contains Pfam profile PF02458 transferase family   chr3:23025183-23026814 REVERSE   Aliases: T17J13.120	3.1	3.0	0.1	0.4	100.0%	-4.3
14498	AT5G67030.2   Symbol: ABA1   zeaxanthin epoxidase (ZEP) (ABA1), identical to GI:9857296 AtABA1; controls Pfam profiles PF01360: Monooxygenase and PF00498: FHA domain; identical to cDNA AtABA1, GI:9857295   chr5:26770748-26774462 REVERSE   Aliases: ABA DEFICIENT 1, ATABA1, IBS3, IMPAIRED IN BABA INDUCED STERILITY 3, K8A10.10, K8A10_10, LOS6, NPQ2, ZEAXANTHIN EPOXIDASE, ZEP	7.5	7.3	0.2	0.4	100.0%	-4.7
14499	AT4G35930.1   expressed protein   chr4:17018978-17021063 FORWARD   Aliases: T19K4.60	2.5	2.4	0.1	0.4	100.0%	-5.5
14500	AT2G42600.2   Symbol: ATPPC2	8.1	8.2	-0.1	-0.4	100.0%	-5.0
14501	NA	2.3	2.3	0.0	0.4	100.0%	-5.5
14502	AT4G23493.1   expressed protein   chr4:12256192-12257049 REVERSE   Aliases: None	6.6	6.5	0.1	0.4	100.0%	-4.7
14503	AT5G04250.1   OTU-like cysteine protease family protein, contains Pfam profile PF02338: OTU-like cysteine protease   chr5:1176014-1178919 FORWARD   Aliases: T19N18.9	6.6	6.5	0.2	0.4	100.0%	-4.6
14504	AT1G08460.1   histone deacetylase family protein (HDA8), identical to HDA8 (Arabidopsis thaliana) GI:21360988low similarity to SP:Q9Z2V5 Histone deacetylase 6 (HD6) (Histone deacetylase mHDA2) {Mus musculus}; contains Pfam profile PF00850: Histone deacetylase family; supporting cDNA gi:21360987:gb:AF510167.1:	8.1	8.2	-0.1	-0.4	100.0%	-5.2
14505	AT3G59110.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:21865697-21869181 FORWARD   Aliases: F17J16.160	4.9	4.8	0.1	0.4	100.0%	-5.0
14506	AT2G12320.1   hypothetical protein   chr2:4942708-4943368 FORWARD   Aliases: T10J7.30, T10J7_30	2.9	2.9	-0.1	-0.4	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14507	AT4G11970.2   YT521-B-like family protein, contains Pfam profile PF04146: YT521-B-like family   chr4:7180431-7184048 FORWARD   Aliases: F16J13.40, F16J13_40	4.4	4.3	0.1	0.4	100.0%	-4.8
14508	AT4G00790.1   expressed protein   chr4:338630-340602 REVERSE   Aliases: A_TM018A10.24, A_TM018A10_24, T18A10.5, T18A10_5	2.5	2.5	-0.1	-0.4	100.0%	-5.5
14509	AT5G27870.1   pectinesterase family protein, similar to pectinesterase (EC 3.1.1.11) from Salix gilgiana GI:6714532, Lycopersicon esculentum SP:Q43143, Phaseolus vulgaris SP:Q43111; contains Pfam profile PF01095 pectinesterase   chr5:9878995-9881810 REVERSE   Aliases: F14I23.30, F14I23_30	2.7	2.7	0.1	0.4	100.0%	-5.5
14510	AT5G25860.1   F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.5	-0.1	-0.4	100.0%	-5.1
14511	AT3G49060.1   protein kinase family protein / U-box domain-containing protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain	5.0	5.1	-0.1	-0.4	100.0%	-5.0
14512	AT1G34210.1   Symbol: SERK2   somatic embryogenesis receptor-like kinase 2 (SERK2), nearly identical to somatic embryogenesis receptor-like kinase 2 (Arabidopsis thaliana) GI:14573457; contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain; identical to cDNA somatic embryogenesis receptor-like kinase 2 (SERK2) GI:14573456   chr1:12458648-12463896 FORWARD   Aliases: ATSERK2, F23M19.11, F23M19_11, SOMATIC EMBRYOGENESIS RECEPTOR LIKE KINASE 2	8.2	8.3	-0.2	-0.4	100.0%	-4.6
14513	AT1G78270.1   UDP-glucose glucosyltransferase, putative, similar to UDP-glucose glucosyltransferase GI:3928543 from (Arabidopsis thaliana)   chr1:29455456-29457310 REVERSE   Aliases: F3F9.19, F3F9_19	5.3	5.4	-0.1	-0.4	100.0%	-5.0
14514	AT5G20620.1   Symbol: UBQ4   polyubiquitin (UBQ4), identical to GI:17677   chr5:6973073-6974945 REVERSE   Aliases: T1M15.20, T1M15_20	8.1	8.3	-0.2	-0.4	100.0%	-4.6
14515	AT2G46380.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g61670.1); similar to extra-large G-protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD45831.1)   chr2:19046450-19049421 FORWARD   Aliases: F11C10.7	2.6	2.7	-0.0	-0.4	100.0%	-5.6
14516	AT1G65340.1   Symbol: CYP96A3   cytochrome P450, putative, similar to cytochrome P450 GI:4688670 from (Catharanthus roseus)   chr1:24271798-24273309 REVERSE   Aliases: T8F5.12, T8F5_12	2.8	2.7	0.1	0.4	100.0%	-5.4
14517	AT4G05420.1   Symbol: DDB1A   UV-damaged DNA-binding protein, putative, similar to UV-damaged DNA binding protein (GI:12082087) (Oryza sativa); contains Pfam PF03178 : CPSF A subunit region	4.6	4.7	-0.1	-0.4	100.0%	-4.7
14518	AT2G33480.1   Symbol: ANAC041   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr2:14188283-14189478 FORWARD   Aliases: ANAC041, F4P9.25, F4P9_25	7.1	7.3	-0.3	-0.4	100.0%	-4.8
14519	AT1G47280.1   expressed protein   chr1:17334499-17336846 REVERSE   Aliases: T3F24.20, T3F24_20	3.1	3.2	-0.1	-0.4	100.0%	-5.2
14520	AT1G14920.1   Symbol: GAI   gibberellin response modulator (GAI) (RGA2) / gibberellin-responsive modulator, identical to GAI GB:CAA75492 GI:2569938 (Arabidopsis thaliana) (Genes Dev. In press)   chr1:5149221-5151349 FORWARD   Aliases: F10B6.34, F10B6_34, GA INSENSITIVE, GAI PROTEIN, RESTORATION ON GROWTH ON AMMONIA, RGA2	5.2	5.0	0.2	0.4	100.0%	-4.7
14521	AT1G05577.1   expressed protein   chr1:1662642-1664287 REVERSE   Aliases: None	2.5	2.4	0.1	0.4	100.0%	-5.5
14522	AT1G21060.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr1:7371788-7374093 FORWARD   Aliases: T22I11.12, T22I11_12	3.8	3.9	-0.1	-0.4	100.0%	-4.8
14523	AT4G37290.1   expressed protein   chr4:17549678-17550251 REVERSE   Aliases: F6G17.7	3.5	3.6	-0.1	-0.4	100.0%	-5.0
14524	AT3G54680.1   proteophosphoglycan-related, contains similarity to proteophosphoglycan (Leishmania major) gi:5420389:emb:CAB46680   chr3:20255367-20257051 FORWARD   Aliases: T5N23.40	3.2	3.1	0.1	0.4	100.0%	-5.1
14525	AT2G05790.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr2:2199389-2201480 FORWARD   Aliases: T25M19.1, T25M19_1	7.8	7.6	0.2	0.4	100.0%	-4.5
14526	AT5G59370.1   Symbol: ACT4   actin 4 (ACT4), identical to SP:P53494 Actin 4 {Arabidopsis thaliana}   chr5:23967049-23969048 FORWARD   Aliases: ACTIN 4, F2O15.3, F2O15_3	3.2	3.3	-0.1	-0.4	100.0%	-5.4
14527	AT1G35513.1   isochorismate synthase-related / isochorismate mutase-related, similar to SP:Q9S7H8 Isochorismate synthase 1, chloroplast precursor (EC 5.4.99.6) (Icsl) (Isochorismate mutase) (Salicylic acid induction deficient 2) (Sid2) (Enhanced disease susceptibility 16) (Eds16) {Arabidopsis thaliana}   chr1:13076823-13077491 FORWARD   Aliases: F15O4.44	4.4	4.3	0.1	0.4	100.0%	-5.3
14528	AT5G12370.3   similar to Brain secretory protein SEC10P [Homo sapiens] (GB:AAH41126.1)	5.1	5.2	-0.1	-0.4	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14529	AT3G14790.1   Symbol: RHM3   NAD-dependent epimerase/dehydratase family protein, similar to dTDP-glucose 4,6-dehydratase from Aneurinibacillus thermoaerophilus GI:16357461, Saccharopolyspora spinosa GI:15077647, RmlB from Leptospira borgpetersenii GI:4234803; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family   chr3:4964162-4967066 FORWARD   Aliases: RHAMNOSE BIOSYNTHESIS 3, T21E2.5	7.0	7.1	-0.1	-0.4	100.0%	-4.8
14530	AT4G14695.1   expressed protein, contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)   chr4:8419828-8420871 FORWARD   Aliases: None	3.1	3.2	-0.1	-0.4	100.0%	-5.4
14531	AT1G74560.2   similar to nucleosome assembly protein (NAP) family protein [Arabidopsis thaliana] (TAIR:At1g18800.1); similar to nucleosome/chromatin assembly factor A [Zea mays] (GB:AAK67146.1); contains InterPro domain Nucleosome assembly protein (NAP) (InterPro:IPR002164)   chr1:28021245-28023702 REVERSE   Aliases: F1M20.24, F1M20_24	6.2	6.4	-0.2	-0.4	100.0%	-5.0
14532	AT2G44200.1   expressed protein   chr2:18283286-18285703 FORWARD   Aliases: F411.1, F411_1	7.7	7.4	0.2	0.4	100.0%	-4.8
14533	AT3G25150.1   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain); similar to ras-GTPase-activating protein (GAP<120>) SH3-domain-binding protein 2 GB:NP_035946 (Mus musculus)   chr3:9156964-9159910 REVERSE   Aliases: MJL12.17	6.2	6.3	-0.1	-0.4	100.0%	-4.9
14534	AT1G40230.1   expressed protein   chr1:15417336-15418247 FORWARD   Aliases: F9D18.23, F9D18_23	2.1	2.2	-0.0	-0.4	100.0%	-5.7
14535	AT3G56240.1   Symbol: CCH   copper homeostasis factor / copper chaperone (CCH) (ATX1), identical to gi:3168840 Pfam profile PF00403: Heavy-metal-associated domain   chr3:20874236-20875470 REVERSE   Aliases: ATX1, COPPER CHAPERONE, COPPER HOMEOSTASIS FACTOR, F18021.200	9.0	9.1	-0.1	-0.4	100.0%	-4.9
14536	AT4G03960.1   tyrosine specific protein phosphatase family protein, contains tyrosine specific protein phosphatases active site, PROSITE:PS00383   chr4:1887526-1889209 FORWARD   Aliases: T24M8.4, T24M8_4	7.4	7.3	0.2	0.4	100.0%	-4.5
14537	AT1G26480.1   Symbol: GRF12   14-3-3 protein GF14 iota (GRF12), identical to 14-3-3 protein GF14iota GI:12963453 from (Arabidopsis thaliana)   chr1:9156319-9157937 REVERSE   Aliases: GF14 IOTA, T1K7.15, T1K7_15	2.5	2.5	-0.0	-0.4	100.0%	-5.8
14538	AT2G22080.1   expressed protein   chr2:9393621-9395263 FORWARD   Aliases: T16B14.7, T16B14_7	8.1	7.9	0.2	0.4	100.0%	-4.9
14539	AT1G64060.1   Symbol: ATRBOH F F   respiratory burst oxidase protein F (RbohF) (RbohAp108) / NADPH oxidase, identical to cytochrome b245 beta chain homolog RbohAp108 (GI:2654868), respiratory burst oxidase protein F (gi:3242456), from Arabidopsis thaliana   chr1:23773437-23780594 FORWARD   Aliases: ATRBOH F, CYTOCHROME B245 BETA CHAIN HOMOLOG RBOHAP108, F22C12.18, F22C12_18, RBOHAP108	5.6	5.4	0.2	0.4	100.0%	-4.6
14540	AT1G30360.1   early-responsive to dehydration stress protein (ERD4), nearly identical to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr1:10715647-10718979 FORWARD   Aliases: T4K22.4, T4K22_4	7.5	7.7	-0.3	-0.4	100.0%	-4.4
14541	AT2G32430.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr2:13778373-13781579 FORWARD   Aliases: T32F6.5, T32F6_5	5.5	5.4	0.1	0.4	100.0%	-4.9
14542	AT1G47790.1   F-box family protein, contains Pfam:PF00646 F-box domain	2.9	2.7	0.1	0.4	100.0%	-5.1
14543	AT4G33640.1   expressed protein   chr4:16159551-16160306 REVERSE   Aliases: T16L1.130, T16L1_130	10.9	10.9	0.1	0.4	100.0%	-5.4
14544	AT1G03960.2   calcium-binding EF hand family protein, contains Pfam profile: PF00036 EF hand   chr1:1013714-1017901 FORWARD   Aliases: F21M11.11, F21M11_11	2.6	2.5	0.1	0.4	100.0%	-5.3
14545	AT1G80330.1   gibberellin 3-beta-dioxygenase, putative / gibberellin 3 beta-hydroxylase, putative, similar to gibberellin 3 beta-hydroxylase GA4H GB:AAK83647 (Arabidopsis thaliana), GA4 (GI:2160454)	3.6	3.6	0.1	0.4	100.0%	-5.1
14546	AT5G14880.1   potassium transporter, putative, similar to potassium transporter HAK2p (Mesembryanthemum crystallinum) gi:14091471:gb:AAK53759; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter   chr5:4814247-4817670 FORWARD   Aliases: T9L3.180, T9L3_180	4.6	4.7	-0.1	-0.4	100.0%	-4.7
14547	AT1G53000.1   cytidylyltransferase family, contains Pfam profile: PF02348 cytidylyltransferase	7.8	7.6	0.2	0.4	100.0%	-4.5
14548	AT5G44180.1   homeobox transcription factor, putative, similar to homeobox transcription factor Hox7/homeotic protein Hox7 (GI:19486)	6.5	6.9	-0.4	-0.4	100.0%	-4.5
14549	AT4G08470.1   Symbol: MAPKKK10   mitogen-activated protein kinase, putative, similar to mitogen-activated protein kinase (Arabidopsis thaliana) gi:1255448:dbj:BAA09057; contains Pfam PF00069: Protein kinase domain	3.9	4.1	-0.2	-0.4	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14550	AT1G27190.1   leucine-rich repeat transmembrane protein kinase, putative, similar to CLV1 receptor kinase GB:AAB58929 GI:2160756 from (Arabidopsis thaliana)   chr1:9446644-9448715 REVERSE   Aliases: T7N9.25, T7N9_25	4.8	4.7	0.1	0.4	100.0%	-4.9
14551	AT1G80010.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282   chr1:30102649-30104739 FORWARD   Aliases: F18B13.10, F18B13_10	5.0	4.9	0.1	0.4	100.0%	-5.0
14552	AT5G28520.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	4.0	3.9	0.1	0.4	100.0%	-5.0
14553	AT4G13190.1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g07070.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g24790.1); similar to putative serine/threonine kinase PBS1 protein [Oryza sativa (japonica cultivar-group)] (GB:NP_914952.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:7659431-7661102 REVERSE   Aliases: F17N18.80, F17N18_80	3.3	3.4	-0.1	-0.4	100.0%	-5.2
14554	AT1G11900.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:4013120-4014680 REVERSE   Aliases: F12F1.26, F12F1_26	5.0	5.2	-0.1	-0.4	100.0%	-4.7
14555	AT1G79870.1   oxidoreductase family protein, contains Pfam profile: PF02826 D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain; similar to glyoxylate reductase from Thermococcus litoralis (gi:13515409)   chr1:30049639-30050920 FORWARD   Aliases: F19K16.17, F19K16_17	7.7	7.6	0.2	0.4	100.0%	-5.0
14556	AT3G51190.1   60S ribosomal protein L8 (RPL8B), ribosomal protein L8, cytosolic - Arabidopsis thaliana, PIR:T04582   chr3:19027585-19028526 REVERSE   Aliases: F24M12.230	2.9	2.9	0.1	0.4	100.0%	-5.1
14557	AT1G57870.1   shaggy-related protein kinase kappa, putative / ASK-kappa, putative, similar to shaggy-related protein kinase kappa SP:Q39019 GI:717180 from (Arabidopsis thaliana)   chr1:21435023-21438637 REVERSE   Aliases: F12K22.12, F12K22_12	5.9	6.0	-0.1	-0.4	100.0%	-4.8
14558	AT5G47740.1   similar to protein kinase family protein / U-box domain-containing protein [Arabidopsis thaliana] (TAIR:At2g45910.1); similar to putative protein kinase [Oryza sativa (japonica cultivar-group)] (GB:AAP55019.1)   chr5:19355737-19357636 FORWARD   Aliases: MCA23.6, MCA23_6	2.7	2.9	-0.2	-0.4	100.0%	-4.4
14559	AT5G62930.1   GDSL-motif lipase/hydrolase family protein, similar to SP:P41734 Isoamyl acetate-hydrolyzing esterase (EC 3.1.-.-) {Saccharomyces cerevisiae}; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:25272114-25273843 FORWARD   Aliases: MQB2.25, MQB2_25	7.7	7.9	-0.2	-0.4	100.0%	-4.6
14560	AT1G17340.1   phosphoinositide phosphatase family protein, contains similarity to phosphoinositide phosphatase SAC1 (Rattus norvegicus) gi:11095248:gb:AAG29810; contains Pfam domain, PF02383: SacI homology domain; identical to cDNA SAC domain protein 5 (SAC5) GI:31415726   chr1:5933893-5938754 FORWARD   Aliases: F28G4.21, F28G4_21	2.9	2.8	0.1	0.4	100.0%	-4.9
14561	AT3G10390.1   Symbol: FLD   amine oxidase family protein / SWIRM domain-containing protein, contains Pfam profile: PF01593 Flavin containing amine oxidase   chr3:3229298-3231824 FORWARD   Aliases: F13M14.34, FLOWERING LOCUS D	2.8	2.9	-0.1	-0.4	100.0%	-5.3
14562	AT3G19230.1   leucine-rich repeat family protein, contains Pfam profile:PF00560 LRR:Leucine Rich Repeat domains; similar to light repressible receptor protein kinase (GI:1321686)(Arabidopsis thaliana)   chr3:6661094-6663525 REVERSE   Aliases: MVI11.14	2.7	2.6	0.1	0.4	100.0%	-5.3
14563	AT3G15940.1   glycosyl transferase family 1 protein, contains Pfam profile:PF00534 Glycosyl transferases group 1   chr3:5393519-5396765 REVERSE   Aliases: MVC8.8	6.1	5.9	0.1	0.4	100.0%	-5.0
14564	AT5G57400.1   expressed protein   chr5:23280048-23280443 REVERSE   Aliases: MSF19.6, MSF19_6	2.7	2.8	-0.0	-0.4	100.0%	-5.6
14565	AT1G26470.1   expressed protein   chr1:9155080-9156233 FORWARD   Aliases: T1K7.16, T1K7_16	7.3	7.2	0.2	0.4	100.0%	-4.4
14566	AT3G09670.1   PWWP domain-containing protein   chr3:2966435-2968973 FORWARD   Aliases: F11F8.26	4.0	4.1	-0.1	-0.4	100.0%	-5.3
14567	AT3G62410.1   Symbol: CP12 2	5.7	5.5	0.2	0.4	100.0%	-4.4
14568	AT1G55300.2   similar to TATA-binding protein-associated factor TAFII55-like [Oryza sativa (japonica cultivar-group)] (GB:BAD68329.1); contains InterPro domain TAFII55 protein conserved region (InterPro:IPR006751)   chr1:20631690-20633359 REVERSE   Aliases: F7A10.3, F7A10_3	5.1	5.2	-0.1	-0.4	100.0%	-4.7
14569	AT4G32300.1   lectin protein kinase family protein, contains Pfam domains, PF01453: Lectin (probable mannose binding) and PF00069: Protein kinase domain   chr4:15599481-15602601 FORWARD   Aliases: F10M6.60, F10M6_60	7.8	7.9	-0.2	-0.4	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14570	AT3G19880.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr3:6911441-6912610 REVERSE   Aliases: MPN9.12	2.7	2.8	-0.1	-0.4	100.0%	-5.5
14571	AT3G60760.1   expressed protein   chr3:22469591-22470177 REVERSE   Aliases: T4C21.170	2.8	2.9	-0.1	-0.4	100.0%	-5.4
14572	AT5G63480.1   expressed protein   chr5:25434491-25436095 FORWARD   Aliases: MLE2.11, MLE2_11	5.9	6.1	-0.2	-0.4	100.0%	-4.6
14573	AT5G03270.1   expressed protein, contains Pfam profile PF03641: decarboxylase family protein   chr5:781869-783996 FORWARD   Aliases: F15A17.300, F15A17_300	3.4	3.4	0.1	0.4	100.0%	-5.4
14574	AT4G30050.1   expressed protein, ; expression supported by MPSS   chr4:14687212-14688757 REVERSE   Aliases: F6G3.80, F6G3_80	2.5	2.5	0.1	0.4	100.0%	-5.3
14575	AT5G61340.1   expressed protein   chr5:24679230-24680343 REVERSE   Aliases: MFB13.11, MFB13_11	2.8	2.9	-0.2	-0.4	100.0%	-4.5
14576	AT5G48930.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus (GI:3288180, GI:2239091); contains Pfam profile PF02458 transferase family   chr5:19853525-19855371 REVERSE   Aliases: K19E20.4, K19E20_4	9.9	10.2	-0.3	-0.4	100.0%	-4.6
14577	AT5G55090.1   Symbol: MAPKKK15   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:22374078-22375424 REVERSE   Aliases: MCO15.4, MCO15_4	3.4	3.4	0.1	0.4	100.0%	-5.2
14578	AT3G21300.1   RNA methyltransferase family protein, contains TIGRfam TIGR00479: RNA methyltransferase, TrmA family   chr3:7493445-7496295 REVERSE   Aliases: MXL8.18	3.0	3.0	-0.1	-0.4	100.0%	-5.3
14579	AT4G01100.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr4:477155-479935 FORWARD   Aliases: F2N1.16, F2N1_16	5.9	5.7	0.2	0.4	100.0%	-4.9
14580	AT1G78940.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:29685750-29688855 REVERSE   Aliases: YUP8H12R.45, YUP8H12R_45	2.5	2.6	-0.0	-0.4	100.0%	-5.7
14581	AT2G29940.1   ABC transporter family protein, similar to ABC1 protein GI:14331118 from (Nicotiana glauca)   chr2:12767216-12773700 FORWARD   Aliases: F23F1.14, F23F1_14	2.8	2.7	0.0	0.4	100.0%	-5.9
14582	AT4G16030.1   60S ribosomal protein L19, putative, similar to 60S ribosomal protein L19-3 (Swiss-Prot:P49693) (Arabidopsis thaliana)   chr4:9083753-9084115 FORWARD   Aliases: DL4055W, FCAALL.264	3.2	3.3	-0.1	-0.4	100.0%	-5.4
14583	AT1G02140.1   mago nashi family protein, similar to Mago Nashi, Genbank Accession Number U03559; contains Pfam PF02792: Mago nashi protein domain   chr1:403195-404439 REVERSE   Aliases: T7I23.7, T7I23_7	9.8	9.5	0.2	0.4	100.0%	-4.6
14584	AT4G10220.1   expressed protein, IB1C3-1 protein, Arabidopsis thaliana, AJ011845   chr4:6362185-6365075 FORWARD   Aliases: T9A4.9	2.3	2.2	0.1	0.4	100.0%	-5.3
14585	AT2G15860.1   expressed protein, and genefinder   chr2:6912470-6916477 REVERSE   Aliases: F19G14.14, F19G14_14	5.9	6.0	-0.1	-0.4	100.0%	-5.0
14586	AT5G20010.1   Symbol: RAN 1   Ras-related GTP-binding nuclear protein (RAN-1), identical to GTP-binding nuclear protein RAN-1 SP:P41916 from (Arabidopsis thaliana)   chr5:6760286-6762096 FORWARD   Aliases: ATRAN1, F28I16.160, F28I16_160, RAN1	11.5	11.7	-0.2	-0.4	100.0%	-4.8
14587	AT5G20020.1   Symbol: RAN2   Ras-related GTP-binding nuclear protein (RAN-2), identical to GTP-binding nuclear protein RAN-2 SP:P41917 from (Arabidopsis thaliana)   chr5:6762754-6764673 FORWARD   Aliases: F28I16.170, F28I16_170	11.5	11.7	-0.2	-0.4	100.0%	-4.8
14588	AT2G24570.1   Symbol: WRKY17	3.7	3.9	-0.2	-0.4	100.0%	-4.6
14589	AT3G54480.2   Symbol: SKIP5   SKP1 interacting partner 5 (SKIP5), identical to GP:14348816 SKP1-interacting partner 5 {Arabidopsis thaliana}   chr3:20182812-20184394 REVERSE   Aliases: SKP1 INTERACTING PARTNER 5, T14E10.50	7.5	7.4	0.1	0.4	100.0%	-5.0
14590	AT1G30140.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g27260.1)   chr1:10598611-10599680 FORWARD   Aliases: T2H7.6, T2H7_6	3.1	3.1	0.1	0.4	100.0%	-5.5
14591	AT1G68430.1   expressed protein   chr1:25658568-25659107 REVERSE   Aliases: T2E12.2, T2E12_2	4.3	4.2	0.1	0.4	100.0%	-4.6
14592	AT5G24620.1   thaumatin-like protein, putative, similar to thaumatin-like protein (Arabidopsis thaliana) GI:2435406; contains Pfam profile PF00314: Thaumatin family   chr5:8430771-8432417 FORWARD   Aliases: K18P6.16, K18P6_16	4.6	4.8	-0.2	-0.4	100.0%	-4.4
14593	AT5G22970.1   expressed protein   chr5:7686276-7686782 REVERSE   Aliases: MRN17.20, MRN17_20	2.3	2.3	0.1	0.4	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14594	AT3G32280.1   hypothetical protein   chr3:13237545-13243867 FORWARD   Aliases: F6H5.21	2.7	2.7	0.0	0.4	100.0%	-5.8
14595	AT2G05900.1   SET domain-containing protein / YDG/SRA domain-containing protein, contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain   chr2:2256967-2257905 FORWARD   Aliases: T6P5.10, T6P5_10	3.4	3.3	0.1	0.4	100.0%	-5.1
14596	AT2G47610.1   60S ribosomal protein L7A (RPL7aA)   chr2:19536860-19538725 FORWARD   Aliases: T30B22.8	9.5	9.7	-0.2	-0.4	100.0%	-4.9
14597	AT1G02810.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr1:618270-620480 FORWARD   Aliases: F22D16.20, F22D16_20	2.5	2.6	-0.1	-0.4	100.0%	-4.4
14598	AT2G42790.1   citrate synthase, glyoxysomal, putative, strong similarity to SP:P49299 Citrate synthase, glyoxysomal precursor {Cucurbita maxima}; contains Pfam profile PF00285: Citrate synthase   chr2:17809933-17813126 REVERSE   Aliases: F7D19.21, F7D19_21	8.8	9.0	-0.2	-0.4	100.0%	-5.0
14599	AT5G52450.1   MATE efflux protein-related, strong similarity to unknown protein (pir::T02324); contains Pfam profile PF01554 Uncharacterized membrane protein family   chr5:21306125-21309088 REVERSE   Aliases: K24M7.20, K24M7_20	7.1	7.2	-0.2	-0.4	100.0%	-4.7
14600	AT2G32470.1   F-box family protein-related, contains TIGRFAM TIGR01640 : F-box protein interaction domain; similar to F-box protein Fbx8 (GI:6164735) (Homo sapiens)   chr2:13794670-13795536 FORWARD   Aliases: T26B15.3, T26B15_3	3.0	2.9	0.1	0.4	100.0%	-5.3
14601	AT1G04880.1   high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein, low similarity to SP:O15347:HMG4_HUMAN High mobility group protein 4 (HMG-4) (High mobility group protein 2a) (HMG-2a) {Homo sapiens}; contains Pfam profiles PF00505: HMG (high mobility group) box, PF01388: ARID/BRIGHT DNA binding domain   chr1:1375960-1379175 REVERSE   Aliases: F13M7.13, F13M7_13	3.4	3.4	0.1	0.4	100.0%	-5.5
14602	AT5G53690.1   hypothetical protein   chr5:21817713-21817943 FORWARD   Aliases: MGN6.4, MGN6_4	2.4	2.4	-0.1	-0.4	100.0%	-5.9
14603	AT4G23300.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:12181979-12184714 FORWARD   Aliases: F21P8.190, F21P8_190	2.8	2.7	0.1	0.4	100.0%	-5.6
14604	AT2G38360.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr2:16076693-16077667 REVERSE   Aliases: T19C21.15, T19C21_15	5.2	5.3	-0.1	-0.4	100.0%	-5.1
14605	AT2G26850.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr2:11456391-11458317 REVERSE   Aliases: F12C20.11, F12C20_11	2.3	2.3	-0.0	-0.4	100.0%	-5.7
14606	AT5G38470.1   DNA repair protein RAD23, putative, similar to DNA repair by nucleotide excision (NER) RAD23 protein, isoform I GI:1914683 from (Daucus carota)   chr5:15421872-15424941 FORWARD   Aliases: MXI10.20, MXI10_20	8.6	8.3	0.3	0.4	100.0%	-4.5
14607	AT1G48095.1   expressed protein   chr1:17763811-17765667 FORWARD   Aliases: F21D18.19, F21D18_19	2.6	2.7	-0.1	-0.4	100.0%	-5.2
14608	AT1G30760.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:10918260-10920659 FORWARD   Aliases: T17H7.1	8.7	9.0	-0.2	-0.4	100.0%	-4.5
14609	AT4G37510.1   ribonuclease III family protein, contains Pfam profile PF00636 RNase3 domain   chr4:17626098-17628941 REVERSE   Aliases: F6G17.160, F6G17_160	5.4	5.6	-0.1	-0.4	100.0%	-4.6
14610	AT5G58590.1   Symbol: RANBP1	11.4	11.2	0.2	0.4	100.0%	-4.6
14611	AT1G29260.1   Symbol: PEX7   peroxisomal targeting signal type 2 receptor (PEX7), identical to peroxisomal targeting signal type 2 receptor (Pex7p) (GI:9502414) (Arabidopsis thaliana); WD-40 repeat protein family member; contains 6 WD-40 repeats (PF00400); similar to peroxisomal targeting signal 2 receptor (PTS2R) (Peroxin-7) (PEX7)(SP:O00628) (Homo sapiens)   chr1:10224801-10226191 FORWARD   Aliases: F28N24.6, F28N24_6, PEROXISOMAL TARGETING SIGNAL TYPE 2 RECEPTOR	6.2	6.1	0.1	0.4	100.0%	-5.0
14612	AT5G10460.1   haloacid dehalogenase-like hydrolase family protein, contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase	6.8	6.6	0.2	0.4	100.0%	-4.8
14613	AT5G45190.1   cyclin family protein, similar to cyclin T1 (Equus caballus) GI:5052355; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr5:18294847-18299078 REVERSE   Aliases: K18C1.7, K18C1_7	8.5	8.3	0.2	0.4	100.0%	-5.1
14614	AT5G59210.2   myosin heavy chain-related, contains weak similarity to Myosin heavy chain, gizzard smooth muscle (Swiss-Prot:P10587) (Gallus gallus)   chr5:23907862-23910891 REVERSE   Aliases: MNC17.12, MNC17_12	7.9	7.8	0.2	0.4	100.0%	-5.0
14615	AT1G04480.1   60S ribosomal protein L23 (RPL23A), identical to GB:AAB80655   chr1:1216094-1217457 FORWARD   Aliases: F19P19.5, F19P19_5	11.1	11.2	-0.1	-0.4	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14616	AT2G23800.1   Symbol: GGPS2   geranylgeranyl pyrophosphate synthase (GGPS2) (GGPS5) / GGPP synthetase / farnesyltranstransferase, identical to GB:U44876; sequence disagrees at N-Terminus, sequence submitted has been confirmed from three electropherograms.   chr2:10138569-10139859 REVERSE   Aliases: F27L4.2, F27L4_2, GERANYLGERANYL PYROPHOSPHATE SYNTHASE 5, GGPS5, PREGERANYLGERANYL PYROPHOSPHATE SYNTHASE	2.5	2.6	-0.1	-0.4	100.0%	-5.7
14617	AT3G57170.1   N-acetylglucosaminyl transferase component family protein / Gpi1 family protein, similar to SP:O14357 N-acetylglucosaminyl-phosphatidylinositol biosynthetic protein gpi1 {Schizosaccharomyces pombe}; contains Pfam profile PF05024: N-acetylglucosaminyl transferase component (Gpi1)   chr3:21170400-21174163 REVERSE   Aliases: F24I3.250	4.1	4.0	0.1	0.4	100.0%	-4.9
14618	AT5G59710.1   Symbol: VIP2   transcription regulator NOT2/NOT3/NOT5 family protein, contains Pfam domain PF04153: NOT2 / NOT3 / NOT5 family   chr5:24075560-24079144 FORWARD   Aliases: MTH12.8, MTH12_8	5.3	5.5	-0.2	-0.4	100.0%	-4.7
14619	AT5G43130.1   similar to transcription initiation factor IID (TFIID) component TAF4 family protein [Arabidopsis thaliana] (TAIR:At1g27720.1); similar to putative protein [Oryza sativa] (GB:CAC39055.1); contains InterPro domain Transcription initiation factor TFIID component TAF4 (InterPro:IPR007900)   chr5:17332677-17338391 REVERSE   Aliases: MMG4.16, MMG4_16	8.6	8.7	-0.1	-0.4	100.0%	-4.8
14620	AT2G30240.1   Symbol: ATCHX13   cation/hydrogen exchanger, putative (CHX13), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr2:12906984-12909856 REVERSE   Aliases: CHX13, T9D9.5, T9D9_5	2.8	2.7	0.1	0.4	100.0%	-5.2
14621	AT4G15950.1   expressed protein   chr4:9040758-9041898 FORWARD   Aliases: DL4012W, FCAALL.240	3.7	3.8	-0.1	-0.4	100.0%	-4.8
14622	AT2G29490.1   Symbol: ATGSTU1   glutathione S-transferase, putative, similar to glutathione S-transferase 103-1A (Arabidopsis thaliana) SWISS-PROT:P46421   chr2:12638556-12639550 REVERSE   Aliases: F16P2.13, F16P2_13, GLUTATHIONE S TRANSFERASE 19, GST19	5.9	5.7	0.2	0.4	100.0%	-4.9
14623	AT5G01820.1   Symbol: ATSR1   CBL-interacting protein kinase 14 (CIPK14), identical to CBL-interacting protein kinase 14 (Arabidopsis thaliana) gi:13249127;gb:AAK16689; contains Pfam profiles PF00069: Protein kinase domain and PF03822: NAF domain; identical to cDNA CBL-interacting protein kinase 14 (CIPK14) GI:13249126   chr5:313190-314997 REVERSE   Aliases: CBL INTERACTING PROTEIN KINASE 14, CIPK14, SERINE/THREONINE PROTEIN KINASE 1, T20L15.90, T20L15_90	6.9	6.7	0.2	0.4	100.0%	-4.9
14624	AT5G45070.1   Symbol: ATPP2 A8   disease resistance protein (TIR class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr5:18205126-18206589 REVERSE   Aliases: ATPP2 A8, K17O22.3, K17O22_3	3.5	3.7	-0.2	-0.4	100.0%	-4.1
14625	AT2G27600.1   AAA-type ATPase family protein / vacuolar sorting protein-related, similar to SP:P46467 SKD1 protein (Vacuolar sorting protein 4b) {Mus musculus}; contains Pfam profiles PF00004: ATPase AAA family, PF04212: MIT domain   chr2:11788115-11791008 FORWARD   Aliases: F10A12.27, F10A12_27	9.0	9.3	-0.3	-0.4	100.0%	-4.6
14626	AT1G21970.1   Symbol: LEC1   CCAAT-box binding transcription factor (LEC1), similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP:P25209) (GI:22380) (Zea mays); identical to GB:AAC39488 GI:3282674 from (Arabidopsis thaliana) (Cell 93 (7), 1195-1205 (1998)); identified in Plant Cell 2003 Jan;15(1):5-18; contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone   chr1:7727569-7729606 REVERSE   Aliases: EMB 212, EMB212, LEAFY COTYLEDON 1, T26F17.20, T26F17_20	3.5	3.4	0.1	0.4	100.0%	-5.3
14627	AT1G10230.1   Symbol: ASK18   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At18), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1a GI:3068807 (Arabidopsis thaliana)   chr1:3355573-3356361 FORWARD   Aliases: ARABIDOPSIS SKP1 LIKE 18, ASK18, F14N23.11, F14N23_11	5.5	5.6	-0.1	-0.4	100.0%	-4.4
14628	AT1G79000.1   Symbol: HAC1   p300/CBP acetyltransferase-related protein 2 (PCAT2), contains Pfam domains PF02135: TAZ zinc finger and PF00569: Zinc finger, ZZ type; identical to cDNA p300/CBP acetyltransferase-related protein 2 GI:12597460   chr1:29721243-29728859 REVERSE   Aliases: PCAT2, YUP8H12R.38, YUP8H12R_38	3.3	3.5	-0.2	-0.4	100.0%	-4.9
14629	AT1G77410.1   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase SP:P45582 from (Asparagus officinalis)   chr1:29093591-29098158 REVERSE   Aliases: F2P24.12, F2P24_12	3.6	3.5	0.1	0.4	100.0%	-5.1
14630	AT3G12230.1   Symbol: SCPL14	2.5	2.7	-0.2	-0.4	100.0%	-4.7
14631	AT3G12240.1   Symbol: SCPL15	2.5	2.7	-0.2	-0.4	100.0%	-4.7
14632	AT3G25890.1   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr3:9477289-9478692 FORWARD   Aliases: MPE11.13	3.9	3.8	0.1	0.4	100.0%	-4.9
14633	AT2G46210.1   delta-8 sphingolipid desaturase, putative, similar to delta-8 sphingolipid desaturase GI:3819708 from (Brassica napus)   chr2:18984417-18986074 FORWARD   Aliases: T3F17.14	4.9	4.8	0.1	0.4	100.0%	-4.4
14634	AT3G26210.1   Symbol: CYP71B23   cytochrome P450 71B23, putative (CYP71B23), Identical to Cytochrome P450 71B23 (SP:Q9LTM0)(Arabidopsis thaliana);contains Pfam profile: PF00067 cytochrome P450   chr3:9594382-9596470 REVERSE   Aliases: MTC11.12	2.8	3.0	-0.1	-0.4	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14635	AT4G10470.1   expressed protein   chr4:6476010-6478339 FORWARD   Aliases: F7L13.50, F7L13_50	3.2	3.2	-0.1	-0.4	100.0%	-5.4
14636	AT3G61720.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr3:22853986-22856373 REVERSE   Aliases: F21F14.8	3.5	3.4	0.1	0.4	100.0%	-5.2
14637	AT4G33220.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr4:16022443-16026364 FORWARD   Aliases: F4I10.150, F4I10_150	2.3	2.3	-0.1	-0.4	100.0%	-5.7
14638	AT2G23830.1   vesicle-associated membrane protein, putative / VAMP, putative, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia)   chr2:10150726-10151591 FORWARD   Aliases: T29E15.3, T29E15_3	2.5	2.5	-0.0	-0.4	100.0%	-5.7
14639	AT5G16500.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:5386678-5389168 REVERSE   Aliases: MQK4.24, MQK4_24	2.7	2.6	0.0	0.4	100.0%	-5.7
14640	AT1G11920.1   pectate lyase family protein, similar to pectate lyase GI:14289169 from (Salix gilgiana)	2.8	2.7	0.1	0.4	100.0%	-4.8
14641	AT4G28530.1   Symbol: ANAC074   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; No apical meristem gene (NAM), required for pattern formation in embryos and flowers-Petunia hybrida, PATCHX:E205713	3.5	3.6	-0.1	-0.4	100.0%	-4.7
14642	AT3G61740.1   PHD finger family protein (ATX3), contains Pfam domains PF00628: PHD-finger and PF00855: PWWP domain; identical to cDNA trithorax 3 (ATX3) partial cds GI:15217142   chr3:22861810-22867947 REVERSE   Aliases: F21F14.13	4.6	4.7	-0.1	-0.4	100.0%	-4.7
14643	AT1G61500.1   S-locus protein kinase, putative, similar to KI domain interacting kinase 1 (Zea mays) gi:2735017:gb:AAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954	3.3	3.2	0.1	0.4	100.0%	-5.4
14644	AT3G10540.1   3-phosphoinositide-dependent protein kinase, putative, similar to 3-phosphoinositide-dependent protein kinase-1 (Oryza sativa) gi:5001830:gb:AAD37166   chr3:3289700-3292707 FORWARD   Aliases: F13M14.18	2.8	2.9	-0.1	-0.4	100.0%	-5.3
14645	AT3G57890.1   tubulin-specific chaperone C-related, contains weak similarity to Tubulin-specific chaperone C (Tubulin-folding cofactor C) (CFC) (Swiss-Prot:Q15814) (Homo sapiens)   chr3:21449180-21452998 FORWARD   Aliases: T10K17.100	8.2	8.4	-0.2	-0.4	100.0%	-4.7
14646	AT1G70870.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:26724682-26725225 REVERSE   Aliases: F15H11.29, F15H11_29	2.6	2.7	-0.1	-0.4	100.0%	-5.5
14647	AT1G14120.1   2-oxoglutarate-dependent dioxygenase, putative, similar to adventitious rooting related oxygenase ARRO-1 from Malus x domestica, gi:3492806; contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr1:4833516-4835083 REVERSE   Aliases: F7A19.20, F7A19_20	2.9	2.9	-0.1	-0.4	100.0%	-5.3
14648	AT1G31620.1   expressed protein   chr1:11316922-11317875 FORWARD   Aliases: F27M3.18, F27M3_18	2.7	2.6	0.1	0.4	100.0%	-5.3
14649	AT3G43500.1   expressed protein   chr3:15411245-15411706 REVERSE   Aliases: T18D12.70	2.2	2.2	0.1	0.4	100.0%	-5.5
14650	AT4G39430.1   expressed protein, ; expression supported by MPSS   chr4:18343008-18345021 FORWARD   Aliases: F23K16.60, F23K16_60	3.9	3.8	0.1	0.4	100.0%	-5.0
14651	AT2G47790.1   transducin family protein / WD-40 repeat family protein, similar to WD-repeat protein 5 (SP:Q9UGP9) (Homo sapiens); The first 3 exons are identical to that of GB:AJ224957. This gene appears to be a truncated version of that in GB:AJ224957; contains 4 WD-40 repeats (PF00400)   chr2:19577641-19580086 REVERSE   Aliases: F17A22.18	8.9	8.7	0.2	0.4	100.0%	-4.6
14652	AT1G19580.1   bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats)   chr1:6774754-6777438 FORWARD   Aliases: None	6.7	7.0	-0.3	-0.4	100.0%	-4.5
14653	AT2G29750.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:12716804-12718773 FORWARD   Aliases: T27A16.15, T27A16_15	3.6	3.8	-0.2	-0.4	100.0%	-4.7
14654	AT4G29960.1   expressed protein   chr4:14660608-14662393 REVERSE   Aliases: F27B13.200, F27B13_200	6.7	6.5	0.2	0.4	100.0%	-4.8
14655	AT3G13180.1   NOL1/NOP2/sun family protein / antitermination NusB domain-containing protein, low similarity to SP:P36929 SUN protein (FMU protein) {Escherichia coli}; contains Pfam profiles PF01189: NOL1/NOP2/sun family, PF01029: NusB family   chr3:4236024-4240016 REVERSE   Aliases: MJG19.14	4.4	4.5	-0.1	-0.4	100.0%	-4.8
14656	AT1G09030.1   histone-like transcription factor (CBF/NF-Y) family protein, contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone; similar to CAAT-box DNA binding protein subunit B (NF-YB) (GI:22380) (Zea mays)   chr1:2908614-2909033 REVERSE   Aliases: F7G19.10, F7G19_10	2.6	2.7	-0.0	-0.4	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14657	AT4G21490.1   pyridine nucleotide-disulphide oxidoreductase family protein, similar to GI:3718005 alternative NADH-dehydrogenase {Yarrowia lipolytica}; contains Pfam profile PF00070: Pyridine nucleotide-disulphide oxidoreductase   chr4:11436507-11438969 REVERSE   Aliases: F18E5.110, F18E5_110	4.4	4.5	-0.1	-0.4	100.0%	-4.8
14658	AT1G10380.1   expressed protein   chr1:3400607-3402325 FORWARD   Aliases: F14N23.27	3.4	3.6	-0.2	-0.4	100.0%	-4.2
14659	AT2G28030.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr2:11941285-11942463 REVERSE   Aliases: T1E2.2	2.5	2.5	0.0	0.4	100.0%	-5.9
14660	AT1G18860.1   Symbol: WRKY61	2.5	2.7	-0.1	-0.4	100.0%	-4.7
14661	AT3G12770.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:4056837-4059200 REVERSE   Aliases: MBK21.13	3.9	4.0	-0.1	-0.4	100.0%	-4.9
14662	AT1G53930.1   ubiquitin family protein, contains Pfam profile: PF00240 ubiquitin family   chr1:20144079-20144555 REVERSE   Aliases: T18A20.19	2.5	2.5	-0.1	-0.4	100.0%	-5.3
14663	AT5G10940.1   transducin family protein / WD-40 repeat family protein, unnamed ORF cDNA FLJ10872, Homo sapiens, EMBL:AK001734; contains Pfam PF00400: WD domain, G-beta repeat (6 copies,1 weak)   chr5:3448649-3454191 REVERSE   Aliases: T30N20.210, T30N20_210	3.8	3.7	0.1	0.4	100.0%	-5.2
14664	AT1G50090.1   aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV   chr1:18558309-18560462 REVERSE   Aliases: F2J10.5, F2J10_5	3.4	3.5	-0.1	-0.4	100.0%	-5.2
14665	AT3G03790.2   ankyrin repeat family protein / regulator of chromosome condensation (RCC1) family protein, similar to hect domain and RLD 2 GB:NP_004658 (Homo sapiens); contains Pfam PF00415: Regulator of chromosome condensation (RCC1); contains Pfam PF00023: Ankyrin repeat; similar to rjs (GI:3414809) (Mus musculus); similar to HERC2 (GI:4079809) (Homo sapiens)   chr3:962004-968156 FORWARD   Aliases: F20H23.18, F20H23_18	5.5	5.3	0.1	0.4	100.0%	-4.7
14666	AT1G56080.1   expressed protein   chr1:20977826-20979956 REVERSE   Aliases: T6H22.12, T6H22_12	4.3	4.1	0.1	0.4	100.0%	-4.8
14667	AT1G33660.1   peroxidase family protein, similar to SP:Q05431 L-ascorbate peroxidase, cytosolic (EC 1.11.1.11) (AP) {Arabidopsis thaliana}; contains Pfam profile PF00141: Peroxidase   chr1:12197681-12198302 REVERSE   Aliases: T1E4.7	4.7	4.6	0.1	0.4	100.0%	-4.7
14668	AT1G53345.1   expressed protein   chr1:19906163-19907549 FORWARD   Aliases: None	3.5	3.6	-0.1	-0.4	100.0%	-5.1
14669	AT3G13672.2   seven in absentia (SINA) family protein, low similarity to SP:P21461 Developmental protein seven in absentia {Drosophila melanogaster}; contains Pfam profile PF03145: Seven in absentia protein family   chr3:4472570-4474371 REVERSE   Aliases: MMM17.8	2.7	2.7	0.0	0.4	100.0%	-5.4
14670	AT1G07270.1   cell division control protein CDC6b, putative (CDC6b), identical to CDC6b protein (GI:18056482) {Arabidopsis thaliana}; contains Prosite PS00017: ATP/GTP-binding site motif A (P-loop); identical to cDNA CDC6b GI:18056481   chr1:2229756-2232896 REVERSE   Aliases: F10K1.2, F10K1_2	3.0	3.0	-0.1	-0.4	100.0%	-5.3
14671	AT1G45110.1   tetrapyrrole methylase family protein, contains Pfam PF00590 : Tetrapyrrole (Corrin/Porphyrin) Methylases domain; contains TIGRFAMS TIGR00522 : diphthine synthase   chr1:17054974-17057232 FORWARD   Aliases: F27F5.18, F27F5_18	4.2	4.3	-0.1	-0.4	100.0%	-4.8
14672	AT4G29240.1   leucine-rich repeat family protein / extensin family protein, contains Pfam PF00560: Leucine Rich Repeat domains; similar to leucine-rich repeat/extensin 1 (GI:13809918) (Arabidopsis thaliana)	4.0	4.1	-0.1	-0.4	100.0%	-5.0
14673	AT1G07890.5   Symbol: APX1   similar to L-ascorbate peroxidase 1b (APX1b) [Arabidopsis thaliana] (TAIR:At3g09640.1); similar to ascorbate peroxidase [Brassica juncea] (GB:AAN60794.1); contains InterPro domain Haem peroxidase (InterPro:IPR002016); contains InterPro domain Plant ascorbate peroxidase (InterPro:IPR002207)   chr1:2437327-2439649 FORWARD   Aliases: ASCORBATE PEROXIDASE, CS1, F24B9.2, F24B9_2	11.8	11.6	0.2	0.4	100.0%	-4.7
14674	AT4G22940.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:12021774-12023478 REVERSE   Aliases: F7H19.120, F7H19_120	2.5	2.4	0.0	0.4	100.0%	-5.5
14675	AT3G52070.2   expressed protein   chr3:19323731-19324444 FORWARD   Aliases: F4F15.180	5.0	4.8	0.2	0.4	100.0%	-4.5
14676	AT1G06930.1   expressed protein, ; expression supported by MPSS   chr1:2129162-2129671 FORWARD   Aliases: F4H5.24, F4H5_24	3.1	3.0	0.1	0.4	100.0%	-5.2
14677	AT3G11180.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to leucoanthocyanidin dioxygenase GB:BAA20143 (Perilla frutescens), Malus domestica, SP:P51091; contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr3:3504220-3507119 FORWARD   Aliases: F11B9.11	2.1	2.2	-0.0	-0.4	100.0%	-5.5
14678	AT5G08230.1   PWWP domain-containing protein, putative transcription factor (HUA2) - Arabidopsis thaliana, EMBL:AF116556   chr5:2643539-2649789 REVERSE   Aliases: F8L15.8	2.4	2.3	0.0	0.4	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14679	AT5G63140.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.0	3.0	-0.1	-0.4	100.0%	-5.3
14680	AT5G58610.1   PHD finger transcription factor, putative   chr5:23703997-23708279 REVERSE   Aliases: MZN1.7, MZN1_7	3.6	3.6	0.1	0.4	100.0%	-5.4
14681	AT3G33080.1   expressed protein, similar to protein prospero GI:1346808 (Drosophila melanogaster)   chr3:13827628-13828157 REVERSE   Aliases: None	1.8	1.7	0.0	0.3	100.0%	-5.9
14682	AT2G23070.1   casein kinase II alpha chain, putative, similar to casein kinase II, alpha chain (CK II) (Zea mays) SWISS-PROT:P28523; contains protein kinase domain, Pfam:PF00069   chr2:9831052-9833978 REVERSE   Aliases: F21P24.13, F21P24_13	10.3	10.5	-0.2	-0.3	100.0%	-4.9
14683	AT3G52600.2   similar to beta-fructosidase, putative / beta-fructofuranosidase, putative [Arabidopsis thaliana] (TAIR:At2g36190.1); similar to acid invertase [Lycopersicon esculentum] (GB:BAA33150.1); similar to beta-fructofuranosidase [Daucus carota] (GB:CAA49162.1); similar to INV1_DAUCA Beta-fructofuranosidase, insoluble isoenzyme 1 precursor (Sucrose hydrolase 1) (Invertase 1) (Cell wall beta-fructosidase 1) (GB:P26792); similar to beta-fructofuranosidase [Solanum tuberosum] (GB:CAA80358.1); similar to cell-wall invertase [Lycopersicon esculentum] (GB:AAM28823.1); contains InterPro domain Glycoside hydrolase, family 32 (InterPro:IPR001362)   chr3:19517630-19520368 REVERSE   Aliases: F3C22.4	2.8	2.8	0.1	0.3	100.0%	-5.3
14684	AT1G06710.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr1:2057278-2060118 REVERSE   Aliases: F4H5.20, F4H5_20	2.9	3.0	-0.1	-0.3	100.0%	-5.3
14685	AT5G40260.2   similar to nodulin MtN3 family protein [Arabidopsis thaliana] (TAIR:At4g10850.1); similar to MtN3-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_917578.1); contains InterPro domain MtN3 and saliva related transmembrane protein (InterPro:IPR004316)   chr5:16106985-16108974 FORWARD   Aliases: MSN9.17, MSN9_17	3.4	3.4	0.1	0.3	100.0%	-5.5
14686	AT3G55440.1   Symbol: ATCTIMC   triosephosphate isomerase, cytosolic, putative, strong similarity to triosephosphate isomerase, cytosolic from Petunia hybrida (SP:P48495), from Coptis japonica (SP:P21820)   chr3:20564671-20567537 FORWARD   Aliases: CYTOSOLIC TRIOSE PHOSPHATE ISOMERASE, T22E16.100	12.9	12.8	0.2	0.3	100.0%	-5.4
14687	AT5G58510.1   expressed protein, KIAA0066, Homo sapiens, EMBL:HSORFKG10   chr5:23665379-23671778 REVERSE   Aliases: MQJ2.13, MQJ2_13	5.5	5.4	0.1	0.3	100.0%	-4.8
14688	AT1G07330.1   expressed protein   chr1:2251130-2253584 FORWARD   Aliases: F22G5.33, F22G5_33	3.0	3.1	-0.1	-0.3	100.0%	-5.4
14689	AT4G04710.1   Symbol: CPK22   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Nicotiana tabacum) gi:3283996;gb:AAC25423; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr4:2389596-2392885 REVERSE   Aliases: T4B21.12, T4B21_12	6.3	6.5	-0.2	-0.3	100.0%	-4.6
14690	AT4G04720.1   Symbol: CPK21   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase(CDPK) (Carrot) SWISS-PROT:P28582   chr4:2394456-2397757 REVERSE   Aliases: T4B21.13, T4B21_13	6.3	6.5	-0.2	-0.3	100.0%	-4.6
14691	AT2G32080.2   Symbol: PUR ALPHA 1   PUR alpha-1 protein, identical to PUR alpha-1 GI:5081612 from (Arabidopsis thaliana); contains Pfam profile: PF04845 PurA ssDNA and RNA-binding protein   chr2:13649314-13651243 REVERSE   Aliases: F22D22.17, F22D22_17, PUR ALPHA 1	4.3	4.4	-0.2	-0.3	100.0%	-4.8
14692	AT1G62910.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23302722-23306827 FORWARD   Aliases: F16P17.6, F16P17_6	2.7	2.7	0.0	0.3	100.0%	-5.7
14693	AT1G52580.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr1:19591306-19592721 FORWARD   Aliases: F6D8.20, F6D8_20	3.9	3.8	0.1	0.3	100.0%	-5.4
14694	AT4G37520.1   peroxidase 50 (PER50) (P50) (PRXR2), identical to SP:Q43731 Peroxidase 50 precursor (EC 1.11.1.7) (Atperox P50) (PRXR2) (ATP9a) {Arabidopsis thaliana}   chr4:17631556-17633243 FORWARD   Aliases: F19F18.10, F19F18_10	3.5	3.2	0.4	0.3	100.0%	-4.9
14695	AT4G37530.1   peroxidase, putative, similar to peroxidase (Arabidopsis thaliana) gi:1402906;emb:CAA66958; identical to Pfam profile PF00141: Peroxidase; identical to cDNA peroxidase ATP37 GI:18874553   chr4:17634778-17636282 FORWARD   Aliases: F19F18.20, F19F18_20	3.5	3.2	0.4	0.3	100.0%	-4.9
14696	AT2G29380.1   protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain; similar to protein phpsphatase 2C (PP2C) (GI:7768151) (Fagus sylvatica).   chr2:12615932-12617201 FORWARD   Aliases: F16P2.24, F16P2_24	2.8	2.7	0.1	0.3	100.0%	-5.3
14697	AT1G22490.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.3	3.2	0.1	0.3	100.0%	-5.3
14698	AT3G17430.1   phosphate translocator-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}   chr3:5965935-5969239 FORWARD   Aliases: MTO12.2	5.8	5.9	-0.1	-0.3	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14699	AT2G26280.1   Symbol: CID7   smr (Small MutS Related) domain-containing protein, weak similarity to PRLI-interacting factor N (Arabidopsis thaliana) GI:11139276; contains Pfam profile PF01713: Smr domain   chr2:11194811-11198415 REVERSE   Aliases: T1D16.8, T1D16_8	9.1	8.9	0.1	0.3	100.0%	-5.0
14700	AT5G48500.1   expressed protein, similar to unknown protein (gb:AAD28645.1)   chr5:19670217-19671470 FORWARD   Aliases: MJE7.14, MJE7_14	5.1	5.0	0.1	0.3	100.0%	-4.9
14701	AT1G69720.1   heme oxygenase 3 (HO3), similar to heme oxygenase 3 (Arabidopsis thaliana) gi:14485563:gb:AAK63006   chr1:26230529-26233294 FORWARD   Aliases: T6C23.8, T6C23_8	2.6	2.6	0.1	0.3	100.0%	-5.6
14702	AT1G37010.1   hypothetical protein   chr1:14043359-14043668 FORWARD   Aliases: T32E20.23, T32E20_23	2.6	2.7	-0.0	-0.3	100.0%	-5.7
14703	AT2G37585.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr2:15772862-15774956 FORWARD   Aliases: None	4.0	4.1	-0.1	-0.3	100.0%	-5.2
14704	AT3G10760.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:3369585-3371232 FORWARD   Aliases: T7M13.16	3.5	3.6	-0.1	-0.3	100.0%	-4.6
14705	AT1G74640.1   expressed protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold   chr1:28036424-28038434 FORWARD   Aliases: F1M20.32, F1M20_32	8.1	8.2	-0.2	-0.3	100.0%	-4.7
14706	AT1G58470.1   Symbol: ATRBP1	3.3	3.3	0.0	0.3	100.0%	-5.4
14707	AT2G28940.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:12433348-12435762 REVERSE   Aliases: T9I4.2, T9I4_2	3.6	3.7	-0.1	-0.3	100.0%	-4.4
14708	AT3G19950.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:6942775-6945199 FORWARD   Aliases: MPN9.20	7.2	7.1	0.1	0.3	100.0%	-5.2
14709	AT2G14390.1   expressed protein   chr2:6117994-6119000 FORWARD   Aliases: T1O16.2, T1O16_2	2.2	2.2	0.0	0.3	100.0%	-5.7
14710	AT5G16110.1   expressed protein, hypothetical protein T26J14.6 - Arabidopsis thaliana, EMBL:AC011915   chr5:5260607-5262843 REVERSE   Aliases: T21H19.30, T21H19_30	5.3	5.1	0.2	0.3	100.0%	-4.8
14711	AT1G19650.1   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, similar to SP:P24859 from (Kluyveromyces lactis) similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus	3.7	3.6	0.1	0.3	100.0%	-5.1
14712	AT3G21180.1   Symbol: ACA9   calcium-transporting ATPase, plasma membrane-type, putative / Ca <sup>2+</sup> -ATPase, putative (ACA9), identical to SP:Q9LU41 Potential calcium-transporting ATPase 9, plasma membrane-type (EC 3.6.3.8) (Ca <sup>2+</sup> )-ATPase isoform 9) {Arabidopsis thaliana}   chr3:7425525-7432204 FORWARD   Aliases: ATACA9, AUTOINHIBITED CA(2+) ATPASE, MXL8.3	3.0	3.1	-0.1	-0.3	100.0%	-5.0
14713	AT5G58890.1   MADS-box family protein, various predicted proteins, Oryza sativa and Arabidopsis thaliana   chr5:23798058-23798942 FORWARD   Aliases: K19M22.9, K19M22_9	2.8	2.7	0.1	0.3	100.0%	-5.2
14714	AT1G12070.1   Rho GDP-dissociation inhibitor family protein, similar to SP:P52565 Rho GDP-dissociation inhibitor 1 (Rho GDI 1) (Rho-GDI alpha) {Homo sapiens}; contains Pfam profile PF02115: RHO protein GDP dissociation inhibitor   chr1:4078911-4080104 REVERSE   Aliases: F12F1.5, F12F1_5	2.4	2.3	0.0	0.3	100.0%	-5.9
14715	AT2G24630.1   Symbol: ATCSLC08   glycosyl transferase family 2 protein, similar to cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	2.8	2.8	0.1	0.3	100.0%	-5.4
14716	AT1G43010.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:16156049-16156908 FORWARD   Aliases: F13A11.14, F13A11_14	2.2	2.2	0.0	0.3	100.0%	-5.8
14717	AT1G70460.1   protein kinase, putative, contains Pfam PF00069: Protein kinase domain   chr1:26559511-26562947 FORWARD   Aliases: F24J13.3, F24J13_3	3.4	3.6	-0.2	-0.3	100.0%	-4.2
14718	AT1G45170.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g42960.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470465.1)   chr1:17098420-17100446 REVERSE   Aliases: F27F5.25, F27F5_25	6.6	6.8	-0.1	-0.3	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14719	AT2G46860.1   inorganic pyrophosphatase, putative (soluble) / pyrophosphate phospho-hydrolase, putative / PPase, putative, strong similarity to SP:Q43187 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase) {Solanum tuberosum}; contains Pfam profile PF00719: inorganic pyrophosphatase   chr2:19260757-19262344 FORWARD   Aliases: F19D11.23, F19D11_23	2.2	2.2	-0.1	-0.3	100.0%	-5.4
14720	AT5G26880.1   tRNA/rRNA methyltransferase (SpoU) family protein, low similarity to tRNA (Gm18) methyltransferase (Thermus thermophilus) GI:11079208; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family   chr5:9457700-9459233 REVERSE   Aliases: F2P16.25, F2P16_25	10.2	10.1	0.1	0.3	100.0%	-5.0
14721	AT3G25585.4   Symbol: AAPT2   similar to aminoalcoholphosphotransferase (AAPT1) [Arabidopsis thaliana] (TAIR:At1g13560.1); similar to aminoalcoholphosphotransferase [Brassica rapa subsp. pekinensis] (GB:AAL46934.3); similar to aminoalcoholphosphotransferase [Pimpinella brachycarpa] (GB:AAC79507.1); similar to aminoalcoholphosphotransferase [Brassica rapa] (GB:AAD56040.1); similar to probable ethanolaminephosphotransferase (EC 2.7.8.1) - soybean (GB:T06384); contains InterPro domain CDP-alcohol phosphatidyltransferase (InterPro:IPR000462)   chr3:9296548-9299983 FORWARD   Aliases: AMINOALCOHOLPHOSPHOTRANSFERASE, MWL2.1	7.1	7.0	0.1	0.3	100.0%	-5.1
14722	AT2G24990.1   RIO1 family protein, similar to extragenic suppressor of the bimD6 mutation (SUDD) (Emericella nidulans) GI:2338556, RIO1 (Saccharomyces cerevisiae) GI:1359602; contains Pfam profile PF01163: RIO1 family   chr2:10632364-10635378 FORWARD   Aliases: F27C12.9, F27C12_9	6.8	7.2	-0.3	-0.3	100.0%	-4.1
14723	AT5G37350.2   RIO1 family protein, similar to extragenic suppressor of the bimD6 mutation (SUDD) (Emericella nidulans) GI:2338556, RIO1 (Saccharomyces cerevisiae) GI:1359602; contains Pfam profile PF01163: RIO1 family   chr5:14810234-14813257 FORWARD   Aliases: MNJ8.10, MNJ8_10	6.8	7.2	-0.3	-0.3	100.0%	-4.1
14724	AT3G22400.1   lipoxygenase, putative, similar to lipoxygenase gi:8649004 (Prunus dulcis), gi:1495802 and gi:1495804 from (Solanum tuberosum)   chr3:7926941-7931358 FORWARD   Aliases: MCB17.13	3.2	3.3	-0.1	-0.3	100.0%	-5.2
14725	AT1G67060.1   expressed protein   chr1:25040279-25043029 FORWARD   Aliases: F1O19.19, F1O19_19	3.5	3.3	0.1	0.3	100.0%	-4.6
14726	AT2G23945.1   chloroplast nucleoid DNA-binding protein-related, contains weak similarity to GP:2541876:dbj:BAA22813.1::D26015 CND41, chloroplast nucleoid DNA binding protein {Nicotiana tabacum}   chr2:10192309-10193685 REVERSE   Aliases: None	3.1	3.0	0.1	0.3	100.0%	-5.2
14727	AT1G73090.1   expressed protein   chr1:27491878-27494427 FORWARD   Aliases: F3N23.29, F3N23_29	3.8	3.7	0.1	0.3	100.0%	-5.3
14728	AT2G13660.1   expressed protein   chr2:5699179-5700098 REVERSE   Aliases: T10F5.25	2.7	2.7	-0.0	-0.3	100.0%	-5.6
14729	AT3G29360.2   similar to UDP-glucose 6-dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At1g26570.1); similar to UDP-glucose 6-dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At5g39320.1); similar to UDP-glucose 6-dehydrogenase, putative [Arabidopsis thaliana] (TAIR:At5g15490.1); similar to putative UDP-glucose dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:AAK16194.1); similar to UDP-glucose dehydrogenase [Cinnamomum osmophloeum] (GB:AAR84297.1); similar to UDP-glucose dehydrogenase [Colocasia esculenta] (GB:AAO62313.1); similar to putative UDP-glucose dehydrogenase 1 [Nicotiana tabacum] (GB:AAT40105.1); similar to putative UDP-glucose dehydrogenase 2 [Nicotiana tabacum] (GB:AAT40106.1); contains InterPro domain UDP-glucose/GDP-mannose dehydrogenase (InterPro:IPR001732)   chr3:11268328-11270465 REVERSE   Aliases: MUO10.18	5.2	5.5	-0.3	-0.3	100.0%	-4.7
14730	AT3G19140.1   expressed protein   chr3:6614916-6615341 REVERSE   Aliases: MVI11.4	2.3	2.3	0.0	0.3	100.0%	-5.9
14731	AT3G61210.1   embryo-abundant protein-related, similar to embryo-abundant protein (Picea glauca) GI:1350531   chr3:22669653-22670845 REVERSE   Aliases: T20K12.110	2.3	2.2	0.0	0.3	100.0%	-5.7
14732	AT3G51940.1   expressed protein   chr3:19284472-19286247 REVERSE   Aliases: F4F15.50	5.6	5.3	0.3	0.3	100.0%	-4.5
14733	AT3G03510.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr3:836046-837714 FORWARD   Aliases: T21P5.7, T21P5_7	4.2	4.1	0.1	0.3	100.0%	-5.0
14734	AT5G60460.1   sec61beta family protein, similar to SP:P52870 Protein transport protein SEC61 beta 1 subunit {Saccharomyces cerevisiae}; contains Pfam profile PF03911: Sec61beta family   chr5:24334663-24335161 REVERSE   Aliases: MUF9.9, MUF9_9	7.6	7.4	0.2	0.3	100.0%	-4.8
14735	AT4G03260.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr4:1428171-1431663 FORWARD   Aliases: F4C21.19, F4C21_19	8.0	8.1	-0.1	-0.3	100.0%	-5.2
14736	AT1G61900.2   expressed protein, contains similarity to glutamic acid/alanine-rich protein GI:6707830 from (Trypanosoma congolense)   chr1:22885880-22888718 REVERSE   Aliases: F8K4.10, F8K4_10	5.0	4.9	0.1	0.3	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14737	AT5G53150.1   similar to DNAJ heat shock N-terminal domain-containing protein [Arabidopsis thaliana] (TAIR:At2g25560.1); similar to OSJNBa0053B21.9 [Oryza sativa (japonica cultivar-group)] (GB:XP_472289.1); contains InterPro domain Heat shock protein DnaJ (InterPro:IPR003095); contains InterPro domain Heat shock protein DnaJ, N-terminal (InterPro:IPR001623)   chr5:21572017-21574717 FORWARD   Aliases: MFH8.9, MFH8_9	4.3	4.4	-0.1	-0.3	100.0%	-4.8
14738	AT3G49620.1   Symbol: DIN11   2-oxoacid-dependent oxidase, putative (DIN11), identical to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554 (Arabidopsis thaliana); identical to cDNA 2-oxoacid-dependent oxidase (din11) GI:10834553; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr3:18404732-18407799 FORWARD   Aliases: DARK INDUCIBLE 11, T9C5.210	2.5	2.5	0.1	0.3	100.0%	-5.4
14739	AT2G02080.1   zinc finger (C2H2 type) family protein, contains Pfam domain PF00096: Zinc finger, C2H2 type   chr2:518158-521706 REVERSE   Aliases: F5O4.15, F5O4_15	2.8	2.7	0.1	0.3	100.0%	-5.0
14740	AT4G39990.1   Symbol: ATGB3   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:303738 from (Pisum sativum)   chr4:18542616-18543972 FORWARD   Aliases: GTP BINDING PROTEIN 3, T5J17.160, T5J17_160	8.7	8.5	0.2	0.3	100.0%	-4.6
14741	AT5G03600.1   GDSL-motif lipase/hydrolase family protein, low similarity to family II lipase EXL3 (Arabidopsis thaliana) GI:15054386; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr5:912806-914225 FORWARD   Aliases: F17C15.20, F17C15_20	2.7	2.7	0.1	0.3	100.0%	-5.4
14742	AT1G16360.1   LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein, Similar to GI:4585976; GI:11994416; GI:4835763; GI:9757735 from (Arabidopsis thaliana)   chr1:5593487-5595173 REVERSE   Aliases: F3O9.16, F3O9_16	3.2	3.1	0.1	0.3	100.0%	-4.8
14743	AT5G66390.1   peroxidase 72 (PER72) (P72) (PRXR8), identical to SP:Q9FJZ9 Peroxidase 72 precursor (EC 1.11.1.7) (Atperox P72) (PRXR8) (ATP6a) {Arabidopsis thaliana}   chr5:26533142-26534610 REVERSE   Aliases: K1F13.4, K1F13_4	2.8	3.0	-0.2	-0.3	100.0%	-4.8
14744	AT4G14850.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At5g09950.1); similar to pentatricopeptide (PPR) repeat-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD52598.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr4:8513854-8516349 FORWARD   Aliases: DL3465W, FCAALL.335	2.7	2.8	-0.1	-0.3	100.0%	-5.5
14745	AT3G50920.2   similar to phosphatidic acid phosphatase-related / PAP2-related [Arabidopsis thaliana] (TAIR:At5g66450.1); similar to phosphatidic acid phosphatase-like [Oryza sativa (japonica cultivar-group)] (GB:XP_467361.1); contains InterPro domain PA-phosphatase related phosphoesterase (InterPro:IPR000326)	5.0	5.1	-0.1	-0.3	100.0%	-4.9
14746	AT4G22310.1   expressed protein, contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)   chr4:11791357-11792848 FORWARD   Aliases: T10I14.140, T10I14_140	10.7	10.4	0.2	0.3	100.0%	-5.0
14747	AT1G59620.1   Symbol: CW9   disease resistance protein (CC-NBS class), putative, domain signature CC-NBS exists, suggestive of a disease resistance protein.   chr1:21906292-21909350 FORWARD   Aliases: CW9, T30E16.18, T30E16_18	2.2	2.2	-0.0	-0.3	100.0%	-5.8
14748	AT4G27980.1   expressed protein   chr4:13921683-13923576 FORWARD   Aliases: T13J8.90, T13J8_90	3.0	3.1	-0.1	-0.3	100.0%	-5.1
14749	AT1G08610.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:2733791-2735470 REVERSE   Aliases: F22O13.9, F22O13_9	4.2	4.3	-0.1	-0.3	100.0%	-4.8
14750	AT4G02080.1   Symbol: ASAR1   GTP-binding protein (SAR1A), identical to SP:O04834 GTP-binding protein SAR1A. (Arabidopsis thaliana)   chr4:921462-922776 FORWARD   Aliases: ATSAR2, ATSARA1C, T10M13.9, T10M13_9	9.3	9.1	0.2	0.3	100.0%	-4.9
14751	AT3G01190.1   peroxidase 27 (PER27) (P27) (PRXR7), identical to SP:Q43735 Peroxidase 27 precursor (EC 1.11.1.7) (Atperox P27) (PRXR7) (ATP12a) {Arabidopsis thaliana}   chr3:67065-68543 REVERSE   Aliases: T4P13.12, T4P13_12	3.4	3.5	-0.1	-0.3	100.0%	-4.7
14752	AT5G15310.1   myb family transcription factor, contains PFAM profile: myb DNA-binding domain PF00249   chr5:4974747-4976230 FORWARD   Aliases: F8M21.200, F8M21_200	2.8	2.9	-0.1	-0.3	100.0%	-5.4
14753	AT2G45590.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:18793732-18796062 FORWARD   Aliases: F17K2.12	6.5	6.3	0.2	0.3	100.0%	-4.8
14754	AT1G05520.1   transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens)   chr1:1630899-1635710 REVERSE   Aliases: T25N20.17	4.0	4.2	-0.2	-0.3	100.0%	-5.0
14755	AT3G49270.1   expressed protein   chr3:18278237-18279255 REVERSE   Aliases: F2K15.130	2.6	2.6	0.1	0.3	100.0%	-5.5
14756	AT1G15140.3   oxidoreductase NAD-binding domain-containing protein, Contains Pfam profile PF00175: Oxidoreductase NAD-binding domain; ESTs gb:H76345 and gb:AA651465 come from this gene   chr1:5210277-5212344 REVERSE   Aliases: F9L1.8, F9L1_8	6.9	6.8	0.1	0.3	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14757	AT1G52690.2   late embryogenesis abundant protein, putative / LEA protein, putative, similar to SP:P13934 Late embryogenesis abundant protein 76 (LEA 76) {Brassica napus}; contains Pfam profile PF02987: Late embryogenesis abundant protein	3.2	2.9	0.2	0.3	100.0%	-4.6
14758	AT1G16950.1   expressed protein   chr1:5796002-5796552 FORWARD   Aliases: F17F16.23	2.4	2.4	-0.0	-0.3	100.0%	-5.6
14759	AT4G09360.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr4:5940183-5943277 FORWARD   Aliases: T15G18.1, T15G18_1	2.0	2.0	-0.0	-0.3	100.0%	-6.0
14760	AT4G02140.1   expressed protein   chr4:949617-950270 REVERSE   Aliases: T10M13.15, T10M13_15	2.9	2.8	0.0	0.3	100.0%	-5.6
14761	AT1G48790.1   mov34 family protein, similar to AMSH (Homo sapiens) GI:4098124; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr1:18047378-18051325 REVERSE   Aliases: F11I4.4, F11I4_4	8.1	8.0	0.1	0.3	100.0%	-4.8
14762	AT5G39420.1   Symbol: CDC2CAT   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr5:15789308-15792399 FORWARD   Aliases: CDC2CAT, MUL8.100, MUL8_100	3.0	2.9	0.1	0.3	100.0%	-5.3
14763	AT2G31130.1   expressed protein   chr2:13270758-13273637 REVERSE   Aliases: T16B12.6, T16B12_6	5.7	5.8	-0.1	-0.3	100.0%	-4.6
14764	AT1G30210.2   TCP family transcription factor, putative, similar to TFPD (GI:6681577) (Arabidopsis thaliana); contains similarity to cyc1A protein GI:6358548 from (Antirrhinum graniticum)   chr1:10627183-10630594 REVERSE   Aliases: F12P21.11, F12P21_11	2.9	2.9	0.1	0.3	100.0%	-5.4
14765	AT2G22920.2   Symbol: SCPL12	3.6	3.7	-0.2	-0.3	100.0%	-4.6
14766	AT5G53660.1   Symbol: AtGRF7	3.3	3.4	-0.1	-0.3	100.0%	-4.9
14767	AT4G31270.1   expressed protein   chr4:15183235-15184967 REVERSE   Aliases: F8F16.90, F8F16_90	5.2	5.4	-0.1	-0.3	100.0%	-4.8
14768	AT4G12110.1   Symbol: SMO1 1	4.7	4.9	-0.2	-0.3	100.0%	-4.9
14769	AT3G19610.1   hypothetical protein   chr3:6812499-6814582 REVERSE   Aliases: MMB12.8	2.3	2.4	-0.0	-0.3	100.0%	-5.9
14770	AT1G03910.1   expressed protein, low similarity to cactin (Drosophila melanogaster) GI:7673675; expression supported by MPSS   chr1:996431-1000230 FORWARD   Aliases: F21M11.16, F21M11_16	7.4	7.3	0.1	0.3	100.0%	-4.8
14771	AT5G56870.1   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase precursor GI:3869280 from (Carica papaya)   chr5:23021422-23025875 FORWARD   Aliases: MPI10.3, MPI10_3	4.4	4.3	0.1	0.3	100.0%	-4.4
14772	AT4G00340.1   Symbol: RLK4   S-locus glycoprotein family protein / curculin-like (mannose-binding) lectin family protein / PAN domain-containing protein, contains Pfam profiles: PF01453 lectin (probable mannose binding), PF00954 S-locus glycoprotein family, PF00024 PAN domain   chr4:148814-151686 FORWARD   Aliases: A_IG005I10.19, A_IG005I10_19, RECEPTOR LIKE PROTEIN KINASE 4	2.2	2.2	0.0	0.3	100.0%	-5.7
14773	AT1G02580.1   Symbol: MEA   maternal embryogenesis control protein / MEDEA (MEA), nearly identical to MEDEA GB:AAC39446 GI:3089625 from (Arabidopsis thaliana); contains Pfam profile PF00856: SET domain   chr1:544783-549202 FORWARD   Aliases: EMB173, EMBRYO DEFECTIVE 173, FERTILIZATION INDEPENDENT SEED, FIS1, MEA, MEDEA, T14P4.11, T14P4_11	3.6	3.7	-0.1	-0.3	100.0%	-5.1
14774	AT1G22880.2   similar to glycosyl hydrolase family 9 protein [Arabidopsis thaliana] (TAIR:At1g71380.1); similar to endo-1,4-beta-glucanase [Malus x domestica] (GB:AAQ55294.1); similar to basic cellulase [Citrus sinensis] (GB:AAB65156.1); contains InterPro domain Glycoside hydrolase, family 9 (InterPro:IPR001701)   chr1:8095491-8097698 FORWARD   Aliases: F19G10.16, F19G10_16	2.7	2.8	-0.1	-0.3	100.0%	-4.9
14775	AT5G06430.1   thioredoxin-related, contains weak similarity to Swiss-Prot:Q9SEU7 thioredoxin M-type 3, chloroplast precursor (TRX-M3) (Arabidopsis thaliana)   chr5:1963581-1964252 REVERSE   Aliases: MHF15.5, MHF15_5	3.7	3.7	-0.1	-0.3	100.0%	-5.3
14776	AT5G55330.1   membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related, contains similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis   chr5:22455051-22456091 REVERSE   Aliases: MTE17.4, MTE17_4	3.7	3.6	0.1	0.3	100.0%	-5.0
14777	AT1G35560.1   TCP family transcription factor, putative, similar to PCF2 (GI:2580440) and PCF1 (GI:2580438) (Oryza sativa)   chr1:13115804-13117213 REVERSE   Aliases: F15O4.35	3.9	3.9	0.1	0.3	100.0%	-5.3
14778	AT1G55080.1   expressed protein   chr1:20556685-20557881 REVERSE   Aliases: T7N22.3, T7N22_3	3.6	3.5	0.1	0.3	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14779	AT4G25040.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:12868184-12869465 FORWARD   Aliases: F24A6.5	2.9	3.0	-0.1	-0.3	100.0%	-5.6
14780	AT3G12190.1   expressed protein   chr3:3886190-3886999 FORWARD   Aliases: F28J15.4	2.8	2.9	-0.0	-0.3	100.0%	-5.7
14781	AT1G74990.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)   chr1:28163376-28164148 REVERSE   Aliases: F25A4.5, F25A4_5	2.8	2.7	0.1	0.3	100.0%	-4.9
14782	AT2G46080.1   expressed protein   chr2:18955190-18957178 REVERSE   Aliases: T3F17.27	7.4	7.5	-0.1	-0.3	100.0%	-4.8
14783	AT4G12860.1   calcium-binding protein, putative, similar to calcium-binding protein GI:6580549 from (Lotus japonicus)   chr4:7538442-7538900 REVERSE   Aliases: T20K18.210, T20K18_210	4.2	4.1	0.1	0.3	100.0%	-5.1
14784	AT1G79680.1   wall-associated kinase, putative, similar to wall-associated kinase 2 GI:4826399 from (Arabidopsis thaliana)   chr1:29984866-29987666 REVERSE   Aliases: F20B17.10, F20B17_10	2.4	2.5	-0.0	-0.3	100.0%	-5.7
14785	AT5G54620.1   ankyrin repeat family protein, contains Pfam domain, PF00023: Ankyrin repeat   chr5:22204987-22206972 REVERSE   Aliases: MRB17.12, MRB17_12	2.4	2.4	0.0	0.3	100.0%	-5.6
14786	AT5G20770.1   hypothetical protein   chr5:7034190-7034885 REVERSE   Aliases: T1M15.170, T1M15_170	2.5	2.4	0.1	0.3	100.0%	-5.2
14787	AT1G35910.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) (Arabidopsis thaliana) GI:2944180; contains Pfam profile PF02358: Trehalose-phosphatase   chr1:13364219-13366270 REVERSE   Aliases: F10O5.8, F10O5_8	5.7	5.5	0.2	0.3	100.0%	-4.4
14788	AT5G17780.1   hydrolase, alpha/beta fold family protein, low similarity to SP:Q02104 Lipase 1 precursor (EC 3.1.1.3) (Triacylglycerol lipase) {Psychrobacter immobilis}, SP:P27747:ACOC_ALCEU Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Ralstonia eutropha) {Alcaligenes eutrophus}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:5867285-5869052 REVERSE   Aliases: MVA3.14, MVA3_14	4.3	4.4	-0.1	-0.3	100.0%	-4.8
14789	AT4G33210.1   F-box family protein (FBL15), contains similarity to F-box protein FBL2 GI:6063090 from (Homo sapiens)   chr4:16015974-16020700 REVERSE   Aliases: F4I10.140, F4I10_140	4.6	4.4	0.2	0.3	100.0%	-4.6
14790	AT1G76900.2   F-box family protein / tubby family protein, similar to Tubby protein (SP:P50586) {Mus musculus}; similar to Chain A, C-Terminal Domain Of Mouse Brain Tubby Protein (GI:6730158) (Mus musculus); similar to Tubby related protein 1 (Tubby-like protein 1) (Swiss-Prot:O00294) (Homo sapiens); similar to phosphodiesterase (GI:467578) (Mus musculus); contains Pfam profile: PF01167: Tub family; contains Pfam PF00646: F-box domain	5.8	5.7	0.1	0.3	100.0%	-4.6
14791	AT3G02630.1   acyl-(acyl-carrier-protein) desaturase, putative / stearoyl-ACP desaturase, putative, similar to Acyl-(acyl-carrier protein) desaturase from Sesamum indicum GI:575942, Cucumis sativus SP:P32061, Ricinus communis SP:P22337; contains Pfam profile PF03405 Fatty acid desaturase   chr3:562038-564877 FORWARD   Aliases: F16B3.26, F16B3_26	9.9	9.6	0.3	0.3	100.0%	-4.6
14792	AT1G06770.2   zinc finger (C3HC4-type RING finger) family protein   chr1:2078910-2081938 REVERSE   Aliases: F4H5.14, F4H5_14	4.1	4.2	-0.1	-0.3	100.0%	-5.1
14793	AT1G07690.1   expressed protein   chr1:2378073-2378997 FORWARD   Aliases: F24B9.22, F24B9_22	3.0	3.1	-0.1	-0.3	100.0%	-5.3
14794	AT3G45420.1   lectin protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, Prosite:PS00108   chr3:16668248-16670251 REVERSE   Aliases: F18N11.180	3.0	2.9	0.1	0.3	100.0%	-5.4
14795	AT4G28350.1   lectin protein kinase family protein, contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr4:14026583-14028628 FORWARD   Aliases: F20O9.40, F20O9_40	3.5	3.4	0.1	0.3	100.0%	-4.8
14796	AT1G01840.1   expressed protein   chr1:303537-304358 FORWARD   Aliases: T1N6.26, T1N6_26	4.7	4.6	0.1	0.3	100.0%	-4.9
14797	AT2G02070.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:505486-509424 FORWARD   Aliases: F5O4.16, F5O4_16	3.0	3.1	-0.1	-0.3	100.0%	-4.8
14798	AT5G24130.1   expressed protein   chr5:8162222-8164069 FORWARD   Aliases: MLE8.5, MLE8_5	3.2	3.1	0.1	0.3	100.0%	-5.1
14799	AT4G09950.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to AIG1 protein SP:P54120 (Arabidopsis thaliana); contains Pfam PF04548: AIG1 family;   chr4:6234759-6236309 FORWARD   Aliases: T5L19.80, T5L19_80	2.8	2.9	-0.1	-0.3	100.0%	-4.7
14800	AT5G20270.1   expressed protein, contains Pfam domain, PF03006: Uncharacterised protein family (Hly-III / UPF0073)   chr5:6840835-6842860 REVERSE   Aliases: F5O24.160, F5O24_160	2.9	3.1	-0.2	-0.3	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14801	AT2G31770.1   zinc finger (C3HC4-type RING finger) family protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam domain, PF01485: IBR domain   chr2:13518656-13520627 FORWARD   Aliases: F20M17.19, F20M17_19	3.1	3.2	-0.1	-0.3	100.0%	-4.8
14802	AT2G15360.1   expressed protein   chr2:6701869-6702247 REVERSE   Aliases: F26H6.12, F26H6_12	2.5	2.6	-0.0	-0.3	100.0%	-5.8
14803	AT3G16440.1   Symbol: ATMLP 300B   jacalin lectin family protein, contains Pfam profile: PF01419 jacalin-like lectin domain; similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767   chr3:5585950-5587753 FORWARD   Aliases: MYROSINASE BINDING PROTEIN LIKE PROTEIN 300B, T2O4.19	3.1	3.2	-0.1	-0.3	100.0%	-4.9
14804	AT5G19910.1   SOH1 family protein, contains Pfam profile: PF05669 SOH1	3.8	3.9	-0.1	-0.3	100.0%	-5.2
14805	AT3G55150.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit; tomato leucine zipper-containing protein, Lycopersicon esculentum, PIR:S21495	3.0	3.1	-0.1	-0.3	100.0%	-4.4
14806	AT1G62420.1   expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506)   chr1:23104084-23108269 REVERSE   Aliases: F24O1.44, F24O1_44	5.3	5.1	0.2	0.3	100.0%	-4.6
14807	AT5G03360.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.7	-0.1	-0.3	100.0%	-5.1
14808	AT4G29790.1   expressed protein   chr4:14582994-14590581 FORWARD   Aliases: F27B13.30, F27B13_30	3.4	3.7	-0.2	-0.3	100.0%	-4.6
14809	AT3G24510.1   Encodes a defensin-like (DEFL) family protein.   chr3:8931984-8932715 FORWARD   Aliases: MOB24.6	2.3	2.3	-0.0	-0.3	100.0%	-5.8
14810	AT2G33460.1   Symbol: RIC1   p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	4.6	4.5	0.1	0.3	100.0%	-5.0
14811	AT1G48290.1   expressed protein, ; expression supported by MPSS   chr1:17846336-17848575 FORWARD   Aliases: F11A17.26, F11A17_26	3.2	3.3	-0.1	-0.3	100.0%	-5.1
14812	AT2G36180.1   calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced SP:P25070 from (Arabidopsis thaliana)   chr2:15180861-15181295 REVERSE   Aliases: F9C22.11, F9C22_11	3.6	3.5	0.1	0.3	100.0%	-5.2
14813	AT5G26740.2   expressed protein, contains Pfam profile PF03619: Domain of unknown function   chr5:9291985-9294690 FORWARD   Aliases: None	7.4	7.2	0.3	0.3	100.0%	-4.5
14814	AT1G75940.1   Symbol: ATA27   glycosyl hydrolase family 1 protein / anther-specific protein ATA27, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; identical to anther-specific protein ATA27 (GI:2746341) (Arabidopsis thaliana)   chr1:28514829-28517945 FORWARD   Aliases: ATA27, T4O12.15, T4O12_15	2.4	2.4	-0.1	-0.3	100.0%	-5.5
14815	AT3G20010.1   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to transcription factor RUSH-1alpha (Oryctolagus cuniculus) GI:1655930; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:6971358-6976346 FORWARD   Aliases: MZE19.6	3.7	3.7	-0.1	-0.3	100.0%	-5.2
14816	AT2G41590.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:17350438-17352083 FORWARD   Aliases: T32G6.11, T32G6_11	2.4	2.5	-0.1	-0.3	100.0%	-5.5
14817	AT4G01240.1   expressed protein   chr4:517795-521972 REVERSE   Aliases: F2N1.7, F2N1_7	2.6	2.5	0.0	0.3	100.0%	-5.7
14818	AT1G20150.1   subtilase family protein, similar to subtilisin-type protease precursor GI:14150446 from (Glycine max)   chr1:6987323-6990352 REVERSE   Aliases: T20H2.7, T20H2_7	2.8	2.7	0.1	0.3	100.0%	-5.3
14819	AT5G03470.1   Symbol: ATB' ALPHA   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'alpha), similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)	5.9	5.8	0.1	0.3	100.0%	-4.9
14820	AT5G49750.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596	2.4	2.5	-0.0	-0.3	100.0%	-5.6
14821	AT4G20760.1   short-chain dehydrogenase/reductase (SDR) family protein, contains Pfam profile: PF00106 short chain dehydrogenase   chr4:11129026-11130781 FORWARD   Aliases: AT4G20750, F21C20.110, F21C20_110	5.7	5.6	0.1	0.3	100.0%	-4.7
14822	AT5G11060.1   Symbol: KNAT4   homeobox protein knotted-1 like 4 (KNAT4), identical to homeobox protein knotted-1 like 4 ( KNAT4) SP:P48001 from (Arabidopsis thaliana)   chr5:3510119-3513306 FORWARD   Aliases: T5K6.50, T5K6_50	5.5	5.4	0.1	0.3	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14823	AT1G71790.1   F-actin capping protein beta subunit family protein, contains Pfam profile: PF01115 F-actin capping protein, beta subunit   chr1:27000531-27002639 FORWARD   Aliases: F14O23.17, F14O23_17	5.4	5.5	-0.1	-0.3	100.0%	-4.6
14824	AT5G27950.1   kinesin motor protein-related, kinesin heavy chain-like protein, potato, PIR:T07397   chr5:9984055-9987994 FORWARD   Aliases: F15F15.20, F15F15_20	3.0	3.1	-0.1	-0.3	100.0%	-5.1
14825	AT2G23890.1   5' nucleotidase family protein, contains Pfam PF05761: 5' nucleotidase family; similar to Cytosolic purine 5'-nucleotidase (EC 3.1.3.5) (5'-nucleotidase cytosolic II) (Swiss-Prot:P49902) (Homo sapiens)   chr2:10177681-10181007 FORWARD   Aliases: T29E15.9, T29E15_9	4.2	4.3	-0.1	-0.3	100.0%	-4.8
14826	AT2G42410.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr2:17665228-17665872 FORWARD   Aliases: MHK10.13, MHK10_13	2.6	2.5	0.0	0.3	100.0%	-5.5
14827	AT1G28270.1   Symbol: RALFL4	2.4	2.4	0.0	0.3	100.0%	-5.6
14828	AT1G73730.1   Symbol: EIL3   ethylene-insensitive3-like3 (EIL3), identical to ethylene-insensitive3-like3 (EIL3) GB:AF004215 (Arabidopsis thaliana) (Cell 89 (7), 1133-1144 (1997))   chr1:27733729-27736175 REVERSE   Aliases: EIL3, ETHYLENE INSENSITIVE3 LIKE3, F25P22.15, F25P22_15	4.1	4.0	0.1	0.3	100.0%	-5.3
14829	AT1G04970.2   lipid-binding serum glycoprotein family protein, low similarity to SP:P17213 Bactericidal permeability-increasing protein precursor (BPI) {Homo sapiens}; contains Pfam profile PF02886: LBP / BPI / CETP family, C-terminal domain   chr1:1411889-1413625 FORWARD   Aliases: F13M7.4, F13M7_4	7.4	7.2	0.2	0.3	100.0%	-4.6
14830	AT5G55700.1   similar to beta-amylase (CT-BMY) / 1,4-alpha-D-glucan maltohydrolase [Arabidopsis thaliana] (TAIR:At4g17090.1); similar to beta-amylase [Glycine max] (GB:CAI39244.1); contains InterPro domain Glycoside hydrolase, family 14 (InterPro:IPR001554); contains InterPro domain Glycoside hydrolase, family 14B, plant (InterPro:IPR001371)   chr5:22568975-22572883 FORWARD   Aliases: MDF20.14, MDF20_14	4.3	4.2	0.1	0.3	100.0%	-5.1
14831	AT1G41770.1   hypothetical protein   chr1:15539662-15539973 FORWARD   Aliases: F9M8.10	4.0	3.9	0.2	0.3	100.0%	-4.8
14832	AT1G71820.1   expressed protein   chr1:27013307-27020770 FORWARD   Aliases: F14O23.20, F14O23_20	4.3	4.4	-0.1	-0.3	100.0%	-5.0
14833	AT4G09650.1   ATP synthase delta chain, chloroplast, putative / H(+)-transporting two-sector ATPase, delta (OSCP) subunit, putative, similar to SP:P32980 ATP synthase delta chain, chloroplast precursor (EC 3.6.3.14) {Nicotiana tabacum}; contains Pfam profile PF00213: ATP synthase F1, delta subunit   chr4:6100740-6101705 FORWARD   Aliases: T25P22.90, T25P22_90	5.1	5.2	-0.1	-0.3	100.0%	-4.7
14834	AT4G38830.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:18122320-18124937 FORWARD   Aliases: T9A14.110, T9A14_110	3.6	3.8	-0.2	-0.3	100.0%	-4.2
14835	AT4G00895.1   ATP synthase delta chain-related, contains weak similarity to Swiss-Prot:P32980 ATP synthase delta chain, chloroplast precursor (Nicotiana tabacum)   chr4:381788-382643 FORWARD   Aliases: None	6.0	5.8	0.2	0.3	100.0%	-5.0
14836	AT4G24930.1   thylakoid lumenal 17.9 kDa protein, chloroplast, SP:Q9SW33;GI:17369630;PMID:11719511; similar to expressed protein gi:12321169 {Oryza sativa}   chr4:12821233-12823752 REVERSE   Aliases: F13M23.70, F13M23_70	5.3	5.1	0.1	0.3	100.0%	-4.3
14837	AT3G32930.1   expressed protein   chr3:13493231-13494548 FORWARD   Aliases: T13O13.1	6.8	6.7	0.1	0.3	100.0%	-5.1
14838	AT4G12910.1   Symbol: SCPL20	4.5	4.7	-0.2	-0.3	100.0%	-4.6
14839	AT1G02205.2   Symbol: CER1   CER1 protein, identical to maize gl1 homolog (glossy1 locus) GI:1209703 and CER1 GI:1199467 from (Arabidopsis thaliana)   chr1:418778-422438 FORWARD   Aliases: AT1G02200, CER1, ECERIFERUM 1, POSSIBLE ALDEHYDE DECARBONYLASE, T6A9.16	2.2	2.2	-0.0	-0.3	100.0%	-6.0
14840	AT2G01800.1   COP1-interacting protein-related, similar to COP1-interacting protein 4 (CIP4) (Arabidopsis thaliana) GI:13160646, COP1-interacting protein 4.1 (CIP4.1) (Arabidopsis thaliana) GI:13160650   chr2:343765-345253 REVERSE   Aliases: T8O11.3, T8O11_3	2.7	2.7	0.0	0.3	100.0%	-5.7
14841	AT1G68120.1   expressed protein   chr1:25529959-25531197 REVERSE   Aliases: T23K23.3, T23K23_3	4.1	4.0	0.1	0.3	100.0%	-4.9
14842	AT5G43120.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr5:17329830-17331596 FORWARD   Aliases: MMG4.15, MMG4_15	3.4	3.4	0.0	0.3	100.0%	-5.4
14843	AT1G33540.1   Symbol: SCPL18	2.7	2.6	0.1	0.3	100.0%	-5.4
14844	AT5G53000.1   Symbol: TAP46   protein phosphatase 2A-associated 46 kDa protein / PP2A regulatory subunit (TAP46), identical to PP2A regulatory subunit (46 kDa protein phosphatase 2A-associated protein) (TAP46) (Arabidopsis thaliana) GI:5107033; contains Pfam profile PF04177: TAP42-like family	7.4	7.5	-0.2	-0.3	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14845	AT5G40350.1   Symbol: MYB24   myb family transcription factor (MYB24), similar to Myb26 GI:1841475 from (Pisum sativum)   chr5:16155774-16158362 REVERSE   Aliases: MPO12.60, MPO12_60	2.6	2.6	-0.0	-0.3	100.0%	-5.7
14846	AT5G09280.1   pectate lyase family protein, similar to major pollen allergen Cup a 1 SP:Q9SCG9 from (Cupressus arizonica)   chr5:2880424-2881598 REVERSE   Aliases: T5E8.80, T5E8_80	2.1	2.2	-0.0	-0.3	100.0%	-6.0
14847	AT5G13080.1   Symbol: WRKY75	3.7	3.9	-0.2	-0.3	100.0%	-4.7
14848	AT2G18610.1   expressed protein   chr2:8083430-8084396 REVERSE   Aliases: F24H14.4, F24H14_4	3.3	3.4	-0.1	-0.3	100.0%	-5.2
14849	AT2G01310.1   expressed protein   chr2:152480-152641 REVERSE   Aliases: F10A8.19, F10A8_19	2.9	3.0	-0.1	-0.3	100.0%	-5.5
14850	AT2G39230.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:16388725-16391328 FORWARD   Aliases: T16B24.13, T16B24_13	3.1	3.1	-0.1	-0.3	100.0%	-5.3
14851	AT2G41780.1   expressed protein   chr2:17435176-17435890 FORWARD   Aliases: T11A7.12, T11A7_12	8.3	8.4	-0.1	-0.3	100.0%	-5.1
14852	AT5G19130.2   GPI transamidase component family protein / Gaa1-like family protein, contains Pfam profile: PF04114 Gaa1-like, GPI transamidase component   chr5:6415154-6419023 REVERSE   Aliases: T24G5.30, T24G5_30	4.1	4.0	0.1	0.3	100.0%	-5.1
14853	AT3G16230.1   expressed protein, similar to ASC-1 complex subunit P50 (GI:12061189) (Homo sapiens)   chr3:5500562-5503549 FORWARD   Aliases: MYA6.4	7.6	7.5	0.1	0.3	100.0%	-4.8
14854	AT5G04970.1   pectinesterase, putative, contains similarity to pectinesterase from Vitis vinifera GI:15081598, Prunus persica SP:Q43062; contains Pfam profile PF01095 pectinesterase   chr5:1464146-1467042 REVERSE   Aliases: MUG13.17, MUG13_17	2.2	2.3	-0.0	-0.3	100.0%	-5.7
14855	AT5G03930.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g03920.1)   chr5:1059503-1060153 FORWARD   Aliases: F8F6.140, F8F6_140	2.5	2.4	0.1	0.3	100.0%	-5.5
14856	AT3G57130.1   Symbol: BOP1   ankyrin repeat family protein / BTB/POZ domain-containing protein, contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain. Lines carrying recessive mutations exhibit a number of visible defects, most pronounced being ectopic outgrowths of in leaf petioles of rosette leaves.   chr3:21158814-21161006 FORWARD   Aliases: BLADE ON PETIOLE 1, BOP1, F24I3.210	2.8	2.8	0.0	0.3	100.0%	-5.6
14857	AT1G56270.1   expressed protein   chr1:21074813-21075301 REVERSE   Aliases: F14G9.12, F14G9_12	3.0	2.9	0.1	0.3	100.0%	-5.1
14858	AT1G35670.1   Symbol: ATCDPK2   calcium-dependent protein kinase 2 (CDPK2), identical to calcium-dependent protein kinase (Arabidopsis thaliana) gi:604881:dbj:BAA04830; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr1:13206593-13209463 FORWARD   Aliases: CALCIUM DEPENDENT PROTEIN KINASE 2, CPK11, F15O4.8	7.4	7.6	-0.2	-0.3	100.0%	-4.9
14859	AT3G27090.1   expressed protein, similar to gda-1 (Pisum sativum) GI:2765418   chr3:9990780-9993063 FORWARD   Aliases: MOJ10.16	8.0	8.2	-0.2	-0.3	100.0%	-5.0
14860	AT5G38170.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam profile: PF00234 protease inhibitor/seed storage/LTP family   chr5:15244868-15245311 FORWARD   Aliases: MXA21.17, MXA21_17	3.6	3.5	0.1	0.3	100.0%	-5.2
14861	AT2G24880.1   self-incompatibility protein-related, low similarity to self-incompatibility from (Papaver nudicaule) GI:3097262, (Papaver rhoeas) GI:3097260   chr2:10597633-10597941 REVERSE   Aliases: F27C12.20, F27C12_20	2.6	2.6	-0.0	-0.3	100.0%	-5.9
14862	AT5G42270.1   Symbol: VAR1   FtsH protease, putative, similar to FtsH protease GI:13183728 from (Medicago sativa)   chr5:16919714-16923100 FORWARD   Aliases: FTSH5, K5J14.13, K5J14_13, VARIEGATED 1	9.2	9.0	0.2	0.3	100.0%	-4.9
14863	AT2G30780.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:13123551-13125136 FORWARD   Aliases: T11J7.17, T11J7_17	3.7	3.7	0.1	0.3	100.0%	-5.3
14864	AT2G40730.1   HEAT repeat-containing protein, contains INTERPRO:IPR000357 HEAT repeat   chr2:16996914-17003295 REVERSE   Aliases: T7D17.9, T7D17_9	2.8	2.9	-0.0	-0.3	100.0%	-5.4
14865	AT5G33380.1   hypothetical protein   chr5:12625040-12625592 FORWARD   Aliases: F19N2.100, F19N2_100	3.1	3.1	-0.1	-0.3	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14866	AT1G14030.1   ribulose-1,5 biphosphate carboxylase oxygenase large subunit N-methyltransferase, putative, strong similarity to SP:P94026 Ribulose-1,5 biphosphate carboxylase/oxygenase large subunit N- methyltransferase, chloroplast precursor (EC 2.1.1.127) ((Ribulose- biphosphate-carboxylase)-lysine N-methyltransferase) {Nicotiana tabacum}; contains Pfam profile PF00856: SET domain; Rare GC intron splice site at 49572 is inferred from protein alignment and is not confirmed experimentally   chr1:4805303-4807514 REVERSE   Aliases: F7A19.12, F7A19_12	4.5	4.4	0.1	0.3	100.0%	-4.8
14867	AT4G32780.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g43870.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP55003.1); contains InterPro domain Plant protein of unknown function DUF828 (InterPro:IPR008546); contains InterPro domain Antifreeze protein, type I (InterPro:IPR000104)	2.5	2.6	-0.1	-0.3	100.0%	-5.4
14868	AT1G42190.1   expressed protein   chr1:15763523-15763717 FORWARD   Aliases: F19C17.40, F19C17_40	2.9	2.9	-0.0	-0.3	100.0%	-5.6
14869	AT3G08920.1   rhodanese-like domain-containing protein, contains rhodanese-like domain PF:00581   chr3:2712242-2713272 FORWARD   Aliases: T16O11.14	4.9	5.0	-0.1	-0.3	100.0%	-4.6
14870	AT1G50470.1   hypothetical protein   chr1:18703668-18704112 REVERSE   Aliases: F11F12.24, F11F12_24	4.1	4.3	-0.1	-0.3	100.0%	-4.9
14871	AT2G10050.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr2:3820372-3820734 REVERSE   Aliases: F7B19.19, F7B19_19	2.5	2.5	-0.0	-0.3	100.0%	-5.6
14872	AT3G56660.1   bZIP transcription factor family protein, similar to AtbZIP transcription factor GI:17065880 from (Arabidopsis thaliana); contains Pfam profile: PF00170 bZIP transcription factor   chr3:20997196-20999192 REVERSE   Aliases: T5P19.310	3.8	3.9	-0.1	-0.3	100.0%	-5.0
14873	AT3G62220.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 (Pti1)(Lycopersicon esculentum) gi:3668069:gb:AAC61805   chr3:23040075-23042130 REVERSE   Aliases: T17J13.180	5.8	5.9	-0.1	-0.3	100.0%	-5.0
14874	AT2G43970.2   La domain-containing protein, contains Pfam profile PF05383: La domain   chr2:18212311-18215294 REVERSE   Aliases: F6E13.10	11.4	11.3	0.1	0.3	100.0%	-5.2
14875	AT2G42830.2   Symbol: SHP2   agamous-like MADS box protein AGL5 / floral homeodomain transcription factor (AGL5), identical to SP:P29385 Agamous-like MADS box protein AGL5 {Arabidopsis thaliana}   chr2:17827443-17831090 FORWARD   Aliases: AGAMOUS LIKE 5, AGL5, F7D19.17, F7D19_17, SHATTERPROOF 2	3.1	3.0	0.1	0.3	100.0%	-5.1
14876	AT1G28230.1   Symbol: PUP1   purine permease (PUP1), identical to purine permease GI:7620007 from (Arabidopsis thaliana)   chr1:9862060-9864593 REVERSE   Aliases: ATPUP1, F3H9.22, F3H9_22, PURINE PERMEASE 1	4.0	3.8	0.1	0.3	100.0%	-5.2
14877	AT1G80930.1   MIF4G domain-containing protein / MA3 domain-containing protein, similar to SP:Q9P6R9 Cell cycle control protein cwf22 {Schizosaccharomyces pombe}; contains Pfam profiles PF02854: MIF4G domain, PF02847: MA3 domain   chr1:30410324-30414602 REVERSE   Aliases: F23A5.29, F23A5_29	5.3	5.4	-0.1	-0.3	100.0%	-4.9
14878	AT3G29750.1   expressed protein   chr3:11581604-11583079 REVERSE   Aliases: MOD1.18	2.5	2.5	-0.0	-0.3	100.0%	-5.4
14879	AT1G26410.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:9138662-9140426 REVERSE   Aliases: T1K7.21, T1K7_21	2.5	2.4	0.0	0.3	100.0%	-5.5
14880	AT1G05920.1   expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)   chr1:1797043-1797990 FORWARD   Aliases: T20M3.20, T20M3_20	2.8	2.7	0.1	0.3	100.0%	-5.3
14881	AT5G35680.2   eukaryotic translation initiation factor 1A, putative / eIF-1A, putative / eIF-4C, putative, strong similarity to translation initiation factor (eIF-1A) (Beta vulgaris) GI:17977975; contains Pfam profile PF01176: Eukaryotic initiation factor 1A   chr5:13875151-13876207 REVERSE   Aliases: MXH1.2, MXH1_2	9.8	9.6	0.2	0.3	100.0%	-5.3
14882	AT2G06120.1   expressed protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287	4.8	4.7	0.1	0.3	100.0%	-5.2
14883	AT1G71697.1   Symbol: ATCK1   choline kinase, putative, similar to GmCK2p choline kinase gi:1438881:gb:AAC49375   chr1:26974885-26977126 FORWARD   Aliases: CHOLINE KINASE, CK, F14O23.8, F14O23_8	4.6	4.5	0.1	0.3	100.0%	-4.7
14884	AT1G50990.1   protein kinase-related, low similarity to SP:Q06548:APKA_ARATH Protein kinase APK1A Arabidopsis thaliana; contains Pfam profile: PF00069: Eukaryotic protein kinase domain; contains non-consensus (GC) splice site at intron 6   chr1:18906598-18908872 FORWARD   Aliases: F8A12.21, F8A12_21	2.6	2.6	0.0	0.3	100.0%	-5.4
14885	AT4G32360.1   NADP adrenodoxin-like ferredoxin reductase, identical to NADP adrenodoxin-like ferredoxin reductase GI:28192433 from (Arabidopsis thaliana)   chr4:15621307-15624889 FORWARD   Aliases: F8B4.60	5.2	5.3	-0.1	-0.3	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14886	AT3G55580.1   regulator of chromosome condensation (RCC1) family protein, UVB-resistance protein UVR8, Arabidopsis thaliana, EMBL:AF130441; contains Pfam PF00415: Regulator of chromosome condensation (RCC1) domain   chr3:20623679-20626899 FORWARD   Aliases: F1I16.1	3.5	3.5	0.1	0.3	100.0%	-5.2
14887	AT1G70210.1   Symbol: CYCD1;1   cyclin delta-1 (CYCD1), nearly identical to SP:P42751 Cyclin delta-1 {Arabidopsis thaliana}   chr1:26443560-26446492 FORWARD   Aliases: CYCD1;1, Cyclin D1;1, F20P5.7, F20P5_7	2.7	2.8	-0.1	-0.3	100.0%	-5.3
14888	AT3G01900.1   Symbol: CYP94B2   cytochrome P450 family protein, similar to Cytochrome P450 94A1 (P450-dependent fatty acid omega-hydroxylase) (SP:O81117) {Vicia sativa}; contains Pfam profile: PF00067 cytochrome P450   chr3:312366-313856 REVERSE   Aliases: F1C9.32, F1C9_32	3.0	3.1	-0.1	-0.3	100.0%	-5.3
14889	AT4G03160.1   hypothetical protein   chr4:1397979-1398685 FORWARD   Aliases: F4C21.8, F4C21_8	2.3	2.4	-0.0	-0.3	100.0%	-6.0
14890	AT3G13290.1   transducin family protein / WD-40 repeat family protein, contains 2 WD-40 repeats (PF00400); autoantigen locus HUMAUTANT (GI:533202) (Homo sapiens) and autoantigen locus HSU17474 (GI:596134) (Homo sapiens)   chr3:4297388-4303515 FORWARD   Aliases: MDC11.12	8.4	8.6	-0.2	-0.3	100.0%	-4.3
14891	AT3G13300.2   Symbol: VCS   transducin family protein / WD-40 repeat family protein, contains 2 WD-40 repeats (PF00400); autoantigen locus HUMAUTANT (GI:533202) (Homo sapiens) and autoantigen locus HSU17474 (GI:596134) (Homo sapiens)   chr3:4303881-4310220 FORWARD   Aliases: MDC11.13, VARICOSE	8.4	8.6	-0.2	-0.3	100.0%	-4.3
14892	AT2G23180.1   Symbol: CYP96A1   cytochrome P450, putative   chr2:9881987-9883674 FORWARD   Aliases: T20D16.19, T20D16_19	2.9	2.9	0.1	0.3	100.0%	-5.3
14893	AT5G20310.1   expressed protein   chr5:6857555-6859003 FORWARD   Aliases: F5O24.200, F5O24_200	3.1	3.0	0.1	0.3	100.0%	-5.2
14894	AT4G00232.1   expressed protein   chr4:100257-100721 REVERSE   Aliases: None	4.0	4.1	-0.1	-0.3	100.0%	-5.0
14895	AT1G32670.1   expressed protein   chr1:11815644-11815956 FORWARD   Aliases: F6N18.7, F6N18_7	2.7	2.6	0.1	0.3	100.0%	-5.7
14896	AT5G40730.1   Symbol: AGP24   arabinogalactan-protein (AGP24)	9.6	9.5	0.1	0.3	100.0%	-5.1
14897	AT1G55950.1   hypothetical protein, contains Pfam profile: PF04504 protein of unknown function, DUF573   chr1:20930504-20931115 REVERSE   Aliases: F14J16.23, F14J16_23	2.6	2.6	0.0	0.3	100.0%	-5.7
14898	AT4G25150.1   acid phosphatase, putative, similar to acid phosphatase-1(1); Apase-1(1) (Lycopersicon esculentum) GI:7705154, acid phosphatase (Glycine max) GI:3341443; contains Pfam profile PF03767: HAD superfamily (subfamily IIIB) phosphatase   chr4:12901631-12903135 REVERSE   Aliases: F24A6.12	5.8	5.9	-0.2	-0.3	100.0%	-4.3
14899	AT3G19990.1   expressed protein   chr3:6965653-6967254 FORWARD   Aliases: MZE19.4	8.1	8.0	0.1	0.3	100.0%	-5.0
14900	AT5G16580.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max)   chr5:5425892-5427475 REVERSE   Aliases: MTG13.2, MTG13_2	2.5	2.6	-0.1	-0.3	100.0%	-4.8
14901	AT5G60320.1   lectin protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain, PF00139: Legume lectins beta domain, and PF00138: Legume lectins alpha domain   chr5:24288034-24290061 FORWARD   Aliases: K9B18.1, K9B18_1	2.5	2.4	0.0	0.3	100.0%	-5.8
14902	AT5G26360.1   chaperonin, putative, similar to SWISS-PROT:P50143- T-complex protein 1, gamma subunit (TCP-1-gamma) (Xenopus laevis); contains Pfam:PF00118 domain, TCP-1/cpn60 chaperonin family   chr5:9255056-9258979 REVERSE   Aliases: F9D12.18, F9D12_18	6.0	6.2	-0.2	-0.3	100.0%	-4.4
14903	AT4G10350.1   Symbol: ANAC070   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; nap gene, Arabidopsis thaliana, gb:AJ222713   chr4:6415252-6416825 REVERSE   Aliases: ANAC070, F24G24.150, F24G24_150	2.3	2.3	-0.0	-0.3	100.0%	-5.6
14904	AT1G31410.1   putrescine-binding periplasmic protein-related, similar to Chain A, Putrescine Receptor (Potf) (GI:3891734) (Escherichia coli); similar to Chain C, Putrescine Receptor (Potf) (GI:3891736) (Escherichia coli); similar to Putrescine-binding periplasmic protein precursor. (Swiss-Prot:P31133) (Escherichia coli)   chr1:11246895-11249340 REVERSE   Aliases: T8E3.6, T8E3_6	7.0	6.9	0.1	0.3	100.0%	-4.5
14905	AT4G07380.1   expressed protein   chr4:4192426-4193013 REVERSE   Aliases: F28D6.12, F28D6_12	2.9	2.8	0.1	0.3	100.0%	-5.4
14906	AT3G27150.1   kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif, Pfam:PF00646 F-box domain   chr3:10010679-10012878 REVERSE   Aliases: MYF5.2	6.2	6.1	0.2	0.3	100.0%	-4.8
14907	AT1G32680.1   hypothetical protein   chr1:11818014-11818259 FORWARD   Aliases: F6N18.21, F6N18_21	3.1	3.1	-0.1	-0.3	100.0%	-5.3
14908	AT3G44400.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr3:16057318-16060655 REVERSE   Aliases: T22K7.80	2.3	2.4	-0.0	-0.3	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14909	AT1G48970.1   similar to eukaryotic translation initiation factor 2B family protein / eIF-2B family protein [Arabidopsis thaliana] (TAIR:At5g38640.1); similar to novel protein similar to vertebrate eukaryotic translation initiation factor 2B, subunit 4 delta, 67kDa (EIF2B4) [Danio rerio] (GB:CAI11537.1); contains InterPro domain Initiation factor 2B (InterPro:IPR000649)   chr1:18117382-18121501 REVERSE   Aliases: F27K7.2	3.6	3.7	-0.1	-0.3	100.0%	-5.2
14910	AT3G28040.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profiles: PF00560 leucine rich repeat, PF00069 eukaryotic protein kinase domain   chr3:10436294-10439628 FORWARD   Aliases: MMG15.21	3.1	3.0	0.1	0.3	100.0%	-5.0
14911	ATCG00680.1   Symbol: PSBB   encodes for CP47, subunit of the photosystem II reaction center.	7.4	7.7	-0.3	-0.3	100.0%	-4.8
14912	AT3G56840.1   FAD-dependent oxidoreductase family protein, contains Pfam profile PF01266 FAD dependent oxidoreductase   chr3:21055296-21057293 FORWARD   Aliases: T8M16.170	5.8	5.7	0.1	0.3	100.0%	-4.9
14913	AT3G52970.1   Symbol: CYP76G1   cytochrome P450 family protein, cytochrome P450 76A2, eggplant, PIR:S38534   chr3:19652284-19654254 REVERSE   Aliases: F8J2.140	2.1	2.1	0.0	0.3	100.0%	-6.0
14914	AT5G49140.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:19936311-19940641 REVERSE   Aliases: K20J1.12, K20J1_12	2.2	2.2	0.0	0.3	100.0%	-5.8
14915	AT2G45440.1   Symbol: DHDPS2	7.9	7.6	0.3	0.3	100.0%	-4.3
14916	AT3G44960.1   expressed protein, ; expression supported by MPSS   chr3:16438780-16440136 FORWARD   Aliases: F14D17.30	2.2	2.2	0.0	0.3	100.0%	-6.0
14917	AT5G02760.1   protein phosphatase 2C family protein / PP2C family protein, similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain   chr5:625252-627691 FORWARD   Aliases: F9G14.70, F9G14_70	2.8	2.7	0.0	0.3	100.0%	-5.4
14918	AT3G22104.1   phototropic-responsive NPH3 protein-related, contains BTB/POZ domain, INTERPRO:IPR000210	5.2	5.1	0.2	0.3	100.0%	-4.7
14919	AT2G20820.2   expressed protein, .   chr2:8971430-8972505 FORWARD   Aliases: F5H14.21, F5H14_21	11.5	11.6	-0.1	-0.3	100.0%	-4.9
14920	AT1G52250.1   dynein light chain type 1 family protein, similar to SP:O02414 Dynein light chain LC6, flagellar outer arm {Anthocidaris crassispina}; contains Pfam profile PF01221: Dynein light chain type 1   chr1:19462342-19462904 REVERSE   Aliases: F19K6.18	3.1	3.0	0.1	0.3	100.0%	-5.0
14921	AT5G21030.1   PAZ domain-containing protein / piwi domain-containing protein, similar to SP:O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}, SP:Q9XGW1 PINHEAD protein (ZWILLE protein) {Arabidopsis thaliana}; contains Pfam profiles PF02171: Piwi domain, PF02170: PAZ domain   chr5:7139894-7144274 REVERSE   Aliases: T10F18.3	2.3	2.2	0.0	0.3	100.0%	-5.5
14922	AT1G06430.1   Symbol: FTSH8   encodes a FtsH protease that is localized to the chloroplast   chr1:1960057-1963006 REVERSE   Aliases: F12K11.22, FTSH8	5.5	5.4	0.1	0.3	100.0%	-4.9
14923	AT1G04930.1   hydroxyproline-rich glycoprotein family protein, Common family member: At2g32840 (Arabidopsis thaliana)   chr1:1396292-1399052 REVERSE   Aliases: F13M7.8, F13M7_8	4.4	4.5	-0.1	-0.3	100.0%	-5.2
14924	AT3G22910.1   calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA13), identical to SP:Q9LIK7 Potential calcium-transporting ATPase 13, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 13) {Arabidopsis thaliana}; similar to SP:Q9LF79 Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca2+-ATPase, isoform 8) {Arabidopsis thaliana}; contains InterPro Accession IPR006069: Cation transporting ATPase Belongs to plant 2B ATPase??s with an N-terminal autoinhibitor.   chr3:8116342-8119395 REVERSE   Aliases: F5N5.18	3.1	3.0	0.1	0.3	100.0%	-5.2
14925	AT5G55720.1   pectate lyase family protein, similar to pectate lyase 1 GP:6606532 from (Musa acuminata)   chr5:22573273-22574951 FORWARD   Aliases: MDF20.16, MDF20_16	2.5	2.5	-0.0	-0.3	100.0%	-5.7
14926	AT4G00130.1   hypothetical protein, contains Pfam profile PF04504: Protein of unknown function, DUF573	3.5	3.6	-0.1	-0.3	100.0%	-5.3
14927	AT1G74350.1   intron maturase, type II family protein, similar to maturase (Arabidopsis thaliana) GI:6851020; contains Pfam profile: PF01348 Type II intron maturase   chr1:27952683-27954944 REVERSE   Aliases: F1M20.3, F1M20_3	3.4	3.3	0.1	0.3	100.0%	-5.2
14928	AT5G66460.1   (1-4)-beta-mannan endohydrolase, putative, similar to (1-4)-beta-mannan endohydrolase (Coffea arabica) GI:10178872; contains Pfam profile PF00150: Cellulase (glycosyl hydrolase family 5)   chr5:26555621-26558262 REVERSE   Aliases: K1F13.12, K1F13_12	5.6	5.8	-0.2	-0.3	100.0%	-4.3
14929	AT1G50290.1   expressed protein   chr1:18631227-18632102 REVERSE   Aliases: F14I3.24, F14I3_24	3.1	3.0	0.1	0.3	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14930	AT5G11100.1   C2 domain-containing protein, similar to Ca <sup>2+</sup> -dependent lipid-binding protein (CLB1) GI:2789434 from ( <i>Lycopersicon esculentum</i> )   chr5:3532403-3535222 FORWARD   Aliases: T5K6.90, T5K6_90	5.6	5.4	0.1	0.3	100.0%	-4.5
14931	AT2G22070.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:9390682-9393144 FORWARD   Aliases: T16B14.8, T16B14_8	3.0	2.9	0.0	0.3	100.0%	-5.6
14932	AT3G11910.1   ubiquitin-specific protease, putative, strong similarity to ubiquitin-specific protease 12 (UBP12) ( <i>Arabidopsis thaliana</i> ) GI:11993471; contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF00917: MATH domain   chr3:3761394-3770391 REVERSE   Aliases: F26K24.20	8.2	8.1	0.1	0.3	100.0%	-5.0
14933	AT4G14110.1   Symbol: COP9   COP9 signalosome subunit, putative / CSN subunit, putative (CSN8), CSN8, FUS7; identical to cDNA CSN complex subunit 8 (CSN8) GI:18056672   chr4:8132882-8134915 REVERSE   Aliases: CONSTITUTIVE PHOTOMORPHOGENIC 9, CSN8, DL3095C, EMB143, EMBRYO DEFECTIVE 143, FCAALL.131, FUS7, FUSCA 7, FUSCA PROTEIN FUS7	7.6	7.8	-0.2	-0.3	100.0%	-4.6
14934	AT3G07820.1   polygalacturonase 3 (PGA3) / pectinase, identical to polygalacturonase ( <i>Arabidopsis thaliana</i> ) GI:3152948	2.3	2.4	-0.0	-0.3	100.0%	-5.7
14935	AT5G63100.1   expressed protein   chr5:25331363-25332654 REVERSE   Aliases: MDC12.6, MDC12_6	3.3	3.2	0.1	0.3	100.0%	-5.2
14936	AT2G33240.1   Symbol: XID   myosin, putative, similar to myosin (GI:433663) ( <i>Arabidopsis thaliana</i> ); myosin my5A (SP:Q02440) { <i>Gallus gallus</i> }   chr2:14094019-14103991 REVERSE   Aliases: ATXID, F25I18.2, F25I18_2	2.4	2.4	0.0	0.3	100.0%	-5.6
14937	AT3G13782.1   nucleosome assembly protein (NAP) family protein, similar to nucleosome assembly protein 1 ( <i>Glycine max</i> ) GI:1161252; contains Pfam profile PF00956: Nucleosome assembly protein (NAP)   chr3:4526667-4528405 FORWARD   Aliases: MMM17.24	3.3	3.6	-0.2	-0.3	100.0%	-4.5
14938	AT1G24440.1   expressed protein, similar to MTD2 ( <i>Medicago truncatula</i> ) GI:9294812   chr1:8662007-8663952 FORWARD   Aliases: F21J9.10	6.5	6.6	-0.1	-0.3	100.0%	-4.8
14939	AT5G35960.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr5:14125754-14127766 REVERSE   Aliases: MEE13.6, MEE13_6	3.0	3.1	-0.1	-0.3	100.0%	-5.3
14940	AT3G23080.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g14500.1); similar to putative nodule membrane protein [ <i>Medicago sativa</i> ] (GB:AAL57201.1); contains InterPro domain Lipid-binding START (InterPro:IPR002913)	5.3	5.2	0.1	0.3	100.0%	-4.9
14941	AT3G23325.1   splicing factor, putative, similar to Splicing factor 3B subunit 10 (SF3b10) (Pre-mRNA splicing factor SF3b 10 kDa subunit) (Swiss-Prot:Q9BWJ5) ( <i>Homo sapiens</i> )   chr3:8345778-8347056 FORWARD   Aliases: None	9.7	9.8	-0.1	-0.3	100.0%	-4.4
14942	AT5G03420.1   dentin sialophosphoprotein-related, contains weak similarity to Swiss-Prot:Q9NZW4 dentin sialophosphoprotein precursor ( <i>Homo sapiens</i> )   chr5:845640-848601 FORWARD   Aliases: F12E4.170, F12E4_170	6.1	6.0	0.1	0.3	100.0%	-5.1
14943	AT1G62510.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr1:23140036-23140856 REVERSE   Aliases: T3P18.7, T3P18_7	1.9	1.8	0.1	0.3	100.0%	-5.2
14944	AT2G44050.1   Symbol: COS1   6,7-dimethyl-8-ribityllumazine synthase / DMRL synthase / lumazine synthase / riboflavin synthase, identical to 6,7-dimethyl-8-ribityllumazine synthase, chloroplast (precursor) SP:O80575 from ( <i>Arabidopsis thaliana</i> )   chr2:18231342-18233236 FORWARD   Aliases: COI1 SUPPRESSOR1, F6E13.18, F6E13.41, F6E13_41	6.3	6.5	-0.2	-0.3	100.0%	-4.6
14945	AT4G28910.2   expressed protein   chr4:14264073-14266659 REVERSE   Aliases: F25O24.30, F25O24_30	8.0	7.8	0.2	0.3	100.0%	-4.5
14946	AT1G32550.1   ferredoxin family protein, similar to ferredoxin from <i>Synechocystis</i> sp. (GI:48019); contains Pfam profile PF00111 2Fe-2S iron-sulfur cluster binding domain   chr1:11771746-11774158 REVERSE   Aliases: T9G5.4, T9G5_4	6.3	6.2	0.1	0.3	100.0%	-4.6
14947	AT1G52280.1   Ras-related GTP-binding protein, putative, similar to RAB7D GI:1370187 from ( <i>Lotus japonicus</i> ) (Plant J. 11 (2), 237-250 (1997)); contains Pfam PF00071: Ras family   chr1:19471638-19473255 REVERSE   Aliases: F19K6.10, F19K6_10	7.3	7.4	-0.1	-0.3	100.0%	-4.9
14948	AT5G10020.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase ERECTA, <i>Arabidopsis thaliana</i> , EMBL:AC004484   chr5:3133262-3137243 FORWARD   Aliases: T31P16.10, T31P16_10	3.2	3.3	-0.1	-0.3	100.0%	-4.9
14949	AT1G65390.2   Symbol: ATPP2 A5   disease resistance protein (TIR class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:24296153-24298275 FORWARD   Aliases: AT1G65400, ATPP2 A5, T8F5.18, T8F5_18	2.9	2.9	0.1	0.3	100.0%	-5.6
14950	AT3G49520.1   F-box family protein, contains weak hit to Pfam:PF00646 F-box domain and weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr3:18370569-18371735 FORWARD   Aliases: T9C5.110	3.1	3.0	0.1	0.3	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14951	AT1G13930.1   expressed protein, weakly similar to drought-induced protein SDi-6 (PIR:S71562) common sunflower (fragment)   chr1:4761039-4761722 FORWARD   Aliases: F16A14.14	10.9	11.0	-0.1	-0.3	100.0%	-5.0
14952	AT3G13690.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:4485799-4490238 FORWARD   Aliases: MMM17.11	3.5	3.7	-0.1	-0.3	100.0%	-4.8
14953	AT4G33030.1   Symbol: SQD1   UDP-sulfoquinovose synthase / sulfite:UDP-glucose sulfotransferase / sulfolipid biosynthesis protein (SQD1), identical to gi:2736155   chr4:15935432-15937810 FORWARD   Aliases: F4I10.6, UDP SULFOQUINOVOSE SYNTHASE	8.3	8.2	0.1	0.3	100.0%	-4.7
14954	AT2G19070.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus (gi:2239091); contains Pfam profile PF02458: Transferase family   chr2:8267120-8269067 REVERSE   Aliases: T20K24.8, T20K24_8	2.8	2.7	0.1	0.3	100.0%	-5.4
14955	AT4G00860.1   Symbol: ATOZI1	11.7	11.8	-0.1	-0.3	100.0%	-5.3
14956	AT5G18450.1   encodes a member of the DREB subfamily A-2 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are eight members in this subfamily including DREB2A AND DREB2B that are involved in response to drought.   chr5:6116099-6117022 REVERSE   Aliases: F20L16.170, F20L16_170	4.0	4.1	-0.1	-0.3	100.0%	-4.9
14957	AT5G66260.1   auxin-responsive protein, putative, GP:10185816 auxin-induced protein TGSAUR12 {Tulipa gesneriana)   chr5:26488495-26488884 FORWARD   Aliases: K1L20.4, K1L20_4	2.5	2.6	-0.1	-0.3	100.0%	-5.5
14958	AT5G55370.1   long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis	2.5	2.6	-0.0	-0.3	100.0%	-5.9
14959	AT3G28510.1   AAA-type ATPase family protein, contains Pfam profile: PF00004 ATPase family   chr3:10686761-10688601 FORWARD   Aliases: T20D4.2	2.9	2.9	-0.0	-0.3	100.0%	-5.8
14960	AT1G18570.1   Symbol: MYB51   myb family transcription factor (MYB51), contains PFAM profile: PF00249	3.0	2.9	0.1	0.3	100.0%	-4.7
14961	AT4G29390.1   40S ribosomal protein S30 (RPS30B), RIBOSOMAL PROTEIN S30 - Arabidopsis thaliana,PID:e1358183   chr4:14464993-14465989 REVERSE   Aliases: F17A13.210, F17A13_210	11.9	12.0	-0.1	-0.3	100.0%	-5.3
14962	AT5G01590.1   expressed protein   chr5:224173-226923 FORWARD   Aliases: F7A7.110, F7A7_110	3.6	3.7	-0.1	-0.3	100.0%	-5.1
14963	AT4G29450.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr4:14478843-14482632 REVERSE   Aliases: F17A13.270, F17A13_270	2.5	2.6	-0.0	-0.3	100.0%	-5.5
14964	AT5G38330.1   Symbol: LCR80   Encodes a member of a family of small,secreted, cysteine rich protein with sequence similarity to the PCP (pollen coat protein) gene family.   chr5:15334997-15335675 FORWARD   Aliases: LCR80, Low molecular weight cysteine rich 80, MSI17.50, MSI17_50	3.6	3.5	0.1	0.3	100.0%	-5.4
14965	AT1G64180.1   intracellular protein transport protein USO1-related, similar to Rap8 (GI:2326183) (Rhynchosciara americana); contains weak similarity to Swiss-Prot:P25386 intracellular protein transport protein USO1 (Saccharomyces cerevisiae)   chr1:23825179-23828022 FORWARD   Aliases: F22C12.6, F22C12_6	5.8	5.7	0.2	0.3	100.0%	-4.6
14966	AT4G13880.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-0B (Lycopersicon esculentum) gi:3894387:gb:AAC78593	2.9	2.8	0.0	0.3	100.0%	-5.5
14967	AT1G59910.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02128   chr1:22057616-22060717 REVERSE   Aliases: F23H11.22, F23H11_22	6.1	5.9	0.1	0.3	100.0%	-4.5
14968	AT5G49990.1   xanthine/uracil permease family protein, similar to permease 1 (Zea mays) GI:7844006; contains Pfam profile: PF00860 Xanthine/uracil permeases family   chr5:20354867-20359077 REVERSE   Aliases: K9P8.13, K9P8_13	3.9	3.7	0.1	0.3	100.0%	-4.6
14969	AT5G27990.1   expressed protein, predicted proteins, Saccharomyces cerevisiae and Schizosaccharomyces pombe   chr5:10017052-10018445 FORWARD   Aliases: F15F15.60, F15F15_60	6.6	6.7	-0.1	-0.3	100.0%	-4.9
14970	AT5G22850.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr5:7633440-7636570 REVERSE   Aliases: MRN17.8, MRN17_8	7.1	7.0	0.1	0.3	100.0%	-5.1
14971	AT4G36380.1   Symbol: ROT3   cytochrome P450 90C1 (CYP90C1) / rotundifolia3 (ROT3), identical	3.2	3.4	-0.2	-0.3	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14972	AT5G10140.1   Symbol: FLC   MADS-box protein flowering locus F (FLF), identical to FLOWERING LOCUS C protein (MADS box protein FLOWERING LOCUS F) (Swiss-Prot:Q9S7Q7) (Arabidopsis thaliana)   chr5:3173498-3179449 REVERSE   Aliases: AGL25, FLF, FLOWERING LOCUS C, FLOWERING LOCUS F, MADS BOX PROTEIN FLOWERING LOCUS F, T31P16.130, T31P16_130	2.5	2.6	-0.0	-0.3	100.0%	-5.5
14973	AT1G16130.1   Symbol: WAKL2   wall-associated kinase, putative, similar to putative serine/threonine-specific protein kinase Gl:7270012 from (Arabidopsis thaliana)   chr1:5525485-5528206 FORWARD   Aliases: T24D18.21, T24D18_21, WALL ASSOCIATED KINASE LIKE 2	3.8	3.9	-0.1	-0.3	100.0%	-4.9
14974	AT2G01600.1   epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (Gl:6492344) (Xenopus laevis)   chr2:268817-272609 FORWARD   Aliases: F2I9.22, F2I9_22	4.8	4.6	0.2	0.3	100.0%	-4.4
14975	AT5G46240.1   Symbol: KAT1   inward rectifying potassium channel (KAT1), identical to K+ channel (Arabidopsis thaliana) gi:1165000:emb:CAA63601; Shaker-type channel (1P/6TM), PMID:11500563   chr5:18760793-18763957 REVERSE   Aliases: MPL12.2, MPL12_2	2.6	2.5	0.1	0.3	100.0%	-5.9
14976	AT1G35340.3   ATP-dependent protease La (LON) domain-containing protein, contains Pfam profile PF02190: ATP-dependent protease La (LON) domain	7.5	7.6	-0.1	-0.3	100.0%	-4.9
14977	AT2G01770.1   integral membrane family protein, contains integral membrane protein domain, Pfam:PF01988   chr2:334774-336424 REVERSE   Aliases: T8O11.6, T8O11_6	2.5	2.5	0.1	0.3	100.0%	-5.3
14978	AT1G54320.1   LEM3 (ligand-effect modulator 3) family protein / CDC50 family protein, Similar to Gl:11994416; Gl:4966357; Gl:4835763; Gl:9757735 from (Arabidopsis thaliana)   chr1:20279202-20281624 REVERSE   Aliases: F20D21.14, F20D21_14	10.2	10.2	0.1	0.3	100.0%	-5.5
14979	AT4G23980.2   Symbol: ARF9   similar to transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related [Arabidopsis thaliana] (TAIR:At2g46530.1); similar to ARFO_ARATH Putative auxin response factor 15 (GB:Q9LQE3); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340); contains InterPro domain AUX/IAA protein (InterPro:IPR003311)   chr4:12451208-12455277 FORWARD   Aliases: AUXIN RESPONSE FACTOR 9, T32A16.150, T32A16_150	3.9	4.1	-0.2	-0.3	100.0%	-4.6
14980	AT2G40160.1   expressed protein   chr2:16784468-16786486 FORWARD   Aliases: T7M7.25, T7M7_25	3.3	3.5	-0.2	-0.3	100.0%	-4.3
14981	AT2G47830.2   cation efflux family protein / metal tolerance protein, putative (MTPc1), member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr2:19597926-19601067 REVERSE   Aliases: F17A22.22	4.5	4.6	-0.1	-0.3	100.0%	-4.8
14982	AT3G01200.1   expressed protein, contains Pfam domain PF03618: Domain of unknown function (DUF299)   chr3:69518-71369 REVERSE   Aliases: T4P13.11, T4P13_11	6.7	6.6	0.1	0.3	100.0%	-5.1
14983	AT3G56610.1   expressed protein   chr3:20982616-20983063 REVERSE   Aliases: T5P19.260	2.6	2.6	-0.1	-0.3	100.0%	-5.5
14984	AT2G24800.1   peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781338:emb:CAA71496   chr2:10578334-10579649 REVERSE   Aliases: F27C12.28, F27C12_28	2.4	2.4	-0.0	-0.3	100.0%	-5.5
14985	AT1G12950.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) Gl:12231296; contains Pfam profile PF01554: MatE   chr1:4419768-4422632 FORWARD   Aliases: F13K23.21, F13K23_21	3.1	3.0	0.1	0.3	100.0%	-4.9
14986	AT5G36900.1   expressed protein   chr5:14564154-14565433 FORWARD   Aliases: MLF18.2, MLF18_2	3.5	3.4	0.1	0.3	100.0%	-5.1
14987	AT4G14000.1   expressed protein   chr4:8090812-8092662 FORWARD   Aliases: DL3040W, FCAALL.136	6.1	6.3	-0.2	-0.3	100.0%	-4.8
14988	AT3G29430.1   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltransferase, putative, similar to gi:413730; similar to geranylgeranyl pyrophosphate synthase, chloroplast precursor GB:P34802 from (Arabidopsis thaliana)   chr3:11312593-11314029 FORWARD   Aliases: MUO10.10	3.8	3.9	-0.1	-0.3	100.0%	-5.2
14989	AT3G48000.1   Symbol: ALDH2B4   aldehyde dehydrogenase (ALDH2), identical to aldehyde dehydrogenase (Arabidopsis thaliana) Gl:8574427; similar to mitochondrial aldehyde dehydrogenase (Arabidopsis thaliana) gi:19850249:gb:AAL99612; identical to cDNA aldehyde dehydrogenase AtALDH2a Gl:20530140   chr3:17727852-17730999 REVERSE   Aliases: ALDEHYDE DEHYDROGENASE 2, ALDH2, T17F15.130	11.5	11.4	0.1	0.3	100.0%	-4.9
14990	AT3G06260.1   galactinol synthase, putative, contains Pfam profile: PF01501 glycosyl transferase family 8   chr3:1893810-1894865 REVERSE   Aliases: F28L1.20, F28L1_20	2.9	2.8	0.0	0.3	100.0%	-5.7
14991	AT1G54410.1   dehydrin family protein, contains Pfam domain, PF00257: Dehydrin	13.4	13.5	-0.1	-0.3	100.0%	-5.6
14992	AT1G11670.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) Gl:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family; EST gb:W43487 comes from this gene   chr1:3928182-3931576 REVERSE   Aliases: F25C20.18, F25C20_18	3.8	4.0	-0.1	-0.3	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
14993	AT3G42790.1   PHD finger family protein, contains PHD-finger domain, INTERPRO:IPR001965   chr3:14888946-14890755 REVERSE   Aliases: T21C14.10	8.7	8.8	-0.1	-0.3	100.0%	-5.2
14994	AT5G20170.1   expressed protein   chr5:6807392-6810800 REVERSE   Aliases: F5O24.60, F5O24_60	6.2	6.1	0.1	0.3	100.0%	-5.3
14995	AT3G51740.1   Symbol: IMK2   leucine-rich repeat transmembrane protein kinase, putative, brassinosteroid-insensitive protein BRI1 - Arabidopsis thaliana, PIR:T09356   chr3:19200028-19203028 FORWARD   Aliases: INFLORESCENCE MERISTEM RECEPTOR LIKE KINASE 2, T18N14.120	2.4	2.4	-0.0	-0.3	100.0%	-5.3
14996	AT3G24040.1   glycosyltransferase family 14 protein / core-2/I-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/I-Branching enzyme   chr3:8680914-8683280 REVERSE   Aliases: F14O13.23	4.4	4.5	-0.1	-0.3	100.0%	-5.1
14997	AT5G11220.1   expressed protein   chr5:3577058-3577979 FORWARD   Aliases: F2I11.110, F2I11_110	2.3	2.3	-0.0	-0.3	100.0%	-6.0
14998	AT4G14940.1   Symbol: ATAO1   copper amine oxidase, putative, highly similar to copper amine oxidase (Arabidopsis thaliana) gi:2654118:gb:AAB87690   chr4:8541875-8544300 FORWARD   Aliases: DL3510W, FCAALL.145	2.7	2.9	-0.1	-0.3	100.0%	-4.5
14999	AT5G19940.1   plastid-lipid associated protein PAP-related / fibrillin-related, weak hit to Pfam profile PF04755: PAP_fibrillin   chr5:6739626-6740984 FORWARD   Aliases: F28I16.90, F28I16_90	5.3	5.2	0.2	0.3	100.0%	-4.6
15000	AT5G23340.1   expressed protein   chr5:7856195-7859280 FORWARD   Aliases: MKD15.20, MKD15_20	3.8	3.6	0.2	0.3	100.0%	-4.5
15001	AT1G26630.1   eukaryotic translation initiation factor 5A, putative / eIF-5A, putative, strong similarity to SP:Q9AXQ6 Eukaryotic translation initiation factor 5A-1 (eIF-5A 1) {Lycopersicon esculentum}   chr1:9205823-9207402 FORWARD   Aliases: T24P13.1, T24P13_1	11.5	11.3	0.2	0.3	100.0%	-4.7
15002	AT5G42870.1   lipin family protein, contains Pfam profile: PF04571 lipin, N-terminal conserved region   chr5:17202691-17206909 REVERSE   Aliases: MBD2.6, MBD2_6	3.1	3.3	-0.2	-0.3	100.0%	-5.0
15003	AT4G22370.1   expressed protein   chr4:11810859-11811575 REVERSE   Aliases: T10I14.210, T10I14_210	3.0	3.1	-0.0	-0.3	100.0%	-5.6
15004	AT5G60110.1   pumilio/Puf RNA-binding domain-containing protein, contains Pfam profile: PF00806: Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain)   chr5:24219180-24220163 FORWARD   Aliases: MGO3.9, MGO3_9	3.0	3.0	0.1	0.3	100.0%	-5.7
15005	AT3G47790.1   Symbol: ATATH7	2.7	2.6	0.1	0.3	100.0%	-4.8
15006	AT5G46730.1   glycine-rich protein   chr5:18981239-18982295 FORWARD   Aliases: MZA15.15, MZA15_15	10.2	10.4	-0.2	-0.3	100.0%	-4.9
15007	AT3G02520.1   Symbol: GRF7   14-3-3 protein GF14 nu (GRF7), identical to 14-3-3 protein GF14 nu GI:1531631 from (Arabidopsis thaliana)   chr3:526444-528320 REVERSE   Aliases: F16B3.15, F16B3_15, GF14 NU	9.6	9.4	0.2	0.3	100.0%	-4.8
15008	AT1G15490.1   hydrolase, alpha/beta fold family protein, Contains PF 00561 alpha/beta hydrolase fold   chr1:5320610-5323890 REVERSE   Aliases: F9L1.44, F9L1_44	4.0	4.1	-0.1	-0.3	100.0%	-5.1
15009	AT5G56320.1   Symbol: ATEXPA14   expansin, putative (EXP14), similar to alpha-expansin 3 GI:6942322 from (Triphysaria versicolor); alpha-expansin gene family, PMID:11641069   chr5:22825867-22827463 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A14, ATEXP14, ATHEXP ALPHA 1.5, EXP14, MCD7.4, MCD7_4	3.0	3.0	0.1	0.3	100.0%	-5.1
15010	AT2G44420.1   protein N-terminal asparagine amidohydrolase family protein, similar to Protein N-terminal asparagine amidohydrolase (EC 3.5.1.-) (Protein NH2-terminal asparagine deamidase) (NTN-amidase) (PNAD) (Protein NH2-terminal asparagine amidohydrolase) (PNAA) (Swiss-Prot:Q64311) (Mus musculus)   chr2:18337549-18339985 FORWARD   Aliases: F4I1.23	3.5	3.6	-0.1	-0.3	100.0%	-4.9
15011	AT2G18470.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr2:8012367-8014849 REVERSE   Aliases: T30D6.2	2.6	2.6	0.0	0.3	100.0%	-5.5
15012	AT3G52470.1   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 ( GI:1619321) (Nicotiana tabacum)	6.2	5.9	0.3	0.3	100.0%	-4.7
15013	AT2G47050.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pollen-specific pectin esterase (Brassica rapa subsp. pekinensis) GI:1620652; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.9	2.9	-0.0	-0.3	100.0%	-5.6
15014	AT5G46790.1   expressed protein, similar to unknown protein (pir::T05073)   chr5:19001097-19001986 REVERSE   Aliases: MZA15.21, MZA15_21	4.6	4.7	-0.1	-0.3	100.0%	-4.9
15015	AT3G22960.1   pyruvate kinase, putative, similar to pyruvate kinase isozyme A, chloroplast precursor (Ricinus communis) SWISS-PROT:Q43117   chr3:8139242-8141992 FORWARD   Aliases: F5N5.15	9.2	9.3	-0.1	-0.3	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15016	AT5G63530.1   Symbol: ATPF3   copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840); nearly identical to farnesylated protein ATPF3 (GI:4097547); contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:25450469-25453060 FORWARD   Aliases: MLE2.16, MLE2_16	7.7	7.4	0.3	0.3	100.0%	-4.3
15017	AT1G15360.1   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr1:5283536-5284668 FORWARD   Aliases: F9L1.31, F9L1_31	3.0	3.1	-0.1	-0.3	100.0%	-5.2
15018	AT4G17530.1   Symbol: RAB1C   Ras-related GTP-binding protein, putative, very strong similarity to RAB1C (Lotus corniculatus var. japonicus) GI:1370166; contains Pfam profile PF00071: Ras family   chr4:9773094-9775598 REVERSE   Aliases: DL4800C, FCAALL.87	9.4	9.3	0.1	0.3	100.0%	-5.3
15019	AT4G27160.1   2S seed storage protein 3 / 2S albumin storage protein / NWMU2-2S albumin 3, identical to SP:P15459   chr4:13611802-13612569 FORWARD   Aliases: T24A18.110, T24A18_110	2.5	2.6	-0.0	-0.3	100.0%	-5.8
15020	AT5G09400.1   Symbol: KUP7   potassium transporter family protein, similar to K+ transporter HAK5 (Arabidopsis thaliana) GI:7108597; contains Pfam profile PF02705: K+ potassium transporter; KUP/HAK/KT Transporter family member, PMID:11500563; Note: possible sequencing error causes a frameshift in the 4th exon:15810448:gb:AY056263   chr5:2916217-2920760 FORWARD   Aliases: T5E8.200, T5E8_200	2.5	2.6	-0.1	-0.3	100.0%	-5.1
15021	AT4G31740.1   expressed protein, weak similarity to r-sly1 (Rattus norvegicus) GI:1144569   chr4:15363784-15364355 FORWARD   Aliases: F28M20.70, F28M20_70	2.5	2.4	0.1	0.3	100.0%	-5.3
15022	AT3G10120.1   expressed protein   chr3:3130077-3130896 FORWARD   Aliases: T22K18.5	3.9	4.0	-0.1	-0.3	100.0%	-5.2
15023	AT5G40210.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr5:16090848-16093345 REVERSE   Aliases: MSN9.110, MSN9_110	3.1	3.0	0.1	0.3	100.0%	-4.9
15024	AT4G18460.1   D-Tyr-tRNA(Tyr) deacylase family protein, contains Pfam profile: PF02580 D-Tyr-tRNA(Tyr) deacylase   chr4:10195548-10196807 REVERSE   Aliases: F28J12.130	5.2	5.1	0.1	0.3	100.0%	-4.7
15025	AT5G08460.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:2733221-2735456 FORWARD   Aliases: F8L15.13	3.1	3.0	0.1	0.3	100.0%	-5.4
15026	AT4G34610.1   homeodomain-containing protein, similarity to homeotic protein BEL1, Arabidopsis thaliana, PIR2:A57632   chr4:16530551-16532503 REVERSE   Aliases: T4L20.190, T4L20_190	4.9	5.0	-0.1	-0.3	100.0%	-4.9
15027	AT3G46370.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thalian) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	2.8	2.7	0.1	0.3	100.0%	-4.8
15028	AT1G65840.1   amine oxidase family protein, similar to polyamine oxidase SP:O64411 (Zea mays); contains Pfam profile PF01593 amine oxidase, flavin-containing   chr1:24493447-24496687 FORWARD   Aliases: F1E22.18, F1E22_18	7.5	7.7	-0.1	-0.3	100.0%	-4.5
15029	AT4G38230.1   Symbol: CPK26   calcium-dependent protein kinase, putative / CDPK, putative, calmodulin-domain protein kinase CDPK isoform 6 (Arabidopsis thaliana) gi:1399275:gb:AAB03246; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr4:17928671-17931176 REVERSE   Aliases: F20D10.350, F20D10_350	2.8	2.8	0.1	0.3	100.0%	-5.3
15030	AT2G38920.1   SPX (SYG1/Pho81/XPR1) domain-containing protein / zinc finger (C3HC4-type RING finger) protein-related, weak similarity to tripartite motif protein TRIM13 (Mus musculus) GI:12407427; contains Pfam profile PF03105: SPX domain, weak hit to PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:16255224-16258080 REVERSE   Aliases: T7F6.9, T7F6_9	2.9	2.9	-0.0	-0.3	100.0%	-5.9
15031	AT1G34355.1   forkhead-associated domain-containing protein / FHA domain-containing protein   chr1:12536475-12541869 FORWARD   Aliases: None	3.1	3.0	0.1	0.3	100.0%	-5.3
15032	AT5G44720.2   molybdenum cofactor sulfurase family protein, weak similarity to molybdenum cofactor sulfurase (LOS5/ABA3) (Arabidopsis thaliana) GI:15407262; contains Pfam profiles PF03476: MOSC N-terminal beta barrel domain, PF03473: MOSC domain   chr5:18060225-18062156 FORWARD   Aliases: K23L20.6, K23L20_6	6.6	6.8	-0.2	-0.3	100.0%	-4.7
15033	AT3G11480.1   The gene encodes for an enzyme that methylates benzoic acid and salicylic acid to the corresponding methyl esters. It is highly expressed in flowers, induced by biotic and abiotic stress and thought to be involved in direct defense mechanism.   chr3:3614475-3617266 FORWARD   Aliases: F24K9.15	2.2	2.3	-0.0	-0.3	100.0%	-5.7
15034	AT3G09910.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:2723477 from (Arabidopsis thaliana) ;contains Pfam profile: PF00071 Ras family   chr3:3036719-3038434 REVERSE   Aliases: F8A24.4	4.6	4.6	-0.1	-0.3	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15035	AT1G58260.1   Symbol: CYP79C2   cytochrome P450 family protein, similar to cytochrome P450 Gl:984542 from (Sorghum bicolor)   chr1:21609417-21611660 FORWARD   Aliases: CYP79C3P, F19C14.12, F19C14_12	3.9	3.6	0.2	0.3	100.0%	-4.1
15036	AT1G59830.2   Symbol: PP2A 1	6.9	7.0	-0.1	-0.3	100.0%	-4.8
15037	AT3G53360.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:19795480-19797786 FORWARD   Aliases: F4P12.60	3.0	2.9	0.0	0.3	100.0%	-5.6
15038	AT1G12860.1   basic helix-loop-helix (bHLH) family protein / F-box family protein, contains Pfam profiles: PF00646 F-box domain, PF00010 helix-loop-helix DNA-binding domain   chr1:4382221-4386390 FORWARD   Aliases: F13K23.12, F13K23_12	3.5	3.6	-0.1	-0.3	100.0%	-5.1
15039	AT1G29950.2   expressed protein   chr1:10491959-10494582 FORWARD   Aliases: T1P2.2	4.9	4.8	0.1	0.3	100.0%	-5.2
15040	AT5G07480.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase 1 (SP:Q96330), 2-oxoglutarate-dependent dioxygenase - Solanum chacoense, EMBL:AF104925; contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr5:2367168-2369555 FORWARD   Aliases: T2I1.190, T2I1_190	2.6	2.6	-0.0	-0.3	100.0%	-5.5
15041	AT5G65960.1   expressed protein   chr5:26402574-26404630 FORWARD   Aliases: K2A18.2, K2A18_2	6.2	6.1	0.1	0.3	100.0%	-4.8
15042	AT1G23690.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220; expression supported by MPSS   chr1:8377422-8378623 REVERSE   Aliases: F5O8.24, F5O8_24	3.3	3.3	-0.1	-0.3	100.0%	-5.2
15043	AT2G34460.1   flavin reductase-related, low similarity to SP:P30043 Flavin reductase {Homo sapiens}   chr2:14536687-14538037 FORWARD   Aliases: F13P17.33	7.4	7.6	-0.2	-0.3	100.0%	-4.4
15044	AT5G41650.1   lactoylglutathione lyase family protein / glyoxalase I family protein, contains Pfam profile PF00903: glyoxalase family protein   chr5:16672141-16673027 FORWARD   Aliases: MBK23.15, MBK23_15	3.5	3.6	-0.1	-0.3	100.0%	-4.9
15045	AT1G64490.1   expressed protein   chr1:23955801-23956376 FORWARD   Aliases: F1N19.6, F1N19_6	7.9	8.1	-0.2	-0.3	100.0%	-4.9
15046	AT3G46170.1   short-chain dehydrogenase/reductase (SDR) family protein, contains similarity to 3-oxoacyl-(acyl-carrier protein) reductase SP:P51831 from (Bacillus subtilis)   chr3:16963708-16964574 REVERSE   Aliases: F12M12.140	2.8	2.9	-0.0	-0.3	100.0%	-5.7
15047	AT2G43250.1   expressed protein, and genefinder   chr2:17984305-17986685 FORWARD   Aliases: F14B2.19	4.1	4.1	-0.1	-0.3	100.0%	-5.2
15048	AT5G11020.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:3486440-3488381 REVERSE   Aliases: None	3.2	3.4	-0.2	-0.3	100.0%	-4.7
15049	AT1G20560.1   AMP-dependent synthetase and ligase family protein, similar to AMP-binding protein Gl:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501; identical to adenosine monophosphate binding protein 1 AMPBP1 (AMPBP1) Gl:20799710   chr1:7119666-7121804 REVERSE   Aliases: F5M15.12, F5M15_12	8.3	8.2	0.1	0.3	100.0%	-5.2
15050	AT4G11090.1   expressed protein, other hypothetical proteins - Arabidopsis thaliana   chr4:6764533-6766264 REVERSE   Aliases: T22B4.70, T22B4_70	5.5	5.4	0.1	0.3	100.0%	-5.0
15051	AT5G15780.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam profile PF01190: Pollen proteins Ole e I family   chr5:5144730-5146369 REVERSE   Aliases: F14F8.160, F14F8_160	2.2	2.2	0.1	0.3	100.0%	-5.7
15052	AT1G78840.1   F-box family protein, contains F-box domain Pfam:PF00646	3.0	2.9	0.1	0.3	100.0%	-5.0
15053	AT3G06860.1   Symbol: MFP2   fatty acid multifunctional protein (MFP2), identical to fatty acid multifunctional protein (AtMFP2) GB:AF123254 (gi:4337027) (Arabidopsis thaliana) (fatty acid beta-oxidation); contains Pfam profiles PF02737 (3-hydroxyacyl-CoA dehydrogenase, NAD binding domain), PF00378 (enoyl-CoA hydratase/isomerase family protein), PF00725 (3-hydroxyacyl-CoA dehydrogenase)	7.4	7.6	-0.2	-0.3	100.0%	-4.4
15054	AT1G75580.1   auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (Gl:10185820) (Tulipa gesneriana)   chr1:28381122-28381839 FORWARD   Aliases: F10A5.21, F10A5_21	2.7	2.7	-0.1	-0.3	100.0%	-5.5
15055	AT2G20960.1   Symbol: PEARLI4   expressed protein, pEARLI 4 gene product (Arabidopsis thaliana) Gl:871782   chr2:9013729-9016844 FORWARD   Aliases: F26H11.28, F26H11_28, PEARLI4	4.2	4.3	-0.1	-0.3	100.0%	-4.6
15056	AT4G04080.1   Symbol: ATISU3/ISU3   Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster, which is subsequently transferred to a target apoprotein.   chr4:1963384-1964306 FORWARD   Aliases: ATISU3, ISU3, T24H24.11, T24H24_11	3.9	3.9	-0.0	-0.3	100.0%	-5.5
15057	AT2G20142.1   expressed protein   chr2:8702451-8703727 FORWARD   Aliases: None	2.6	2.5	0.1	0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15058	AT2G20145.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr2:8702451-8703031 FORWARD   Aliases: None	2.6	2.5	0.1	0.3	100.0%	-5.3
15059	AT1G55360.1   expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr1:20669888-20672392 REVERSE   Aliases: F7A10.1, F7A10_1	5.0	4.8	0.2	0.3	100.0%	-4.7
15060	AT5G27440.1   expressed protein   chr5:9689501-9690314 REVERSE   Aliases: F21A20.150, F21A20_150	3.5	3.6	-0.1	-0.3	100.0%	-5.4
15061	AT3G21190.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;   chr3:7432305-7434651 REVERSE   Aliases: MXL8.4	7.5	7.7	-0.2	-0.3	100.0%	-4.8
15062	AT3G12270.1   protein arginine N-methyltransferase family protein, similar to protein arginine N-methyltransferase 3 from {Rattus norvegicus} SP:O70467, {Homo sapiens} SP:O60678   chr3:3910661-3913261 FORWARD   Aliases: F28J15.7	5.4	5.3	0.1	0.3	100.0%	-4.7
15063	AT2G39160.1   expressed protein   chr2:16340568-16341251 REVERSE   Aliases: T16B24.20, T16B24_20	4.1	4.0	0.1	0.3	100.0%	-5.2
15064	AT1G60200.1   splicing factor PWI domain-containing protein / RNA recognition motif (RRM)-containing protein, contains Pfam profiles PF01480: PWI domain, PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr1:22204547-22208953 REVERSE   Aliases: T13D8.9, T13D8_9	5.8	5.8	-0.1	-0.3	100.0%	-5.5
15065	AT3G16030.1   lectin protein kinase family protein, contains Pfam domains PF00069: Protein kinase domain and PF01453: Lectin (probable mannose binding)   chr3:5439615-5442808 FORWARD   Aliases: MSL1.2	2.6	2.5	0.1	0.3	100.0%	-4.8
15066	AT3G09550.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr3:2932468-2934359 FORWARD   Aliases: F11F8.13	3.1	3.1	0.1	0.3	100.0%	-5.3
15067	AT5G12870.1   myb family transcription factor (MYB46), contains PFAM profile: myb DNA binding domain PF00249   chr5:4062727-4064995 REVERSE   Aliases: T24H18.40, T24H18_40	2.6	2.6	-0.1	-0.3	100.0%	-5.1
15068	AT5G46795.1   expressed protein   chr5:19004215-19005424 REVERSE   Aliases: None	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15069	AT5G58580.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:23694132-23695058 REVERSE   Aliases: MZN1.3, MZN1_3	3.9	4.1	-0.1	-0.3	100.0%	-5.0
15070	AT5G16420.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:5368037-5369644 FORWARD   Aliases: MQK4.15, MQK4_15	4.7	4.8	-0.1	-0.3	100.0%	-4.9
15071	AT5G19580.1   glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594   chr5:6607373-6609628 REVERSE   Aliases: T20D1.100, T20D1_100	3.4	3.3	0.1	0.3	100.0%	-5.2
15072	ATMG00710.1   Symbol: ORF120	3.2	3.3	-0.1	-0.3	100.0%	-5.2
15073	AT5G18570.1   GTP1/OBG family protein, similar to SP:P20964 Spo0B-associated GTP-binding protein {Bacillus subtilis}; contains Pfam profile PF01018: GTP1/OBG family   chr5:6171663-6174835 REVERSE   Aliases: T28N17.50, T28N17_50	5.7	5.6	0.1	0.3	100.0%	-4.5
15074	AT5G56040.2   similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At5g48940.1); similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g24240.1); similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g34110.1); similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At2g33170.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At4g26540.1); similar to putative receptor-like protein kinase INRPK1 [Oryza sativa (japonica cultivar-group)] (GB:XP_550272.1); similar to putative receptor protein kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_462812.1); similar to putative Receptor-like protein kinase precursor [Oryza sativa (japonica cultivar-group)] (GB:BAD46328.1); similar to putative leucine-rich repeat protein kinase [Oryza sativa (japonica cultivar-group)] (GB:XP_476051.1); similar to receptor protein kinase [Pinus sylvestris] (GB:CAC20842.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr5:22712104-22715854 FORWARD   Aliases: MDA7.8, MDA7_8	5.8	5.9	-0.1	-0.3	100.0%	-5.1
15075	AT3G17330.1   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr3:5916946-5920194 REVERSE   Aliases: MGD8.17	4.4	4.4	-0.1	-0.3	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15076	AT3G28610.1   similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At3g28600.1); similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At5g40000.1); similar to ATPase 2 [Hordeum vulgare subsp. vulgare] (GB:AAV49983.1); similar to putative ATPase protein [Solanum demissum] (GB:AAT39939.1); similar to Cell Division Protein AAA ATPase family [Triticum turgidum] (GB:CAH10071.1); similar to Cell Division Protein AAA ATPase family [Triticum turgidum] (GB:CAH10065.1); similar to Cell Division Protein AAA ATPase family [Triticum aestivum] (GB:CAH10201.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr3:10726227-10727651 FORWARD   Aliases: MZN14.16	3.0	2.9	0.0	0.3	100.0%	-5.7
15077	AT3G22435.1   XS domain-containing protein, contains Pfam profile PF03468: XS domain   chr3:7956255-7957891 FORWARD   Aliases: None	3.6	3.5	0.1	0.3	100.0%	-5.0
15078	AT4G13630.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr4:7933904-7936025 REVERSE   Aliases: F18A5.20, F18A5_20	5.9	5.8	0.1	0.3	100.0%	-5.2
15079	AT5G47840.1   adenylate kinase, chloroplast, putative / ATP-AMP transphosphorylase, putative, similar to SP:P43188 Adenylate kinase, chloroplast (EC 2.7.4.3) (ATP-AMP transphosphorylase) {Zea mays}; contains Pfam profile PF00406: Adenylate kinase	8.5	8.7	-0.2	-0.3	100.0%	-4.5
15080	AT5G03860.1   malate synthase, putative, strong similarity to glyoxysomal malate synthase from Brassica napus (SP:P13244)   chr5:1032103-1034569 REVERSE   Aliases: MED24.5	2.9	3.0	-0.1	-0.3	100.0%	-5.2
15081	AT2G33220.1   expressed protein   chr2:14085948-14087213 FORWARD   Aliases: F25I18.4, F25I18_4	10.2	10.1	0.1	0.3	100.0%	-5.0
15082	AT5G46500.1   expressed protein   chr5:18873681-18875014 FORWARD   Aliases: K11I1.9, K11I1_9	2.5	2.5	-0.0	-0.3	100.0%	-5.8
15083	AT4G00755.2   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr4:324994-326964 FORWARD   Aliases: None	5.5	5.6	-0.1	-0.3	100.0%	-5.2
15084	AT1G18620.1   expressed protein   chr1:6410025-6414443 FORWARD   Aliases: F25I16.3, F25I16_3	3.8	4.0	-0.2	-0.3	100.0%	-4.6
15085	AT4G08685.1   Symbol: SAH7   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr4:5550426-5551816 FORWARD   Aliases: None	9.0	9.2	-0.2	-0.3	100.0%	-4.5
15086	AT2G30520.2   Symbol: RPT2   similar to phototropic-responsive NPH3 family protein [Arabidopsis thaliana] (TAIR:At5g48800.1); similar to Hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAN77296.1); contains InterPro domain NPH3 (InterPro:IPR004249)   chr2:13009819-13012672 REVERSE   Aliases: AT2G30510, ROOT PHOTOTROPISM 2, RPT2, T6B20.13, T6B20_13	3.0	2.9	0.0	0.3	100.0%	-5.6
15087	AT4G10480.1   nascent polypeptide associated complex alpha chain protein, putative / alpha-NAC, putative, similar to alpha-NAC, non-muscle form (Mus musculus) GI:1666690; contains Pfam profiles PF01849: NAC domain, PF00627: UBA/TS-N domain   chr4:6477872-6479160 REVERSE   Aliases: F7L13.60, F7L13_60	11.6	11.8	-0.1	-0.3	100.0%	-5.3
15088	AT1G15320.1   expressed protein   chr1:5272463-5273694 REVERSE   Aliases: F9L1.26, F9L1_26	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15089	AT4G00110.1   Symbol: GAE3   NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	4.5	4.6	-0.1	-0.3	100.0%	-4.9
15090	AT3G23460.1   cyclopropane fatty acid synthase-related, similar to cyclopropane synthase (Sterculia foetida) GI:21069167   chr3:8412326-8414326 FORWARD   Aliases: MLM24.19	2.7	2.8	-0.0	-0.3	100.0%	-5.8
15091	AT2G38710.2   similar to DUF51 family protein [Dictyostelium discoideum] (GB:EAL65703.1); contains InterPro domain Protein of unknown function DUF51 (InterPro:IPR002733)   chr2:16191447-16194213 REVERSE   Aliases: T6A23.9, T6A23_9	9.7	9.8	-0.1	-0.3	100.0%	-5.2
15092	AT1G54090.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit   chr1:20193235-20195568 FORWARD   Aliases: F15I1.17, F15I1_17	3.3	3.4	-0.1	-0.3	100.0%	-4.8
15093	AT2G18670.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:8100302-8102046 FORWARD   Aliases: MSF3.5, MSF3_5	3.3	3.2	0.1	0.3	100.0%	-5.1
15094	AT4G29890.1   choline monooxygenase, putative (CMO-like), similar to Choline monooxygenase, chloroplast precursor (EC 1.14.15.7) from {Amaranthus tricolor} SP:Q93XE1, {Beta vulgaris} SP:O22553; contains Pfam Rieske (2Fe-2S) domain PF00355	5.0	4.9	0.1	0.3	100.0%	-4.6
15095	AT1G68480.1   Symbol: JAG   similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At1g13400.1); similar to zinc finger protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD38321.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr1:25687977-25689828 REVERSE   Aliases: JAGGED, T26J14.5, T26J14_5	2.5	2.5	-0.0	-0.3	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15096	AT3G14720.1   Symbol: ATMPK19   mitogen-activated protein kinase, putative / MAPK, putative (MPK19), identical to mitogen-activated protein kinase (MAPK)(AtMPK19), PMID:12119167;   chr3:4946192-4949049 FORWARD   Aliases: MIE1.22	5.7	5.9	-0.1	-0.3	100.0%	-4.8
15097	AT5G35380.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:13610659-13613523 REVERSE   Aliases: T26D22.11, T26D22_11	2.1	2.2	-0.0	-0.3	100.0%	-5.8
15098	AT3G13050.1   transporter-related, low similarity to apical organic cation transporter (Sus scrofa) GI:2062135, SP:Q02563 Synaptic vesicle protein 2 (SV2) {Rattus norvegicus}; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:4176518-4179073 FORWARD   Aliases: MGH6.18	4.7	4.8	-0.1	-0.3	100.0%	-4.8
15099	AT5G15440.1   circadian clock coupling factor-related, similar to circadian clock coupling factor ZGT (Nicotiana tabacum) GI:14210079   chr5:5012073-5014649 FORWARD   Aliases: T20K14.50, T20K14_50	6.4	6.4	0.1	0.3	100.0%	-5.2
15100	AT3G47140.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:17368011-17368786 FORWARD   Aliases: F13I12.190	2.6	2.5	0.1	0.3	100.0%	-5.5
15101	AT1G17050.1   geranyl diphosphate synthase, putative / GPPS, putative / dimethylallyltransferase, putative / prenyl transferase, putative, similar to GI:11322965; Except for first 55 amino acids, 52% identical to Prenyl transferase (Cyanophora paradoxa) (gi 99282). Location of est 120E9T7 (gb:T43950)   chr1:5829092-5831326 FORWARD   Aliases: F20D23.25, F20D23_25	6.6	6.8	-0.2	-0.3	100.0%	-4.9
15102	AT2G15500.1   hypothetical protein   chr2:6770789-6771833 FORWARD   Aliases: F9O13.5	3.5	3.5	0.1	0.3	100.0%	-5.1
15103	AT5G44480.1   Symbol: DUR   NAD-dependent epimerase/dehydratase family protein, similar to SP:P55180 UDP-glucose 4-epimerase (EC 5.1.3.2) from Bacillus subtilis, GI:3021357 UDP-galactose 4-epimerase from Cyamopsis tetragonoloba; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	3.5	3.6	-0.1	-0.3	100.0%	-4.7
15104	AT4G27190.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr4:13620983-13623940 REVERSE   Aliases: T24A18.140, T24A18_140	2.1	2.1	-0.0	-0.3	100.0%	-5.9
15105	AT1G49050.1   aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease; contains similarity to nucellin GI:2290203 from (Hordeum vulgare)	6.9	6.8	0.2	0.3	100.0%	-4.6
15106	AT2G22490.1   Symbol: CYCD2;1   cyclin delta-2 (CYCD2), identical to SP:P42752 Cyclin delta-2 {Arabidopsis thaliana}   chr2:9560883-9563221 REVERSE   Aliases: CYCD2;1, Cyclin D2;1, F14M13.11, F14M13_11	7.2	7.1	0.1	0.3	100.0%	-4.7
15107	AT1G70500.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase (Cucumis sativus) GI:6624205; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)	3.0	3.1	-0.1	-0.3	100.0%	-5.0
15108	AT5G61320.1   Symbol: CYP89A3   cytochrome P450, putative, Similar to	2.9	3.0	-0.1	-0.3	100.0%	-5.5
15109	AT3G47270.1   expressed protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At3g30450, At4g03990, At5g34895, At2g02200   chr3:17420777-17424798 FORWARD   Aliases: T21L8.20	2.1	2.0	0.1	0.3	100.0%	-6.0
15110	AT1G55370.2   expressed protein   chr1:20678449-20680014 FORWARD   Aliases: T18I3.2	4.1	4.0	0.1	0.3	100.0%	-5.3
15111	AT1G21200.1   expressed protein   chr1:7421206-7423132 FORWARD   Aliases: F16F4.11, F16F4_11	3.2	3.0	0.2	0.3	100.0%	-4.8
15112	AT3G59070.1   auxin-responsive protein, putative, similar to auxin-induced protein AIR12 (GI:11357190) (Arabidopsis thaliana)   chr3:21843341-21845491 REVERSE   Aliases: F17J16.120	2.5	2.4	0.0	0.3	100.0%	-5.7
15113	AT5G12190.1   RNA recognition motif (RRM)-containing protein, similar to SP:P52298 20 kDa nuclear cap binding protein (NCBP 20 kDa subunit) (CBP20) (NCBP interacting protein 1) (NIP1) {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:3940533-3941206 REVERSE   Aliases: MXC9.15, MXC9_15	8.5	8.4	0.2	0.3	100.0%	-4.8
15114	AT2G36020.1   abscisic acid-responsive HVA22 family protein, weak similarity to SP:Q00765 Polyposis locus protein 1 (TB2 protein) {Homo sapiens}; contains Pfam profile PF03134: TB2/DP1, HVA22 family	2.2	2.2	-0.0	-0.3	100.0%	-5.8
15115	AT4G03090.1   expressed protein   chr4:1366495-1371155 REVERSE   Aliases: T4I9.3, T4I9_3	3.9	3.9	-0.1	-0.3	100.0%	-5.1
15116	AT3G61570.1   intracellular protein transport protein USO1-related, contains weak similarity to intracellular protein transport protein USO1 (Swiss-Prot:P25386) (Saccharomyces cerevisiae)   chr3:22790461-22794809 REVERSE   Aliases: F2A19.170	6.8	6.7	0.1	0.3	100.0%	-5.2
15117	AT1G35620.1   Symbol: ATPDIL5 2   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	8.3	8.3	0.1	0.3	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15118	AT5G41440.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:16604463-16604837 REVERSE   Aliases: MYC6.14, MYC6_14	3.4	3.4	0.1	0.3	100.0%	-5.2
15119	AT1G04290.1   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein; EST gb:T45093 comes from this gene   chr1:1147566-1148532 REVERSE   Aliases: F19P19.27, F19P19_27	7.6	7.7	-0.1	-0.3	100.0%	-4.6
15120	AT1G07340.1   Symbol: ATSTP2	2.5	2.5	0.1	0.3	100.0%	-5.3
15121	AT4G14980.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.9	3.8	0.1	0.3	100.0%	-4.8
15122	AT5G06080.1   LOB domain protein 33 / lateral organ boundaries domain protein 33 (LBD33), identical to SP:Q9LHS8 LOB domain protein 33 {Arabidopsis thaliana}   chr5:1830797-1831428 REVERSE   Aliases: K16F4.4, K16F4_4	2.6	2.5	0.0	0.3	100.0%	-5.5
15123	AT3G42540.1   expressed protein   chr3:14656093-14657428 FORWARD   Aliases: T32A11.110	3.3	3.4	-0.1	-0.3	100.0%	-5.2
15124	AT1G34245.1   expressed protein   chr1:12472846-12473731 FORWARD   Aliases: None	2.4	2.4	-0.0	-0.3	100.0%	-5.8
15125	AT1G65930.1   isocitrate dehydrogenase, putative / NADP+ isocitrate dehydrogenase, putative, strong similarity to isocitrate dehydrogenase SP:Q40345 from (Medicago sativa)   chr1:24542587-24545790 FORWARD   Aliases: F12P19.10, F12P19_10	12.2	12.3	-0.1	-0.3	100.0%	-5.8
15126	AT1G62050.1   similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At1g11740.1); similar to ankyrin repeat protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_468329.1); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr1:22939792-22942689 REVERSE   Aliases: F8K4.24	3.1	3.2	-0.1	-0.3	100.0%	-5.1
15127	AT4G01190.1   Type I phosphatidylinositol-4-phosphate 5-kinase, subfamily A. Preferentially phosphorylates PtdIns4P. Expressed in flowers and inflorescence stems.   chr4:504211-506131 REVERSE   Aliases: F2N1.9, F2N1_9	2.5	2.4	0.1	0.3	100.0%	-5.4
15128	AT1G27690.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr1:9636581-9638564 FORWARD   Aliases: T22C5.14, T22C5_14	5.1	5.0	0.1	0.3	100.0%	-5.0
15129	AT1G68795.1   Symbol: CLE12   CLE12, CLAVATA3/ESR-Related 12   chr1:25844518-25845315 REVERSE   Aliases: CLAVATA3/ESR RELATED 12	2.9	3.0	-0.1	-0.3	100.0%	-5.1
15130	AT1G14570.2   UBX domain-containing protein, contains Pfam profiles PF00789: UBX domain, PF02809: Ubiquitin interaction motif   chr1:4983562-4987355 FORWARD   Aliases: T5E21.7, T5E21_7	8.3	8.4	-0.1	-0.3	100.0%	-5.3
15131	AT1G20780.1   armadillo/beta-catenin repeat protein-related / U-box domain-containing protein, low similarity to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain	2.8	2.8	0.1	0.3	100.0%	-5.1
15132	AT1G55670.1   photosystem I reaction center subunit V, chloroplast, putative / PSI-G, putative (PSAG), identical to SP:Q9S7N7; similar to SP:Q00327 Photosystem I reaction center subunit V, chloroplast precursor (PSI-G) (Photosystem I 9 kDa protein) {Hordeum vulgare}; contains Pfam profile PF01241: Photosystem I psaG / psaK   chr1:20806336-20807115 REVERSE   Aliases: F20N2.33, F20N2_33	8.4	8.1	0.2	0.3	100.0%	-4.0
15133	AT4G18870.1   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr4:10346180-10347238 FORWARD   Aliases: F13C5.40, F13C5_40	2.2	2.2	0.0	0.3	100.0%	-5.7
15134	AT2G28210.1   carbonic anhydrase family protein, similar to storage protein (dioscorin) (Dioscorea cayenensis) GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase   chr2:12037074-12039497 FORWARD   Aliases: T3B23.12, T3B23_12	2.0	2.2	-0.2	-0.3	100.0%	-4.4
15135	AT3G51000.1   epoxide hydrolase, putative, similar to epoxide hydrolase (Glycine max) GI:2764806; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr3:18956006-18957511 REVERSE   Aliases: F24M12.40	7.4	7.5	-0.2	-0.3	100.0%	-4.5
15136	AT4G02530.1   chloroplast thylakoid lumen protein, SP:022773 ;TL16_ARATH   chr4:1112146-1114026 REVERSE   Aliases: T10P11.17, T10P11_17	7.0	6.9	0.1	0.3	100.0%	-4.4
15137	AT1G32340.1   Symbol: NHL8   zinc finger (C3HC4-type RING finger) family protein, contains a Zinc finger, C3HC4 type (RING finger) signature, PROSITE:PS00518	6.8	6.7	0.1	0.3	100.0%	-5.0
15138	AT5G62360.1   invertase/pectin methylesterase inhibitor family protein, similar to pectinesterase from Arabidopsis thaliana SP:Q42534, Lycopersicon esculentum SP:Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:25057882-25058687 FORWARD   Aliases: MMI9.1, MMI9_1	3.3	3.3	0.1	0.3	100.0%	-5.2
15139	AT4G33990.1   Symbol: EMB2758   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:16290146-16292617 REVERSE   Aliases: EMB2758, EMBRYO DEFECTIVE 2758, F17I5.180, F17I5_180	2.4	2.4	0.0	0.3	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15140	AT3G16360.1   Symbol: AHP4   phosphotransfer family protein, similar to two-component phosphorelay mediators ATHP1 (GI:4156241), ATHP3 (GI:4156245) (Arabidopsis thaliana), histidine-containing phosphotransfer protein (Catharanthus roseus) GI:13774348   chr3:5554480-5555399 FORWARD   Aliases: HPT PHOSPHOTRANSMITTER 4, T2O4.20	2.4	2.3	0.0	0.3	100.0%	-6.0
15141	AT3G20160.1   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative, similar to gi:2578821; similar to geranyl geranyl pyrophosphate synthase GB:BAA23157 (Arabidopsis thaliana)   chr3:7039001-7040035 FORWARD   Aliases: MAL21.19	3.6	3.5	0.1	0.3	100.0%	-5.0
15142	AT5G66190.1   ferredoxin--NADP(+) reductase, putative / adrenodoxin reductase, putative, strong similarity to Ferredoxin--NADP reductase, chloroplast precursor (EC 1.18.1.2) (FNR) from {Pisum sativum} SP:P10933, {Mesembryanthemum crystallinum} SP:P41343, {Spinacia oleracea} SP:P00455; identical to cDNA ferredoxin-NADP+ reductase precursor (pethH) GI:5730138   chr5:26467983-26470388 REVERSE   Aliases: K2A18.27, K2A18_27	5.3	5.2	0.1	0.3	100.0%	-5.1
15143	AT4G34510.1   Symbol: KCS2   fatty acid elongase, putative, similar to fatty acid elongase 1, Arabidopsis thaliana,gb:U29142 (GI:881615)   chr4:16491801-16493423 FORWARD   Aliases: T4L20.90, T4L20_90	2.4	2.3	0.0	0.3	100.0%	-5.6
15144	AT3G52190.1   transducin family protein / WD-40 repeat family protein, similar to St12p protein (GI:166878) {Arabidopsis thaliana}; contains Pfam profile: PF00400 WD domain, G-beta repeat   chr3:19364950-19368036 REVERSE   Aliases: T25B15.3	5.7	5.8	-0.1	-0.3	100.0%	-4.7
15145	AT4G31430.3   similar to nucleoporin-related [Arabidopsis thaliana] (TAIR:At5g20200.1); similar to OSJNBa0071113.9 [Oryza sativa (japonica cultivar-group)] (GB:CAE03408.3)   chr4:15248462-15252843 FORWARD   Aliases: F3L17.8	2.7	2.8	-0.1	-0.3	100.0%	-5.3
15146	AT5G13140.1   expressed protein   chr5:4170563-4171797 REVERSE   Aliases: T19L5.100, T19L5_100	2.3	2.3	-0.0	-0.3	100.0%	-5.7
15147	AT2G29620.1   expressed protein   chr2:12670277-12672880 REVERSE   Aliases: T27A16.28, T27A16_28	2.4	2.5	-0.1	-0.3	100.0%	-5.2
15148	AT3G57700.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr3:21395894-21396916 FORWARD   Aliases: F15B8.110	2.8	2.8	-0.0	-0.3	100.0%	-5.7
15149	AT5G48560.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.3	3.5	-0.2	-0.3	100.0%	-4.6
15150	AT1G72770.1   Symbol: HAB1   protein phosphatase 2C P2C-HA / PP2C P2C-HA (P2C-HA), identical to protein phosphatase 2C (AtP2C-HA) GB:AJ003119 (Arabidopsis thaliana) (Plant Mol. Biol. 38 (5), 879-883 (1998))   chr1:27393720-27396943 FORWARD   Aliases: F28P22.4, F28P22_4, HOMOLOGY TO ABI1	8.6	8.5	0.1	0.3	100.0%	-5.2
15151	AT1G68840.1   Symbol: RAV2   DNA-binding protein RAV2 (RAV2) / AP2 domain-containing protein RAP2.8, identical to RAV2 GI:3868859 from (Arabidopsis thaliana), AP2 domain containing protein RAP2.8 (Arabidopsis thaliana) GI:2281641; contains Pfam profile: PF00847 AP2-domain   chr1:25883990-25885399 FORWARD   Aliases: RAP2.8, RAV2, T6L1.3, T6L1_3	4.8	4.7	0.1	0.3	100.0%	-5.0
15152	AT1G60320.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:22238756-22239271 FORWARD   Aliases: T13D8.20, T13D8_20	3.1	3.0	0.1	0.3	100.0%	-5.1
15153	AT4G25760.1   expressed protein   chr4:13116085-13116847 FORWARD   Aliases: F14M19.40, F14M19_40	4.6	4.5	0.1	0.3	100.0%	-4.7
15154	AT5G40470.1   expressed protein   chr5:16225237-16227125 REVERSE   Aliases: K21I16.4, K21I16_4	5.5	5.4	0.1	0.3	100.0%	-4.9
15155	AT2G27940.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:11905019-11905944 FORWARD   Aliases: T1E2.14, T1E2_14	2.5	2.4	0.0	0.3	100.0%	-5.8
15156	AT3G44680.1   Symbol: HDA9   histone deacetylase, putative, similar to histone deacetylase-1 (HD-1) (Gallus gallus) GI:2791684; contains Pfam profile PF00850: Histone deacetylase family; identical to cDNA histone deacetylase partial cds GI:21637258   chr3:16237549-16240906 REVERSE   Aliases: HDA09, HISTONE DEACETYLASE, T18B22.80	4.7	4.5	0.1	0.3	100.0%	-4.9
15157	AT4G04740.1   Symbol: CPK23   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Lycopersicon esculentum) gi:19171502:emb:CAC87494   chr4:2404199-2408565 REVERSE   Aliases: T4B21.15, T4B21_15	2.3	2.3	-0.1	-0.3	100.0%	-6.0
15158	AT5G66970.1   signal recognition particle-related / SRP-related, low similarity to SP:P49966_ARATH Signal recognition particle 54 kDa protein 2 (SRP54) {Arabidopsis thaliana}	3.0	3.1	-0.1	-0.3	100.0%	-5.3
15159	AT2G17700.1   protein kinase family protein, similar to protein kinase (gi:170047) from Glycine max; contains a protein kinase domain profile (PDOC00100) (PF00069)   chr2:7692470-7696477 REVERSE   Aliases: T17A5.2, T17A5_2	4.2	4.1	0.1	0.3	100.0%	-5.0
15160	AT3G59410.1   protein kinase family protein, low similarity to GCN2 eIF2alpha kinase (Mus musculus) GI:6066585; contains Pfam profiles PF03129: Anticodon binding domain, PF00069: Protein kinase domain   chr3:21961546-21970243 FORWARD   Aliases: F25L23.270	5.5	5.4	0.1	0.3	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15161	AT1G23720.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:8388644-8391529 FORWARD   Aliases: F5O8.27, F5O8_27	2.9	3.2	-0.3	-0.3	100.0%	-4.1
15162	AT1G51450.1   SP1a/Ryanodine receptor (SPRY) domain-containing protein, low similarity to DEAD box protein DDX1 (Gallus gallus) GI:16323037, ryanodine receptor (Caenorhabditis elegans) GI:1871447; contains Pfam profile PF00622: SPRY domain   chr1:19078039-19080188 FORWARD   Aliases: F5D21.18, F5D21_18	3.6	3.6	-0.1	-0.3	100.0%	-5.1
15163	AT3G59940.1   kelch repeat-containing F-box family protein, contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain	3.6	3.4	0.2	0.3	100.0%	-4.3
15164	AT2G20230.1   expressed protein   chr2:8732622-8735101 FORWARD   Aliases: F11A3.22, F11A3_22	8.7	8.5	0.2	0.3	100.0%	-4.9
15165	AT2G29060.1   scarecrow transcription factor family protein   chr2:12489068-12494060 FORWARD   Aliases: T9I4.14, T9I4_14	4.0	3.9	0.1	0.3	100.0%	-5.4
15166	AT1G28375.1   expressed protein   chr1:9961041-9961646 FORWARD   Aliases: None	2.7	2.8	-0.1	-0.3	100.0%	-5.5
15167	AT1G19740.1   ATP-dependent protease La (LON) domain-containing protein, weak similarity to SP:P36774 ATP-dependent protease La 2 (EC 3.4.21.53) {Myxococcus xanthus}; contains Pfam profile PF02190: ATP-dependent protease La (LON) domain   chr1:6824313-6825450 FORWARD   Aliases: F14P1.10, F14P1_10	4.0	4.1	-0.1	-0.3	100.0%	-4.8
15168	AT2G27680.1   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr2:11810892-11813065 REVERSE   Aliases: F15K20.22, F15K20_22	7.6	7.5	0.1	0.3	100.0%	-4.7
15169	AT5G06330.1   hairpin-responsive protein, putative (HIN1), similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)   chr5:1934740-1935645 REVERSE   Aliases: MHF15.15, MHF15_15	3.2	3.3	-0.1	-0.3	100.0%	-4.5
15170	AT4G25830.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:13133645-13135033 FORWARD   Aliases: F14M19.9	2.8	2.8	-0.1	-0.3	100.0%	-5.4
15171	AT4G20770.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:11130773-11132995 REVERSE   Aliases: F21C20.120, F21C20_120	2.9	2.9	-0.0	-0.3	100.0%	-5.6
15172	ATCG01090.1   Symbol: NDHI   Encodes subunit of the chloroplast NAD(P)H dehydrogenase complex	8.7	8.9	-0.2	-0.3	100.0%	-4.5
15173	AT1G80630.1   leucine-rich repeat family protein   chr1:30313588-30315548 REVERSE   Aliases: T21F11.4, T21F11_4	4.6	4.7	-0.1	-0.3	100.0%	-4.9
15174	AT1G12700.1   helicase domain-containing protein / pentatricopeptide (PPR) repeat-containing protein, contains Pfam profiles PF01535: PPR repeat, PF00271: Helicase conserved C-terminal domain   chr1:4322911-4326195 REVERSE   Aliases: T12C24.31, T12C24_31	2.8	2.9	-0.1	-0.3	100.0%	-5.4
15175	AT5G21050.1   expressed protein   chr5:7147892-7148959 FORWARD   Aliases: T10F18.80, T10F18_80	3.9	3.8	0.1	0.3	100.0%	-5.3
15176	AT4G00180.1   Symbol: YAB3   axial regulator YABBY3 (YABBY3), identical to YABBY3 (Arabidopsis thaliana) GI:4928753   chr4:72619-75381 REVERSE   Aliases: F6N15.22, F6N15_22, YAB3, YABBY3	2.7	2.6	0.1	0.3	100.0%	-5.4
15177	AT5G08370.2   similar to alpha-galactosidase, putative / melibiase, putative / alpha-D-galactoside galactohydrolase, putative [Arabidopsis thaliana] (TAIR:At5g08380.1); similar to alpha galactosidase [Coffea arabica] (GB:CAI47559.1); contains InterPro domain Glycoside hydrolase, clan GH-D (InterPro:IPR000111); contains InterPro domain Glycoside hydrolase, family 27 (InterPro:IPR002241)   chr5:2690560-2693551 REVERSE   Aliases: F8L15.100, F8L15_100	5.3	5.4	-0.2	-0.3	100.0%	-4.6
15178	AT3G14225.1   Symbol: EMB1474   GDSL-motif lipase/hydrolase family protein, contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr3:4734623-4736000 REVERSE   Aliases: EMB1474, EMBRYO DEFECTIVE 1474, MLE3.2	3.3	3.4	-0.1	-0.3	100.0%	-4.4
15179	AT3G21480.1   transcription activation domain-interacting protein-related, contains weak similarity to Pax transcription activation domain interacting protein PTIP (GI:4336734) (Mus musculus)   chr3:7567736-7572104 FORWARD   Aliases: MIL23.5	3.3	3.3	-0.1	-0.3	100.0%	-5.2
15180	AT4G35240.1   expressed protein, contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Protein of unknown function (DUF630)   chr4:16761484-16764329 REVERSE   Aliases: F23E12.200, F23E12_200	4.2	4.0	0.2	0.3	100.0%	-4.9
15181	AT2G06230.1   expressed protein   chr2:2440434-2440730 REVERSE   Aliases: F18P14.2, F18P14_2	2.7	2.8	-0.1	-0.3	100.0%	-5.5
15182	AT3G26932.2   similar to double-stranded RNA-binding domain (DsRBD)-containing protein [Arabidopsis thaliana] (TAIR:At5g41070.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD07039.1); contains InterPro domain Double-stranded RNA binding (DsRBD) domain (InterPro:IPR001159)   chr3:9931522-9933310 REVERSE   Aliases: MQP17.7	2.2	2.3	-0.0	-0.3	100.0%	-6.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15183	AT3G51560.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr3:19132787-19136892 REVERSE   Aliases: T18N14.3	4.4	4.3	0.1	0.3	100.0%	-5.4
15184	AT3G55730.1   Symbol: MYB109	5.0	4.9	0.1	0.3	100.0%	-5.0
15185	AT4G37880.1   expressed protein   chr4:17809697-17811574 FORWARD   Aliases: T28I19.160, T28I19_160	5.9	5.8	0.1	0.3	100.0%	-5.1
15186	AT2G15130.1   plant basic secretory protein (BSP) family protein, similar to NtPRp27 (Nicotiana tabacum) GI:5360263; contains Pfam profile PF04450: Plant Basic Secretory Protein   chr2:6572027-6573086 FORWARD   Aliases: T15J14.17, T15J14_17	4.5	4.4	0.1	0.3	100.0%	-5.1
15187	AT2G01070.1   expressed protein, similar to membrane protein PTM1 precursor isolog GB:AAB65479	4.8	4.7	0.1	0.3	100.0%	-4.8
15188	AT3G09560.2   lipin family protein, contains Pfam profile: PF04571 lipin, N-terminal conserved region   chr3:2934622-2939461 REVERSE   Aliases: F11F8.14	3.3	3.4	-0.1	-0.3	100.0%	-5.2
15189	AT4G27580.1   expressed protein   chr4:13765667-13766603 REVERSE   Aliases: T29A15.70, T29A15_70	3.1	3.0	0.1	0.3	100.0%	-5.4
15190	AT1G66350.1   Symbol: RGL1   gibberellin regulatory protein (RGL1), similar to GB:CAA75492 from (Arabidopsis thaliana); contains Pfam profile PF03514: GRAS family transcription factor; identical to cDNA RGL1 protein GI:15777856, RGL1 protein (Arabidopsis thaliana) GI:15777857   chr1:24751858-24753705 FORWARD   Aliases: RGA LIKE 1, RGL, T27F4.10, T27F4_10	3.8	3.8	0.1	0.3	100.0%	-5.3
15191	AT4G28810.1   expressed protein, PMID: 12679534, putative bHLH127 transcription factor	2.4	2.4	-0.0	-0.3	100.0%	-5.8
15192	AT1G36320.1   expressed protein, similar to hypothetical protein GB:CAB37532 from (Arabidopsis thaliana),   chr1:13673029-13675310 FORWARD   Aliases: F7F23.4, F7F23_4	7.8	7.7	0.1	0.3	100.0%	-4.9
15193	AT3G05520.1   F-actin capping protein alpha subunit family protein, contains Pfam profile: PF01267 F-actin capping protein alpha subunit   chr3:1598556-1601306 FORWARD   Aliases: F22F7.25	7.5	7.6	-0.1	-0.3	100.0%	-5.0
15194	AT1G60000.2   29 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein cp29, putative, similar to 29 kDa ribonucleoprotein chloroplast precursor {Nicotiana sylvestris} SP:Q08935, SP:Q08937; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM) contains an AG-donor site at intron.   chr1:22097238-22098227 REVERSE   Aliases: T2K10.5, T2K10_5	9.1	9.3	-0.1	-0.3	100.0%	-4.5
15195	ATCG00190.1   Symbol: RPOB   Chloroplast DNA-dependent RNA polymerase B subunit.   chrC:23111-26329 REVERSE   Aliases: RPOB	4.1	4.2	-0.1	-0.3	100.0%	-4.9
15196	AT2G33410.1   heterogeneous nuclear ribonucleoprotein, putative / hnRNP, putative   chr2:14162963-14164838 FORWARD   Aliases: F4P9.18, F4P9_18	7.2	7.4	-0.2	-0.3	100.0%	-4.6
15197	AT4G15380.1   Symbol: CYP705A4   cytochrome P450 family protein, similar to CYTOCHROME P450 93A3 (P450 CP5) (SP:O81973) (Glycine max)   chr4:8788739-8790422 FORWARD   Aliases: DL3735W, FCAALL.280	3.0	3.1	-0.1	-0.3	100.0%	-4.4
15198	AT1G68020.2   Symbol: ATTPS6	4.0	4.0	0.1	0.3	100.0%	-5.2
15199	AT2G20310.1   expressed protein   chr2:8768409-8770233 REVERSE   Aliases: F11A3.14, F11A3_14	3.7	3.8	-0.1	-0.3	100.0%	-5.3
15200	AT3G18710.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain   chr3:6434089-6435567 REVERSE   Aliases: MVE11.7	6.3	6.4	-0.1	-0.3	100.0%	-5.2
15201	AT5G09450.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile: PF01535 PPR repeat   chr5:2941813-2943669 FORWARD   Aliases: T5E8.250, T5E8_250	6.2	6.0	0.2	0.3	100.0%	-4.8
15202	AT5G59350.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:23958008-23959433 FORWARD   Aliases: F2O15.1, F2O15_1	3.4	3.3	0.1	0.3	100.0%	-5.1
15203	AT5G03670.1   expressed protein   chr5:947145-950170 FORWARD   Aliases: F17C15.90, F17C15_90	2.3	2.4	-0.1	-0.3	100.0%	-5.4
15204	AT2G30760.1   expressed protein   chr2:13112847-13115298 REVERSE   Aliases: T11J7.15, T11J7_15	2.3	2.3	0.0	0.3	100.0%	-5.7
15205	AT4G02910.1   expressed protein   chr4:1288486-1289615 REVERSE   Aliases: T4I9.21	3.4	3.5	-0.1	-0.3	100.0%	-4.9
15206	AT5G14300.1   prohibitin, putative, similar to prohibitin (Arabidopsis thaliana) GI:1946331; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr5:4613105-4614026 FORWARD   Aliases: F18O22.90, F18O22_90	2.2	2.3	-0.0	-0.3	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15207	AT3G51140.1   expressed protein   chr3:19008748-19010883 FORWARD   Aliases: F24M12.180	7.2	7.0	0.2	0.3	100.0%	-4.4
15208	AT5G66340.1   hypothetical protein   chr5:26519728-26520379 FORWARD   Aliases: K1L20.12, K1L20_12	4.3	4.2	0.1	0.3	100.0%	-5.1
15209	AT1G27140.1   Symbol: ATGSTU14   glutathione S-transferase, putative, similar to glutathione S-transferase GB: AAF22517 GI:6652870 from (Papaver somniferum) GB:AY050343.   chr1:9427845-9428703 FORWARD   Aliases: GLUTATHIONE S TRANSFERASE 13, GST13, T7N9.20, T7N9_20	3.9	3.8	0.1	0.3	100.0%	-5.3
15210	AT1G01090.1   Symbol: PDH E1 ALPHA   pyruvate dehydrogenase E1 component alpha subunit, chloroplast, identical to pyruvate dehydrogenase E1 alpha subunit GB:AAB86803 GI:2454182 from (Arabidopsis thaliana); identical to cDNA pyruvate dehydrogenase E1 alpha subunit mRNA, nuclear gene encoding plastid protein GI:2454181   chr1:47485-49279 REVERSE   Aliases: PYRUVATE DEHYDROGENASE E1 ALPHA, T25K16.8, T25K16_8	10.9	10.7	0.2	0.3	100.0%	-4.9
15211	AT5G59750.1   riboflavin biosynthesis protein, putative, similar to SP:P50855 Riboflavin biosynthesis protein ribA (Includes: GTP cyclohydrolase II (EC 3.5.4.25); 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase)) {Actinobacillus pleuropneumoniae}; contains Pfam profiles PF00925: GTP cyclohydrolase II, PF00926: 3,4-dihydroxy-2-butanone 4-phosphate synthase   chr5:24090515-24092765 FORWARD   Aliases: MTH12.13, MTH12_13	7.2	7.1	0.2	0.3	100.0%	-4.4
15212	AT1G59780.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	3.1	-0.1	-0.3	100.0%	-5.2
15213	AT3G28830.1   expressed protein   chr3:10832470-10834521 FORWARD   Aliases: T19N8.13	2.8	2.8	0.1	0.3	100.0%	-5.2
15214	AT1G60350.1   Symbol: ANAC024   no apical meristem (NAM) protein-related, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to CUP-SHAPED COTYLEDON1 (CUC1) (GI:12060422) (Arabidopsis thaliana)   chr1:22244938-22245900 REVERSE   Aliases: ANAC024, T13D8.22, T13D8_22	2.4	2.5	-0.0	-0.3	100.0%	-5.7
15215	AT4G34940.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr4:16639603-16641950 FORWARD   Aliases: F11I11.180, F11I11_180	2.3	2.3	-0.0	-0.3	100.0%	-5.6
15216	AT3G22850.1   expressed protein, similar to auxin down-regulated protein ARG10 (Vigna radiata) GI:2970051, wali7 (aluminum-induced protein) (Triticum aestivum) GI:451193   chr3:8089010-8090462 FORWARD   Aliases: F5N5.2	9.0	9.2	-0.2	-0.3	100.0%	-4.9
15217	AT4G32930.1   expressed protein, predicted protein, Caenorhabditis elegans, gb:Z70780   chr4:15898840-15900824 FORWARD   Aliases: F26P21.50, F26P21_50	8.4	8.5	-0.1	-0.3	100.0%	-4.7
15218	AT2G41990.1   expressed protein   chr2:17534335-17536015 FORWARD   Aliases: T6D20.12, T6D20_12	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15219	AT5G04390.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:1239101-1240518 FORWARD   Aliases: T19N18.120, T19N18_120	2.7	2.6	0.0	0.3	100.0%	-5.5
15220	AT5G67530.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr5:26958408-26962200 FORWARD   Aliases: K9I9.9, K9I9_9	7.2	7.4	-0.1	-0.3	100.0%	-5.2
15221	AT5G56160.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus) and SEC14 cytosolic factor (SP:P45816) (Candida lipolytica)   chr5:22749712-22752765 FORWARD   Aliases: MDA7.22, MDA7_22	4.0	4.1	-0.1	-0.3	100.0%	-4.9
15222	AT5G42170.1   family II extracellular lipase, putative, similar to family II lipase EXL3 (Arabidopsis thaliana) GI:15054386; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr5:16867114-16868935 FORWARD   Aliases: MJC20.28, MJC20_28	2.8	2.8	-0.0	-0.3	100.0%	-5.5
15223	AT4G38860.1   auxin-responsive protein, putative, auxin-induced protein 10A, Glycine max., PIR2:JQ1099	2.5	2.5	0.0	0.3	100.0%	-5.8
15224	AT1G72100.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to embryogenic gene (Betula pendula) GI:4539485; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr1:27130874-27132640 FORWARD   Aliases: F28P5.13, F28P5_13	2.5	2.4	0.1	0.3	100.0%	-5.3
15225	AT3G03560.1   expressed protein   chr3:853976-856493 REVERSE   Aliases: T21P5.2	3.9	4.0	-0.1	-0.3	100.0%	-4.9
15226	AT2G37710.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr2:15821796-15824082 REVERSE   Aliases: F13M22.21, F13M22_21	3.6	3.5	0.1	0.3	100.0%	-5.1
15227	AT5G38910.1   germin-like protein, putative, similar to SP:Q9LEA7; contains PS00725 germin family signature   chr5:15596041-15596814 FORWARD   Aliases: K15E6.90, K15E6_90	2.3	2.4	-0.0	-0.3	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15228	AT2G27880.1   argonaute protein, putative / AGO, putative, similar to SP:O04379 Argonaute protein (AGO1) {Arabidopsis thaliana}; contains Pfam profiles PF02170: PAZ domain, PF02171: Piwi domain   chr2:11878565-11883789 FORWARD   Aliases: T1E2.20, T1E2_20	2.7	2.7	0.1	0.3	100.0%	-5.3
15229	AT5G17220.1   Symbol: ATGSTF12   glutathione S-transferase, putative   chr5:5658462-5659388 FORWARD   Aliases: GLUTATHIONE S TRANSFERASE 26, GST26, MKP11.22, MKP11_22, TRANSPARENT TESTA 19, TT19	3.3	3.3	0.1	0.3	100.0%	-5.4
15230	AT4G09670.1   oxidoreductase family protein, similar to AX110P (Daucus carota) GI:285739; contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain	5.5	5.7	-0.2	-0.3	100.0%	-4.8
15231	ATMG00690.1   Symbol: ORF240A   hypothetical protein   chrM:203588-204310 REVERSE   Aliases: ORF240A	7.0	6.6	0.4	0.3	100.0%	-4.4
15232	AT1G76910.1   expressed protein   chr1:28892112-28892998 FORWARD   Aliases: F22K20.20, F22K20_20	3.2	3.2	0.1	0.3	100.0%	-4.8
15233	AT1G55920.1   Symbol: AtSerat2;1   serine O-acetyltransferase, putative, identical to GI:608677 from (Arabidopsis thaliana)   chr1:20915781-20917112 FORWARD   Aliases: F14J16.18, F14J16_18, SAT1, SAT5, SERINE ACETYLTRANSFERASE, SERINE ACETYLTRANSFERASE 1	6.8	6.6	0.1	0.3	100.0%	-4.5
15234	AT2G15900.1   phox (PX) domain-containing protein, weak similarity to SP:Q9Y5W8 Sorting nexin 13 {Homo sapiens}; contains Pfam profiles PF00787: PX domain, PF02194: PXA domain   chr2:6934472-6939784 FORWARD   Aliases: F19G14.10, F19G14_10	2.9	2.8	0.1	0.3	100.0%	-5.1
15235	AT1G02260.1   transmembrane protein, putative, similar to P protein (Melanocyte-specific transporter protein) (SP:Q04671) {Homo sapiens}; contains 8 transmembrane domains   chr1:440441-442877 REVERSE   Aliases: T6A9.21	4.6	4.5	0.2	0.3	100.0%	-4.4
15236	AT4G24780.1   pectate lyase family protein, similar to pectate lyase GP:14289169 from (Salix gilgiana)	11.4	11.2	0.2	0.3	100.0%	-4.5
15237	AT1G31800.1   cytochrome P450 family protein, similar to Cytochrome P450 97B2 (SP:048921) (Glycine max); contains Pfam profile: PF00067: Cytochrome P450   chr1:11396383-11400071 FORWARD   Aliases: F5M6.19, F5M6_19	7.0	7.1	-0.1	-0.3	100.0%	-4.7
15238	AT5G55040.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr5:22347146-22347986 REVERSE   Aliases: K13P22.4, K13P22_4	3.1	3.1	-0.1	-0.3	100.0%	-5.5
15239	AT4G03340.1   glycosyltransferase family 14 protein / core-2/l-branching enzyme family protein, contains Pfam profile: PF02485 Core-2/l-Branching enzyme   chr4:1467749-1470062 REVERSE   Aliases: F4C21.27, F4C21_27	4.3	4.4	-0.1	-0.3	100.0%	-4.7
15240	AT5G04330.1   cytochrome P450, putative / ferulate-5-hydroxylase, putative, Similar to	3.8	3.7	0.1	0.3	100.0%	-4.8
15241	AT5G13630.1   Symbol: GUN5   magnesium-chelatase subunit chlH, chloroplast, putative / Mg-protoporphyrin IX chelatase, putative (CHLH), nearly identical to magnesium chelatase subunit GI:1154627 from (Arabidopsis thaliana); contains Pfam profile: PF02514 CobN/magnesium chelatase family protein   chr5:4387337-4392230 REVERSE   Aliases: CCH, CCH1, CHLH, CONDITIONAL CHLORINA, GENOMES UNCOUPLED 5, T6I14.12	9.5	9.7	-0.2	-0.3	100.0%	-4.7
15242	AT3G14020.1   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr3:4642975-4644308 FORWARD   Aliases: MDC16.15	5.3	5.2	0.1	0.3	100.0%	-4.9
15243	AT5G65000.2   nucleotide-sugar transporter family protein, low similarity to SP:Q9Y2D2 UDP N-acetylglucosamine transporter {Homo sapiens}; contains Pfam profile PF04142: Nucleotide-sugar transporter	7.7	7.8	-0.1	-0.3	100.0%	-5.0
15244	AT5G51630.2   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:20986847-20991926 FORWARD   Aliases: K17N15.18, K17N15_18	3.2	3.1	0.2	0.3	100.0%	-4.6
15245	AT5G25140.1   Symbol: CYP71B13   cytochrome P450 family protein, CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438   chr5:8672427-8674632 FORWARD   Aliases: F21J6.4	2.9	2.9	0.1	0.3	100.0%	-5.3
15246	AT1G54040.2   Symbol: ESP   kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (4 repeats); similar to jsimilar to epithiospecifier (GI:16118838) (Arabidopsis thaliana) isoform contains AT-AG splice sites at intron   chr1:20174383-20177617 REVERSE   Aliases: EPITHIOSPECIFIER PROTEIN, F15I1.12, F15I1_12, TASTY	2.5	2.5	0.1	0.3	100.0%	-5.6
15247	AT5G05920.2   Symbol: DHS   similar to deoxyhypusine synthase [Crotalaria retusa] (GB:CAG28987.1); contains InterPro domain Deoxyhypusine synthase (InterPro:IPR002773)   chr5:1777553-1779823 REVERSE   Aliases: K18J17.7, K18J17_7, deoxyhypusine synthase	4.8	4.8	-0.1	-0.3	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15248	AT5G13910.1   Symbol: LEP   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (LEAFY PETIOLE). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.   chr5:4482452-4483087 REVERSE   Aliases: LEAFY PETIOLE, LEP, MAC12.13, MAC12_13	3.1	3.1	-0.1	-0.3	100.0%	-5.0
15249	AT1G26580.1   expressed protein, similar to putative MYB family transcription factor GB:AAD17429 GI:4335752 from (Arabidopsis thaliana)   chr1:9184593-9187492 FORWARD   Aliases: T1K7.5, T1K7_5	5.7	5.5	0.2	0.3	100.0%	-4.6
15250	AT5G62030.1   diphthamide synthesis DPH2 family protein, contains InterPro accession IPR002728: Diphthamide synthesis DPH2 protein   chr5:24935705-24938102 FORWARD   Aliases: MTG10.5, MTG10_5	3.9	3.8	0.1	0.3	100.0%	-5.0
15251	AT5G59030.1   Symbol: COPT1   copper transporter 1 (COPT1), nearly identical to SP:Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}	4.3	4.2	0.1	0.3	100.0%	-4.7
15252	AT1G59850.1   expressed protein   chr1:22032174-22033872 REVERSE   Aliases: F23H11.17, F23H11_17	3.1	3.0	0.1	0.3	100.0%	-4.9
15253	AT4G15680.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	4.3	4.2	0.1	0.3	100.0%	-5.1
15254	AT1G49410.1   Symbol: TOM6   expressed protein   chr1:18289409-18290570 REVERSE   Aliases: F13F21.16, F13F21_16, TOM6	6.9	6.7	0.2	0.3	100.0%	-4.6
15255	AT1G17010.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase (Petunia x hybrida)(GI:311658), (Solanum tuberosum)(GI:1039356); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:5817565-5819345 FORWARD   Aliases: F20D23.29, F20D23_29	2.2	2.3	-0.0	-0.3	100.0%	-5.7
15256	AT1G66030.1   Symbol: CYP96A14P   cytochrome P450-related, weak similarity to cytochrome P450 (Catharanthus roseus) GI:4688670   chr1:24586812-24587315 FORWARD   Aliases: F15E12.16, F15E12_16	3.1	3.2	-0.0	-0.3	100.0%	-5.6
15257	AT5G54720.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:22249521-22250078 REVERSE   Aliases: K5F14.7, K5F14_7	2.3	2.3	-0.0	-0.3	100.0%	-6.0
15258	AT4G02660.1   WD-40 repeat family protein / beige-related, contains Pfam PF00400: WD domain, G-beta repeat; similar to BEIGE (GI:3928547) (Rattus norvegicus); lysosomal trafficking regulator - Bos taurus, EMBL: AF114785   chr4:1159667-1174321 REVERSE   Aliases: T10P11.5, T10P11_5	3.5	3.5	-0.1	-0.3	100.0%	-5.2
15259	AT2G14060.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri) and to SAM:benzoic acid carboxyl methyltransferase (BAMT)(GI:9789277)(Antirrhinum majus)   chr2:5921596-5922849 REVERSE   Aliases: F9B22.17, F9B22_17	2.4	2.5	-0.1	-0.3	100.0%	-5.6
15260	AT2G30290.1   vacuolar sorting receptor, putative, similar to vacuolar sorting receptor homolog (Arabidopsis thaliana) GI:1737218   chr2:12919967-12922858 REVERSE   Aliases: T9D9.10, T9D9_10	2.5	2.6	-0.0	-0.3	100.0%	-5.4
15261	AT1G68250.1   expressed protein   chr1:25583036-25583857 REVERSE   Aliases: T22E19.12, T22E19_12	2.6	2.5	0.1	0.3	100.0%	-5.4
15262	AT2G40470.1   LOB domain protein 15 / lateral organ boundaries domain protein 15 (LBD15), identical to SP:Q8L5T5 LOB domain protein 15 {Arabidopsis thaliana}; similar to ASYMMETRIC LEAVES2 (Arabidopsis thaliana) GI:19918971   chr2:16909382-16910730 REVERSE   Aliases: T2P4.18, T2P4_18	2.2	2.2	-0.0	-0.3	100.0%	-5.5
15263	AT5G30490.1   expressed protein   chr5:11629213-11631760 FORWARD   Aliases: None	5.1	5.0	0.1	0.3	100.0%	-5.0
15264	AT5G47280.1   Symbol: ADR1 L3   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr5:19210384-19212786 FORWARD   Aliases: ADR1 L3, ADR1 LIKE 3, MQL5.14, MQL5_14	2.2	2.2	-0.0	-0.3	100.0%	-5.9
15265	AT3G05170.1   phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family   chr3:1466579-1468406 FORWARD   Aliases: T12H1.14, T12H1_14	4.6	4.8	-0.2	-0.3	100.0%	-4.4
15266	AT2G03800.1   Symbol: GEK1   expressed protein   chr2:1156774-1158930 FORWARD   Aliases: F19B11.25, F19B11_25, GEK01	7.0	6.9	0.1	0.3	100.0%	-4.9
15267	AT2G44430.1   DNA-binding bromodomain-containing protein, contains Pfam domains, Pfam PF00439: Bromodomain and PF00249: Myb-like DNA-binding domain   chr2:18340623-18343440 FORWARD   Aliases: F4I1.24	4.9	5.1	-0.2	-0.3	100.0%	-4.5
15268	AT3G58800.1   expressed protein, proline-rich protein A41R, Chlorella virus PBCV-1, PIR:T17531	4.0	3.9	0.1	0.3	100.0%	-4.7
15269	AT3G63230.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana);   chr3:23370608-23371097 FORWARD   Aliases: F16M2.80	2.5	2.5	0.0	0.3	100.0%	-5.8
15270	AT5G50850.1   pyruvate dehydrogenase E1 component beta subunit, mitochondrial / PDHE1-B (PDH2), identical to SP:Q38799 Pyruvate dehydrogenase E1 component beta subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-B) {Arabidopsis thaliana}	11.5	11.6	-0.1	-0.3	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15271	AT1G06470.2   phosphate translocator-related, low similarity to SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275   chr1:1969751-1973755 FORWARD   Aliases: F12K11.18, F12K11_18	5.6	5.7	-0.1	-0.3	100.0%	-4.8
15272	AT1G62890.1   expressed protein   chr1:23298642-23299229 FORWARD   Aliases: F16P17.24, F16P17_24	3.0	2.9	0.1	0.3	100.0%	-5.2
15273	AT1G30710.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:10895262-10896975 FORWARD   Aliases: T5I8.16, T5I8_16	2.3	2.3	-0.0	-0.3	100.0%	-5.9
15274	NA	2.2	2.2	0.0	0.3	100.0%	-6.2
15275	AT4G32460.2   expressed protein, contains Pfam profile PF04862: Protein of unknown function, DUF642   chr4:15662272-15664954 REVERSE   Aliases: F8B4.160, F8B4_160	5.4	5.3	0.1	0.3	100.0%	-4.7
15276	AT3G19050.1   kinesin motor protein-related, contains Pfam profile: PF00225 Kinesin motor domain; contains non-consensus splice site (GC) at intron 12	2.6	2.6	-0.0	-0.3	100.0%	-5.6
15277	AT2G14100.1   Symbol: CYP705A13   cytochrome P450 family protein, contains Pfam profile PF00067: Cytochrome P450   chr2:5941638-5943453 REVERSE   Aliases: T22C12.3, T22C12_3	3.5	3.6	-0.1	-0.3	100.0%	-4.3
15278	AT5G27420.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 zinc finger protein ATL6 (Arabidopsis thaliana) gi:4928403:gb:AAD33584.1:AF132016_1(4928403); contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:9684075-9685564 FORWARD   Aliases: F21A20.130, F21A20_130	3.8	3.9	-0.1	-0.3	100.0%	-4.6
15279	AT4G03040.1   expressed protein   chr4:1341083-1343140 FORWARD   Aliases: T4I9.8, T4I9_8	2.8	2.8	-0.0	-0.3	100.0%	-5.7
15280	AT1G33490.1   expressed protein   chr1:12150675-12152374 REVERSE   Aliases: F10C21.22, F10C21_22	6.1	5.9	0.2	0.3	100.0%	-4.8
15281	AT1G47740.2   expressed protein   chr1:17570148-17572599 FORWARD   Aliases: T2E6.19, T2E6_19	6.5	6.6	-0.1	-0.3	100.0%	-4.9
15282	AT1G27640.1   expressed protein   chr1:9614450-9614893 REVERSE   Aliases: T22C5.9	4.4	4.3	0.1	0.3	100.0%	-5.0
15283	AT1G66960.1   lupeol synthase, putative / 2,3-oxidosqualene-triterpenoid cyclase, putative, similar to lupeol synthase GI:1762150 from (Arabidopsis thaliana), 2,3-oxidosqualene-triterpenoid cyclase (Arabidopsis thaliana) GI:2738027   chr1:24988604-24993460 REVERSE   Aliases: F1O19.4, F1O19_4	3.2	3.3	-0.1	-0.3	100.0%	-5.3
15284	AT1G51110.1   plastid-lipid associated protein PAP / fibrillin family protein, similar to plastid-lipid associated protein PAP2 (Brassica rapa) GI:14248550; contains Pfam profile PF04755: PAP_fibrillin   chr1:18939016-18941327 FORWARD   Aliases: AT1G51115, F23H24.16, F23H24_16	4.2	4.1	0.1	0.3	100.0%	-4.9
15285	AT5G63380.1   Encodes a peroxisomal protein involved in the activation of fatty acids through esterification with CoA. At5g63380 preferentially activates fatty acids with increased chain length (C9:0 to C8:0) and thus shares characteristics with long-chain fatty acyl-CoA synthases. Also able to catalyze the conversion of OPDA to its CoA ester and is therefore thought to be involved in the peroxisomal &#946;-oxidation steps of jasmonic acid biosynthesis.   chr5:25404637-25407289 REVERSE   Aliases: K9H21.11, K9H21_11	6.8	6.9	-0.1	-0.3	100.0%	-4.8
15286	AT5G61700.1   Symbol: ATATH16   ABC transporter family protein, ABC family transporter, Entamoeba histolytica, EMBL:EH058   chr5:24811090-24815170 FORWARD   Aliases: K11J9.11, K11J9_11	3.4	3.4	0.1	0.3	100.0%	-5.2
15287	AT2G34830.1   Symbol: WRKY35	3.4	3.3	0.1	0.3	100.0%	-4.3
15288	AT5G48530.1   expressed protein   chr5:19685796-19686056 REVERSE   Aliases: MJE7.17, MJE7_17	2.6	2.6	-0.0	-0.3	100.0%	-5.7
15289	AT2G24070.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g30710.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g30710.1); similar to putative streptococcal hemagglutinin [Oryza sativa (japonica cultivar-group)] (GB:XP_468240.1); contains InterPro domain Protein of unknown function DUF566 (InterPro:IPR007573)   chr2:10238902-10242556 REVERSE   Aliases: T29E15.27, T29E15_27	2.4	2.5	-0.0	-0.3	100.0%	-5.5
15290	AT1G68270.1   AMP-dependent synthetase and ligase family protein, similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501   chr1:25591854-25593917 REVERSE   Aliases: T22E19.10, T22E19_10	2.4	2.5	-0.0	-0.3	100.0%	-5.8
15291	AT2G31085.1   Symbol: CLE6   Clavata3 / ESR-Related-6 (CLE6), CLAVATA3/ESR-Related 6 (CLE6)   chr2:13261255-13261783 FORWARD   Aliases: CLAVATA3/ESR RELATED 6	2.6	2.6	-0.1	-0.3	100.0%	-5.3
15292	AT5G20180.2   ribosomal protein L36 family protein, contains Pfam profile: PF00444 ribosomal protein L36   chr5:6810966-6812148 FORWARD   Aliases: F5O24.70, F5O24_70	10.3	10.2	0.1	0.3	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15293	AT1G55940.1   Symbol: CYP708A1   cytochrome P450, putative, similar to SP:Q42569 from (Arabidopsis thaliana)   chr1:20926133-20929284 REVERSE   Aliases: F14J16.21, F14J16_21	2.5	2.6	-0.1	-0.3	100.0%	-4.5
15294	AT5G57450.2   Symbol: XRCC3   DNA repair family protein, contains similarity to Swiss-Prot:O43542 DNA-repair protein XRCC3 (X-ray repair cross-complementing protein 3) (Homo sapiens)   chr5:23290988-23292202 REVERSE   Aliases: ATXRCC3, MUA2.3, MUA2_3	3.6	3.5	0.1	0.3	100.0%	-5.2
15295	AT5G50500.1   expressed protein   chr5:20579376-20579783 REVERSE   Aliases: MBA10.5, MBA10_5	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15296	AT5G17970.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:5949001-5951621 REVERSE   Aliases: MCM23.4, MCM23_4	3.0	2.9	0.1	0.3	100.0%	-5.2
15297	AT1G03770.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to polycomb-M33 interacting protein Ring1B (Mus musculus) GI:2239142; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:944771-947334 FORWARD   Aliases: F21M11.32, F21M11_32	3.6	3.6	0.1	0.3	100.0%	-5.2
15298	AT5G56330.1   carbonic anhydrase family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase	2.2	2.3	-0.0	-0.3	100.0%	-5.5
15299	AT2G17920.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:7789794-7791369 FORWARD   Aliases: T13L16.6, T13L16_6	2.5	2.5	0.0	0.3	100.0%	-5.6
15300	AT2G07300.1   expressed protein   chr2:3030795-3031771 FORWARD   Aliases: T13E11.7, T13E11_7	2.5	2.5	-0.0	-0.3	100.0%	-5.4
15301	AT3G47295.1   expressed protein   chr3:17438935-17439496 FORWARD   Aliases: None	2.4	2.5	-0.0	-0.3	100.0%	-5.5
15302	AT3G16100.1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family   chr3:5459178-5460783 FORWARD   Aliases: MSL1.14	9.2	9.1	0.1	0.3	100.0%	-4.5
15303	AT5G60230.2   Symbol: SEN2   tRNA-splicing endonuclease, putative, contains similarity to Swiss-Prot:P16658 tRNA-splicing endonuclease subunit SEN2 (tRNA-intron endonuclease) (Saccharomyces cerevisiae); contains Pfam domain PF01974: tRNA intron endonuclease, catalytic C-terminal domain   chr5:24267317-24268821 REVERSE   Aliases: ATSEN2, F15L12.18, F15L12_18, SPLICING ENDONUCLEASE 2	5.7	5.8	-0.1	-0.3	100.0%	-4.6
15304	AT3G06370.1   Symbol: NHX4   sodium proton exchanger, putative (NHX3), similar to sodium proton exchanger (Nhx1) GB:AAD16946 (Arabidopsis thaliana); Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563   chr3:1930402-1934079 REVERSE   Aliases: ATNHX4, F24P17.16, F24P17_16	3.2	3.1	0.0	0.3	100.0%	-5.4
15305	AT1G69830.1   Symbol: ATAMY3	7.0	7.2	-0.2	-0.3	100.0%	-4.7
15306	AT3G44500.1   Ulp1 protease family protein, similar to At1g32840, At4g04010, At2g06430, At2g15140, At2g04980, At2g14130, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210, At3g32900   chr3:16112404-16117068 FORWARD   Aliases: F14L2.50	2.7	2.7	-0.0	-0.3	100.0%	-5.9
15307	AT1G74480.1   RWP-RK domain-containing protein, contains Pfam profile: PF02042 RWP-RK domain   chr1:27996693-27997839 REVERSE   Aliases: F1M20.16, F1M20_16	2.8	2.7	0.0	0.3	100.0%	-5.7
15308	AT4G16430.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	8.1	8.3	-0.1	-0.3	100.0%	-5.0
15309	AT5G56370.2   F-box family protein, contains F-box domain Pfam:PF00646	2.2	2.2	-0.0	-0.3	100.0%	-5.8
15310	AT1G31000.1   F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.7	0.1	0.3	100.0%	-5.2
15311	AT4G00480.1   Symbol: ATMYC1	2.7	2.6	0.0	0.3	100.0%	-5.5
15312	AT3G14580.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:4903019-4904236 FORWARD   Aliases: MIE1.8	3.5	3.5	-0.1	-0.3	100.0%	-5.4
15313	AT4G35730.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g34220.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_480332.1); contains InterPro domain Eukaryotic protein of unknown function DUF292 (InterPro:IPR005061)   chr4:16931044-16933361 FORWARD   Aliases: F8D20.240, F8D20_240	4.5	4.5	-0.1	-0.3	100.0%	-4.8
15314	AT3G53210.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575; contains Pfam profile PF00892: Integral membrane protein   chr3:19731143-19732849 FORWARD   Aliases: T4D2.140	4.3	4.2	0.1	0.3	100.0%	-5.1
15315	AT4G21390.1   S-locus lectin protein kinase family protein, contains Pfam profiles: PF00954 S-locus glycoprotein family, PF00069 protein kinase domain, PF01453 lectin (probable mannose binding)   chr4:11394368-11397594 REVERSE   Aliases: T6K22.120, T6K22_120	4.4	4.5	-0.1	-0.3	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15316	AT2G28050.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:11945342-11946730 REVERSE   Aliases: T1E2.3, T1E2_3	3.7	3.8	-0.1	-0.3	100.0%	-4.8
15317	AT5G57520.1   Symbol: ZFP2   zinc finger (C2H2 type) family protein (ZFP2), identical to zinc finger protein 2 (ZFP2) GI:790674 from (Arabidopsis thaliana); contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:23313195-23313909 FORWARD   Aliases: MUA2.9, MUA2_9, ZFP2, ZINC FINGER PROTEIN 2	2.7	2.7	0.0	0.3	100.0%	-5.5
15318	AT1G66760.2   MATE efflux family protein, contains TIGRfam profile: TIGR00797: MATE efflux family protein, Pfam profile PF01554: Uncharacterized membrane protein family   chr1:24905641-24908066 FORWARD   Aliases: F4N21.11, F4N21_11	3.0	3.1	-0.1	-0.3	100.0%	-5.3
15319	AT1G23240.2   caleosin-related family protein, similar to caleosin GB:AAF13743 GI:6478218 from (Sesamum indicum); similar to Ca+2-binding EF hand protein GB:AAB71227 (Glycine max); contains Pfam profile PF05042: Caleosin related protein   chr1:8252744-8254610 REVERSE   Aliases: F26F24.33, F26F24_33	2.8	2.7	0.0	0.3	100.0%	-5.3
15320	AT2G41230.1   expressed protein   chr2:17202004-17202752 REVERSE   Aliases: F13H10.22, F13H10_22	7.6	7.5	0.1	0.3	100.0%	-5.1
15321	AT2G39540.1   gibberellin-regulated family protein, similar to SP:P27057 GAST1 protein precursor {Lycopersicon esculentum}; contains Pfam profile PF02704: Gibberellin regulated protein   chr2:16507944-16508319 FORWARD   Aliases: F12L6.20, F12L6_20	3.0	3.1	-0.1	-0.3	100.0%	-5.2
15322	AT2G01900.1   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr2:405917-409013 FORWARD   Aliases: T23K3.9, T23K3_9	2.5	2.3	0.2	0.3	100.0%	-4.3
15323	AT5G28410.1   hypothetical protein, DYNAMIN-LIKE PROTEIN- Arabidopsis thaliana, EMBL:L36939   chr5:10358377-10359442 FORWARD   Aliases: F21B23.2, F21B23_2	2.5	2.5	-0.0	-0.3	100.0%	-5.9
15324	AT4G01330.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.0	4.0	0.1	0.3	100.0%	-4.9
15325	AT5G66000.1   expressed protein   chr5:26413171-26414726 REVERSE   Aliases: K2A18.6, K2A18_6	4.8	4.9	-0.1	-0.3	100.0%	-4.6
15326	AT1G68765.1   Symbol: IDA   expressed protein	3.9	3.9	0.1	0.3	100.0%	-5.4
15327	AT5G39910.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase PG1 (Glycine max) GI:5669846; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr5:15996640-15998899 REVERSE   Aliases: MYH19.70, MYH19_70	2.5	2.5	0.0	0.3	100.0%	-5.7
15328	AT5G30520.1   hypothetical protein   chr5:11653422-11653868 REVERSE   Aliases: None	2.9	3.0	-0.0	-0.3	100.0%	-5.4
15329	AT2G18060.1   Symbol: ANAC037   no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.8	2.9	-0.1	-0.3	100.0%	-4.9
15330	AT5G40160.1   Symbol: EMB506	3.4	3.3	0.1	0.3	100.0%	-5.2
15331	AT3G15760.1   expressed protein   chr3:5337560-5338470 FORWARD   Aliases: MSJ11.16	2.9	3.0	-0.1	-0.3	100.0%	-5.1
15332	AT5G66300.1   Symbol: ANAC105   no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751)	2.9	3.0	-0.1	-0.3	100.0%	-5.2
15333	AT1G59900.1   Symbol: AT E1 ALPHA   pyruvate dehydrogenase E1 component alpha subunit, mitochondrial (PDHE1-A), identical to SP:P52901 Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) {Arabidopsis thaliana}   chr1:22054960-22057550 FORWARD   Aliases: PYRUVATE DEHYDROGENASE E1 ALPHA SUBUNIT	10.9	10.9	0.1	0.3	100.0%	-5.3
15334	AT5G26240.1   Symbol: CLC D   chloride channel protein (CLC-d), identical to CLC-d chloride channel protein (Arabidopsis thaliana) GI:1742959	3.6	3.5	0.1	0.3	100.0%	-4.8
15335	AT1G75660.1   Symbol: XRN3   5'-3' exoribonuclease (XRN3), identical to XRN3 (Arabidopsis thaliana) gi:11875628:gb:AAG40732   chr1:28411808-28418778 FORWARD   Aliases: F10A5.15, F10A5_15, XRN3	4.5	4.4	0.1	0.3	100.0%	-5.1
15336	AT1G11630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3912902-3914407 REVERSE   Aliases: F25C20.22, F25C20_22	4.5	4.6	-0.1	-0.3	100.0%	-4.8
15337	AT3G61630.1   AP2 domain-containing transcription factor, putative, transcription factor Pti6 - Lycopersicon esculentum, PIR:T07728   chr3:22816155-22817499 FORWARD   Aliases: F15G16.20	2.3	2.2	0.1	0.3	100.0%	-5.2
15338	AT4G38190.1   Symbol: ATCSLD4   cellulose synthase family protein, similar to cellulose synthase catalytic subunit gi:2827143 from (Arabidopsis thaliana), cellulose synthase-5 (gi:9622882) from Zea mays   chr4:17909913-17913635 REVERSE   Aliases: CSLD4, F20D10.310, F20D10_310	5.2	5.1	0.1	0.3	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15339	AT2G39120.1   expressed protein   chr2:16328872-16330035 FORWARD   Aliases: T7F6.29, T7F6_29	3.9	4.0	-0.1	-0.3	100.0%	-5.1
15340	AT1G14950.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:294060) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:5157331-5158248 REVERSE   Aliases: F10B6.38, F10B6_38	3.5	3.4	0.1	0.3	100.0%	-5.2
15341	AT5G20540.1   expressed protein   chr5:6947845-6952040 FORWARD   Aliases: F7C8.130, F7C8_130	4.0	4.1	-0.1	-0.3	100.0%	-5.2
15342	AT4G23210.2   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:12148786-12151429 REVERSE   Aliases: F21P8.100, F21P8_100	2.8	2.7	0.1	0.3	100.0%	-5.3
15343	AT1G51800.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19217817-19221639 FORWARD   Aliases: F19C24.3, F19C24_3	3.0	3.1	-0.2	-0.3	100.0%	-4.4
15344	AT1G05670.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, similar to UDP-glucose:salicylic acid glucosyltransferase (Nicotiana tabacum) GI:7385017; contains Pfam profiles PF00201: UDP-glucuronosyl and UDP-glucosyl transferase, PF01535: PPR repeat   chr1:1698573-1702719 REVERSE   Aliases: F3F20.12, F3F20_12	2.6	2.7	-0.1	-0.3	100.0%	-5.3
15345	AT3G62270.1   anion exchange family protein, contains similarity to anion exchanger 3, cardiac splice form - Rattus norvegicus, PIR:A42497   chr3:23053259-23057023 REVERSE   Aliases: T17J13.230	3.3	3.5	-0.2	-0.3	100.0%	-4.6
15346	AT1G13130.1   glycosyl hydrolase family 5 protein / cellulase family protein   chr1:4474718-4477939 FORWARD   Aliases: F3F19.15, F3F19_15	2.6	2.5	0.1	0.3	100.0%	-5.4
15347	AT1G52070.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.4	3.5	-0.1	-0.3	100.0%	-5.3
15348	AT4G14530.1   expressed protein   chr4:8343472-8343879 REVERSE   Aliases: DL3305C, FCAALL.249	3.7	3.8	-0.1	-0.3	100.0%	-5.3
15349	AT1G03430.1   Symbol: AHP5   two-component phosphorelay mediator, putative, strong similarity to ATHP1 (Arabidopsis thaliana) GI:4156241   chr1:847874-849495 FORWARD   Aliases: F21B7.5, HISTIDINE CONTAINING PHOSPHOTRANSFER FACTOR 5	4.5	4.4	0.1	0.3	100.0%	-4.8
15350	AT3G20130.1   Symbol: CYP705A22   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr3:7026935-7028842 FORWARD   Aliases: MAL21.17	2.4	2.4	-0.1	-0.3	100.0%	-5.1
15351	AT5G18000.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr5:5959480-5961639 REVERSE   Aliases: MCM23.7, MCM23_7	3.4	3.4	0.1	0.3	100.0%	-5.2
15352	AT4G20320.1   similar to CTP synthase, putative / UTP--ammonia ligase, putative [Arabidopsis thaliana] (TAIR:At2g34890.1); similar to CTP synthase, putative / UTP--ammonia ligase, putative [Arabidopsis thaliana] (TAIR:At3g12670.1); similar to CTP synthase, putative / UTP--ammonia ligase, putative [Arabidopsis thaliana] (TAIR:At4g02120.1); similar to CTP synthase, putative / UTP--ammonia ligase, putative [Arabidopsis thaliana] (TAIR:At1g30820.1); similar to putative CTP synthase [Oryza sativa (japonica cultivar-group)] (GB:NP_917689.1); similar to putative CTP synthase [Oryza sativa (japonica cultivar-group)] (GB:NP_917309.1); similar to putative CTP synthase [Oryza sativa (japonica cultivar-group)] (GB:AAU44105.1); similar to putative CTP synthase [Oryza sativa (japonica cultivar-group)] (GB:BAD68695.1); similar to MGC81822 protein [Xenopus laevis] (GB:AAH74125.1); contains InterPro domain Glutamine amidotransferase class-I (InterPro:IPR000991); contains InterPro domain CTP synthase (InterPro:IPR004468)   chr4:10974589-10979475 FORWARD   Aliases: F1C12.230, F1C12_230	2.7	2.6	0.1	0.3	100.0%	-5.3
15353	AT5G35010.1   hypothetical protein, similar to At3g24380, At5g36840, At3g42740, At4g05290, At2g14770, At3g43390, At2g05560, At4g08880, At1g34730, At1g27790   chr5:13293901-13294593 FORWARD   Aliases: MSK10.5, MSK10_5	1.8	1.8	-0.0	-0.3	100.0%	-5.9
15354	AT1G08500.1   plastocyanin-like domain-containing protein   chr1:2689057-2690048 FORWARD   Aliases: T27G7.18, T27G7_18	3.9	3.8	0.1	0.3	100.0%	-4.3
15355	AT2G31780.1   zinc finger (C3HC4-type RING finger) family protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam:PF01485 IBR domain   chr2:13522276-13524490 FORWARD   Aliases: F20M17.18, F20M17_18	2.7	2.8	-0.1	-0.3	100.0%	-5.3
15356	AT2G32370.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to HD-Zip homeo domain OCL5 protein (GI:8920427) (Zea mays); contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain   chr2:13749485-13753363 FORWARD   Aliases: T32F6.11, T32F6_11	3.3	3.3	0.0	0.3	100.0%	-5.5
15357	AT3G20450.1   expressed protein   chr3:7130668-7131280 REVERSE   Aliases: MQC12.24	4.2	4.0	0.1	0.3	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15358	AT5G04380.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri) and to SAM:benzoic acid carboxyl methyltransferase (BAMT)(GI:9789277)(Antirrhinum majus)   chr5:1234884-1236318 FORWARD   Aliases: T19N18.110, T19N18_110	2.5	2.5	-0.0	-0.3	100.0%	-5.7
15359	AT2G25565.1   expressed protein   chr2:10891140-10892373 REVERSE   Aliases: F3N11.20	3.0	2.9	0.1	0.3	100.0%	-5.4
15360	AT1G18560.1   hAT dimerisation domain-containing protein / BED zinc finger domain-containing protein / transposase-related, weak similarity to Tam3-transposase (Antirrhinum majus) GI:16064; contains Pfam profiles PF02892: BED zinc finger, PF05699: hAT family dimerisation domain	3.5	3.6	-0.1	-0.3	100.0%	-5.1
15361	AT1G54480.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to disease resistance protein GI:3894383 from (Lycopersicon esculentum)   chr1:20351047-20352699 FORWARD   Aliases: F20D21.29, F20D21_29	2.7	2.6	0.1	0.3	100.0%	-5.5
15362	AT1G74630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:28034182-28036113 FORWARD   Aliases: F1M20.31, F1M20_31	2.9	2.9	-0.1	-0.3	100.0%	-5.2
15363	AT3G24630.1   expressed protein   chr3:8988405-8990744 FORWARD   Aliases: MSD24.1	3.1	3.2	-0.1	-0.3	100.0%	-5.2
15364	AT5G64060.1   Symbol: ANAC103   no apical meristem (NAM) family protein, similar to NAC1 (GI:7716952)	3.1	3.2	-0.1	-0.3	100.0%	-5.2
15365	AT2G19580.1   senescence-associated protein-related, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855; contains a transmembrane 4 family signature; rare (GC) splice donor consensus found instead of (GT) at intron 2.   chr2:8479216-8482173 REVERSE   Aliases: F3P11.18, F3P11_18	7.1	7.0	0.1	0.3	100.0%	-5.1
15366	AT1G01650.2   similar to protease-associated (PA) domain-containing protein [Arabidopsis thaliana] (TAIR:At1g63690.2); similar to growth-on protein GRO10 [Euphorbia esula] (GB:AAL14629.1); contains InterPro domain Presenilin signal peptide peptidase (InterPro:IPR006639); contains InterPro domain Membrane protein of unknown function DUF435 (InterPro:IPR007369)   chr1:232841-237817 REVERSE   Aliases: T1N6.3, T1N6_3	7.1	7.0	0.2	0.3	100.0%	-4.7
15367	AT2G44350.2   Symbol: ATCS   citrate synthase, mitochondrial, putative, strong similarity to SP:P20115 Citrate synthase, mitochondrial precursor {Arabidopsis thaliana}; contains Pfam profile PF00285: Citrate synthase   chr2:18323354-18328158 FORWARD   Aliases: F4I1.16	11.1	11.3	-0.2	-0.3	100.0%	-5.2
15368	AT1G69740.1   porphobilinogen synthase, putative / delta-aminolevulinic acid dehydratase, putative, similar to delta-aminolevulinic acid dehydratase (Alad) GI:493019 (SP:P43210) from Glycine max, SP:P24493 from Spinacia oleracea, SP:P30124 from Pisum sativum   chr1:26235499-26238626 FORWARD   Aliases: T6C23.6, T6C23_6	8.0	7.9	0.1	0.3	100.0%	-4.8
15369	AT5G07960.1   expressed protein, contains Pfam PF03669: Uncharacterised protein family (UPF0139)   chr5:2542247-2543460 FORWARD   Aliases: F13G24.160	6.6	6.5	0.1	0.3	100.0%	-5.0
15370	AT1G03160.1   expressed protein, similar to hypothetical protein DDB0187425 [Dictyostelium discoideum] (GB:EAL63733.1)	3.2	3.1	0.0	0.3	100.0%	-5.3
15371	NA	9.6	9.3	0.4	0.3	100.0%	-4.4
15372	AT1G12930.1   importin-related, similar to late gestation lung 2 protein (GI:7274209) {Rattus norvegicus}; similar to Ran binding protein 13 (importin 13)) (GI:8133102) {Homo sapiens}; contains weak hit to Pfam PF03810: Importin-beta N-terminal domain   chr1:4398373-4405602 REVERSE   Aliases: F13K23.18, F13K23_18	4.8	4.7	0.1	0.3	100.0%	-4.7
15373	AT5G15150.1   Symbol: ATHB 3	2.3	2.4	-0.0	-0.3	100.0%	-6.0
15374	AT3G26390.1   hypothetical protein   chr3:9664687-9665187 REVERSE   Aliases: F20C19.11	2.8	2.7	0.0	0.3	100.0%	-5.5
15375	AT5G43970.1   Symbol: TOM22 V   expressed protein   chr5:17710034-17710630 FORWARD   Aliases: ATTOM22 V, MRH10.8, MRH10_8, TOM22, TOM9 2	8.1	8.2	-0.1	-0.3	100.0%	-4.8
15376	AT3G15570.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr3:5270171-5271860 REVERSE   Aliases: MQD17.2	3.2	3.3	-0.1	-0.3	100.0%	-5.2
15377	AT5G06920.1   expressed protein   chr5:2142859-2143920 FORWARD   Aliases: MOJ9.9, MOJ9_9	3.4	3.3	0.1	0.3	100.0%	-5.3
15378	AT4G00416.1   Symbol: MBD3   methyl-CpG-binding domain-containing protein, contains Pfam profile PF01429: Methyl-CpG binding domain   chr4:179022-179513 FORWARD   Aliases: None	2.2	2.3	-0.0	-0.3	100.0%	-6.0
15379	AT4G35220.1   cyclase family protein, contains Pfam profile: PF04199 putative cyclase   chr4:16752618-16754310 FORWARD   Aliases: F23E12.220, F23E12_220	9.2	9.0	0.2	0.3	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15380	AT1G49210.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:18205626-18206339 FORWARD   Aliases: F27J15.3, F27J15_3	2.5	2.4	0.0	0.3	100.0%	-5.5
15381	AT4G28210.1   Symbol: EMB1923   expressed protein   chr4:13990626-13992084 FORWARD   Aliases: EMB1923, EMBRYO DEFECTIVE 1923, F26K10.90, F26K10_90	6.9	7.0	-0.2	-0.3	100.0%	-4.2
15382	AT5G47010.1   RNA helicase, putative, similar to type 1 RNA helicase pNORF1 (Homo sapiens) GI:1885356   chr5:19089236-19096561 FORWARD   Aliases: MQD22.15, MQD22_15	5.2	5.3	-0.1	-0.3	100.0%	-5.2
15383	AT5G20730.3   Symbol: NPH4   auxin-responsive factor (ARF7), identical to auxin response factor 7 GI:4104929 from (Arabidopsis thaliana)   chr5:7016472-7022115 REVERSE   Aliases: ARF7, AUXIN RESPONSE FACTOR 7, AUXIN REGULATED TRANSCRIPTIONAL ACTIVATOR 7, AUXIN RESPONSIVE TRANSCRIPTIONAL ACTIVATOR 7, BIP, BIPOSTO, IAA21, MASSUGU1, MSG1, NON PHOTOTROPHIC HYPOCOTYL, T1M15.130, T1M15_130, TIR5, TRANSPORT INHIBITOR RESPONSE 5	8.3	8.2	0.1	0.3	100.0%	-5.1
15384	AT3G42680.1   expressed protein   chr3:14773857-14774386 REVERSE   Aliases: T12K4.130	3.3	3.3	0.0	0.3	100.0%	-5.4
15385	AT4G15320.1   Symbol: ATCSLB06   cellulose synthase family protein, similar to Zea mays cellulose synthase-5 (gi:9622882), -2 (gi:9622876), -1 (gi:9622874)   chr4:8742639-8747981 REVERSE   Aliases: ATCSLB6, CSLB06, DL3705C, FCAALL.268	2.9	2.9	-0.1	-0.3	100.0%	-5.3
15386	AT2G45400.1   dihydroflavonol 4-reductase family / dihydrokaempferol 4-reductase family, similar to dihydroflavonol 4-reductase (SP:P51102), vestitone reductase (Medicago sativa, GI:973249)   chr2:18710903-18713319 REVERSE   Aliases: F4L23.9	4.3	4.1	0.2	0.3	100.0%	-4.3
15387	AT3G12100.2   similar to cation efflux family protein [Arabidopsis thaliana] (TAIR:At2g04620.1); similar to cation efflux protein, putative [Entamoeba histolytica HM-1:IMSS] (GB:EAL49993.1); contains InterPro domain Cation efflux protein (InterPro:IPR002524)   chr3:3854521-3857325 REVERSE   Aliases: T21B14.8	4.7	4.6	0.1	0.3	100.0%	-4.8
15388	AT3G21960.1   receptor-like protein kinase-related, contains Pfam profile: PF01657 Domain of unknown function that is usually associated with protein kinase domain Pfam:PF00069; belongs to a family which includes receptor-like kinase family proteins   chr3:7737163-7738155 FORWARD   Aliases: MZN24.11	2.7	2.7	-0.0	-0.3	100.0%	-5.5
15389	AT4G05300.1   hypothetical protein   chr4:2705668-2708156 FORWARD   Aliases: C17L7.220, C17L7_220	3.4	3.4	0.0	0.3	100.0%	-5.6
15390	AT4G10920.1   Symbol: KELP   transcriptional coactivator p15 (PC4) family protein (KELP), similar to SP:P53999 Activated RNA polymerase II transcriptional coactivator p15 (PC4) (p14) {Homo sapiens}; contains Pfam profile PF02229: Transcriptional Coactivator p15 (PC4); supporting cDNA gi:2997685:gb:AF053303.1:AF053303   chr4:6697672-6699189 REVERSE   Aliases: F25I24.130, F25I24_130	5.5	5.7	-0.1	-0.3	100.0%	-4.6
15391	AT2G34400.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:14523317-14525265 FORWARD   Aliases: F13P17.24	4.3	4.2	0.1	0.3	100.0%	-5.0
15392	AT3G59120.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.9	-0.1	-0.3	100.0%	-5.0
15393	AT4G01070.1   the glycosyltransferase (UGT72B1) is involved in metabolizing xenobiotica (chloroaniline and chlorophenole). Comparison between wild type and knock-out mutant demonstrates the central role of this gene for metabolizing chloroaniline but significantly less for chlorophenole. The glucosyltransferase preferred UDP-xylose over UDP-glucose indicating its (additional) functioning as a xylosyltransferase in planta   chr4:461592-463449 REVERSE   Aliases: F2N1.15, F2N1_15, GT72B1	5.1	5.3	-0.2	-0.3	100.0%	-4.6
15394	AT5G03520.2   similar to Ras-related GTP-binding protein, putative [Arabidopsis thaliana] (TAIR:At3g09900.1); similar to ras-related protein RAB8-3 [Nicotiana tabacum] (GB:BA84324.1); similar to small GTP-binding protein [Daucus carota] (GB:CAA04701.1); similar to small GTP-binding protein [Pisum sativum] (GB:CAA90081.1); contains InterPro domain Small GTP-binding protein domain (InterPro:IPR005225); contains InterPro domain Ras small GTPase, Rab type (InterPro:IPR003579); contains InterPro domain Ras small GTPase, Rho type (InterPro:IPR003578); contains InterPro domain Ras small GTPase, Ras type (InterPro:IPR003577); contains InterPro domain Ras GTPase superfamily (InterPro:IPR001806); contains InterPro domain GTP-binding nuclear protein Ran (InterPro:IPR002041)	8.1	7.9	0.2	0.3	100.0%	-4.8
15395	AT5G46440.1   expressed protein   chr5:18851870-18852380 FORWARD   Aliases: K11I1.3, K11I1_3	3.1	3.0	0.1	0.3	100.0%	-5.5
15396	AT3G26760.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to sex determination protein tasselseed 2 SP:P50160 from (Zea mays)   chr3:9844828-9846413 FORWARD   Aliases: MDJ14.5	4.4	4.3	0.1	0.3	100.0%	-4.9
15397	AT4G10760.1   Symbol: EMB1706   methyltransferase MT-A70, putative, similar to (N6-adenosine)-methyltransferase (Mus musculus) GI:10179948, m6A methyltransferase (MT-A70) (Homo sapiens) GI:2460037; contains Pfam profile PF05063: MT-A70 (S-adenosylmethionine-binding subunit of human mRNA:m6A methyltransferase (MTase))   chr4:6619480-6623347 REVERSE   Aliases: EMB1706, EMBRYO DEFECTIVE 1706, T12H20.6, T12H20_6	8.3	8.1	0.2	0.3	100.0%	-4.4
15398	AT2G47660.1   expressed protein   chr2:19550022-19550230 FORWARD   Aliases: F17A22.5	3.0	3.0	0.1	0.3	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15399	AT2G26180.1   calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr2:11150511-11152175 REVERSE   Aliases: T1D16.18, T1D16_18	3.2	3.3	-0.1	-0.3	100.0%	-5.0
15400	AT4G35260.1   Symbol: IDH1   isocitrate dehydrogenase subunit 1 / NAD+ isocitrate dehydrogenase subunit 1, nearly identical to NAD+ dependent isocitrate dehydrogenase subunit 1 (Arabidopsis thaliana) GI:1766046   chr4:16774200-16776330 REVERSE   Aliases: F23E12.180, F23E12_180, ISOCITRATE DEHYDROGENASE 1, NAD+ DEPENDENT ISOCITRATE DEHYDROGENASE SUBUNIT 1	8.5	8.3	0.2	0.3	100.0%	-5.0
15401	AT2G17440.1   leucine-rich repeat family protein, contains Pfam PF00560: Leucine Rich Repeats   chr2:7578222-7580838 FORWARD   Aliases: F5J6.20, F5J6_20	3.9	4.0	-0.1	-0.3	100.0%	-4.7
15402	AT4G18960.1   Symbol: AG   floral homeotic protein AGAMOUS (AG), contains an ACG start codon (Riechmann, Ito, and Meyerowitz, Mol Cell Biol, 1999); supported by cDNA gi:16155:emb:X53579   chr4:10382867-10388550 FORWARD   Aliases: AGAMOUS, AGAMOUS PROTEIN, F13C5.130, F13C5_130	3.2	3.3	-0.0	-0.3	100.0%	-5.5
15403	AT1G75430.1   homeodomain-containing protein, contains 'Homeobox' domain signature, Prosite:PS00027   chr1:28311782-28313178 REVERSE   Aliases: F1B16.4, F1B16_4	2.5	2.6	-0.0	-0.3	100.0%	-5.5
15404	AT5G09630.1   expressed protein   chr5:2985871-2987653 REVERSE   Aliases: F17I14.180, F17I14_180	4.6	4.6	-0.1	-0.3	100.0%	-5.2
15405	AT4G19030.1   Symbol: NLM1   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230; identical to cDNA NLM1 protein GI:2677613   chr4:10421543-10423498 REVERSE   Aliases: AT NLM1, F13C5.200, F13C5_200	2.6	2.6	-0.0	-0.3	100.0%	-5.4
15406	AT1G11300.1   S-locus lectin protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:3794389-3800719 FORWARD   Aliases: T28P6.6, T28P6_6	2.6	2.6	-0.0	-0.3	100.0%	-5.4
15407	AT1G17420.1   Symbol: LOX3   lipoxygenase, putative, similar to lipoxygenase gi:1495804 (Solanum tuberosum), gi:1654140 (Lycopersicon esculentum)   chr1:5977404-5981473 FORWARD   Aliases: F28G4.10	3.2	3.1	0.1	0.3	100.0%	-4.9
15408	AT2G14140.1   hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At3g30450, At4g03990, At5g34895, At3g47270, At2g02200   chr2:5974260-5978569 FORWARD   Aliases: T22C12.7, T22C12_7	2.0	1.9	0.1	0.3	100.0%	-6.1
15409	AT5G45200.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18301194-18307559 REVERSE   Aliases: K18C1.8, K18C1_8	2.3	2.3	-0.0	-0.3	100.0%	-5.7
15410	AT3G15370.1   Symbol: ATEXPA12   expansin, putative (EXP12), similar to expansin GI:11191999 from (Lycopersicon esculentum); alpha-expansin gene family, PMID:11641069   chr3:5190579-5191989 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN 12, ATEXP12, ATHEXP ALPHA 1.24, EXP12, MJK13.3	3.8	3.8	0.1	0.3	100.0%	-5.5
15411	AT1G19430.1   dehydration-responsive protein-related, low similarity to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr1:6724564-6728031 REVERSE   Aliases: F18O14.20, F18O14_20	5.3	5.4	-0.1	-0.3	100.0%	-4.8
15412	AT2G41460.1   Symbol: ARP   apurinic endonuclease-redox protein / DNA-(apurinic or apyrimidinic site) lyase, identical to apurinic endonuclease-redox protein SP: P45951 from (Arabidopsis thaliana)   chr2:17292809-17296006 FORWARD   Aliases: T26J13.5, T26J13_5	6.9	7.0	-0.1	-0.3	100.0%	-4.8
15413	AT1G32610.2   similar to VQ motif-containing protein [Arabidopsis thaliana] (TAIR:At2g35230.1); similar to AGR285Wp [Ashbya gossypii ATCC 10895] (GB:AAS54775.1); similar to Wal1 protein [Eremothecium gossypii] (GB:AAN28957.1)   chr1:11795679-11797120 REVERSE   Aliases: F6N18.2, F6N18_2	2.9	2.9	0.1	0.3	100.0%	-5.1
15414	AT5G67050.1   lipase class 3 family protein, similar to lipase precursor (Rhizopus arrhizus) GI:6942320; contains Pfam profile PF01764: Lipase	3.0	3.1	-0.1	-0.3	100.0%	-5.1
15415	AT3G30440.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr3:12080396-12084354 FORWARD   Aliases: MSJ3.5	2.3	2.3	0.0	0.3	100.0%	-6.0
15416	AT1G51160.2   similar to synbindin, putative [Arabidopsis thaliana] (TAIR:At5g02280.1); similar to putative trafficking protein particle complex 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD73086.1); contains InterPro domain Sybindin-like protein (InterPro:IPR007233)   chr1:18953259-18955431 FORWARD   Aliases: F23H24.18, F23H24_18	7.8	7.9	-0.1	-0.3	100.0%	-4.9
15417	AT5G45320.1   expressed protein, ; expression supported by MPSS   chr5:18379581-18380280 REVERSE   Aliases: K9E15.10, K9E15_10	2.7	2.8	-0.1	-0.3	100.0%	-5.3
15418	AT4G11330.1   Symbol: ATMPK5	4.7	4.5	0.1	0.3	100.0%	-4.8
15419	AT4G16880.1   disease resistance protein-related, contains weak similarity to disease resistance protein RPP4 (Arabidopsis thaliana) gi:20270890:gb:AAM18462   chr4:9496206-9498945 REVERSE   Aliases: DL4470C, FCAALL.50	2.5	2.6	-0.1	-0.3	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15420	AT5G57390.1   similar to ovule development protein, putative [Arabidopsis thaliana] (TAIR:At1g51190.1); similar to OSJNBb0022F16.3 [Oryza sativa (japonica cultivar-group)] (GB:XP_474162.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr5:23270685-23273676 REVERSE   Aliases: MSF19.5, MSF19_5	5.1	5.0	0.1	0.3	100.0%	-4.6
15421	AT1G17890.3   GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase, putative, similar to GDP-4-keto-6-deoxy-D-mannose-3,5-epimerase-4-reductase (GER1)GI:6016479 from (Arabidopsis thaliana)	6.3	6.4	-0.1	-0.3	100.0%	-5.0
15422	AT1G27160.1   valyl-tRNA synthetase / valine--tRNA ligase-related, similar to valyl tRNA synthetase GI:1890130 from (Arabidopsis thaliana)   chr1:9432405-9433177 FORWARD   Aliases: T7N9.22, T7N9_22	2.9	3.0	-0.1	-0.3	100.0%	-5.2
15423	AT4G29630.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase 3 (CDA3) (Arabidopsis thaliana) GI:3818577, cytidine deaminase homolog DesF (Arabidopsis thaliana) GI:4836448; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14522575-14523246 FORWARD   Aliases: T16L4.140, T16L4_140	2.8	2.8	0.1	0.3	100.0%	-5.3
15424	AT2G21070.2   expressed protein, similar to hypothetical protein DDB0203108 [Dictyostelium discoideum] (GB:EAL69882.1)	3.4	3.5	-0.1	-0.3	100.0%	-5.3
15425	AT3G19390.1   cysteine proteinase, putative / thiol protease, putative, contains similarity to cysteine proteinase RD21A (thiol protease) GI:435619, SP:P43297 from (Arabidopsis thaliana)   chr3:6722995-6724957 FORWARD   Aliases: MLD14.3	6.0	5.9	0.1	0.3	100.0%	-4.7
15426	AT5G64150.1   methylase family protein, contains TIGRfam TIGR00536: modification methylase, HemK family   chr5:25686057-25688444 REVERSE   Aliases: MHJ24.13, MHJ24_13	4.9	4.8	0.1	0.3	100.0%	-5.0
15427	AT4G12720.3   MutT/nudix family protein, similar to SP:P53370 Nucleoside diphosphate-linked moiety X motif 6 {Homo sapiens}; contains Pfam profile PF00293: NUDIX domain   chr4:7487540-7490073 FORWARD   Aliases: T20K18.70, T20K18_70	9.0	8.9	0.0	0.3	100.0%	-5.6
15428	AT1G51100.1   expressed protein   chr1:18937976-18938812 FORWARD   Aliases: F23H24.6, F23H24_6	2.6	2.7	-0.1	-0.3	100.0%	-5.5
15429	AT3G19516.1   expressed protein   chr3:6770167-6771084 REVERSE   Aliases: T31J18.1	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15430	AT3G15170.1   Symbol: CUC1   cup-shaped cotyledon1 protein / CUC1 protein (CUC1), identical to CUP-SHAPED COTYLEDON1 (CUC1) (GI:12060422) (Arabidopsis thaliana)   chr3:5109903-5111454 FORWARD   Aliases: ANAC054, CUP SHAPED COTYLEDON1, F4B12.8	3.0	3.0	0.0	0.3	100.0%	-5.7
15431	AT4G28010.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:13930365-13933276 FORWARD   Aliases: T13J8.120, T13J8_120	2.8	2.8	-0.0	-0.3	100.0%	-5.6
15432	AT2G31010.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:13201288-13207205 FORWARD   Aliases: F7F1.22, F7F1_22	3.3	3.2	0.1	0.3	100.0%	-5.3
15433	AT3G14190.1   expressed protein   chr3:4710490-4711976 FORWARD   Aliases: MAG2.18	8.4	8.3	0.1	0.3	100.0%	-4.6
15434	AT4G21310.1   expressed protein, predicted protein, Arabidopsis thaliana   chr4:11339058-11340080 REVERSE   Aliases: T6K22.40, T6K22_40	4.2	4.1	0.1	0.3	100.0%	-4.7
15435	AT5G10220.1   Symbol: ANN6   annexin 6 (ANN6), nearly identical to calcium-binding protein annexin 6 (Arabidopsis thaliana) GI:12667518   chr5:3206876-3208808 REVERSE   Aliases: F18D22.3, annexin 6	2.8	2.7	0.0	0.3	100.0%	-5.5
15436	AT3G18460.1   expressed protein, similar to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr3:6333054-6333954 REVERSE   Aliases: MYF24.18	2.6	2.5	0.1	0.3	100.0%	-5.5
15437	AT3G09960.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	3.5	3.6	-0.1	-0.3	100.0%	-4.6
15438	AT3G46200.1   MutT/nudix family protein, similar to head organizer protein P17F11 GI:17976973 from (Xenopus laevis); contains a NUDIX hydrolase domain IPR000086   chr3:16980251-16982189 FORWARD   Aliases: F12M12.170	5.9	5.9	0.1	0.3	100.0%	-5.1
15439	AT4G27140.1   2S seed storage protein 1 / 2S albumin storage protein / NWMU1-2S albumin 1, identical to SP:P15457   chr4:13607335-13608037 FORWARD   Aliases: T24A18.90, T24A18_90	2.7	2.7	-0.0	-0.3	100.0%	-5.7
15440	AT4G24580.1   pleckstrin homology (PH) domain-containing protein-related / RhoGAP domain-containing protein, contains Pfam domain, PF00620: RhoGAP domain   chr4:12687889-12694258 REVERSE   Aliases: F22K18.220, F22K18_220	2.8	2.8	0.1	0.3	100.0%	-5.0
15441	AT1G74090.1   sulfotransferase family protein, similar to SP:P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) {Flaveria chloraefolia}; contains Pfam profile PF00685: Sulfotransferase domain   chr1:27866570-27867854 FORWARD   Aliases: F2P9.4, F2P9_4	9.7	9.6	0.1	0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15442	AT5G11800.1   Symbol: KEA6   K+ efflux antiporter, putative (KEA6), Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563; similar to glutathione-regulated potassium-efflux system protein KEFB, Escherichia coli, SWISSPROT:P45522   chr5:3803337-3808197 REVERSE   Aliases: ATKEA6, T22P22.190, T22P22_190	5.5	5.5	-0.1	-0.3	100.0%	-4.9
15443	AT4G37340.1   Symbol: CYP81D3   cytochrome P450 family protein, Similar to Cytochrome P450 91A1 (SP:Q9FG65) (Arabidopsis thaliana);   chr4:17564845-17566719 REVERSE   Aliases: F6G17.1	2.8	2.8	0.1	0.3	100.0%	-4.8
15444	AT3G06630.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain, PF00989 PAS domain, and PF00785 PAC motif   chr3:2070394-2073797 REVERSE   Aliases: T8E24.13, T8E24_13	2.6	2.5	0.0	0.3	100.0%	-6.3
15445	AT3G17230.1   invertase/pectin methylesterase inhibitor family protein, similar to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr3:5886387-5889242 REVERSE   Aliases: MGD8.6	2.8	2.9	-0.1	-0.3	100.0%	-5.2
15446	AT2G22640.1   Symbol: BRK1   Component of the WAVE protein complex which act as activators of ARP2/3 complex involved in actin nucleation. Required for trichome morphogenesis.   chr2:9630148-9631298 FORWARD   Aliases: BRICK1, HSPC300, T9I22.8, T9I22_8	8.4	8.3	0.2	0.3	100.0%	-4.8
15447	AT4G36050.2   similar to apurinic endonuclease-redox protein / DNA-(apurinic or apyrimidinic site) lyase [Arabidopsis thaliana] (TAIR:At2g41460.1); similar to Hypothetical protein MGC55889 [Danio rerio] (GB:AAH44527.1); contains InterPro domain Endonuclease/exonuclease/phosphatase family (InterPro:IPR005135); contains InterPro domain Exodeoxyribonuclease III xth (InterPro:IPR004808)   chr4:17051985-17055062 REVERSE   Aliases: T19K4.180, T19K4_180	5.1	5.2	-0.1	-0.3	100.0%	-4.8
15448	AT3G29150.1   expressed protein   chr3:11108985-11115588 REVERSE   Aliases: MXE2.13	2.9	3.0	-0.1	-0.3	100.0%	-5.2
15449	AT2G29390.3   Symbol: SMO2 1	6.8	6.6	0.2	0.3	100.0%	-4.7
15450	AT3G28930.1   Symbol: AIG2   avrRpt2-induced AIG2 protein (AIG2), identical to SP:P54121 AIG2 protein (avrRpt2-induced gene) {Arabidopsis thaliana}   chr3:10960944-10961991 REVERSE   Aliases: AIG2, AVRRPT2 INDUCED GENE 2, K5K13.3	4.2	4.1	0.1	0.3	100.0%	-4.5
15451	AT5G54930.2   similar to AT hook motif-containing protein [Arabidopsis thaliana] (TAIR:At5g52890.1); contains InterPro domain HMG-I and HMG-Y DNA-binding domain (A+T-hook) (InterPro:IPR000637)   chr5:22322959-22324787 REVERSE   Aliases: MBG8.20, MBG8_20	7.6	7.7	-0.1	-0.3	100.0%	-4.7
15452	AT5G38500.1   hypothetical protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)	2.3	2.3	-0.0	-0.3	100.0%	-5.8
15453	AT1G61390.1   S-locus protein kinase, putative, contains protein kinase domain, Pfam:PF00069; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22654003-22657304 REVERSE   Aliases: T1F9.12, T1F9_12	2.5	2.4	0.0	0.3	100.0%	-5.9
15454	AT3G10870.1   hydrolase, alpha/beta fold family protein, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, SP:Q43360 PIR7B protein {Oryza sativa}; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr3:3401083-3402677 REVERSE   Aliases: T7M13.5	3.6	3.5	0.1	0.3	100.0%	-5.3
15455	AT1G30380.1   photosystem I reaction center subunit psaK, chloroplast, putative / photosystem I subunit X, putative / PSI-K, putative (PSAK), identical to SP:Q9SUI5; strong similarity to SP:P36886 Photosystem I reaction center subunit psaK, chloroplast precursor (Photosystem I subunit X) (PSI-K) (Light-harvesting complex I 7 kDa protein){Hordeum vulgare}; contains Pfam profile PF01241: Photosystem I psaG / psaK	9.1	9.0	0.1	0.3	100.0%	-4.7
15456	AT2G22810.1   Symbol: ACS4   1-aminocyclopropane-1-carboxylate synthase 4 / ACC synthase 4 (ACS4), identical to gi:940370 (GB:U23481)   chr2:9724871-9726552 REVERSE   Aliases: 1 AMINOCYCLOPROPANE 1 CARBOXYLATE SYNTHASE, 1 AMINOCYCLOPROPANE 1 CARBOXYLATE SYNTHASE 4, ACC4, T30L20.7	4.3	4.4	-0.1	-0.3	100.0%	-4.5
15457	AT4G18000.1   expressed protein   chr4:9989765-9990148 REVERSE   Aliases: T6K21.180, T6K21_180	3.3	3.4	-0.1	-0.3	100.0%	-5.1
15458	AT2G06090.1   self-incompatibility protein-related, similar to S1 self-incompatibility protein (Papaver rhoeas) GI:452430   chr2:2371604-2372011 REVERSE   Aliases: F5K7.15, F5K7_15	2.6	2.6	0.1	0.3	100.0%	-5.4
15459	AT4G18510.1   Symbol: CLE2   Clavata3 / ESR-Related-2 (CLE2), CLAVATA3/ESR-Related-2 (CLE2)   chr4:10211880-10212412 FORWARD   Aliases: CLAVATA3/ESR RELATED, F28J12.170, F28J12_170	2.8	2.9	-0.1	-0.3	100.0%	-4.4
15460	AT5G56700.1   F-box protein-related, contains a partial F-box domain Pfam:PF00646   chr5:22959020-22960604 FORWARD   Aliases: MIK19.15, MIK19_15	2.8	2.7	0.1	0.3	100.0%	-5.4
15461	AT5G04950.1   nicotianamine synthase, putative, similar to nicotianamine synthase (Lycopersicon esculentum)(GI:4753801), nicotianamine synthase 2 (Hordeum vulgare)(GI:4894912)   chr5:1457646-1458891 REVERSE   Aliases: MUG13.19, MUG13_19	3.0	3.2	-0.2	-0.3	100.0%	-4.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15462	AT3G49460.1   60S acidic ribosomal protein-related, contains weak similarity to Swiss-Prot:52855 60S acidic ribosomal protein P1 (L12) (Zea mays)   chr3:18351336-18351601 REVERSE   Aliases: T9C5.60	2.4	2.4	-0.0	-0.3	100.0%	-5.5
15463	AT1G08270.2   expressed protein, low similarity to SP:P46467 SKD1 protein (Vacuolar sorting protein 4b) {Mus musculus}	3.8	3.9	-0.0	-0.3	100.0%	-5.5
15464	AT5G46850.1   expressed protein, ; expression supported by MPSS   chr5:19027941-19029237 FORWARD   Aliases: MSD23.3, MSD23_3	4.8	4.7	0.1	0.3	100.0%	-4.9
15465	AT1G12830.1   expressed protein   chr1:4374248-4375168 REVERSE   Aliases: F13K23.8, F13K23_8	7.4	7.5	-0.2	-0.3	100.0%	-4.6
15466	AT2G15535.1   Symbol: LCR10   SLR1 binding pollen coat protein-related, contains weak similarity to SLR1 binding pollen coat protein (Brassica juncea) gi:7649936:dbj:BAA94096   chr2:6785277-6785935 FORWARD   Aliases: LCR10, Low molecular weight cysteine rich 10	2.5	2.5	-0.0	-0.3	100.0%	-5.6
15467	AT4G21750.2   Symbol: ATML1   similar to anthocyaninless2 (ANL2) [Arabidopsis thaliana] (TAIR:At4g00730.1); similar to homeobox-leucine zipper family protein / lipid-binding START domain-containing protein [Arabidopsis thaliana] (TAIR:At1g05230.1); similar to homeobox-leucine zipper protein protodermal factor 2 (PDF2) [Arabidopsis thaliana] (TAIR:At4g04890.1); similar to homeobox-leucine zipper family protein / lipid-binding START domain-containing protein [Arabidopsis thaliana] (TAIR:At1g05230.2); similar to homeobox-leucine zipper family protein / homeodomain GLABRA2 like protein 1 (HD-GL2-1) [Arabidopsis thaliana] (TAIR:At3g61150.1); similar to homeobox protein (GB:AAB37230.1); similar to OSJNBb0060E08.16 [Oryza sativa (japonica cultivar-group)] (GB:XP_473974.1); similar to GL2-type homeodomain protein [Oryza sativa (japonica cultivar-group)] (GB:BAC77155.1); similar to homeobox 1 [Picea abies] (GB:AAG43405.1); similar to roc1(homeobox protein) [Oryza sativa (japonica cultivar-group)] (GB:XP_480435.1); contains InterPro domain Homeobox (InterPro:IPR001356); contains InterPro domain Lipid-binding START (InterPro:IPR002913)   chr4:11555199-11560745 FORWARD   Aliases: F17L22.210, F17L22_210, MERISTEM LAYER 1	4.2	4.1	0.1	0.3	100.0%	-5.2
15468	AT5G01490.1   Symbol: CAX4   cation exchanger, putative (CAX4), identical to cation/proton antiporter (Arabidopsis thaliana) gi:15426028:gb:AAK97656; similar to high affinity calcium antiporter CAX1 (Arabidopsis thaliana) gi:9256741:gb:AAB05913; Ca <sup>2+</sup> :Cation Antiporter (CaCA) Family member PMID:11500563   chr5:195588-198523 FORWARD   Aliases: ATCAX4, F7A7.10, F7A7_10	4.0	4.1	-0.1	-0.3	100.0%	-4.5
15469	AT1G71030.1   Symbol: ATMYBL2   Encodes a putative myb family transcription factor. In contrast to most other myb-like proteins its myb domain consists of a single repeat. A proline-rich region potentially involved in transactivation is found in the C-terminal part of the protein. Its transcript accumulates mainly in leaves.   chr1:26798785-26800026 REVERSE   Aliases: ATMYBL2, F23N20.2, F23N20_2	2.8	2.7	0.0	0.3	100.0%	-5.7
15470	AT3G50860.1   clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	3.6	3.8	-0.1	-0.3	100.0%	-4.9
15471	AT5G63120.2   ethylene-responsive DEAD box RNA helicase, putative (RH30), strong similarity to ethylene-responsive RNA helicase (Lycopersicon esculentum) GI:5669638; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr5:25335978-25339491 REVERSE   Aliases: MDC12.8, MDC12_8	2.9	2.8	0.0	0.3	100.0%	-5.4
15472	AT5G20340.1   Symbol: BG5   beta-1,3-glucanase (BG5), identical to plant beta-1,3-glucanase bg5 GI:2808439 (Arabidopsis thaliana)   chr5:6874789-6875853 FORWARD   Aliases: BETA 1,3 GLUCANASE 5, F5O24.230, F5O24_230	2.0	2.1	-0.0	-0.3	100.0%	-5.9
15473	AT1G30850.1   expressed protein   chr1:10985097-10985999 FORWARD   Aliases: T17H7.17, T17H7_17	2.6	2.6	0.1	0.3	100.0%	-4.7
15474	AT3G33073.1   expressed protein   chr3:13652020-13652925 REVERSE   Aliases: T25F15.5	3.6	3.5	0.1	0.3	100.0%	-4.9
15475	AT1G76010.1   expressed protein   chr1:28531744-28534427 REVERSE   Aliases: T4O12.22, T4O12_22	6.7	6.8	-0.2	-0.3	100.0%	-4.8
15476	AT5G63050.1   Symbol: EMB2759   expressed protein   chr5:25309661-25312221 FORWARD   Aliases: EMB2759, EMBRYO DEFECTIVE 2759, MDC12.1, MDC12_1	4.2	4.3	-0.1	-0.3	100.0%	-5.0
15477	AT2G20360.1   expressed protein   chr2:8793096-8796554 FORWARD   Aliases: F11A3.9, F11A3_9	9.3	9.6	-0.3	-0.3	100.0%	-4.5
15478	AT4G15030.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g56660.1); similar to chromosome 10 open reading frame 4 [Homo sapiens] (GB:CAH73836.1); similar to C10orf4 protein [Homo sapiens] (GB:AAH18007.1); similar to FRA10AC1 protein [Homo sapiens] (GB:CAD24470.1)   chr4:8578972-8581326 FORWARD   Aliases: DL3556W, FCAALL.175	5.2	5.0	0.2	0.3	100.0%	-4.6
15479	AT4G09580.1   expressed protein   chr4:6052349-6054382 REVERSE   Aliases: T25P22.20, T25P22_20	3.0	3.0	-0.0	-0.3	100.0%	-5.4
15480	AT3G26630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr3:9792608-9794222 REVERSE   Aliases: MLJ15.2	3.6	3.5	0.1	0.3	100.0%	-5.2
15481	AT4G37220.1   stress-responsive protein, putative, similar to cold acclimation WCOR413-like protein gamma form (Hordeum vulgare) gi:18449100:gb:AAL69988; similar to stress-regulated protein SAP1 (Xerophyta viscosa) gi:21360378:gb:AAM47505	3.8	3.9	-0.1	-0.3	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15482	AT2G30000.1   expressed protein, contains Pfam domain PF03660: Uncharacterised protein family (UPF0123)   chr2:12810932-12812054 REVERSE   Aliases: F23F1.8, F23F1_8	10.9	10.9	-0.1	-0.3	100.0%	-5.2
15483	AT3G54590.1   Symbol: ATHRGP1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965	2.9	3.1	-0.2	-0.3	100.0%	-4.1
15484	AT2G20595.1   expressed protein   chr2:8878632-8879142 REVERSE   Aliases: None	3.4	3.5	-0.1	-0.3	100.0%	-5.2
15485	AT3G45230.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; related to vegetative cell wall protein gp1 (Chlamydomonas reinhardtii) gi:12018147:gb:AAG45420   chr3:16580036-16580812 FORWARD   Aliases: T14D3.170	5.8	5.8	0.1	0.3	100.0%	-4.8
15486	AT1G26760.1   SET domain-containing protein, contains Pfam profiles PF00856: SET domain, PF00515: tetratricopeptide repeat (TPR) domain   chr1:9248291-9251590 REVERSE   Aliases: T24P13.14, T24P13_14	4.3	4.2	0.1	0.3	100.0%	-5.1
15487	AT3G57790.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to SP:P15922 Exo-poly-alpha-D-galacturonosidase precursor (EC 3.2.1.82) (Exo-PG) {Erwinia chrysanthemi}; contains PF00295: Glycosyl hydrolases family 28   chr3:21416364-21418065 REVERSE   Aliases: F15B8.20	5.7	5.6	0.1	0.3	100.0%	-4.5
15488	AT3G17060.1   pectinesterase family protein, similar to pectinesterase GB:AAB57669 (Citrus sinensis); contains Pfam profile: PF01095 pectinesterase   chr3:5816683-5818504 REVERSE   Aliases: K14A17.1	2.9	2.8	0.1	0.3	100.0%	-5.2
15489	AT5G55530.3   C2 domain-containing protein, low similarity to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain   chr5:22510660-22513182 FORWARD   Aliases: MTE17.25, MTE17_25	7.6	7.4	0.2	0.3	100.0%	-4.7
15490	AT5G35730.1   EXS family protein / ERD1/XPR1/SYG1 family protein, low similarity to xenotropic and polytropic murine leukemia virus receptor (Mus spretus) GI:6093318; contains Pfam profile PF03124: EXS family   chr5:13910937-13914204 FORWARD   Aliases: MXH1.10, MXH1_10	5.4	5.5	-0.1	-0.3	100.0%	-4.9
15491	AT3G33064.1   hypothetical protein   chr3:13623922-13624638 FORWARD   Aliases: T25F15.11	2.4	2.4	0.0	0.3	100.0%	-5.3
15492	AT4G22070.1   Symbol: WRKY31	2.0	2.0	0.0	0.3	100.0%	-5.2
15493	AT4G35440.1   Symbol: CLC E   voltage-gated chloride channel family protein, contains Pfam profile PF00654: Voltage gated chloride channel   chr4:16835991-16839380 REVERSE   Aliases: ATCLC E, CHLORIDE CHANNEL E, F15J1.10, F15J1_10	2.7	2.7	-0.0	-0.3	100.0%	-5.4
15494	AT5G51520.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Lycopersicon esculentum SP:Q43143, Arabidopsis thaliana SP:Q42534; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:20943206-20943820 FORWARD   Aliases: K17N15.7, K17N15_7	2.2	2.1	0.0	0.3	100.0%	-5.9
15495	AT1G65445.1   transferase-related, similar to N-hydroxycinnamoyl/benzoyltransferase (GI:6469032) (Ipomoea batatas);similar to hydroxycinnamoyl transferase (GI:27475616) (Nicotiana tabacum)   chr1:24319477-24320415 FORWARD   Aliases: None	3.1	3.2	-0.1	-0.3	100.0%	-5.4
15496	AT5G39860.1   bHLH protein, putative DNA-binding protein - Arabidopsis thaliana, EMBL:AC011765	2.4	2.4	-0.0	-0.3	100.0%	-5.5
15497	AT4G34820.1   expressed protein   chr4:16599610-16602044 REVERSE   Aliases: F11I11.60, F11I11_60	3.9	4.0	-0.1	-0.3	100.0%	-4.6
15498	AT5G27410.1   aminotransferase class IV family protein, contains Pfam profile: PF01063 aminotransferase class IV   chr5:9678795-9682943 FORWARD   Aliases: F21A20.120, F21A20_120	4.4	4.5	-0.1	-0.3	100.0%	-4.9
15499	AT5G23680.1   sterile alpha motif (SAM) domain-containing protein, contains Pfam profile PF00536: SAM domain (Sterile alpha motif)   chr5:7984957-7986854 REVERSE   Aliases: MQM1.5, MQM1_5	5.4	5.7	-0.3	-0.3	100.0%	-4.7
15500	AT1G77180.2   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At2g16940.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At5g67320.1); similar to GAMYB-binding protein [Hordeum vulgare subsp. vulgare] (GB:AAO25542.1); contains InterPro domain SKIP/SNW domain (InterPro:IPR004015)   chr1:29004502-29007019 REVERSE   Aliases: T14N5.5, T14N5_5	9.2	9.1	0.1	0.3	100.0%	-5.1
15501	AT1G20880.1   RNA recognition motif (RRM)-containing protein, similar to RRM-containing protein SEB-4 (Xenopus laevis) GI:8895698; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); is the location of EST 197B1T7 , gb:AA597386   chr1:7262032-7265427 REVERSE   Aliases: F9H16.14, F9H16_14	2.9	2.8	0.1	0.3	100.0%	-5.0
15502	ATCG00220.1   Symbol: PSBM   PSII low MW protein   chrC:28707-28811 REVERSE   Aliases: PSBM	10.3	10.6	-0.2	-0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15503	AT1G26400.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:9133278-9134861 REVERSE   Aliases: T1K7.22, T1K7_22	2.8	2.9	-0.0	-0.3	100.0%	-5.8
15504	AT4G08340.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr4:5264212-5271145 REVERSE   Aliases: T28D5.30, T28D5_30	2.2	2.2	-0.0	-0.3	100.0%	-5.8
15505	AT2G22970.2   Symbol: SCPL11	2.8	2.8	-0.0	-0.3	100.0%	-5.7
15506	AT4G10440.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) Gl:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr4:6459724-6461928 REVERSE   Aliases: F7L13.20, F7L13_20	3.1	3.1	-0.1	-0.3	100.0%	-5.1
15507	AT1G03030.1   phosphoribulokinase/uridine kinase family protein, contains Pfam PF00485: Phosphoribulokinase / Uridine kinase family; Belongs to Interpro IPR006083 Phosphoribulokinase/uridine kinase family; similar to Uridine kinase (Uridine monophosphokinase) (SP:P27515) {Saccharomyces cerevisiae}; ESTs gb:AA585719, gb:AA728503 and gb:T22272 come from this gene   chr1:701489-703864 FORWARD   Aliases: F1003.15, F1003_15	6.8	6.6	0.2	0.3	100.0%	-4.7
15508	AT4G16060.1   expressed protein   chr4:9094437-9096293 FORWARD   Aliases: DL4070W, FCAALL.269	8.1	8.2	-0.1	-0.3	100.0%	-4.7
15509	AT1G13370.1   histone H3, putative, strong similarity to Histone H3.2, minor Medicago sativa SP:P11105, histone H3 Rubus idaeus Gl:10732809; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:4587777-4588610 REVERSE   Aliases: T6J4.12, T6J4_12	4.1	3.9	0.2	0.3	100.0%	-4.5
15510	AT5G25170.1   expressed protein   chr5:8693187-8695098 FORWARD   Aliases: F21J6.101, F21J6_101	5.9	5.8	0.1	0.3	100.0%	-4.9
15511	AT3G51490.1   sugar transporter family protein, similar to D-xylose proton-symporter (Lactobacillus brevis) Gl:2895856; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:19115997-19118541 REVERSE   Aliases: F26O13.130	3.2	3.3	-0.1	-0.3	100.0%	-5.1
15512	AT2G29300.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12595274-12596616 FORWARD   Aliases: F16P2.32, F16P2_32	3.0	3.1	-0.1	-0.3	100.0%	-5.2
15513	AT1G75360.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g27670.1)   chr1:28278249-28279651 FORWARD   Aliases: F1B16.16, F1B16_16	3.6	3.7	-0.1	-0.3	100.0%	-5.4
15514	AT4G14160.3   transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens)   chr4:8167421-8173363 FORWARD   Aliases: DL3120W, FCAALL.112	4.4	4.5	-0.1	-0.3	100.0%	-5.0
15515	AT1G50650.1   stigma-specific Stig1 family protein, low similarity to stigma-specific protein STIG1 (Nicotiana tabacum) Gl:496647; contains Pfam profile PF04885: Stigma-specific protein, Stig1   chr1:18767441-18767965 REVERSE   Aliases: F11F12.3, F11F12_3	3.0	3.1	-0.0	-0.3	100.0%	-5.3
15516	AT2G42920.1   pentatricopeptide (PPR) repeat-containing protein, and genefinder   chr2:17865775-17867461 FORWARD   Aliases: F23E6.4	4.1	4.0	0.1	0.3	100.0%	-4.9
15517	AT4G15300.1   Symbol: CYP702A2   cytochrome P450 family protein, similar to Cytochrome P450 90C1 (ROTUNDIFOLIA3) (SP:Q9M066) (Arabidopsis thaliana); contains Pfam profile: PF00067: Cytochrome P450   chr4:8730723-8732748 REVERSE   Aliases: DL3695C, FCAALL.257	2.9	2.8	0.1	0.3	100.0%	-5.3
15518	AT5G37640.1   Symbol: UBQ9   polyubiquitin (UBQ9), identical to polyubiquitin (ubq9) gene sequence Gl:304120 from (Arabidopsis thaliana)   chr5:14970012-14970980 REVERSE   Aliases: K12B20.90, K12B20_90	3.3	3.4	-0.0	-0.3	100.0%	-5.5
15519	AT2G46850.1   expressed protein   chr2:19258135-19260437 FORWARD   Aliases: F19D11.13	2.7	2.8	-0.1	-0.3	100.0%	-5.2
15520	AT3G08600.1   expressed protein   chr3:2612400-2613829 FORWARD   Aliases: F17O14.7	4.7	4.7	-0.1	-0.3	100.0%	-4.8
15521	AT3G17160.1   expressed protein   chr3:5852158-5853694 FORWARD   Aliases: K14A17.24	8.3	8.4	-0.1	-0.3	100.0%	-4.8
15522	AT1G67730.1   b-keto acyl reductase, putative (GLOSSY8), similar to b-keto acyl reductase Gl:2586127 from (Hordeum vulgare)   chr1:25395123-25397273 FORWARD   Aliases: F12A21.14, F12A21_14	8.8	8.8	-0.1	-0.3	100.0%	-5.0
15523	AT3G57930.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g42190.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_467479.1)   chr3:21458084-21458936 REVERSE   Aliases: T10K17.140	7.3	7.1	0.2	0.3	100.0%	-4.6
15524	AT2G42590.3   Symbol: GRF9   similar to 14-3-3 protein GF14 iota (GRF12) [Arabidopsis thaliana] (TAIR:At1g26480.1); similar to 14-3-3 protein homolog [Maackia amurensis] (GB:AAC15418.1); similar to SGF14D [Glycine max] (GB:AAB09583.1); contains InterPro domain 14-3-3 protein (InterPro:IPR000308)   chr2:17738933-17741045 REVERSE   Aliases: F14N22.14, F14N22_14, GF14 MU	8.9	9.1	-0.1	-0.3	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15525	AT1G54420.1   expressed protein   chr1:20315286-20316085 FORWARD   Aliases: F20D21.41, F20D21_41	2.3	2.3	-0.0	-0.3	100.0%	-5.4
15526	AT3G18800.1   expressed protein   chr3:6479694-6480384 FORWARD   Aliases: MVE11.18	3.6	3.5	0.1	0.3	100.0%	-5.0
15527	AT5G52620.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr5:21365780-21366907 REVERSE   Aliases: F6N7.11, F6N7_11	2.4	2.4	-0.0	-0.3	100.0%	-5.8
15528	AT2G42350.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:17646323-17646976 FORWARD   Aliases: MHK10.7, MHK10_7	4.0	4.2	-0.2	-0.3	100.0%	-4.0
15529	AT5G03700.1   PAN domain-containing protein, contains Pfam profile: PF00024 PAN domain	5.1	5.0	0.1	0.3	100.0%	-4.8
15530	AT2G44770.1   phagocytosis and cell motility protein ELMO1-related, contains weak similarity to ELMO1 (Mus musculus) gi:16118551:gb:AAL14464   chr2:18464397-18467458 FORWARD   Aliases: F16B22.26	5.1	5.0	0.1	0.3	100.0%	-5.1
15531	AT5G01840.1   ovate family protein, 59% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.8	4.9	-0.0	-0.3	100.0%	-5.4
15532	AT1G20696.2   Symbol: HMGB3   similar to high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 [Arabidopsis thaliana] (TAIR:At1g20693.1); similar to DNA-binding protein [Nicotiana tabacum] (GB:AAB61215.1); similar to high mobility group protein 2 HMG2 [Ipomoea nil] (GB:AAC50019.1); contains InterPro domain HMG1/2 (high mobility group) box (InterPro:IPR000910)   chr1:7179443-7181489 FORWARD   Aliases: HIGH MOBILITY GROUP B 3, HMG BETA 2, NFD03, NFD3	5.7	5.5	0.2	0.3	100.0%	-4.5
15533	AT3G56650.1   thylakoid luminal 20 kDa protein, SP:Q9LXX5; PMID:11719511; F22K20.16 - Arabidopsis thaliana, EMBL:AC002291;   chr3:20995786-20996892 FORWARD   Aliases: T5P19.300	3.9	3.8	0.1	0.3	100.0%	-5.2
15534	AT1G29110.1   cysteine proteinase, putative, contains similarity to cysteine protease SPCP1 GI:13491750 from (Ipomoea batatas)	4.1	4.0	0.1	0.3	100.0%	-4.8
15535	AT5G27360.1   Symbol: SFP2   sugar-porter family protein 2 (SFP2), identical to sugar-porter family protein 2 (Arabidopsis thaliana) GI:14585701   chr5:9657029-9662562 FORWARD   Aliases: F21A20.70, F21A20_70, sugar porter family protein 2	2.6	2.5	0.1	0.3	100.0%	-5.4
15536	AT3G43990.1   bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain   chr3:15793525-15796165 REVERSE   Aliases: T15B3.130	2.4	2.4	0.0	0.3	100.0%	-5.8
15537	AT3G26090.1   Symbol: RGS1   expressed protein   chr3:9533985-9536866 FORWARD   Aliases: ATRGS1, MPE11.28, REGULATOR OF G PROTEIN SIGNALING 1	7.9	8.0	-0.1	-0.3	100.0%	-4.8
15538	AT5G45210.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18312748-18315661 FORWARD   Aliases: K18C1.9, K18C1_9	2.2	2.1	0.0	0.3	100.0%	-5.8
15539	AT5G12430.1   DNAJ heat shock N-terminal domain-containing protein, similarity to TETRATRICOPEPTIDE REPEAT PROTEIN 2 , human, SWISSPROT:TTC2_HUMAN; contains Pfam profiles PF00226: DnaJ domain, PF00515: TPR Domain   chr5:4027980-4034087 REVERSE   Aliases: None	2.9	2.8	0.1	0.3	100.0%	-5.1
15540	AT5G15725.1   expressed protein   chr5:5127407-5128340 FORWARD   Aliases: None	2.8	2.8	0.0	0.3	100.0%	-5.6
15541	AT5G37600.1   Symbol: ATGSR1	12.7	12.6	0.1	0.3	100.0%	-5.3
15542	AT3G23390.1   60S ribosomal protein L36a/L44 (RPL36aA), similar to ribosomal protein L41 GB:AAA34366 from (Candida maltosa)   chr3:8375382-8376397 FORWARD   Aliases: MLM24.22	11.1	11.1	-0.1	-0.3	100.0%	-5.4
15543	AT3G08670.1   expressed protein   chr3:2633743-2636542 FORWARD   Aliases: F17O14.14	2.5	2.5	0.0	0.3	100.0%	-5.6
15544	AT3G50720.1   protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi:1054633:emb:CAA63387   chr3:18858500-18860411 REVERSE   Aliases: T3A5.100	3.2	3.1	0.1	0.3	100.0%	-5.2
15545	AT5G38850.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:15572386-15575962 FORWARD   Aliases: K15E6.30, K15E6_30	2.7	2.8	-0.0	-0.3	100.0%	-5.3
15546	AT3G25850.1   DC1 domain-containing protein, similar to unknown protein GB:AAC79144 from (Arabidopsis thaliana)   chr3:9459415-9460191 REVERSE   Aliases: K9I22.1	2.1	2.1	0.0	0.3	100.0%	-6.0
15547	AT1G67080.1   expressed protein   chr1:25048888-25050523 REVERSE   Aliases: F1O19.13, F1O19_13	7.9	7.8	0.1	0.3	100.0%	-4.9
15548	AT3G30350.1   expressed protein   chr3:11962896-11964265 REVERSE   Aliases: T6J22.14	2.8	2.8	0.0	0.3	100.0%	-5.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15549	AT1G75010.1   similar to phosphatidylinositol-4-phosphate 5-kinase family protein [Arabidopsis thaliana] (TAIR:At1g60890.1); similar to putative phosphatidylinositol-4-phosphate 5-kinase [Bacteroides thetaiotaomicron VPI-5482] (GB:AAO75854.1); contains InterPro domain MORN motif (InterPro:IPR003409)   chr1:28168501-28173705 REVERSE   Aliases: F25A4.3, F25A4_3	5.1	5.2	-0.1	-0.3	100.0%	-4.6
15550	AT1G26700.1   Symbol: MLO14   seven transmembrane MLO family protein / MLO-like protein 14 (MLO14), identical to membrane protein Mlo14 (Arabidopsis thaliana) gi:14091598:gb:AAK53807; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr1:9228222-9232227 FORWARD   Aliases: T24P13.8, T24P13_8	3.3	3.3	-0.1	-0.3	100.0%	-5.4
15551	AT2G47820.1   expressed protein   chr2:19594478-19597892 FORWARD   Aliases: F17A22.21	2.8	2.8	-0.0	-0.3	100.0%	-5.3
15552	AT1G71900.1   expressed protein   chr1:27065150-27068158 FORWARD   Aliases: F17M19.5, F17M19_5	5.8	5.7	0.2	0.3	100.0%	-4.8
15553	AT3G59540.1   60S ribosomal protein L38 (RPL38B), 60S RIBOSOMAL PROTEIN L38 - Lycopersicon esculentum, EMBL:X69979   chr3:22006655-22007783 REVERSE   Aliases: T16L24.90	10.2	10.4	-0.2	-0.3	100.0%	-4.8
15554	AT5G14890.1   NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	3.5	3.5	0.1	0.3	100.0%	-5.2
15555	AT1G72040.1   deoxynucleoside kinase family, contains Pfam profile: PF01712 deoxynucleoside kinase   chr1:27115559-27118004 REVERSE   Aliases: F28P5.7, F28P5_7	6.8	6.9	-0.2	-0.3	100.0%	-4.5
15556	AT3G07020.2   UDP-glucose:sterol glucosyltransferase (UGT80A2), identical to UDP-glucose:sterol glucosyltransferase (Arabidopsis thaliana) GI:2462931; contains Pfam profile: PF03033 glycosyltransferase family 28 N-terminal domain   chr3:2217659-2221708 REVERSE   Aliases: F17A9.17	6.3	6.4	-0.1	-0.3	100.0%	-4.6
15557	AT4G12270.1   copper amine oxidase family protein, contains similarity to copper amine oxidase (Cicer arietinum) gi:3819099:emb:CAA08855; contains Pfam domains PF02728: Copper amine oxidase, N3 domain and PF02727: Copper amine oxidase, N2 domain   chr4:7297802-7299924 FORWARD   Aliases: T4C9.110, T4C9_110	2.1	2.2	-0.0	-0.3	100.0%	-5.8
15558	AT4G25910.1   Symbol: NFU3   nitrogen fixation protein, putative, nitrogen fixation protein nifU (SP:Q43885) (Anabaena sp.); contains Pfam profile: PF01106 NifU-like domain   chr4:13163982-13165173 FORWARD   Aliases: ATCNFU3, F20B18.20, F20B18_20	8.1	8.0	0.1	0.3	100.0%	-4.4
15559	AT1G67670.1   expressed protein   chr1:25369136-25369330 FORWARD   Aliases: F12A21.18, F12A21_18	3.5	3.4	0.1	0.3	100.0%	-5.2
15560	AT3G13445.2   Symbol: TBP1   similar to transcription initiation factor IID-2 (TFIID-2) / TATA-box factor 2 / TATA sequence-binding protein 2 (TBP2) [Arabidopsis thaliana] (TAIR:At1g55520.2); similar to transcription initiation factor IID-2 (TFIID-2) / TATA-box factor 2 / TATA sequence-binding protein 2 (TBP2) [Arabidopsis thaliana] (TAIR:At1g55520.1); similar to TATA-binding protein [Zea mays] (GB:AAA65942.1); contains InterPro domain Transcription factor TFIID (InterPro:IPR000814)   chr3:4379805-4382231 FORWARD   Aliases: MRP15.22, TATA BINDING PROTEIN 1, TFIID 1, TRANSCRIPTION FACTOR IID 1	5.2	5.0	0.1	0.3	100.0%	-4.5
15561	AT4G26750.1   hydroxyproline-rich glycoprotein family protein   chr4:13475700-13478503 REVERSE   Aliases: F10M23.90, F10M23_90	5.6	5.5	0.1	0.3	100.0%	-5.4
15562	AT5G51870.2   MADS-box protein (AGL71), contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr5:21103322-21105149 REVERSE   Aliases: MJM18.2, MJM18_2	3.0	2.9	0.0	0.3	100.0%	-5.4
15563	AT1G72990.2   similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At4g36360.2); similar to beta-galactosidase, putative / lactase, putative [Arabidopsis thaliana] (TAIR:At4g36360.1); similar to BGAL_MACFA Beta-galactosidase precursor (Lactase) (Acid beta-galactosidase) (GB:Q60HF6); similar to lysosomal beta-galactosidase [Felis catus] (GB:NP_001009860.1); contains InterPro domain Glycoside hydrolase, family 35 (InterPro:IPR001944)   chr1:27460943-27466053 REVERSE   Aliases: F3N23.19, F3N23_19	6.2	6.3	-0.1	-0.3	100.0%	-4.9
15564	AT4G27590.1   copper-binding protein-related, low similarity to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain   chr4:13771191-13771891 FORWARD   Aliases: T29A15.80, T29A15_80	3.1	3.2	-0.1	-0.3	100.0%	-5.3
15565	AT1G09720.1   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia)   chr1:3144440-3147305 REVERSE   Aliases: F21M12.11, F21M12_11	2.2	2.2	-0.0	-0.3	100.0%	-6.1
15566	AT1G54060.1   expressed protein, similar to 6b-interacting protein 1 (NtSIP1) (Nicotiana tabacum) GI:18149189   chr1:20184347-20185992 FORWARD   Aliases: F15I1.14, F15I1_14	6.7	6.9	-0.1	-0.3	100.0%	-4.9
15567	AT3G32050.1   expressed protein   chr3:13071339-13072295 REVERSE   Aliases: F1M23.5	3.4	3.5	-0.1	-0.3	100.0%	-5.0
15568	AT4G00820.1   calmodulin-binding protein-related, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr4:349116-351550 FORWARD   Aliases: A_TM018A10.13, A_TM018A10_13, T18A10.11, T18A10_11	2.3	2.3	0.0	0.3	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15569	AT2G16970.1   expressed protein, ; expression supported by MPSS   chr2:7376631-7382610 FORWARD   Aliases: F12A24.15, F12A24_15	4.0	3.9	0.1	0.3	100.0%	-4.4
15570	AT5G67220.1   nitrogen regulation family protein, similar to unknown protein (gb:AAF51525.1) ; contains Pfam domain PF01207: Dihydrouridine synthase (Dus); similar to (SP:P45672) NIFR3-like protein (SP:P45672) (Azospirillum brasilense)   chr5:26836684-26839190 REVERSE   Aliases: K21H1.18, K21H1_18	10.2	10.2	-0.1	-0.3	100.0%	-5.0
15571	AT1G31950.1   terpene synthase/cyclase family protein, similar to sesquiterpene synthases (GI:11934937)(Lycopersicon hirsutum), (GI:11934933)(Lycopersicon esculentum); contains Pfam profile: PF01397: Terpene synthase family   chr1:11475787-11478174 FORWARD   Aliases: F5M6.5	2.4	2.3	0.1	0.3	100.0%	-5.5
15572	AT5G11990.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:3872652-3873197 REVERSE   Aliases: F14F18.160, F14F18_160	2.9	3.0	-0.1	-0.3	100.0%	-4.9
15573	AT3G13420.1   expressed protein   chr3:4364534-4366798 FORWARD   Aliases: MRP15.5	3.2	3.3	-0.1	-0.3	100.0%	-5.0
15574	AT2G34360.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr2:14514373-14517138 FORWARD   Aliases: F13P17.20, F13P17_20	3.0	3.1	-0.1	-0.3	100.0%	-5.3
15575	AT2G22930.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	3.0	3.0	0.1	0.3	100.0%	-4.6
15576	AT4G16590.1   Symbol: ATCSLA01   glycosyltransferase-related, low similarity to beta-(1-3)-glucosyl transferase (Bradyrhizobium japonicum) GI:3687658	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15577	AT4G12770.1   auxilin-related, low similarity to SP:Q27974 Auxilin {Bos taurus}   chr4:7506378-7511563 REVERSE   Aliases: T20K18.120, T20K18_120	3.9	3.7	0.1	0.3	100.0%	-4.4
15578	AT5G39080.1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family   chr5:15658886-15660389 FORWARD   Aliases: MXF12.90, MXF12_90	4.3	4.4	-0.1	-0.3	100.0%	-5.0
15579	AT4G17930.1   hypothetical protein   chr4:9964631-9964852 FORWARD   Aliases: T6K21.110, T6K21_110	2.4	2.5	-0.0	-0.3	100.0%	-5.6
15580	AT5G54060.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	4.5	4.4	0.1	0.3	100.0%	-4.9
15581	AT1G33840.1   hypothetical protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr1:12283842-12285330 REVERSE   Aliases: F14M2.3, F14M2_3	2.8	2.6	0.1	0.3	100.0%	-4.4
15582	AT1G49040.2   Symbol: SCD1   stomatal cytokinesis defective / SCD1 protein (SCD1), contains Pfam PF02141: DENN (AEX-3) domain; contains Pfam PF00400: WD domain, G-beta repeat (8 copies); identical to stomatal cytokinesis defective (Arabidopsis thaliana) GI:19743728; supporting cDNA gi:19743727:gb:AY082605.1.; PMID 12874123   chr1:18145470-18152601 REVERSE   Aliases: F27J15.17, F27J15_17, STOMATAL CYTOKINESIS DEFECTIVE 1	7.4	7.4	-0.1	-0.3	100.0%	-5.1
15583	AT3G42100.1   AT hook motif-containing protein-related, very low similarity to SP:Q9UUA2 DNA repair and recombination protein pif1, mitochondrial precursor {Schizosaccharomyces pombe}; weak hit to Pfam profile PF02178: AT hook motif   chr3:14286145-14292264 REVERSE   Aliases: F4M19.60	2.4	2.4	0.1	0.3	100.0%	-5.4
15584	AT4G19150.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr4:10471346-10472753 REVERSE   Aliases: T18B16.120, T18B16_120	7.7	7.6	0.1	0.3	100.0%	-4.7
15585	AT1G09700.1   Symbol: HYL1   double-stranded RNA-binding domain (DsRBD)-containing protein, contains Pfam profile PF00035: Double-stranded RNA binding motif; supporting cDNA gi:12247456:gb:AF276440.1:AF276440   chr1:3137769-3140236 REVERSE   Aliases: F21M12.9, F21M12_9, HYPONASTIC LEAVES 1	5.1	5.2	-0.1	-0.3	100.0%	-4.5
15586	AT4G39390.2   transporter-related, low similarity to glucose-6-phosphate/phosphate-translocator precursor (Solanum tuberosum) GI:2997593   chr4:18315625-18318018 FORWARD   Aliases: F23K16.20, F23K16_20	4.8	4.9	-0.1	-0.3	100.0%	-4.9
15587	AT3G23680.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:8526373-8527180 REVERSE   Aliases: MYM9.1	2.9	2.9	-0.1	-0.3	100.0%	-5.4
15588	AT4G20000.1   VQ motif-containing protein, contains PF05678: VQ motif   chr4:10838320-10839152 FORWARD   Aliases: F18F4.100, F18F4_100	2.7	2.7	0.1	0.3	100.0%	-5.3
15589	AT4G24170.1   kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain   chr4:12543216-12546815 FORWARD   Aliases: T19F6.1	2.3	2.3	-0.1	-0.3	100.0%	-5.2
15590	AT5G58460.1   Symbol: ATCHX25   cation/hydrogen exchanger, putative (CHX25), similar to Na+/H+-exchanging protein slr1595, Synechocystis sp., PIR:S74951; monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr5:23649587-23652263 REVERSE   Aliases: CHX25, MQJ2.3, MQJ2_3	4.2	4.2	0.0	0.3	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15591	AT1G27530.1   expressed protein, Similar to gb:AF151884 CGI-126 protein from Homo sapiens. EST gb:Z18048 comes from this gene   chr1:9562586-9563926 REVERSE   Aliases: T17H3.3, T17H3_3	11.8	11.9	-0.1	-0.3	100.0%	-5.0
15592	AT4G29560.1   expressed protein   chr4:14503879-14506020 REVERSE   Aliases: T16L4.70, T16L4_70	3.8	3.8	-0.1	-0.3	100.0%	-5.0
15593	AT1G44446.3   Symbol: CH1   chlorophyll a oxygenase (CAO) / chlorophyll b synthase, identical to chlorophyll a oxygenase GI:5853117 from (Arabidopsis thaliana); contains Pfam PF00355 Rieske (2Fe-2S) domain	4.1	4.2	-0.1	-0.3	100.0%	-4.7
15594	AT2G45340.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:18698796-18701776 FORWARD   Aliases: F4L23.15	4.1	4.0	0.1	0.3	100.0%	-4.8
15595	AT5G14020.1   expressed protein   chr5:4523524-4525865 REVERSE   Aliases: MAC12.31, MAC12_31	2.7	2.7	0.0	0.3	100.0%	-5.6
15596	AT1G70070.1   Symbol: PDE317	5.6	5.7	-0.1	-0.3	100.0%	-4.6
15597	AT2G19550.1   esterase/lipase/thioesterase family protein, low similarity to cinnamoyl ester hydrolase Cln1 (Butyrivibrio fibrisolvens) GI:1622732; contains esterase/lipase/thioesterase active site serine (PS50187) (Interpro entry IPR000379) and alpha/beta hydrolase fold (PF00561).   chr2:8471615-8472613 REVERSE   Aliases: F3P11.15, F3P11_15	3.7	3.6	0.1	0.3	100.0%	-5.0
15598	AT1G54470.1   expressed protein   chr1:20348405-20348743 FORWARD   Aliases: F20D21.44, F20D21_44	2.3	2.4	-0.0	-0.3	100.0%	-5.5
15599	AT5G53110.1   expressed protein   chr5:21546248-21546970 FORWARD   Aliases: MFH8.3, MFH8_3	3.0	3.1	-0.1	-0.3	100.0%	-4.9
15600	AT5G58130.1   RNA recognition motif (RRM)-containing protein   chr5:23538276-23541022 REVERSE   Aliases: K21L19.13, K21L19_13	6.9	7.0	-0.1	-0.3	100.0%	-5.1
15601	AT3G55790.1   expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	2.5	2.5	-0.0	-0.3	100.0%	-5.5
15602	AT5G53350.1   Symbol: CLPX   ATP-dependent Clp protease ATP-binding subunit ClpX1 (CLPX), identical to CLP protease regulatory subunit CLPX GI:2674203 from (Arabidopsis thaliana)   chr5:21661124-21664933 FORWARD   Aliases: K19E1.15, K19E1_15	10.3	10.3	0.1	0.3	100.0%	-5.3
15603	AT2G04800.2   expressed protein   chr2:1687193-1687686 REVERSE   Aliases: F28I8.16, F28I8_16	7.1	7.2	-0.1	-0.3	100.0%	-4.6
15604	AT1G23510.2   expressed protein   chr1:8341438-8342732 REVERSE   Aliases: F28C11.14, F28C11_14	2.8	2.8	0.0	0.3	100.0%	-5.5
15605	AT1G05590.1   glycosyl hydrolase family 20 protein, similar to beta-hexosaminidase precursor SP:P43077 from (Candida albicans)	5.4	5.4	0.1	0.3	100.0%	-4.7
15606	AT3G61930.1   expressed protein   chr3:22946485-22947156 FORWARD   Aliases: F21F14.100	4.1	4.3	-0.2	-0.3	100.0%	-4.3
15607	AT1G62560.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 SP:P32417 from (Oryctolagus cuniculus); contains Pfam profile PF00743 Flavin-binding monooxygenase-like   chr1:23163488-23166314 FORWARD   Aliases: T3P18.12, T3P18_12	3.3	3.4	-0.1	-0.3	100.0%	-5.2
15608	AT5G38390.1   F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.3	-0.1	-0.3	100.0%	-5.2
15609	AT2G14850.1   expressed protein   chr2:6392954-6394652 FORWARD   Aliases: F26C24.1	4.8	4.8	0.1	0.3	100.0%	-5.1
15610	AT1G27920.1   microtubule associated protein (MAP65/ASE1) family protein, low similarity to protein regulating cytokinesis 1 (PRC1) (Homo sapiens) GI:2865521; contains Pfam profile PF03999: Microtubule associated protein (MAP65/ASE1 family)   chr1:9726935-9729835 FORWARD   Aliases: F13K9.3, F13K9_3	2.8	3.0	-0.2	-0.3	100.0%	-4.4
15611	AT4G13650.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:7938963-7942894 REVERSE   Aliases: F18A5.40, F18A5_40	2.6	2.7	-0.0	-0.3	100.0%	-5.7
15612	AT5G17050.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, similar to UDP glucose:flavonoid 3-o-glucosyltransferase, Vitis vinifera, EMBL:AF000372   chr5:5607791-5609495 REVERSE   Aliases: F2K13.200, F2K13_200	9.0	9.2	-0.2	-0.3	100.0%	-4.7
15613	AT4G31080.1   expressed protein   chr4:15120927-15121977 FORWARD   Aliases: F6I18.10, F6I18_10	3.9	3.7	0.2	0.3	100.0%	-4.9
15614	AT2G41900.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat   chr2:17497490-17501000 FORWARD   Aliases: T6D20.20, T6D20_20	4.9	4.7	0.1	0.3	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15615	AT2G33990.1   similar to calmodulin-binding family protein [Arabidopsis thaliana] (TAIR:At3g15050.1); similar to putative SF16 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73780.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048)   chr2:14367355-14369257 REVERSE   Aliases: T14G11.11, T14G11_11	4.8	4.7	0.1	0.3	100.0%	-4.8
15616	AT2G19400.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr2:8406239-8409682 REVERSE   Aliases: F27F23.20, F27F23_20	3.6	3.6	0.1	0.3	100.0%	-5.2
15617	AT2G40020.2   expressed protein   chr2:16718064-16720148 FORWARD   Aliases: T28M21.18, T28M21_18	4.6	4.5	0.1	0.3	100.0%	-4.7
15618	AT5G25840.1   expressed protein   chr5:9010727-9011501 REVERSE   Aliases: F18A17.90, F18A17_90	2.4	2.4	0.0	0.3	100.0%	-5.6
15619	AT5G40360.1   Symbol: MYB115	2.9	3.0	-0.0	-0.3	100.0%	-5.5
15620	AT5G23540.1   26S proteasome regulatory subunit, putative, similar to 26S proteasome-associated pad1 homolog (Homo sapiens) GI:1923256, 26S proteasome, non-ATPase subunit (Mus musculus) GI:2505940; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family   chr5:7937672-7939578 FORWARD   Aliases: MQM1.19, MQM1_19	10.4	10.6	-0.2	-0.3	100.0%	-4.9
15621	AT2G01450.4   Symbol: ATPMK17   similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK16) [Arabidopsis thaliana] (TAIR:At5g19010.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK8) [Arabidopsis thaliana] (TAIR:At1g18150.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK9) [Arabidopsis thaliana] (TAIR:At3g18040.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK8) [Arabidopsis thaliana] (TAIR:At1g18150.2); similar to putative MAPK protein kinase [Triticum aestivum] (GB:AAX20166.1); similar to putative MAP kinase [Oryza sativa (japonica cultivar-group)] (GB:BAD53616.1); similar to putative MAP kinase [Hordeum vulgare subsp. vulgare] (GB:CAD42638.1); similar to blast and wounding induced mitogen-activated protein kinase [Oryza sativa] (GB:AAD52659.1); similar to putative MAPK protein kinase [Triticum aestivum] (GB:AAX20165.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr2:199510-203125 REVERSE   Aliases: F2I9.7, F2I9_7	7.4	7.6	-0.2	-0.3	100.0%	-4.5
15622	AT3G18360.1   VQ motif-containing protein, contains PF05678: VQ motif   chr3:6300833-6301690 REVERSE   Aliases: MYF24.8	2.5	2.5	0.0	0.3	100.0%	-5.4
15623	AT2G04060.1   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase precursor SP:P49676 from (Brassica oleracea)   chr2:1342134-1345161 REVERSE   Aliases: F3L12.16, F3L12_16	2.6	2.6	0.1	0.3	100.0%	-5.5
15624	AT5G58690.1   phosphoinositide-specific phospholipase C family protein, contains Pfam profile: PF00388 phosphatidylinositol-specific phospholipase C   chr5:23726755-23729357 REVERSE   Aliases: MZN1.15, MZN1_15	6.6	6.8	-0.2	-0.3	100.0%	-4.6
15625	AT1G72760.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:27389083-27391936 REVERSE   Aliases: F28P22.5, F28P22_5	2.9	2.9	-0.1	-0.3	100.0%	-5.3
15626	AT4G26820.1   hypothetical protein   chr4:13493459-13494187 REVERSE   Aliases: F10M23.160, F10M23_160	3.3	3.4	-0.1	-0.3	100.0%	-5.5
15627	AT1G62440.1   Symbol: LRX2   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	2.3	2.4	-0.1	-0.3	100.0%	-5.6
15628	AT5G11630.1   expressed protein   chr5:3740461-3742140 FORWARD   Aliases: T22P22.20, T22P22_20	4.6	4.7	-0.1	-0.3	100.0%	-5.0
15629	AT2G03110.1   similar to KH domain-containing protein [Arabidopsis thaliana] (TAIR:At1g14170.1); similar to putative KH domain containing protein [Solanum demissum] (GB:AAU90323.1); contains InterPro domain KH domain (InterPro:IPR004087); contains InterPro domain KH domain, type 1 (InterPro:IPR004088)	3.2	3.1	0.1	0.3	100.0%	-5.3
15630	AT3G24982.1   similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:At3g25010.1); similar to disease resistance family protein [Arabidopsis thaliana] (TAIR:At2g32680.1); similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:At2g33020.1); similar to disease resistance family protein / LRR family protein [Arabidopsis thaliana] (TAIR:At3g24900.1); similar to leucine-rich repeat family protein [Arabidopsis thaliana] (TAIR:At2g33060.1); similar to verticillium wilt disease resistance protein precursor [Solanum torvum] (GB:AAQ82053.1); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)	2.9	2.9	0.1	0.3	100.0%	-5.4
15631	AT1G51960.1   calmodulin-binding family protein, contains IQ calmodulin-binding motif, Pfam:PF00612   chr1:19314024-19315352 FORWARD   Aliases: T14L22.17	2.5	2.6	-0.0	-0.3	100.0%	-5.6
15632	AT5G16470.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr5:5379419-5380043 FORWARD   Aliases: MQK4.20, MQK4_20	10.4	10.3	0.1	0.3	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15633	AT5G20240.1   Symbol: PI   floral homeotic protein PISTILLATA (PI), contains Pfam profiles PF01486: K-box region and PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr5:6829123-6831456 FORWARD   Aliases: F5O24.130, F5O24_130, FLORAL HOMEOTIC PROTEIN PISTILLATA, PISTILLATA	3.1	3.2	-0.1	-0.3	100.0%	-5.0
15634	AT3G49340.1   cysteine proteinase, putative, contains PS00640: Eukaryotic thiol (cysteine) proteases asparagine active site; similar to cysteine proteinase GI:535454 from (Alnus glutinosam)   chr3:18304332-18305562 REVERSE   Aliases: F2K15.200	3.8	3.9	-0.1	-0.3	100.0%	-5.3
15635	AT4G30590.1   plastocyanin-like domain-containing protein   chr4:14935629-14936568 REVERSE   Aliases: F17I23.70, F17I23_70	3.6	3.6	0.1	0.3	100.0%	-5.1
15636	AT1G32560.1   late embryogenesis abundant group 1 domain-containing protein / LEA group 1 domain-containing protein, contains Pfam domain, PF03760: Late embryogenesis abundant (LEA) group 1   chr1:11774464-11775259 FORWARD   Aliases: T9G5.2, T9G5_2	2.9	2.8	0.1	0.3	100.0%	-5.3
15637	AT5G49710.3   expressed protein, similar to unknown protein (pir::T05575)   chr5:20212653-20214579 FORWARD   Aliases: K2I5.7, K2I5_7	5.1	5.0	0.1	0.3	100.0%	-4.3
15638	AT4G39110.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:18222477-18225113 REVERSE   Aliases: T22F8.10, T22F8_10	2.6	2.6	0.0	0.3	100.0%	-5.5
15639	AT5G07310.1   encodes a member of the ERF (ethylene response factor) subfamily B-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	3.1	3.1	-0.0	-0.3	100.0%	-5.4
15640	AT1G12750.1   rhomboid family protein, contains PFAM domain PF01694, Rhomboid family   chr1:4344983-4348325 REVERSE   Aliases: T12C24.28, T12C24_28	4.9	4.8	0.1	0.3	100.0%	-4.8
15641	AT5G19550.1   Symbol: ASP2   aspartate aminotransferase, cytoplasmic isozyme 1 / transaminase A (ASP2), identical to SP:P46645 Aspartate aminotransferase, cytoplasmic isozyme 1 (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}	10.4	10.2	0.2	0.3	100.0%	-4.6
15642	AT4G25950.1   vacuolar ATP synthase, putative / V-ATPase, putative / vacuolar proton pump, putative, similar to Swiss-Prot:O82629 vacuolar ATP synthase subunit G 2 (V-ATPase G subunit 2, Vacuolar proton pump G subunit 2) (Arabidopsis thaliana)   chr4:13173762-13174344 REVERSE   Aliases: F20B18.60, F20B18_60	3.0	3.0	0.0	0.3	100.0%	-5.6
15643	AT5G06790.1   expressed protein, similar to unknown protein (emb:CAB67623.1); expression supported by MPSS   chr5:2098089-2098718 REVERSE   Aliases: MPH15.15, MPH15_15	2.4	2.4	-0.0	-0.3	100.0%	-5.5
15644	AT1G61630.1   equilibrative nucleoside transporter, putative (ENT7), identical to putative equilibrative nucleoside transporter ENT7 (Arabidopsis thaliana) GI:16518989; contains similarity to SWISS-PROT:Q99808 equilibrative nucleoside transporter 1 (Equilibrative nitrobenzylmercaptapurine riboside-sensitive nucleoside transporter, Equilibrative NBMPR-sensitive nucleoside transporter, Nucleoside transporter, es-type) (Homo sapiens); contains Pfam profile PF01733: Nucleoside transporter   chr1:22747872-22749776 FORWARD   Aliases: T25B24.2, T25B24_2	3.0	3.1	-0.1	-0.3	100.0%	-5.1
15645	AT4G38850.1   Symbol: SAUR_AC1   auxin-responsive protein / small auxin up RNA (SAUR-AC1), identical to GP:546362 small auxin up RNA {Arabidopsis thaliana}; belongs to auxin-induced (indole-3-acetic acid induced) protein family   chr4:18126165-18126674 FORWARD   Aliases: ATSR15AU, F19H22.6, SAUR15, SMALL AUXIN UP RNA 1 FROM ARABIDOPSIS THALIANA ECOTYPE COLUMBIA	3.9	3.9	-0.1	-0.3	100.0%	-5.5
15646	AT2G29540.2   Symbol: ATRPC14   similar to DNA-directed RNA polymerase II 13.6 kDa subunit (RPB13.6) [Arabidopsis thaliana] (TAIR:At3g52090.1); similar to Polymerase (RNA) I polypeptide C [Homo sapiens] (GB:CAI16933.1); contains InterPro domain DNA-directed RNA polymerase, 13 to 16 kDa subunit (InterPro:IPR008193)   chr2:12649598-12651021 FORWARD   Aliases: ATRPAC14, F16P2.8, F16P2_8, RNA POLYMERASE 14 KDA SUBUNIT	8.5	8.3	0.1	0.3	100.0%	-4.7
15647	AT4G13730.2   RabGAP/TBC domain-containing protein, low similarity to SP:Q08484 GTPase-activating protein GYP1 {Saccharomyces cerevisiae}; contains Pfam profile PF00566: TBC domain   chr4:7970275-7974244 FORWARD   Aliases: F18A5.120, F18A5_120	6.4	6.3	0.1	0.3	100.0%	-4.9
15648	AT2G26520.1   expressed protein   chr2:11287103-11288018 FORWARD   Aliases: T9J22.19, T9J22_19	3.1	3.0	0.0	0.3	100.0%	-5.4
15649	AT1G30970.1   zinc finger (C2H2 type) family protein, contains Pfam domain PF00096: Zinc finger, C2H2 type   chr1:11040262-11043732 REVERSE   Aliases: F17F8.14	3.5	3.6	-0.1	-0.3	100.0%	-5.0
15650	AT2G20660.1   Symbol: RALFL14   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr2:8916548-8916853 FORWARD   Aliases: F23N11.2, F23N11_2, RALF LIKE 14	2.7	2.7	-0.0	-0.3	100.0%	-5.6
15651	AT1G21270.1   Symbol: WAK2   wall-associated kinase 2 (WAK2), identical to wall-associated kinase 2 (Arabidopsis thaliana) GI:4826399; induced by salicylic acid or INA (PMID:10380805)   chr1:7444919-7448447 FORWARD   Aliases: F16F4.5, F16F4_5	3.6	3.6	0.1	0.3	100.0%	-5.2
15652	AT5G26020.1   hypothetical protein   chr5:9093598-9094880 REVERSE   Aliases: T1N24.102, T1N24_102	3.7	3.6	0.1	0.3	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15653	AT3G16350.1   myb family transcription factor, ; contains Pfam profile: PF00249 Myb-like DNA-binding domain   chr3:5547724-5549666 FORWARD   Aliases: T2O4.10	5.2	5.1	0.1	0.3	100.0%	-4.8
15654	AT3G13040.2   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:4172149-4175255 REVERSE   Aliases: MGH6.22	8.5	8.6	-0.1	-0.3	100.0%	-5.0
15655	AT5G15760.1   plastid-specific 30S ribosomal protein 3, putative / PSRP-3, putative, similar to SP:P82412 Plastid-specific 30S ribosomal protein 3, chloroplast precursor (PSRP-3) {Spinacia oleracea}; contains Pfam profile PF04839: Plastid and cyanobacterial ribosomal protein (PSRP-3 / Ycf65)   chr5:5143056-5144056 FORWARD   Aliases: F14F8.140, F14F8_140	2.4	2.4	0.0	0.3	100.0%	-5.4
15656	AT5G51160.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:20809506-20811000 FORWARD   Aliases: MWD22.10, MWD22_10	3.8	3.6	0.2	0.3	100.0%	-4.6
15657	AT3G60560.1   hypothetical protein, 04.05.01.01   chr3:22393433-22393753 FORWARD   Aliases: T8B10.220	2.2	2.2	-0.0	-0.3	100.0%	-6.0
15658	AT1G66840.1   expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827); expression supported by MPSS   chr1:24937661-24939779 REVERSE   Aliases: F4N21.22, F4N21_22	3.9	3.8	0.1	0.3	100.0%	-4.9
15659	AT5G37500.1   Symbol: GORK   guard cell outward rectifying K+ channel (GORK), identical to guard cell outward rectifying K+ channel (Arabidopsis thaliana) gi:11414742:emb:CAC17380; member of the 1 pore, 6 transmembrane (1P/6TM) Shaker K+ channel family, PMID:11500563   chr5:14906923-14912134 REVERSE   Aliases: GATED OUTWARDLY RECTIFYING K+ CHANNEL, MPA22.4, MPA22_4	3.4	3.5	-0.1	-0.3	100.0%	-4.6
15660	AT3G23930.1   expressed protein   chr3:8646904-8647915 FORWARD   Aliases: F14O13.11	3.3	3.4	-0.1	-0.3	100.0%	-5.4
15661	AT2G19230.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:8351841-8355513 REVERSE   Aliases: F27F23.3, F27F23_3	3.1	3.1	0.0	0.3	100.0%	-5.7
15662	AT1G68490.1   expressed protein   chr1:25697112-25699139 FORWARD   Aliases: T26J14.6, T26J14_6	6.7	6.8	-0.2	-0.3	100.0%	-4.8
15663	AT1G50300.1   zinc finger (Ran-binding) family protein / RNA recognition motif (RRM)-containing protein, similar to SP:Q27294 RNA-binding protein cabeza {Drosophila melanogaster}; contains Pfam profiles: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain), PF00641: Zn-finger in Ran binding protein and others   chr1:18632356-18635610 REVERSE   Aliases: F14I3.10, F14I3_10	8.9	8.7	0.2	0.3	100.0%	-4.9
15664	AT2G02515.1   expressed protein   chr2:675255-675655 FORWARD   Aliases: None	3.6	3.7	-0.1	-0.3	100.0%	-5.0
15665	AT1G76960.1   expressed protein   chr1:28925351-28925850 REVERSE   Aliases: F22K20.6, F22K20_6	2.1	2.2	-0.0	-0.3	100.0%	-6.0
15666	AT4G03205.2   similar to coproporphyrinogen III oxidase, putative / coproporphyrinogenase, putative / coprogen oxidase, putative [Arabidopsis thaliana] (TAIR:At1g03475.1); similar to coproporphyrinogen oxidase [Glycine max] (GB:CAA50401.1); contains InterPro domain Coproporphyrinogen III oxidase (InterPro:IPR001260)   chr4:1412785-1414782 FORWARD   Aliases: None	2.7	2.8	-0.0	-0.3	100.0%	-5.4
15667	AT3G46830.1   Ras-related protein (RAB11A) / small GTP-binding protein, putative, identical to SP:Q96283 Ras-related protein Rab11A {Arabidopsis thaliana}; identical to cDNA Rab11 protein GI:2598228	7.4	7.6	-0.2	-0.3	100.0%	-4.8
15668	AT5G52070.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr5:21178537-21182251 FORWARD   Aliases: MSG15.17, MSG15_17	3.1	3.3	-0.2	-0.3	100.0%	-4.6
15669	AT5G04670.1   expressed protein, BRL protein, Homo sapiens, EMBL:AF005067   chr5:1337840-1340885 REVERSE   Aliases: T1E3.30, T1E3_30	5.1	5.0	0.1	0.3	100.0%	-4.7
15670	AT5G54020.1   expressed protein   chr5:21939090-21940760 REVERSE   Aliases: K19P17.19, K19P17_19	2.8	2.9	-0.2	-0.3	100.0%	-4.3
15671	AT3G30610.1   hypothetical protein   chr3:12189170-12189508 REVERSE   Aliases: MQP15.14	3.0	3.0	0.1	0.3	100.0%	-4.8
15672	AT1G79840.1   Symbol: GL2   homeobox-leucine zipper protein 10 (HB-10) / HD-ZIP transcription factor 10 / homeobox protein (GLABRA2), identical to homeobox protein (GLABRA2) (homeobox-leucine zipper protein ATHB-10) (HD-ZIP protein ATHB-10) GB:P46607 (Arabidopsis thaliana)   chr1:30042308-30045984 FORWARD   Aliases: F19K16.20, F19K16_20, GLABRA 2, HOMEBOX PROTEIN GLABRA 2	2.8	2.9	-0.1	-0.3	100.0%	-4.8
15673	AT1G43020.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g21060.1); similar to putative ternary complex factor MIP1 [Antirrhinum majus] (GB:AAO59425.1); contains domain SER_RICH (PS50324)   chr1:16157843-16159570 FORWARD   Aliases: F13A11.7, F13A11_7	2.5	2.3	0.1	0.3	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15674	AT3G04160.1   expressed protein, ; expression supported by MPSS   chr3:1091654-1094303 REVERSE   Aliases: T6K12.22, T6K12_22	2.9	2.9	0.1	0.3	100.0%	-5.4
15675	AT4G01480.1   inorganic pyrophosphatase, putative (soluble) / pyrophosphate phospho-hydrolase, putative / PPase, putative, strong similarity to SP:Q43187 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase) {Solanum tuberosum}; contains Pfam profile PF00719: inorganic pyrophosphatase   chr4:626118-628036 FORWARD   Aliases: F11O4.12, F11O4_12	5.8	6.0	-0.2	-0.3	100.0%	-4.6
15676	AT3G08640.1   alphavirus core protein family, contains Pfam profile: PF00944 alphavirus core protein   chr3:2622886-2624314 FORWARD   Aliases: F17O14.11	8.4	8.2	0.2	0.3	100.0%	-4.5
15677	AT4G16563.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr4:9329679-9331545 REVERSE   Aliases: None	3.7	3.6	0.2	0.3	100.0%	-4.3
15678	AT5G24316.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:8278780-8279967 REVERSE   Aliases: None	3.0	2.9	0.1	0.3	100.0%	-5.2
15679	AT1G03740.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g44290.1); similar to putative CRK1 protein(cdc2-related kinase 1) [Oryza sativa (japonica cultivar-group)] (GB:NP_910987.1); similar to CRK1 protein [Beta vulgaris subsp. vulgaris] (GB:CAB89665.1); similar to putative CRK1 protein [Oryza sativa (japonica cultivar-group)] (GB:NP_918694.1); similar to putative CRK1 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD89473.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:933512-937042 FORWARD   Aliases: F21B7.34	3.0	3.2	-0.1	-0.3	100.0%	-4.9
15680	AT3G03370.1   expressed protein   chr3:797126-798480 REVERSE   Aliases: T21P5.21, T21P5_21	2.6	2.7	-0.1	-0.3	100.0%	-5.2
15681	AT5G36960.1   expressed protein, ; expression supported by MPSS   chr5:14615975-14616959 FORWARD   Aliases: MLF18.14, MLF18_14	3.2	3.2	-0.0	-0.3	100.0%	-5.6
15682	AT2G37950.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger); contains PROSITE PS00190: Cytochrome c family heme-binding site signature   chr2:15889566-15891057 REVERSE   Aliases: T8P21.14, T8P21_14	3.6	3.4	0.2	0.3	100.0%	-4.1
15683	AT5G49310.1   importin alpha-1 subunit, putative, similar to importin alpha-1 subunit (Karyopherin alpha-1 subunit, KAP alpha) (Arabidopsis thaliana) SWISS-PROT:Q96321   chr5:20009242-20011742 REVERSE   Aliases: K21P3.21, K21P3_21	3.3	3.4	-0.1	-0.3	100.0%	-5.2
15684	AT2G42480.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr2:17692883-17696929 REVERSE   Aliases: MHK10.20, MHK10_20	3.5	3.6	-0.1	-0.3	100.0%	-5.3
15685	AT4G38600.2   Symbol: KAK   HECT-domain-containing protein / ubiquitin-transferase family protein, similar to SP:Q14669Thyroid receptor interacting protein 12 (TRIP12) {Homo sapiens}; contains Pfam profile PF00632: HECT-domain (ubiquitin-transferase)   chr4:18041025-18049246 REVERSE   Aliases: AT4G38610, F20M13.160, F20M13_160, KAKTUS, UBIQUITIN PROTEIN LIGASE 3, UBIQUITIN_PROTEIN LIGASE, UPL3	4.1	4.2	-0.1	-0.3	100.0%	-5.1
15686	AT5G24890.1   expressed protein, weak similarity to MTD1 (Medicago truncatula) GI:9294810   chr5:8558207-8559409 REVERSE   Aliases: F6A4.100, F6A4_100	5.6	5.4	0.2	0.3	100.0%	-4.6
15687	AT1G22520.1   expressed protein, contains Pfam PF04418: Domain of unknown function (DUF543)   chr1:7953011-7954391 REVERSE   Aliases: F12K8.27, F12K8_27	7.6	7.7	-0.1	-0.3	100.0%	-4.7
15688	AT1G10580.1   transducin family protein / WD-40 repeat family protein, similar to splicing factor hPRP17 (gi:3283220); contains 7 WD-40 repeats (PF00400);similar to ESTs emb:F15435 and dbj:AUO62661   chr1:3491282-3493738 REVERSE   Aliases: T10O24.21, T10O24_21	5.4	5.6	-0.1	-0.3	100.0%	-4.5
15689	AT1G77610.1   glucose-6-phosphate/phosphate translocator-related, similar to glucose-6-phosphate/phosphate-translocators from (Mesembryanthemum crystallinum) GI:9295277, (Solanum tuberosum) GI:2997593, (Pisum sativum) GI:2997591; contains Pfam profile PF00892: Integral membrane protein	4.4	4.6	-0.2	-0.3	100.0%	-5.0
15690	AT1G49750.1   leucine-rich repeat family protein, contains leucine-rich repeats, Pfam:PF00560   chr1:18414597-18416469 REVERSE   Aliases: F14J22.4, F14J22_4	3.4	3.5	-0.1	-0.3	100.0%	-5.0
15691	AT5G02860.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:654100-656559 FORWARD   Aliases: F9G14.170, F9G14_170	3.7	3.8	-0.1	-0.3	100.0%	-5.2
15692	AT2G06520.1   membrane protein, putative, contains 2 transmembrane domains;   chr2:2587781-2588355 REVERSE   Aliases: T12H3.7, T12H3_7	9.6	9.4	0.2	0.3	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15693	AT5G06800.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:2103172-2105899 FORWARD   Aliases: MPH15.16, MPH15_16	2.8	3.0	-0.2	-0.3	100.0%	-4.4
15694	AT5G59305.1   expressed protein   chr5:23940428-23941128 FORWARD   Aliases: None	2.7	2.7	-0.1	-0.3	100.0%	-5.5
15695	ATCG01100.1   Symbol: NDHA   NADH dehydrogenase ND1   chrC:119847-122009 REVERSE   Aliases: NDHA	5.9	6.2	-0.3	-0.3	100.0%	-4.6
15696	AT1G74740.1   Symbol: CPK30   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Arabidopsis thaliana) gi:604880:dbj:BAA04829; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr1:28083104-28086305 REVERSE   Aliases: CDPK1A, F25A4.29, F25A4_29	3.8	3.9	-0.1	-0.3	100.0%	-4.8
15697	AT1G66490.1   F-box family protein, contains weak hit to Pfam PF00646: F-box domain;; contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr1:24813084-24814212 REVERSE   Aliases: F28G11.7, F28G11_7	3.1	3.1	0.0	0.3	100.0%	-5.7
15698	AT3G10570.1   Symbol: CYP77A6   cytochrome P450, putative, similar to cytochrome P450 77A3 GB:O48928 (Glycine max)   chr3:3302109-3303844 FORWARD   Aliases: F13M14.15	2.6	2.6	0.1	0.3	100.0%	-5.4
15699	AT1G72940.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27445899-27447517 FORWARD   Aliases: F3N23.14, F3N23_14	4.6	4.6	-0.1	-0.3	100.0%	-4.9
15700	AT2G26140.1   Symbol: FTSH4   encodes an FtsH protease that is localized to the mitochondrion	6.7	6.9	-0.2	-0.3	100.0%	-4.7
15701	AT3G12060.1   expressed protein, similar to hypothetical protein GB:CAB82953 GI:7340710 from (Arabidopsis thaliana)   chr3:3843148-3845156 FORWARD   Aliases: MEC18.19	2.9	2.8	0.0	0.3	100.0%	-5.6
15702	AT5G41150.2   Symbol: UVH1   similar to ERCC4_CRIGR DNA repair endonuclease XPF (DNA excision repair protein ERCC-4) (GB:Q9QYM7); similar to ERCC4 [Cricetulus griseus] (GB:BAA89229.1)   chr5:16491281-16494179 REVERSE   Aliases: ATRAD1, MEE6.22, MEE6_22, RAD1, REPAIR ENDONUCLEASE, ULTRAVIOLET HYPERSENSITIVE 1	3.5	3.4	0.1	0.3	100.0%	-4.9
15703	AT1G49290.1   expressed protein, ; expression supported by MPSS   chr1:18236276-18237292 REVERSE   Aliases: F13F21.27, F13F21_27	3.1	3.0	0.1	0.3	100.0%	-5.3
15704	AT3G14750.1   expressed protein, weak similarity to Septation ring formation regulator (Swiss-Prot:O34894) (Bacillus subtilis)	7.5	7.6	-0.1	-0.3	100.0%	-5.1
15705	AT3G60690.1   auxin-responsive family protein, similar to auxin-induced protein SAUR-AC1 (GP:546362) (PIR:T06084)(Arabidopsis thaliana) PIR:T06084   chr3:22446096-22446924 FORWARD   Aliases: T4C21.100	5.3	5.2	0.1	0.3	100.0%	-4.8
15706	AT2G39430.1   disease resistance-responsive protein-related / dirigent protein-related, contains similarity to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669; contains similarity to dirigent protein (Thuja plicata) gi:6694709:gb:AAF25365	3.2	3.4	-0.2	-0.3	100.0%	-4.4
15707	AT4G13170.1   60S ribosomal protein L13A (RPL13aC), ribosomal protein L13a -Lupinus luteus,PID:e1237871   chr4:7654940-7656561 REVERSE   Aliases: F17N18.60, F17N18_60	10.2	10.3	-0.1	-0.3	100.0%	-4.7
15708	AT1G26680.1   transcriptional factor B3 family protein, low similarity to reproductive meristem gene 1 from (Brassica oleracea var. botrytis) GI:3170424, (Arabidopsis thaliana) GI:13604227; contains Pfam profile PF02362: B3 DNA binding domain   chr1:9219459-9223636 FORWARD   Aliases: T24P13.6, T24P13_6	2.8	2.9	-0.1	-0.3	100.0%	-5.2
15709	AT3G13226.1   regulatory protein RecX family protein, contains Pfam PF02631: regulatory protein RecX   chr3:4264311-4266369 REVERSE   Aliases: None	7.4	7.5	-0.1	-0.3	100.0%	-4.8
15710	AT5G62540.1   ubiquitin-conjugating enzyme 3 (UBC3), E2; identical to gi:431261, SP:P42746   chr5:25121160-25122845 FORWARD   Aliases: K19B1.15, K19B1_15	9.0	8.9	0.1	0.3	100.0%	-4.7
15711	AT3G48920.1   myb family transcription factor (MYB45), similar to MybHv33 GI:456214 from (Hordeum vulgare); contains PFAM profile: myb DNA binding domain PF00249   chr3:18150377-18151546 FORWARD   Aliases: T2J13.240	2.4	2.4	0.1	0.3	100.0%	-4.8
15712	AT1G78720.1   protein transport protein sec61, putative, similar to SP:P38377 Protein transport protein Sec61 alpha subunit isoform 1 (Sec61 alpha- 1) {Canis familiaris}; contains Pfam profile PF00344: eubacterial secY protein   chr1:29610522-29612403 FORWARD   Aliases: F9K20.24, F9K20_24	2.5	2.4	0.0	0.3	100.0%	-5.3
15713	AT3G43530.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr3:15438133-15441064 REVERSE   Aliases: T18D12.100	3.6	3.5	0.1	0.3	100.0%	-5.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15714	AT1G65080.1   OXA1 family protein, contains Pfam PF02096: 60Kd inner membrane protein; similar to AtOXA1 (GI:6624207) (Arabidopsis thaliana)   chr1:24180246-24184534 FORWARD   Aliases: F16G16.8, F16G16_8	4.6	4.6	0.1	0.3	100.0%	-4.9
15715	AT1G44030.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.8	0.1	0.3	100.0%	-5.1
15716	AT3G27160.1   Symbol: GHS1   ribosomal protein S21 family protein, contains Pfam profile: PF01165 ribosomal protein S21   chr3:10018713-10020327 FORWARD   Aliases: GLUCOSE HYPERSENSITIVE 1, MYF5.3	6.9	7.0	-0.1	-0.3	100.0%	-4.8
15717	AT1G07250.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, similar to UDP-glucose glucosyltransferase GI:453245 from (Manihot esculenta)   chr1:2225899-2227565 FORWARD   Aliases: F10K1.4, F10K1_4	8.3	8.2	0.1	0.3	100.0%	-5.2
15718	AT2G25920.1   expressed protein   chr2:11061369-11063120 REVERSE   Aliases: F17H15.5, F17H15_5	5.2	5.1	0.1	0.3	100.0%	-5.0
15719	AT5G10780.1   expressed protein, HSPC184, Homo sapiens, EMBL:AF151018   chr5:3408347-3410044 FORWARD   Aliases: T30N20.50, T30N20_50	9.5	9.3	0.2	0.3	100.0%	-4.5
15720	AT4G29230.1   Symbol: ANAC075   no apical meristem (NAM) family protein, similar to NAM family proteins GP:12751304.; GP:6223650.; GP:9758909 - Arabidopsis thaliana, PIR2:T04621   chr4:14410344-14414962 FORWARD   Aliases: ANAC075, F17A13.50, F17A13_50	2.8	2.7	0.1	0.3	100.0%	-5.2
15721	AT5G19700.1   MATE efflux protein-related, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr5:6660823-6662349 REVERSE   Aliases: T29J13.120, T29J13_120	6.7	6.6	0.2	0.3	100.0%	-4.0
15722	AT1G70820.1   phosphoglucomutase, putative / glucose phosphomutase, putative, similar to phosphoglucomutase GI:534981 from (Spinacia oleracea), phosphomannomutase (Pseudomonas aeruginosa) GI:150994; contains InterPro accession IPR006352: Phosphoglucosamine mutase   chr1:26709180-26711926 FORWARD   Aliases: F15H11.7, F15H11_7	4.4	4.4	0.1	0.3	100.0%	-5.0
15723	AT4G33480.1   expressed protein   chr4:16105614-16108649 REVERSE   Aliases: F17M5.240, F17M5_240	3.0	3.0	0.0	0.3	100.0%	-5.5
15724	AT5G57760.1   expressed protein   chr5:23417951-23418480 FORWARD   Aliases: MRI1.12, MRI1_12	2.6	2.6	0.0	0.3	100.0%	-5.5
15725	AT1G79320.1   latex abundant protein, putative (AMC5) / caspase family protein, similar to latex-abundant protein (Hevea brasiliensis) gb:AAD13216; contains Pfam domain, PF00656: ICE-like protease (caspase) p20 domain   chr1:29841579-29842801 FORWARD   Aliases: YUP8H12R.6, YUP8H12R_6	3.2	3.4	-0.1	-0.3	100.0%	-4.2
15726	AT1G58070.1   expressed protein   chr1:21506570-21507739 FORWARD   Aliases: T15M6.8, T15M6_8	3.0	2.9	0.1	0.3	100.0%	-4.7
15727	AT3G47810.3   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	11.7	11.6	0.1	0.3	100.0%	-5.3
15728	AT5G48790.1   expressed protein   chr5:19797086-19799266 REVERSE   Aliases: K24G6.12, K24G6_12	7.6	7.5	0.1	0.3	100.0%	-4.5
15729	AT1G45688.2   expressed protein   chr1:17193844-17195598 FORWARD   Aliases: F2G19.25, F2G19_25	5.9	5.8	0.1	0.3	100.0%	-4.6
15730	AT1G64780.1   Symbol: ATAMT1;2   ammonium transporter 1, member 2 (AMT1.2), nearly identical to SP:Q9ZPJ8 Ammonium transporter 1, member 2 (AtAMT1;2) {Arabidopsis thaliana}   chr1:24064433-24066293 REVERSE   Aliases: None	2.9	2.7	0.2	0.3	100.0%	-4.2
15731	AT3G25720.1   expressed protein   chr3:9381471-9382642 FORWARD   Aliases: K13N2.4	3.1	3.2	-0.1	-0.3	100.0%	-4.9
15732	AT1G67070.1   Symbol: DIN9   phosphomannose isomerase, putative (DIN9), contains Pfam profile: PF01238 phosphomannose isomerase type I ;similar to phosphomannose isomerase GI:10834550 from (Arabidopsis thaliana); identical to cDNA phosphomannose isomerase (din9) partial cds GI:10834549   chr1:25045956-25048250 FORWARD   Aliases: DARK INDUCIBLE 9, F1O19.12, F1O19_12	3.0	3.0	0.1	0.3	100.0%	-5.3
15733	AT3G08000.1   RNA-binding protein, putative, similar to RNA-binding protein from (Nicotiana tabacum) GI:15822703, (Nicotiana glauca) GI:624925; contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:2554840-2555847 REVERSE   Aliases: F17A17.34	4.1	4.0	0.0	0.3	100.0%	-5.2
15734	AT5G60030.1   expressed protein   chr5:24189308-24190201 REVERSE   Aliases: MGO3.1	7.2	7.6	-0.3	-0.3	100.0%	-4.6
15735	AT3G29370.1   expressed protein   chr3:11279826-11280345 FORWARD   Aliases: MUO10.6	2.9	2.9	0.1	0.3	100.0%	-5.4
15736	AT3G59280.1   Symbol: TXR1   signaling molecule-related, contains similarity to mitochondria-associated granulocyte macrophage CSF signaling molecule, mitochondrial precursor (CGI-136) (Mus musculus) SWISS-PROT:Q9CQV1   chr3:21919890-21921699 REVERSE   Aliases: F25L23.140, THAXTOMIN A RESISTANT 1	10.6	10.4	0.1	0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15737	AT5G09290.1   3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP:Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family   chr5:2882429-2884099 FORWARD   Aliases: T5E8.90, T5E8_90	2.9	2.8	0.1	0.3	100.0%	-4.7
15738	AT1G80670.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400) (1 weak); similar to Hypothetical RAE1-like protein.(SP:Q38942) (Arabidopsis thaliana); similar to mRNA-associated protein mrnp 41 ((mRNA export protein) (GB:AAC28126) (GI:1903456)(RAE1) (MRNP41) (SP:P78406) (Homo sapiens)   chr1:30325468-30328640 REVERSE   Aliases: F23A5.2, F23A5_2	5.5	5.4	0.1	0.3	100.0%	-4.5
15739	AT4G02090.1   expressed protein   chr4:923100-923916 FORWARD   Aliases: T10M13.10, T10M13_10	3.7	3.8	-0.1	-0.3	100.0%	-4.4
15740	AT2G43640.1   signal recognition particle 14 kDa family protein / SRP14 family protein, similar to SP:P16254 Signal recognition particle 14 kDa protein (SRP14) {Mus musculus}; contains Pfam profile: PF02290 signal recognition particle 14kD protein   chr2:18104578-18106139 REVERSE   Aliases: F18O19.25	8.5	8.6	-0.1	-0.3	100.0%	-5.0
15741	AT1G01770.1   expressed protein   chr1:278615-282891 FORWARD   Aliases: T1N6.18, T1N6_18	5.7	5.6	0.1	0.3	100.0%	-4.8
15742	AT1G78070.2   WD-40 repeat family protein, contains Pfam profile PF00400: WD domain, G-beta repeat   chr1:29359926-29363883 FORWARD   Aliases: F28K19.28, F28K19_28	2.8	2.7	0.1	0.3	100.0%	-5.1
15743	AT4G29580.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase homolog DesB (Arabidopsis thaliana) GI:4836444, cytidine deaminase 9 (CDA9) (Arabidopsis thaliana) GI:5080715; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14510153-14511049 FORWARD   Aliases: T16L4.90, T16L4_90	2.2	2.2	-0.0	-0.3	100.0%	-5.7
15744	AT1G11915.1   expressed protein   chr1:4021823-4023290 FORWARD   Aliases: None	2.9	2.9	0.0	0.3	100.0%	-5.8
15745	AT3G62320.1   expressed protein   chr3:23072780-23073373 REVERSE   Aliases: T12C14.20	2.7	2.7	-0.0	-0.3	100.0%	-5.3
15746	AT2G44240.1   expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr2:18296900-18299421 FORWARD   Aliases: F4I1.5	3.1	3.0	0.0	0.3	100.0%	-5.4
15747	AT4G17060.1   expressed protein   chr4:9593548-9595268 REVERSE   Aliases: None	5.9	5.8	0.1	0.3	100.0%	-4.8
15748	AT3G12220.1   Symbol: SCPL16	2.6	2.6	0.0	0.3	100.0%	-5.4
15749	AT2G29370.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to SP:P50162 Tropinone reductase-I (EC 1.1.1.206) (TR-I) (Tropine dehydrogenase) {Datura stramonium}   chr2:12613136-12614695 FORWARD   Aliases: F16P2.25, F16P2_25	3.6	3.5	0.1	0.3	100.0%	-4.7
15750	AT1G08020.1   expressed protein   chr1:2489773-2490304 REVERSE   Aliases: T6D22.10, T6D22_10	3.5	3.5	-0.1	-0.3	100.0%	-5.0
15751	ATCG00520.1   Symbol: YCF4   hypothetical protein   chrC:59772-60326 FORWARD   Aliases: YCF4	6.5	6.8	-0.4	-0.3	100.0%	-4.6
15752	AT5G45770.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611   chr5:18580795-18582148 FORWARD   Aliases: MRA19.20, MRA19_20	3.4	3.4	0.0	0.3	100.0%	-5.5
15753	AT4G24810.2   similar to ABC1 family protein [Arabidopsis thaliana] (TAIR:At5g50330.1); similar to ABC transporter-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_915227.1); contains InterPro domain ABC1 protein (InterPro:IPR004147)   chr4:12786637-12789723 REVERSE   Aliases: F6I7.20, F6I7_20	4.0	4.1	-0.1	-0.3	100.0%	-4.8
15754	AT2G29900.1   presenilin family protein, similar to presenilin (Drosophila melanogaster) GI:2062395; contains Pfam profile PF01080: Presenilin	5.8	5.8	0.1	0.3	100.0%	-5.1
15755	AT5G16770.2   myb family transcription factor (MYB9), contains Pfam profile: PF00249 Myb-like DNA-binding domain   chr5:5514887-5516939 FORWARD   Aliases: F5E19.110, F5E19_110	3.1	3.2	-0.1	-0.3	100.0%	-5.5
15756	ATCG00490.1   Symbol: RBCL   large subunit of RUBISCO.   chrC:54958-56397 FORWARD   Aliases: RBCL	10.0	9.7	0.3	0.3	100.0%	-5.1
15757	AT5G23060.1   expressed protein   chr5:7736593-7738518 REVERSE   Aliases: MYJ24.5, MYJ24_5	6.1	6.2	-0.1	-0.3	100.0%	-4.3
15758	AT5G14370.1   expressed protein   chr5:4631894-4633716 REVERSE   Aliases: F18O22.160, F18O22_160	3.5	3.5	-0.1	-0.3	100.0%	-4.8
15759	AT5G42780.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, similar to unknown protein (pir::T05568)   chr5:17172004-17172985 FORWARD   Aliases: MJB21.16, MJB21_16	2.9	3.0	-0.1	-0.3	100.0%	-5.2
15760	AT5G28560.1   expressed protein   chr5:10566850-10567134 FORWARD   Aliases: T10I18.20, T10I18_20	3.2	3.2	-0.0	-0.3	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15761	AT3G09410.3   pectinacylesterase family protein, similar to pectinacylesterase precursor GB:CAA67728 (Vigna radiata); contains Pfam profile: PF03283 pectinacylesterase   chr3:2897644-2900990 REVERSE   Aliases: F3L24.30	3.4	3.3	0.1	0.3	100.0%	-4.9
15762	AT3G42070.1   expressed protein   chr3:14268855-14270078 FORWARD   Aliases: F4M19.30	2.6	2.6	0.0	0.3	100.0%	-5.4
15763	AT3G03810.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'auxin-independent growth promoter protein -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr3:972197-976348 REVERSE   Aliases: F20H23.17, F20H23_17	3.3	3.3	0.0	0.3	100.0%	-5.3
15764	AT3G14310.1   Symbol: ATPME3	9.3	9.5	-0.2	-0.3	100.0%	-4.8
15765	AT2G46090.1   Encodes a putative sphingosine kinase (SphK) containing the five conserved domains (C1-C5) previously identified in SphKs.   chr2:18957980-18960347 FORWARD   Aliases: T3F17.26	7.6	7.5	0.1	0.3	100.0%	-4.9
15766	AT3G13580.3   60S ribosomal protein L7 (RPL7D), similar to 60S ribosomal protein L7 GB:AAD14525 GI:4262232 from (Arabidopsis thaliana)	10.2	10.3	-0.1	-0.3	100.0%	-4.9
15767	AT3G45430.1   lectin protein kinase family protein, contains Pfam domains PF00138: Legume lectins alpha domain and PF00069: Protein kinase domain   chr3:16671744-16673585 REVERSE   Aliases: F9K21.10	3.0	2.9	0.0	0.3	100.0%	-5.5
15768	AT1G33400.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr1:12104764-12109500 REVERSE   Aliases: F10C21.7, F10C21_7	5.5	5.4	0.1	0.3	100.0%	-4.9
15769	AT3G10600.1   Symbol: CAT7   amino acid permease family protein, similar to SP:Q09143 High-affinity cationic amino acid transporter-1 (CAT-1) {Mus musculus}; contains Pfam profile PF00324: Amino acid permease   chr3:3313974-3317167 FORWARD   Aliases: CATIONIC AMINO ACID TRANSPORTER 7, F13M14.11	3.0	3.0	-0.1	-0.3	100.0%	-5.1
15770	AT2G44180.1   Symbol: MAP2A   methionyl aminopeptidase, putative / methionine aminopeptidase, putative / peptidase M, putative, similar to SP:P50579 Methionine aminopeptidase 2 (EC 3.4.11.18) (MetAP 2) {Homo sapiens}; contains Pfam profile PF00557: metallopeptidase family M24   chr2:18276351-18278919 REVERSE   Aliases: F6E13.31, METHIONINE AMINOPEPTIDASE 2A	6.5	6.6	-0.1	-0.3	100.0%	-4.9
15771	AT1G06250.1   lipase class 3 family protein, similar to lipase GB:AAD01804 GI:4103627 from (Dianthus caryophyllus); contains Pfam profile PF01764: Lipase   chr1:1913255-1914894 REVERSE   Aliases: F9P14.11, F9P14_11	2.4	2.4	-0.0	-0.3	100.0%	-5.6
15772	AT5G52720.1   similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:At5g52670.1); contains InterPro domain Heavy metal transport/detoxification protein (InterPro:IPR006121)   chr5:21396083-21396970 FORWARD   Aliases: F6N7.21, F6N7_21	2.7	2.7	-0.1	-0.3	100.0%	-5.5
15773	AT4G37330.1   Symbol: CYP81D4   cytochrome P450 family protein   chr4:17562339-17564590 REVERSE   Aliases: F6G17.5	5.8	5.6	0.1	0.3	100.0%	-5.1
15774	AT1G67930.1   Golgi transport complex protein-related, similar to golgi transport complex protein (GTC90) GB:5453670 (Homo sapiens) (stimulates in vitro Golgi transport J. Biol. Chem. 273 (45), 29565-29576 (1998))   chr1:25477222-25481083 REVERSE   Aliases: T23K23.22, T23K23_22	6.3	6.5	-0.2	-0.3	100.0%	-4.7
15775	AT5G46100.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:18711543-18712961 REVERSE   Aliases: MCL19.15, MCL19_15	3.3	3.2	0.1	0.3	100.0%	-5.2
15776	AT1G48960.1   universal stress protein (USP) family protein, contains Pfam PF00582: universal stress protein family; similar to hypothetical protein GI:7770340 from (Arabidopsis thaliana)   chr1:18116154-18117284 FORWARD   Aliases: F27K7.3	5.2	5.1	0.2	0.3	100.0%	-4.5
15777	AT5G59840.1   Ras-related GTP-binding family protein, contains Pfam profile: PF00071 Ras family   chr5:24124441-24126477 REVERSE   Aliases: MMN10.12, MMN10_12	4.7	4.7	0.1	0.3	100.0%	-5.2
15778	AT1G61000.1   Nuf2 family protein, contains Pfam PF03800: Nuf2 family domain; similar to Myosin-like protein NUF2 (Nuclear filament-containing protein 2) (Nuclear division protein nuf2) (Swiss-Prot:Q10173) (Schizosaccharomyces pombe)   chr1:22469433-22477711 REVERSE   Aliases: T7P1.14, T7P1_14	3.7	3.7	0.1	0.3	100.0%	-5.2
15779	AT3G19340.1   expressed protein   chr3:6701279-6704232 REVERSE   Aliases: MLD14.7	7.2	7.3	-0.1	-0.3	100.0%	-4.8
15780	AT3G21175.2   Symbol: ZML1   zinc finger (GATA type) family protein, similar to zinc finger protein ZIM gi:8918533 from (Arabidopsis thaliana); contains Pfam PF00320: GATA zinc finger   chr3:7422045-7424895 FORWARD   Aliases: ZIM LIKE 1	6.0	5.9	0.1	0.3	100.0%	-4.9
15781	AT2G35460.1   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum);   chr2:14912867-14913583 FORWARD   Aliases: T32F12.16, T32F12_16	3.4	3.5	-0.1	-0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15782	AT2G04920.1   F-box family protein (FBX9), identical to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana); contains F-box domain PF:00646; contains TIGRFAM TIGR01640 : F-box protein interaction domain   chr2:1726135-1727265 FORWARD   Aliases: F1O13.5, F1O13_5	3.0	2.9	0.1	0.3	100.0%	-5.3
15783	AT5G64290.1   oxoglutarate/malate translocator, putative, similar to SWISS-PROT:Q41364 2-oxoglutarate/malate translocator, chloroplast precursor. (Spinach){Spinacia oleracea}	7.8	7.5	0.3	0.3	100.0%	-4.6
15784	AT1G33340.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (GI:6492344) (Xenopus laevis)   chr1:12087608-12088938 FORWARD   Aliases: F10C21.3	2.4	2.4	-0.0	-0.3	100.0%	-5.5
15785	AT5G51740.1   peptidase M48 family protein, contains Pfam domain, PF01435: Peptidase family M48   chr5:21034253-21036447 FORWARD   Aliases: MIO24.13, MIO24_13	6.7	6.5	0.2	0.3	100.0%	-4.9
15786	AT5G01310.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain, weak hit to PF01661: Appr-1-p processing enzyme family	3.0	3.1	-0.0	-0.3	100.0%	-5.6
15787	AT4G29720.1   amine oxidase family protein, similar to polyamine oxidase isoform-2 (Homo sapiens) GI:16554963; contains Pfam profile PF01593: amine oxidase, flavin-containing	3.8	3.8	-0.1	-0.3	100.0%	-4.7
15788	AT2G13510.1   hypothetical protein, low similarity to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:5637083-5638189 REVERSE   Aliases: T10F5.5, T10F5_5	3.4	3.3	0.1	0.3	100.0%	-5.0
15789	AT3G46490.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to hyoscyamine 6 beta-hydroxylase from Atropa belladonna (GI:4996123) and Hyoscyamus niger (SP:P24397), gibberellin 20-oxidase (GI:9791186); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr3:17126614-17130275 FORWARD   Aliases: F12A12.10	3.5	3.4	0.1	0.3	100.0%	-5.0
15790	AT1G52320.2   expressed protein, contains Pfam profile: PF04782 protein of unknown function (DUF632)   chr1:19489368-19491102 FORWARD   Aliases: F19K6.7, F19K6_7	5.9	5.7	0.1	0.3	100.0%	-4.8
15791	AT1G07860.1   expressed protein   chr1:2428908-2429428 REVERSE   Aliases: F24B9.36, F24B9_36	2.4	2.5	-0.1	-0.3	100.0%	-5.5
15792	AT3G30310.1   hypothetical protein   chr3:11931181-11931706 FORWARD   Aliases: T6J22.6	2.3	2.3	0.0	0.3	100.0%	-5.8
15793	AT2G15610.1   expressed protein   chr2:6813115-6814534 FORWARD   Aliases: F9O13.16	2.3	2.3	0.0	0.3	100.0%	-5.5
15794	AT5G66950.1   expressed protein   chr5:26750559-26753372 FORWARD   Aliases: K8A10.2, K8A10_2	6.1	6.0	0.1	0.3	100.0%	-4.7
15795	AT3G51410.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g35680.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483701.1); contains InterPro domain Arabidopsis conserved protein (InterPro:IPR004320)   chr3:19092236-19093191 REVERSE   Aliases: F26O13.50	2.6	2.6	-0.1	-0.3	100.0%	-5.2
15796	AT3G28320.1   expressed protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	4.3	4.3	0.1	0.3	100.0%	-5.0
15797	AT5G26760.2   expressed protein   chr5:9403683-9407304 REVERSE   Aliases: F2P16.20, F2P16_20	5.0	5.1	-0.1	-0.3	100.0%	-4.7
15798	AT2G43790.1   Symbol: ATMPK6	4.5	4.3	0.2	0.3	100.0%	-4.9
15799	AT4G31680.1   transcriptional factor B3 family protein, low similarity to reproductive meristem gene 1 (Brassica oleracea var. botrytis) GI:3170424; contains Pfam profile PF02362: B3 DNA binding domain   chr4:15340295-15342086 REVERSE   Aliases: F28M20.130, F28M20_130	2.5	2.5	0.0	0.3	100.0%	-5.4
15800	AT5G54890.1   expressed protein   chr5:22310572-22312370 FORWARD   Aliases: MBG8.16, MBG8_16	5.0	5.1	-0.1	-0.3	100.0%	-5.1
15801	AT5G19050.1   expressed protein   chr5:6369269-6371901 FORWARD   Aliases: T16G12.90, T16G12_90	6.0	5.9	0.1	0.3	100.0%	-4.6
15802	AT1G47420.1   expressed protein, identical to hypothetical protein GB:AAD46040 GI:5668814 from (Arabidopsis thaliana)   chr1:17397958-17399693 REVERSE   Aliases: T3F24.12	12.6	12.4	0.2	0.3	100.0%	-4.8
15803	AT1G34760.1   Symbol: GRF11   14-3-3 protein GF14 omicron (GRF11), identical to SP:Q9S9Z8, 14-3-3-like protein GF14 omicron (General regulatory factor 11){Arabidopsis thaliana}   chr1:12743826-12745581 REVERSE   Aliases: 14 3 3 PROTEIN GF14OMICRON, F11O6.13, GF14 OMICRON	3.4	3.6	-0.2	-0.3	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15804	AT1G69730.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr1:26232295-26235002 REVERSE   Aliases: T6C23.7, T6C23_7	3.6	3.6	0.1	0.3	100.0%	-5.2
15805	AT3G10930.1   expressed protein   chr3:3420135-3420837 REVERSE   Aliases: F9F8.25	6.8	6.6	0.2	0.3	100.0%	-4.8
15806	AT4G38740.1   Symbol: ROC1   peptidyl-prolyl cis-trans isomerase / cyclophilin / rotamase / cyclosporin A-binding protein (ROC1), identical to SP:P34790 Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin) (Cyclosporin A-binding protein) {Arabidopsis thaliana}   chr4:18083389-18084245 REVERSE   Aliases: CYCLOPHILIN, T9A14.20, T9A14_20	9.8	10.1	-0.3	-0.3	100.0%	-4.5
15807	AT3G01380.1   phosphatidylinositolglycan class N (PIG-N) family protein, similar to phosphatidylinositolglycan class N short form GB:BAA82620 (gi:5631308) (Mus musculus)   chr3:144295-149835 REVERSE   Aliases: T13O15.2, T13O15_2	3.4	3.5	-0.0	-0.3	100.0%	-5.4
15808	AT1G19340.1   methyltransferase MT-A70 family protein, contains Pfam profile PF05063: MT-A70 (S-adenosylmethionine-binding subunit of human mRNA:m6A methyltransferase (MTase))   chr1:6684742-6687107 FORWARD   Aliases: F18O14.6, F18O14_6	2.8	2.9	-0.0	-0.3	100.0%	-5.3
15809	ATCG00380.1   Symbol: RPS4   Chloroplast encoded ribosomal protein S4	11.8	11.6	0.2	0.3	100.0%	-5.0
15810	AT5G47570.1   expressed protein   chr5:19309839-19311962 REVERSE   Aliases: MNJ7.16, MNJ7_16	12.3	12.2	0.1	0.3	100.0%	-5.2
15811	AT2G33040.1   ATP synthase gamma chain, mitochondrial (ATPC), identical to SP:Q96250 ATP synthase gamma chain, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; contains Pfam profile: PF00231 ATP synthase   chr2:14025857-14028257 REVERSE   Aliases: F25I18.22, F25I18_22, T21L14.5	12.0	12.1	-0.1	-0.3	100.0%	-5.3
15812	AT1G32940.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr1:11937576-11940958 FORWARD   Aliases: F9L11.11, F9L11_11	4.8	4.7	0.1	0.3	100.0%	-5.0
15813	AT1G54190.1   zinc finger protein-related, similar to zinc finger protein (Arabidopsis thaliana) GI:15811367   chr1:20232705-20234243 FORWARD   Aliases: F20D21.1, F20D21_1	3.2	3.2	0.0	0.3	100.0%	-5.4
15814	AT4G38540.1   monooxygenase, putative (MO2), identical to GI:3426064   chr4:18023173-18025021 FORWARD   Aliases: F20M13.100, F20M13_100	7.4	7.4	-0.1	-0.3	100.0%	-4.8
15815	AT1G52900.1   disease resistance protein (TIR class), putative, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:19705879-19706584 REVERSE   Aliases: F14G24.17, F14G24_17	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15816	AT1G48220.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 (Pti1)(Lycopersicon esculentum) gi:3668069:gb:AAC61805   chr1:17806532-17808623 FORWARD   Aliases: F11A17.22, F11A17_22	2.8	2.8	0.0	0.3	100.0%	-5.3
15817	AT1G65980.2   Symbol: TPX1   similar to peroxiredoxin type 2, putative [Arabidopsis thaliana] (TAIR:At1g65970.1); similar to thioredoxin peroxidase 1 [Lycopersicon esculentum] (GB:AAP34571.1); similar to thioredoxin-dependent peroxidase [Plantago major] (GB:CAH58634.1); contains InterPro domain Alkyl hydroperoxide reductase/ Thiol specific antioxidant/ Mal allergen (InterPro:IPR000866)   chr1:24562969-24564599 REVERSE   Aliases: F12P19.14, F12P19_14, PEROXIREDOXIN TPX1	12.4	12.5	-0.0	-0.3	100.0%	-5.4
15818	AT4G33690.1   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At3g23900.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_480486.1); contains domain LYS_RICH (PS50318)   chr4:16174821-16176241 FORWARD   Aliases: T16L1.180, T16L1_180	6.0	6.2	-0.2	-0.3	100.0%	-4.8
15819	AT3G56990.1   glycine-rich protein, conserved hypothetical protein SPCC330.09 - Schizosaccharomyces pombe, PIR:T41319   chr3:21099242-21103036 REVERSE   Aliases: F24I3.70	4.6	4.5	0.1	0.3	100.0%	-5.1
15820	AT2G17030.1   F-box family protein, similar to hypothetical protein GB:AAB81667 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr2:7406185-7408003 FORWARD   Aliases: F6P23.19, F6P23_19	4.4	4.3	0.1	0.3	100.0%	-4.9
15821	AT2G41940.1   Symbol: ZFP8   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:17514587-17515694 FORWARD   Aliases: T6D20.16, T6D20_16, ZFP8, ZINC FINGER PROTEIN 8	2.7	2.6	0.1	0.3	100.0%	-5.4
15822	AT1G35320.1   expressed protein   chr1:12960432-12962831 REVERSE   Aliases: T9I1.9, T9I1_9	4.6	4.7	-0.1	-0.3	100.0%	-4.7
15823	AT1G16460.3   Symbol: ATRDH2	9.5	9.3	0.2	0.3	100.0%	-4.9
15824	AT1G15990.1   Symbol: ATCNGC7   cyclic nucleotide-regulated ion channel, putative (CNGC7), similar to cyclic nucleotide and calmodulin-regulated ion channel protein GI:4581207 from (Arabidopsis thaliana)   chr1:5491298-5493766 REVERSE   Aliases: CNGC7, CYCLIC NUCLEOTIDE GATED CHANNEL 7, T24D18.9, T24D18_9	2.7	2.6	0.0	0.3	100.0%	-5.4
15825	AT2G05910.1   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr2:2258297-2259378 REVERSE   Aliases: T6P5.11, T6P5_11	4.9	5.0	-0.0	-0.3	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15826	AT5G05690.2   Symbol: CPD   similar to steroid 22-alpha-hydroxylase (CYP90B1) (DWF4) [Arabidopsis thaliana] (TAIR:At3g50660.1); similar to cytochrome P450 [Nicotiana tabacum] (GB:CAD27417.1); contains InterPro domain E-class P450, group I (InterPro:IPR002401); contains InterPro domain Cytochrome P450 (InterPro:IPR001128)   chr5:1702689-1706788 REVERSE   Aliases: CABBAGE 3, CBB3, CONSTITUTIVE PHOTOMORPHOGENIC DWARF, CYP90, CYP90A, CYP90A1, CYTOCHROME P450, CYTOCHROME P450 MONOOXYGENASE, DWARF 3, DWF3, MJJ3.9, MJJ3_9	6.3	6.4	-0.1	-0.3	100.0%	-4.6
15827	AT1G63400.1   pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR-repeats Pfam profile: PF01535   chr1:23510985-23512718 FORWARD   Aliases: F2K11.22, F2K11_22	3.2	3.1	0.0	0.3	100.0%	-5.3
15828	AT5G44070.1   Symbol: CAD1   phytochelatin synthase 1 (PCS1), identical to phytochelatin synthase (Arabidopsis thaliana) gi:18254401:gb:AAL66747; identical to cDNA phytochelatin synthase, GI:18254400   chr5:17751985-17755066 FORWARD   Aliases: ARA8, ATPCS1, CADMIUM SENSITIVE 1, MRH10.18, MRH10_18, PCS1, PHYTOCHELATIN SYNTHASE	7.9	8.0	-0.1	-0.3	100.0%	-5.0
15829	AT2G36030.1   expressed protein   chr2:15134638-15134850 REVERSE   Aliases: F11F19.6, F11F19_6	3.6	3.5	0.1	0.3	100.0%	-5.3
15830	AT5G51250.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr5:20847969-20849075 FORWARD   Aliases: MWD22.20, MWD22_20	3.7	3.8	-0.0	-0.3	100.0%	-5.5
15831	AT1G65210.1   hypothetical protein   chr1:24228475-24229478 FORWARD   Aliases: T23K8.12, T23K8_12	2.3	2.3	-0.0	-0.3	100.0%	-5.9
15832	AT4G01150.1   expressed protein   chr4:493548-494795 FORWARD   Aliases: F2N1.18, F2N1_18	10.0	10.2	-0.2	-0.3	100.0%	-4.6
15833	AT1G30240.1   similar to proline-, glutamic acid-, leucine-rich protein 1 [Mus musculus] (GB:NP_083507.2)   chr1:10641083-10645919 REVERSE   Aliases: F12P21.4, F12P21_4	5.6	5.7	-0.1	-0.3	100.0%	-4.5
15834	AT1G16810.2   similar to CGI-144-like protein [Lycopersicon esculentum] (GB:CAC81814.1)   chr1:5755610-5756888 FORWARD   Aliases: F17F16.25	10.5	10.4	0.1	0.3	100.0%	-5.2
15835	AT2G16960.1   importin beta-2 subunit family protein, contains weak hit to Pfam PF02985: HEAT repeat (4 copies); contains weak hit to Pfam PF03130: PBS lyase HEAT-like repeat (2 copies); supported by tandem duplication of importin beta family protein (TIGR_Ath1:At2g16950) (Arabidopsis thaliana); similar to Importin beta-2 subunit (Karyopherin beta-2 subunit) (Transportin) (M9 region interaction protein) (MIP) (Swiss-Prot:Q92973) (Homo sapiens)   chr2:7371765-7376045 FORWARD   Aliases: F12A24.14, F12A24_14	3.4	3.4	0.1	0.3	100.0%	-5.4
15836	AT1G13400.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type. Activated by AGAMOUS in a cal-1, ap1-1 background. Expressed in stamen primordia and the placental region of carpels.   chr1:4597624-4598908 FORWARD   Aliases: T6J4.23, T6J4_23	2.5	2.4	0.1	0.3	100.0%	-5.3
15837	AT2G27870.1   expressed protein   chr2:11874328-11875272 REVERSE   Aliases: T1E2.21	2.5	2.4	0.1	0.3	100.0%	-5.3
15838	AT1G66770.1   nodulin MtN3 family protein, contains Pfam PF03083 MtN3/saliva family; similar to LIM7 (cDNAs induced in meiotic prophase in lily microsporocytes) GI:431154 from (Lilium longiflorum)   chr1:24910114-24910899 REVERSE   Aliases: F4N21.10, F4N21_10	3.3	3.2	0.1	0.3	100.0%	-5.3
15839	AT1G26640.1   aspartate/glutamate/uridylate kinase family protein, contains Pfam amino acid kinase family PF00696   chr1:9206978-9209887 REVERSE   Aliases: T24P13.2, T24P13_2	7.7	7.9	-0.2	-0.3	100.0%	-4.8
15840	AT4G14780.1   protein kinase, putative, similar to protein kinase ATMRK1 (Arabidopsis thaliana) gi:2351097:dbj:BAA22079   chr4:8492827-8494586 FORWARD   Aliases: DL3430W, FCAALL.308	3.9	3.9	0.1	0.3	100.0%	-4.9
15841	AT2G46760.1   FAD-binding domain-containing protein, strong similarity to At1g32300, At2g46740, At2g46750, At5g56490; contains PF01565: FAD binding domain   chr2:19220098-19222236 REVERSE   Aliases: F19D11.4	3.1	3.2	-0.1	-0.3	100.0%	-4.6
15842	AT4G18590.1   expressed protein   chr4:10236256-10237196 FORWARD   Aliases: F28J12.250, F28J12_250	6.2	6.3	-0.1	-0.3	100.0%	-4.8
15843	AT3G16880.1   F-box protein-related, contains weak hit to Pfam PF00646: F-box domain; contains weak hit to TIGRFAM TIGR01640: F-box protein interaction domain	2.8	2.9	-0.1	-0.3	100.0%	-5.3
15844	AT3G22190.1   calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:7831668-7833519 REVERSE   Aliases: MKA23.10	4.1	4.1	0.1	0.3	100.0%	-5.1
15845	AT3G14380.1   integral membrane family protein, similar to unknown protein GB:AAD50013 from (Arabidopsis thaliana); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588); contains 4 transmembrane domains   chr3:4802959-4803818 REVERSE   Aliases: MLN21.16	4.7	4.6	0.1	0.3	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15846	AT2G31680.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:289370 from ( <i>Brassica napus</i> )   chr2:13480671-13482129 REVERSE   Aliases: T9H9.20, T9H9_20	4.5	4.4	0.1	0.3	100.0%	-5.2
15847	AT4G15200.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr4:8663499-8665759 REVERSE   Aliases: DL3645C, FCAALL.218	2.3	2.3	0.0	0.3	100.0%	-5.7
15848	AT3G44560.1   acyl CoA reductase, putative, similar to acyl CoA reductase ( <i>Simmondsia chinensis</i> ) GI:5020215; contains Pfam profile PF03015: Male sterility protein   chr3:16162164-16165384 FORWARD   Aliases: F14L2.110	2.0	2.0	-0.0	-0.3	100.0%	-6.1
15849	AT2G20060.1   ribosomal protein L4 family protein, contains Pfam profile PF00573: ribosomal protein L4/L1 family   chr2:8666124-8668562 FORWARD   Aliases: T2G17.14, T2G17_14	9.5	9.7	-0.1	-0.3	100.0%	-4.6
15850	AT1G17640.1   RNA recognition motif (RRM)-containing protein, similar to GB:L02953 from ( <i>Xenopus laevis</i> ) (Nucleic Acids Res. 21, 999-1006 (1993)); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:6067387-6069091 REVERSE   Aliases: F11A6.17	4.4	4.4	-0.1	-0.3	100.0%	-5.2
15851	AT1G21850.1   Symbol: SKS8   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)( <i>Brassica napus</i> ); contains Pfam profile: PF00394 Multicopper oxidase   chr1:7667792-7670519 REVERSE   Aliases: SKS8, T26F17.6, T26F17_6	2.9	2.8	0.1	0.3	100.0%	-5.2
15852	AT4G32980.1   Symbol: ATH1   homeobox protein (ATH1), identical to SWISS-PROT:P48731 homeobox protein ATH1. ( <i>Arabidopsis thaliana</i> )   chr4:15914725-15918047 REVERSE   Aliases: ARABIDOPSIS THALIANA HOMEBOX GENE 1, F26P21.100, F26P21_100	2.8	2.8	0.0	0.3	100.0%	-5.4
15853	AT3G14130.1   (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative, similar to Chain A, Glycolate Oxidase (E.C.1.1.3.15) Mutant With Tyr 24 Replaced By Phe (Y24f) gi:999542   chr3:4685653-4688316 REVERSE   Aliases: MAG2.2	4.3	4.5	-0.1	-0.3	100.0%	-4.5
15854	AT3G14150.1   (S)-2-hydroxy-acid oxidase, peroxisomal, putative / glycolate oxidase, putative / short chain alpha-hydroxy acid oxidase, putative, similar to (S)-2-hydroxy-acid oxidase, peroxisomal (Glycolate oxidase, GOX) (Short chain alpha-hydroxy acid oxidase) ( <i>Spinacia oleracea</i> ) SWISS-PROT:P05414   chr3:4690457-4692997 REVERSE   Aliases: MAG2.11	4.3	4.5	-0.1	-0.3	100.0%	-4.5
15855	AT2G25240.1   serpin, putative / serine protease inhibitor, putative, similar to phloem serpin-1 ( <i>Cucurbita maxima</i> ) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr2:10758847-10760206 REVERSE   Aliases: T22F11.17, T22F11_17	4.9	5.0	-0.1	-0.3	100.0%	-4.9
15856	AT3G03900.1   adenylylsulfate kinase, putative, similar to adenylylsulfate kinase 1, chloroplast precursor (APS kinase, Adenosine-5'-phosphosulfate kinase, ATP adenosine-5'- phosphosulfate 3'-phosphotransferase) ( <i>Arabidopsis thaliana</i> ) SWISS-PROT:Q43295   chr3:1002982-1004278 REVERSE   Aliases: F20H23.5, F20H23_5	6.5	6.4	0.1	0.3	100.0%	-4.7
15857	AT2G32000.2   similar to DNA topoisomerase III alpha, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g63920.1); similar to topoisomerase (DNA) III beta [ <i>Mus musculus</i> ] (GB:NP_035754.1); similar to TOP3B [ <i>Homo sapiens</i> ] (GB:CAG30482.1); similar to Topoisomerase (DNA) III beta [ <i>Homo sapiens</i> ] (GB:AAH02432.1); similar to PREDICTED: similar to topoisomerase III beta [ <i>Rattus norvegicus</i> ] (GB:XP_213564.3); similar to MGC53016 protein [ <i>Xenopus laevis</i> ] (GB:AAH46848.1); contains InterPro domain DNA topoisomerase I, DNA-binding (InterPro:IPR003602); contains InterPro domain DNA topoisomerase I (InterPro:IPR000380); contains InterPro domain DNA topoisomerase I, ATP-binding (InterPro:IPR003601)   chr2:13623013-13628718 REVERSE   Aliases: F22D22.25, F22D22_25	4.7	4.8	-0.1	-0.3	100.0%	-4.8
15858	AT5G01110.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer ( <i>Petunia x hybrida</i> ) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr5:41770-44374 REVERSE   Aliases: F7J8.90, F7J8_90	4.0	3.9	0.1	0.3	100.0%	-4.7
15859	AT4G36780.1   brassinosteroid signalling positive regulator-related, contains similarity to BZR1 protein ( <i>Arabidopsis thaliana</i> ) gi:20270971:gb:AAM18490   chr4:17332523-17334347 REVERSE   Aliases: AP22.34, AP22_34	3.2	3.1	0.0	0.3	100.0%	-5.4
15860	AT1G10810.1   aldo/keto reductase family protein, contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr1:3599370-3600758 FORWARD   Aliases: T16B5.5, T16B5_5	2.6	2.6	0.0	0.3	100.0%	-5.4
15861	AT2G47940.1   Symbol: DEGP2   DegP2 protease (DEGP2), identical to DegP2 protease GI:13172275 from ( <i>Arabidopsis thaliana</i> ); identical to cDNA DegP2 protease (DEGP2) nuclear gene for chloroplast product GI:13172274	4.8	4.9	-0.1	-0.3	100.0%	-4.7
15862	AT3G45820.1   expressed protein   chr3:16851015-16851968 REVERSE   Aliases: F16L2.30	2.2	2.2	0.0	0.3	100.0%	-5.7
15863	AT5G53800.1   expressed protein   chr5:21865361-21867337 FORWARD   Aliases: MGN6.19, MGN6_19	9.7	9.5	0.2	0.3	100.0%	-4.7
15864	AT2G46260.1   BTB/POZ domain-containing protein, contains Pfam PF00651: BTB/POZ domain; contains Interpro IPR000210/ PS50097: BTBB/POZ domain; similar to POZ/BTB containing-protein AtPOB1 (GI:12006855) ( <i>Arabidopsis thaliana</i> ); similar to actinfilin (GI:21667852) ( <i>Rattus norvegicus</i> )   chr2:19003041-19005706 FORWARD   Aliases: T3F17.9	6.0	6.0	-0.1	-0.3	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15865	AT3G50260.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr3:18645558-18646380 FORWARD   Aliases: F11C1.100	4.8	4.6	0.1	0.3	100.0%	-4.6
15866	AT5G64000.1   Symbol: SAL2   3'(2'),5'-bisphosphate nucleotidase, putative / inositol polyphosphate 1-phosphatase, putative, similar to SP:Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family   chr5:25633864-25635850 FORWARD   Aliases: ATSAL2, MBM17.10, MBM17_10	3.4	3.3	0.1	0.3	100.0%	-5.0
15867	AT5G39660.2   Dof-type zinc finger domain-containing protein, similar to H-protein promoter binding factor-2a GI:3386546 from (Arabidopsis thaliana)   chr5:15895954-15898272 FORWARD   Aliases: MIJ24.16, MIJ24_16	6.0	6.0	0.1	0.3	100.0%	-4.8
15868	AT2G45840.1   expressed protein   chr2:18876335-18878561 FORWARD   Aliases: F4I18.18	2.8	2.8	0.1	0.3	100.0%	-5.2
15869	AT4G00940.1   Dof-type zinc finger domain-containing protein, similar to DNA-binding protein DAG1/BBFa GI:4581965 (Arabidopsis thaliana)   chr4:403320-404234 REVERSE   Aliases: A_TM018A10.25, A_TM018A10_25, T18A10.24, T18A10_24	3.2	3.4	-0.1	-0.3	100.0%	-5.0
15870	AT1G63930.1   expressed protein, ; expression supported by MPSS   chr1:23731590-23732837 FORWARD   Aliases: T12P18.5, T12P18_5	3.7	3.5	0.1	0.3	100.0%	-4.7
15871	AT1G11770.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:3975705-3977378 FORWARD   Aliases: F25C20.7, F25C20_7	2.4	2.3	0.0	0.3	100.0%	-5.6
15872	AT2G26650.1   Symbol: AKT1   potassium channel protein 1 (AKT1), identical to AKT1 (Arabidopsis thaliana) gi:563112:gb:AAA96810; member of the 1 pore, 6 transmembrane (1P/6TM- Shaker-type) K+ channel family, PMID:11500563	5.8	5.7	0.1	0.3	100.0%	-4.7
15873	AT5G15710.1   F-box family protein, unusual floral organs protein UFO - Arabidopsis thaliana, PIR:S57710   chr5:5122495-5124374 FORWARD   Aliases: F14F8.90, F14F8_90	4.6	4.7	-0.1	-0.3	100.0%	-4.9
15874	AT2G41930.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:17508708-17509762 FORWARD   Aliases: T6D20.17, T6D20_17	3.6	3.6	0.1	0.3	100.0%	-5.1
15875	AT2G20790.3   expressed protein, weak similarity to clathrin-adaptor medium chain apm 3 (GI:12000359) (Dictyostelium discoideum); weak similarity to Adapter-related protein complex 3 mu 2 subunit (Clathrin coat assembly protein AP47 homolog 2) (Golgi adaptor AP-1 47 kDa protein homolog 2) (HA1 47 kDa subunit homolog 2) (P47B) (Swiss-Prot:P53678) (Rattus norvegicus)   chr2:8957607-8959772 REVERSE   Aliases: F5H14.24, F5H14_24	5.7	5.7	-0.1	-0.3	100.0%	-5.0
15876	AT1G20670.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr1:7164527-7167923 REVERSE   Aliases: F2D10.15, F2D10_15	3.8	3.7	0.1	0.3	100.0%	-4.9
15877	AT3G29160.3   Symbol: AKIN11	6.3	6.2	0.1	0.3	100.0%	-4.9
15878	AT5G03400.1   expressed protein   chr5:837918-839201 REVERSE   Aliases: F12E4.140, F12E4_140	3.6	3.6	0.1	0.3	100.0%	-5.5
15879	AT2G25720.1   expressed protein   chr2:10962597-10963130 REVERSE   Aliases: F3N11.17, F3N11_17	9.8	9.9	-0.1	-0.3	100.0%	-4.6
15880	AT5G03795.1   similar to exostosin family protein [Arabidopsis thaliana] (TAIR:At3g07620.1); similar to EXO [Cucumis melo] (GB:AAU04753.1); contains InterPro domain Exostosin-like (InterPro:IPR004263)   chr5:1007389-1010472 REVERSE   Aliases: None	3.6	3.5	0.1	0.3	100.0%	-4.8
15881	AT5G28890.1   expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr5:10904106-10904804 REVERSE   Aliases: F7P1.70, F7P1_70	2.8	2.8	0.1	0.3	100.0%	-5.6
15882	AT2G41510.1   FAD-binding domain-containing protein / cytokinin oxidase family protein, similar to cytokinin oxidase, Zea mays (gi:3882018) (gi:3441978)   chr2:17321704-17323939 FORWARD   Aliases: T32G6.3, T32G6_3	2.8	2.7	0.1	0.3	100.0%	-5.3
15883	AT1G62680.1   pentatricopeptide (PPR) repeat-containing protein, contains multiple PPR repeats Pfam Profile: PF01535   chr1:23211912-23213540 REVERSE   Aliases: F23N19.22, F23N19_22	3.7	3.7	0.1	0.3	100.0%	-5.2
15884	AT5G28940.1   hypothetical protein   chr5:10985292-10987604 REVERSE   Aliases: F3F24.40, F3F24_40	2.3	2.4	-0.0	-0.3	100.0%	-5.6
15885	AT1G62940.1   4-coumarate--CoA ligase family protein / 4-coumaroyl-CoA synthase family protein, similar to gi:112801 from Petroselinum crispum, GB:AAD40664 from (Solanum tuberosum) (J. Biol. Chem. 266 (13), 8551-8559 (1991)); contains Pfam AMP-binding enzyme domain PF00501   chr1:23314219-23316412 FORWARD   Aliases: F16P17.9, F16P17_9	2.8	2.9	-0.0	-0.3	100.0%	-5.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15886	AT5G49680.1   cell expansion protein, putative, similar to SABRE (Arabidopsis thaliana) GI:719291   chr5:20199258-20205533 FORWARD   Aliases: K2I5.4, K2I5_4	3.8	4.1	-0.2	-0.3	100.0%	-4.6
15887	AT4G28670.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:14151393-14153941 FORWARD   Aliases: T5F17.120, T5F17_120	2.7	2.6	0.1	0.3	100.0%	-5.4
15888	AT1G01010.1   Symbol: ANAC001   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAC domain protein NAM GB: AAD17313 GI:4325282 from (Arabidopsis thaliana)   chr1:3631-5899 FORWARD   Aliases: ANAC001, T25K16.1, T25K16_1	2.5	2.4	0.1	0.3	100.0%	-5.2
15889	AT2G41470.1   embryo-specific protein-related, similar to embryo-specific protein 3 (ATS3) (Arabidopsis thaliana) GI:3335171   chr2:17299223-17303439 REVERSE   Aliases: T26J13.6, T26J13_6	3.9	3.9	-0.0	-0.3	100.0%	-5.6
15890	AT3G08750.1   F-box family protein, contains F-box domain Pfam:PF00646	2.9	3.0	-0.1	-0.3	100.0%	-5.3
15891	AT5G65850.1   F-box family protein   chr5:26363543-26364721 FORWARD   Aliases: K14B20.2, K14B20_2	3.4	3.3	0.1	0.3	100.0%	-5.1
15892	AT3G51070.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr3:18980048-18983271 FORWARD   Aliases: F24M12.110	2.8	2.7	0.1	0.3	100.0%	-5.3
15893	ATCG01020.1   Symbol: RPL32   encodes a chloroplast ribosomal protein L32, a constituent of the large subunit of the ribosomal complex   chrC:113449-113607 FORWARD   Aliases: RPL32	11.0	10.8	0.2	0.3	100.0%	-5.1
15894	AT2G19300.1   expressed protein   chr2:8375122-8375301 REVERSE   Aliases: F27F23.10, F27F23_10	2.7	2.7	0.0	0.3	100.0%	-5.7
15895	AT2G01290.1   expressed protein   chr2:148918-150381 REVERSE   Aliases: F10A8.17, F10A8_17	6.3	6.2	0.1	0.3	100.0%	-4.3
15896	AT4G29380.1   protein kinase family protein / WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; contains Pfam PF00069: Protein kinase domain; contains PF02985: HEAT repeat; similar to adaptor protein (GI:1817584) (Homo sapiens); similar to VPS15 protein (GI:6103009) (Pichia pastoris)   chr4:14458828-14464865 FORWARD   Aliases: F17A13.200, F17A13_200	6.1	6.2	-0.1	-0.3	100.0%	-4.9
15897	AT3G12610.1   Symbol: DRT100	4.0	4.1	-0.1	-0.3	100.0%	-4.5
15898	AT3G43900.1   hypothetical protein, predicted protein, Arabidopsis thaliana   chr3:15757827-15758081 FORWARD   Aliases: T15B3.40	3.3	3.2	0.1	0.3	100.0%	-4.9
15899	AT5G28790.1   hypothetical protein   chr5:10820177-10820529 FORWARD   Aliases: T32B20.80, T32B20_80	2.3	2.3	0.0	0.3	100.0%	-5.8
15900	AT1G23600.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220; expression supported by MPSS   chr1:8361187-8362347 REVERSE   Aliases: F28C11.31	2.8	2.7	0.0	0.3	100.0%	-5.3
15901	AT5G03260.1   laccase, putative / diphenol oxidase, putative, similar to laccase (Pinus taeda)(GI:13661207)   chr5:777020-779423 REVERSE   Aliases: F15A17.290, F15A17_290	4.1	3.9	0.1	0.3	100.0%	-4.8
15902	AT3G56520.1   no apical meristem (NAM) family protein, similar to nam-like protein 5 (GI:21105738 ) (Petunia x hybrida); hypothetical protein SENU5, senescence up-regulated - Lycopersicon esculentum, PIR:T07182   chr3:20958086-20958710 REVERSE   Aliases: T5P19.170	2.4	2.4	-0.0	-0.3	100.0%	-5.9
15903	AT2G27395.1   cysteine protease-related, contains similarity to senescence-specific cysteine protease GI:5823018 from (Brassica napus)	2.9	3.0	-0.1	-0.3	100.0%	-5.4
15904	AT1G15710.1   prephenate dehydrogenase family protein, contains Pfam profile: PF02153 prephenate dehydrogenase	6.9	7.2	-0.2	-0.3	100.0%	-4.3
15905	AT1G55640.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) GI:4877285; contains Pfam profile PF03208: Prenyated rab acceptor (PRA1)   chr1:20797437-20798000 FORWARD   Aliases: F20N2.7	3.3	3.2	0.1	0.3	100.0%	-4.9
15906	AT3G25905.1   Symbol: CLE27   CLE27, putative, CLAVATA3/ESR-Related 27 (CLE27)   chr3:9487405-9488008 REVERSE   Aliases: CLAVATA3/ESR RELATED 27	2.7	2.6	0.1	0.3	100.0%	-5.3
15907	AT1G58390.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	3.1	0.0	0.3	100.0%	-5.5
15908	AT2G18230.1   inorganic pyrophosphatase (soluble) (PPA) / pyrophosphate phospho-hydrolase / PPase, nearly identical to SP:P21216 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase) {Arabidopsis thaliana}   chr2:7939009-7941411 REVERSE   Aliases: T30D6.26, T30D6_26	10.0	10.2	-0.3	-0.3	100.0%	-4.5
15909	AT3G55670.1   hypothetical protein, various predicted proteins, Arabidopsis thaliana   chr3:20668992-20670482 REVERSE   Aliases: F1I16.80	3.1	3.2	-0.0	-0.3	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15910	AT5G47030.1   ATP synthase delta' chain, mitochondrial, identical to SP:Q96252 ATP synthase delta' chain, mitochondrial precursor (EC 3.6.3.14) {Arabidopsis thaliana}; contains Pfam profile PF02823: ATP synthase, Delta/Epsilon chain, beta-sandwich domain	8.6	9.0	-0.4	-0.3	100.0%	-4.4
15911	AT2G25680.1   expressed protein, ; expression supported by MPSS   chr2:10940139-10941615 REVERSE   Aliases: F3N11.13, F3N11_13	4.8	4.7	0.1	0.3	100.0%	-4.3
15912	AT3G26480.1   transducin family protein / WD-40 repeat family protein, contains Pfam profile: PF00400 WD domain, G-beta repeat (5 copies, 2 below cutoff); related to LACK protective antigen (GI:13625467) (Leishmania donovani)   chr3:9688510-9692064 REVERSE   Aliases: F20C19.21	3.6	3.5	0.1	0.3	100.0%	-4.9
15913	AT5G12020.1   17.6 kDa	4.3	4.3	-0.1	-0.3	100.0%	-4.7
15914	AT3G24780.1   expressed protein   chr3:9049453-9051600 FORWARD   Aliases: K7P8.7	2.8	2.9	-0.1	-0.3	100.0%	-5.5
15915	AT4G31920.1   Symbol: ARR10   two-component responsive regulator family protein / response regulator family protein, contains Pfam profile: PF00072 response regulator receiver domain   chr4:15444140-15446929 REVERSE   Aliases: ARABIDOPSIS RESPONSE REGULATOR 10, F11C18.3	8.0	7.8	0.2	0.3	100.0%	-4.7
15916	AT2G03820.1   nonsense-mediated mRNA decay NMD3 family protein, contains Pfam profile: PF04981 NMD3 family   chr2:1164954-1167026 REVERSE   Aliases: T18C20.2, T18C20_2	6.9	7.0	-0.1	-0.3	100.0%	-4.9
15917	AT5G13320.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr5:4268905-4271054 FORWARD   Aliases: T22N19.5	2.5	2.6	-0.0	-0.3	100.0%	-5.4
15918	AT3G53000.1   Symbol: ATPP2 A15   F-box family protein / SKP1 interacting partner 3-related, low similarity to SKP1 interacting partner 3 (Arabidopsis thaliana) GI:10716951; contains Pfam profile PF00646: F-box domain   chr3:19665046-19667058 FORWARD   Aliases: ATPP2 A15, F8J2.170	4.9	4.8	0.1	0.3	100.0%	-4.7
15919	AT3G23690.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	8.7	8.7	-0.1	-0.3	100.0%	-5.0
15920	AT1G71160.1   beta-ketoacyl-CoA synthase family protein, similar to fatty acid elongase 3-ketoacyl-CoA synthase 1 GB:AAC99312, very-long-chain fatty acid condensing enzyme CUT1 (GI:5001734)   chr1:26832363-26833870 REVERSE   Aliases: F23N20.15, F23N20_15	2.7	2.8	-0.1	-0.3	100.0%	-5.5
15921	AT5G46510.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18877678-18884240 FORWARD   Aliases: K11I1.10, K11I1_10	2.6	2.7	-0.0	-0.3	100.0%	-5.6
15922	AT3G26744.4   Symbol: ICE1   similar to basic helix-loop-helix (bHLH) family protein / F-box family protein [Arabidopsis thaliana] (TAIR:At1g12860.1); similar to transcription factor ICE1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD88203.1); similar to OSJNBa0093F16.27 [Oryza sativa (japonica cultivar-group)] (GB:NP_914885.1)   chr3:9834843-9836454 REVERSE   Aliases: INDUCER OF CBF EXPRESSION 1, MDJ14.8	6.6	6.6	0.1	0.3	100.0%	-5.0
15923	AT5G64370.1   Symbol: PYD3   PYD3 encodes a beta-ureidopropionase which, when expressed in E. coli, has been shown to convert beta-ureidopropionate into beta-alanine.   chr5:25756441-25758438 FORWARD   Aliases: MSJ1.21, MSJ1_21, PYD3	8.8	8.7	0.2	0.3	100.0%	-4.9
15924	AT5G42560.1   abscisic acid-responsive HVA22 family protein, weak similarity to SP:Q00765 Polyposis locus protein 1 (TB2 protein) {Homo sapiens}; contains Pfam profile PF03134: TB2/DP1, HVA22 family	4.8	4.9	-0.1	-0.3	100.0%	-4.7
15925	AT1G19830.1   auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR21 (GI:10185818) (Tulipa gesneriana)   chr1:6852146-6852846 FORWARD   Aliases: F14P1.18, F14P1_18	2.6	2.6	-0.0	-0.3	100.0%	-5.5
15926	AT3G62490.1   expressed protein, hypothetical proteins - Arabidopsis thaliana   chr3:23123476-23125975 REVERSE   Aliases: T12C14.190	2.4	2.4	0.0	0.3	100.0%	-6.1
15927	AT2G26950.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:11507907-11509118 REVERSE   Aliases: T20P8.20, T20P8_20	2.5	2.5	0.0	0.3	100.0%	-5.3
15928	AT5G07370.4   Symbol: IPK2a   inositol polyphosphate 6-/3-/5-kinase 2a (IPK2a), contains Pfam domain, PF03770: Inositol polyphosphate kinase   chr5:2330400-2332282 FORWARD   Aliases: ATIPK2A, INOSITOL POLYPHOSPHATE KINASE 2 ALPHA, T2I1.80, T2I1_80	6.4	6.5	-0.1	-0.3	100.0%	-5.1
15929	AT5G66630.1   LIM domain-containing protein, contains low similarity to Pfam profile PF00412: LIM domain   chr5:26609874-26613147 FORWARD   Aliases: K1F13.31, K1F13_31	2.7	2.7	0.0	0.3	100.0%	-5.5
15930	AT1G34550.1   Symbol: EMB2756   expressed protein, contains Pfam profile PF04765: Protein of unknown function (DUF616); expression supported by MPSS   chr1:12646794-12652624 REVERSE   Aliases: EMB2756, EMBRYO DEFECTIVE 2756, F12K21.12, F12K21_12	5.8	5.9	-0.1	-0.3	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15931	AT4G16950.2   Symbol: RPP5   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.; closest homolog in Col-0 to RPP5 of clutivar Landsberg erecta.   chr4:9538821-9544486 REVERSE   Aliases: DISEASE RESISTANCE PROTEIN RPP5, DL4505C, FCAALL.315, RECOGNITION OF PERONOSPORA PARASITICA 5	3.4	3.3	0.1	0.3	100.0%	-4.6
15932	AT5G22940.1   exostosin family protein, contains Pfam profile: PF03016	3.5	3.5	-0.1	-0.3	100.0%	-5.1
15933	AT3G26400.1   Symbol: EIF4B1	5.9	5.9	0.1	0.3	100.0%	-4.7
15934	AT4G07450.1   expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	2.3	2.5	-0.2	-0.3	100.0%	-4.3
15935	AT4G25410.1   basix helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.2	-0.0	-0.3	100.0%	-5.6
15936	AT3G59850.1   polygalacturonase, putative / pectinase, putative, similar to SP:P48979 Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) {Prunus persica}; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr3:22120141-22122586 REVERSE   Aliases: F24G16.120	2.6	2.6	0.0	0.3	100.0%	-5.4
15937	AT3G30150.1   expressed protein   chr3:11784635-11785591 REVERSE   Aliases: T20F20.5	2.8	2.8	0.1	0.3	100.0%	-5.5
15938	AT4G22910.1   similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At4g11920.1); similar to cell cycle switch protein [Medicago sativa subsp. x varia] (GB:AAD22612.1); similar to cell cycle switch protein CCS52a [Lupinus albus] (GB:AAQ54907.1); similar to Putative cell cycle switch protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468588.1); similar to WD-repeat cell cycle regulatory protein [Medicago truncatula] (GB:AAF37386.1); contains InterPro domain Cdc20/Fizzy (InterPro:IPR000002); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr4:12012702-12016022 FORWARD   Aliases: F7H19.90, F7H19_90	4.0	4.1	-0.1	-0.3	100.0%	-5.0
15939	AT1G29770.1   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr1:10424561-10425627 FORWARD   Aliases: F1N18.17, F1N18_17	2.2	2.2	-0.0	-0.3	100.0%	-6.1
15940	AT1G60960.1   Symbol: IRT3   metal transporter, putative (IRT3), identical to putative metal transporter IRT3 (Arabidopsis thaliana) gi:17385796:gb:AAL38438; similar to iron-regulated transporter 1 (Lycopersicon esculentum) gi:9716481:gb:AAF97509; member of the Zinc (Zn <sup>2+</sup> )-Iron (Fe <sup>2+</sup> ) permease (ZIP) family, PMID:11500563   chr1:22448988-22450810 REVERSE   Aliases: T7P1.10, T7P1_10	8.0	8.0	-0.1	-0.3	100.0%	-4.9
15941	AT4G37820.1   expressed protein, Kaposi's sarcoma-associated herpes-like virus ORF73gene, Kaposi's sarcoma-associated herpesvirus, U52064   chr4:17785249-17787465 FORWARD   Aliases: T28I19.100, T28I19_100	5.9	5.8	0.1	0.3	100.0%	-4.5
15942	AT4G26740.1   Symbol: ATS1   embryo-specific protein 1 (ATS1), identical to embryo-specific protein 1 (Arabidopsis thaliana) GI:3335169   chr4:13473522-13475319 REVERSE   Aliases: ARABIDOPSIS THALIANA SEED GENE 1, F10M23.80, F10M23_80	2.4	2.3	0.0	0.3	100.0%	-5.5
15943	AT1G14890.1   invertase/pectin methylesterase inhibitor family protein, similar to pectinesterase GB:X85216 GI:732912 SP:Q43111 (Phaseolus vulgaris), SP:Q42534 from Arabidopsis thaliana; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:5137048-5137926 FORWARD   Aliases: F10B6.30, F10B6_30	6.6	6.4	0.2	0.3	100.0%	-4.6
15944	AT5G44620.1   Symbol: CYP706A3   cytochrome P450 family protein, similar to cytochrome P450 monooxygenase (GI:14334057) (Gossypium arboreum)   chr5:18015006-18016785 REVERSE   Aliases: K15C23.6, K15C23_6	3.2	3.1	0.0	0.3	100.0%	-5.7
15945	AT1G04090.1   expressed protein   chr1:1057150-1059418 FORWARD   Aliases: F20D22.17, F20D22_17	2.7	2.8	-0.0	-0.3	100.0%	-5.5
15946	AT4G28990.1   RNA-binding protein-related, contains weak similarity to Swiss-Prot:Q01844 RNA-binding protein EWS (EWS oncogene)(Ewing sarcoma breakpoint region 1 protein) (Homo sapiens)   chr4:14291157-14293180 FORWARD   Aliases: F19B15.20, F19B15_20	4.0	4.1	-0.1	-0.3	100.0%	-4.9
15947	AT1G09190.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:2966122-2971459 REVERSE   Aliases: T12M4.11, T12M4_11	3.7	3.8	-0.1	-0.3	100.0%	-5.0
15948	AT5G62310.1   Symbol: IRE   incomplete root hair elongation (IRE) / protein kinase, putative, nearly identical to IRE (incomplete root hair elongation) (Arabidopsis thaliana) gi:6729346:dbj:BAA89783   chr5:25040581-25045640 FORWARD   Aliases: INCOMPLETE ROOT HAIR ELONGATION, MMI9.15, MMI9_15	2.8	2.7	0.0	0.3	100.0%	-5.6
15949	AT3G57900.1   expressed protein, hypothetical protein T24P15.12 - Arabidopsis thaliana, PIR:T00930   chr3:21453258-21453551 REVERSE   Aliases: T10K17.110	3.8	3.8	0.0	0.3	100.0%	-5.3
15950	AT5G38290.2   peptidyl-tRNA hydrolase family protein, contains Pfam profile PF01195: peptidyl-tRNA hydrolase   chr5:15320610-15322776 FORWARD   Aliases: MSI17.2, MSI17_2	4.1	4.1	0.1	0.3	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15951	AT4G24950.1   expressed protein   chr4:12826292-12826765 FORWARD   Aliases: F13M23.90, F13M23_90	3.0	3.1	-0.1	-0.3	100.0%	-5.4
15952	AT3G11980.1   Symbol: MS2   male sterility protein 2 (MS2), identical to male sterility protein 2 (MS2) SP:Q08891 (Arabidopsis thaliana)   chr3:3814242-3817123 FORWARD   Aliases: MALE STERILITY 2, MALE STERILITY PROTEIN 2, MEC18.1	2.6	2.7	-0.0	-0.3	100.0%	-5.7
15953	AT1G64300.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g41730.1); similar to putative protein kinase family protein [Oryza sativa (japonica cultivar-group)] (GB:XP_475974.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:23866729-23869708 FORWARD   Aliases: F15H21.13, F15H21_13	3.6	3.6	0.1	0.3	100.0%	-5.2
15954	AT1G70690.1   kinase-related, contains Pfam PF01657:Domain of unknown function; similar to receptor-like protein kinase 4 GI:13506745 (Arabidopsis thaliana)   chr1:26655676-26657287 FORWARD   Aliases: F5A18.13, F5A18_13	3.5	3.7	-0.2	-0.3	100.0%	-4.3
15955	AT2G41050.1   PQ-loop repeat family protein / transmembrane family protein, similar to SP:Q10482 Seven transmembrane protein 1 {Schizosaccharomyces pombe}; contains Pfam profile PF04193: PQ loop repeat   chr2:17130268-17133427 REVERSE   Aliases: T3K9.18, T3K9_18	4.0	3.9	0.1	0.3	100.0%	-5.0
15956	AT2G38830.1   tumor susceptibility protein-related, contains weak similarity to Swiss-Prot:Q99816 tumor susceptibility gene 101 protein (Homo sapiens)	3.0	3.1	-0.1	-0.3	100.0%	-5.5
15957	AT1G80730.1   Symbol: ZFP1   zinc finger (C2H2 type) family protein (ZFP1), identical to zinc finger protein, ZFP1 gi:790673:gb:AAA87297; contains zinc finger, C2H2 type, domain, Prosite:PS00028   chr1:30344215-30345139 REVERSE   Aliases: ATZFP1, F23A5.8, F23A5_8, ZFP1	2.2	2.2	0.0	0.3	100.0%	-5.8
15958	AT3G61940.1   Symbol: MTPA1   zinc transporter, putative, similar to zinc transporter ZAT (Arabidopsis thaliana) gi:4206640:gb:AAD11757; similar to zinc transporter ZnT-2 (Rattus norvegicus) gi:1256378:gb:AAB02775; member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr3:22948145-22949549 FORWARD   Aliases: ATMTPA1, F21F14.110	4.0	3.9	0.2	0.3	100.0%	-4.2
15959	NA	3.6	3.8	-0.2	-0.3	100.0%	-4.6
15960	AT2G17270.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr2:7517182-7519469 FORWARD   Aliases: F5J6.3, F5J6_3	4.8	4.9	-0.1	-0.3	100.0%	-4.7
15961	AT1G79520.1   cation efflux family protein, contains cation efflux family protein domain, Pfam:PF01545	3.9	4.0	-0.1	-0.3	100.0%	-4.7
15962	AT1G52190.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:19438192-19442640 FORWARD   Aliases: F9I5.4, F9I5_4	3.8	3.7	0.1	0.3	100.0%	-5.2
15963	AT2G16720.1   Symbol: MYB7   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:7262671-7263643 REVERSE   Aliases: ATMYB7, T24I21.13, T24I21_13	6.6	6.6	-0.1	-0.3	100.0%	-4.7
15964	AT4G08940.1   expressed protein   chr4:5730400-5732183 REVERSE   Aliases: T3H13.12, T3H13_12	3.6	3.7	-0.1	-0.3	100.0%	-5.0
15965	AT2G45310.1   Symbol: GAE4   NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	2.9	2.9	-0.0	-0.3	100.0%	-5.4
15966	AT1G68260.1   thioesterase family protein, contains Pfam profile: PF03061: thioesterase family protein	5.4	5.5	-0.1	-0.3	100.0%	-4.5
15967	AT1G11690.1   hypothetical protein   chr1:3941469-3942212 FORWARD   Aliases: F25C20.16, F25C20_16	3.6	3.6	-0.1	-0.3	100.0%	-5.2
15968	AT1G65670.1   Symbol: CYP702A1   cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) (Arabidopsis thaliana)   chr1:24425656-24427616 REVERSE   Aliases: F1E22.5	2.7	2.6	0.0	0.3	100.0%	-5.7
15969	ATMG00670.1   Symbol: ORF275	3.9	3.7	0.2	0.3	100.0%	-4.6
15970	AT5G56780.1   expressed protein, contains similarity to transcription repressor   chr5:22981491-22983467 REVERSE   Aliases: MIK19.25, MIK19_25	3.6	3.6	-0.1	-0.3	100.0%	-5.2
15971	AT2G24580.1   sarcosine oxidase family protein, similar to peroxisomal sarcosine oxidase from Homo sapiens (SP:Q9P0Z9), Oryctolagus cuniculus (SP:P79371), Mus musculus (SP:Q9D826)   chr2:10451869-10453321 REVERSE   Aliases: F25P17.12, F25P17_12	8.4	8.3	0.1	0.3	100.0%	-4.8
15972	AT4G26400.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:13344857-13346583 REVERSE   Aliases: M3E9.170, M3E9_170	8.1	8.2	-0.1	-0.3	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15973	AT2G21550.1   bifunctional dihydrofolate reductase-thymidylate synthase, putative / DHFR-TS, putative, similar to THY-1 (SP: Q05762) and THY-2 (SP:Q05763) from Arabidopsis thaliana; contains Pfam profiles PF00303 thymidylate synthase and PF00186 dihydrofolate reductase   chr2:9234289-9237269 FORWARD   Aliases: F2G1.18, F2G1_18	3.6	3.5	0.1	0.3	100.0%	-4.5
15974	AT1G70920.1   homeobox-leucine zipper protein, putative / HD-ZIP transcription factor, putative, similar to homeodomain leucine zipper protein Gl:5006851 from (Oryza sativa)   chr1:26739702-26742241 FORWARD   Aliases: F15H11.30	4.2	4.3	-0.1	-0.3	100.0%	-5.3
15975	AT4G11460.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:6964463-6967088 FORWARD   Aliases: F25E4.80, F25E4_80	2.3	2.3	-0.0	-0.3	100.0%	-5.8
15976	AT5G45880.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr5:18626891-18628393 REVERSE   Aliases: K15I22.8, K15I22_8	3.5	3.6	-0.1	-0.3	100.0%	-4.8
15977	AT1G71180.1   6-phosphogluconate dehydrogenase NAD-binding domain-containing protein, similar to SP:P23523 2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60) (Tartronate semialdehyde reductase) {Escherichia coli}; contains Pfam profile PF03446: NAD binding domain of 6-phosphogluconate dehydrogenase   chr1:26835997-26837371 FORWARD   Aliases: F23N20.17, F23N20_17	7.9	8.0	-0.1	-0.3	100.0%	-5.0
15978	AT2G06020.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:2342532-2346204 FORWARD   Aliases: F5K7.22, F5K7_22	2.1	2.1	-0.0	-0.3	100.0%	-6.0
15979	AT3G03640.1   Symbol: GLUC   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; identical to beta-glucosidase GB:AAC31962 (Arabidopsis thaliana); similar to thioglucoside glucohydrolase (Gl:984052) (Arabidopsis thaliana)   chr3:881031-884163 FORWARD   Aliases: BETA GLUCOSIDASE, T12J13.8, T12J13_8	11.0	10.9	0.1	0.3	100.0%	-4.5
15980	AT1G03440.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611   chr1:852365-854031 FORWARD   Aliases: F21B7.6, F21B7_6	2.8	2.7	0.0	0.3	100.0%	-5.3
15981	AT1G31070.2   UDP-N-acetylglucosamine pyrophosphorylase-related, low similarity to SP:P43123 UDP-N-acetylglucosamine pyrophosphorylase (EC 2.7.7.23) {Saccharomyces cerevisiae}   chr1:11084841-11088543 FORWARD   Aliases: F17F8.1	3.2	3.3	-0.1	-0.3	100.0%	-5.5
15982	AT4G08240.2   expressed protein   chr4:5194672-5196758 FORWARD   Aliases: T12G13.80, T12G13_80	5.7	5.6	0.1	0.3	100.0%	-4.8
15983	AT2G36400.1   Symbol: AtGRF3	3.7	3.7	0.1	0.3	100.0%	-5.1
15984	AT2G19680.1   mitochondrial ATP synthase g subunit family protein, contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit	10.4	10.6	-0.2	-0.3	100.0%	-4.7
15985	AT4G25030.2   expressed protein   chr4:12864838-12866837 FORWARD   Aliases: F13M23.170, F13M23_170	9.3	9.4	-0.1	-0.3	100.0%	-5.0
15986	AT1G66970.1   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family   chr1:24996216-24999780 REVERSE   Aliases: F1O19.5, F1O19_5	2.9	2.8	0.1	0.3	100.0%	-5.1
15987	AT5G60620.1   phospholipid/glycerol acyltransferase family protein, contains Pfam PF01553: Acyltransferase   chr5:24384442-24387015 FORWARD   Aliases: MUP24.4, MUP24_4	9.1	9.3	-0.1	-0.3	100.0%	-4.9
15988	AT4G33666.1   expressed protein   chr4:16169051-16169538 FORWARD   Aliases: None	3.1	3.0	0.2	0.3	100.0%	-4.2
15989	AT5G04810.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr5:1390038-1393931 FORWARD   Aliases: MUK11.12	5.6	5.7	-0.1	-0.3	100.0%	-4.8
15990	AT5G13650.2   elongation factor family protein, contains Pfam profiles: PF00009 elongation factor Tu GTP binding domain,PF00679 elongation factor G C-terminus, PF03144 elongation factor Tu domain 2	5.8	6.0	-0.2	-0.3	100.0%	-4.4
15991	AT3G63470.1   Symbol: SCPL40	2.8	2.8	0.0	0.3	100.0%	-5.5
15992	AT3G25790.1   myb family transcription factor, contains Pfam domain, PF00249: Myb-like DNA-binding domain   chr3:9414364-9416240 FORWARD   Aliases: K13N2.13	5.3	5.1	0.2	0.3	100.0%	-4.3
15993	AT2G38570.1   expressed protein, ; expression supported by MPSS   chr2:16143932-16145495 REVERSE   Aliases: T6A23.23, T6A23_23	3.9	3.9	0.1	0.3	100.0%	-5.1
15994	AT1G08730.1   Symbol: XIC   myosin heavy chain (PCR43), identical to myosin heavy chain PCR43 (PIR:T00727) (Arabidopsis thaliana); similar to ESTs gb:R30087 and gb:AA394762   chr1:2779966-2788398 FORWARD   Aliases: ATXIC, F22O13.200, F22O13_200, PCR43	3.2	3.1	0.1	0.3	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
15995	AT5G39410.1   expressed protein   chr5:15785072-15787638 REVERSE   Aliases: MUL8.9, MUL8_9	8.1	8.3	-0.2	-0.3	100.0%	-4.7
15996	AT4G25750.1   ABC transporter family protein, Bactrocera tryoni membrane transporter (white) gene, PID:g3676298   chr4:13110636-13112369 REVERSE   Aliases: F14M19.30, F14M19_30	2.6	2.5	0.0	0.3	100.0%	-5.6
15997	AT2G40440.1   BTB/POZ domain-containing protein, contains Pfam PF00651: BTB/POZ domain; contains Interpro IPR000210/ PS50097: BTBB/POZ domain;   chr2:16896290-16898370 REVERSE   Aliases: T2P4.21, T2P4_21	2.7	2.7	0.0	0.3	100.0%	-5.7
15998	AT1G76340.1   integral membrane family protein, contains Pfam profile PF00892: Integral membrane protein; similar to GDP-mannose transporter (SP:Q941R4) (Arabidopsis thaliana) and to LPG2 protein (GI:9998817) (Leishmania mexicana)   chr1:28639849-28641200 REVERSE   Aliases: F15M4.16, F15M4_16	5.3	5.4	-0.1	-0.3	100.0%	-4.7
15999	AT3G43140.1   hypothetical protein, predicted proteins, Arabidopsis thaliana   chr3:15123419-15123833 FORWARD   Aliases: F7M19.150	3.4	3.3	0.1	0.3	100.0%	-5.1
16000	AT1G49960.2   xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family   chr1:18502308-18505554 FORWARD   Aliases: F2J10.15, F2J10_15	3.3	3.4	-0.1	-0.3	100.0%	-4.6
16001	AT2G43590.1   chitinase, putative, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus)   chr2:18088408-18089826 REVERSE   Aliases: F18O19.30	4.3	4.4	-0.1	-0.3	100.0%	-5.1
16002	AT5G54030.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.8	0.0	0.3	100.0%	-5.4
16003	AT1G14510.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr1:4961882-4964420 REVERSE   Aliases: F14L17.29, F14L17_29	7.2	7.1	0.1	0.3	100.0%	-4.8
16004	AT3G04030.2   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:1042889-1044685 REVERSE   Aliases: T11I18.14, T11I18_14	2.4	2.4	0.1	0.3	100.0%	-5.0
16005	NA	5.3	5.7	-0.4	-0.3	100.0%	-4.8
16006	AT5G57655.2   xylose isomerase family protein, contains similarity to Xylose isomerase (EC 5.3.1.5) (Swiss-Prot:P22842) (Thermoanaerobacter ethanolicus)   chr5:23363987-23367230 FORWARD   Aliases: None	3.6	3.5	0.1	0.3	100.0%	-4.6
16007	AT5G35580.1   protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821	6.0	6.1	-0.1	-0.3	100.0%	-4.6
16008	AT5G24530.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavanone 3-hydroxylase (Persea americana)(GI:727410); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr5:8378836-8383404 FORWARD   Aliases: K18P6.6, K18P6_6	3.8	4.0	-0.1	-0.3	100.0%	-4.4
16009	AT2G26880.1   MADS-box family protein   chr2:11466984-11468177 REVERSE   Aliases: F12C20.8, F12C20_8	2.6	2.6	-0.0	-0.3	100.0%	-5.6
16010	AT2G05520.5   Symbol: GRP 3   similar to glycine-rich protein (GRP35) [Arabidopsis thaliana] (TAIR:At2g05380.1); similar to glycine-rich protein [Citrus unshiu] (GB:BAA92155.1); contains domain GLY_RICH (PS50315)   chr2:2026159-2027114 FORWARD   Aliases: ATGRP 3, GLYCINE RICH PROTEIN 3, T20G20.13, T20G20_13	7.5	7.4	0.1	0.3	100.0%	-4.8
16011	AT2G37770.2   similar to aldo/keto reductase family protein [Arabidopsis thaliana] (TAIR:At3g53880.1); similar to aldose reductase [Digitalis purpurea] (GB:CAC32835.1); contains InterPro domain Aldo/keto reductase (InterPro:IPR001395)   chr2:15841962-15843959 FORWARD   Aliases: T8P21.32	3.9	3.9	-0.1	-0.3	100.0%	-5.1
16012	AT4G28750.1   Symbol: PSAE1   photosystem I reaction center subunit IV, chloroplast, putative / PSI-E, putative (PSAE1), identical to SP:Q9S831; similar to SP:P12354 Photosystem I reaction center subunit IV, chloroplast precursor (PSI-E) {Spinacia oleracea}; contains Pfam profile PF02427: Photosystem I reaction centre subunit IV / PsaE   chr4:14202779-14203961 REVERSE   Aliases: F16A16.140, F16A16_140, PSA E1 KNOCKOUT	9.2	9.1	0.1	0.3	100.0%	-4.4
16013	AT2G17140.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:7469893-7473439 FORWARD   Aliases: F6P23.26, F6P23_26	3.1	3.2	-0.1	-0.3	100.0%	-5.3
16014	AT2G02100.1   Symbol: LCR69/PDF2.2   plant defensin-fusion protein, putative (PDF2.2), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:O65740   chr2:528349-529107 FORWARD   Aliases: F5O4.13, F5O4_13, LCR69, Low molecular weight cysteine rich 69, PDF2.2	13.2	13.1	0.1	0.3	100.0%	-5.5
16015	AT3G53350.3   myosin heavy chain-related, low similarity to filamin-interacting protein S-FILIP (Rattus norvegicus) GI:21392397, nonmuscle heavy chain myosin II-A (Mus musculus) GI:17978023   chr3:19791053-19792719 REVERSE   Aliases: F4P12.50	4.7	4.8	-0.1	-0.3	100.0%	-4.6
16016	AT1G15330.1   CBS domain-containing protein, low similarity to SP:Q9MYP4 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) {Sus scrofa}; contains Pfam profile PF00571: CBS domain   chr1:5274341-5275597 FORWARD   Aliases: F9L1.27, F9L1_27	3.9	4.1	-0.1	-0.3	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16017	AT5G67550.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g25270.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_549958.1)   chr5:26963980-26966387 REVERSE   Aliases: K9I9.11, K9I9_11	3.1	3.2	-0.0	-0.3	100.0%	-5.4
16018	AT4G35820.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to prolyl 4-hydroxylase, alpha subunit, from Mus musculus (SP:Q60715), Homo sapiens (GI:18073925); contains PF03171 2OG-Fe(II) oxygenase superfamily domain	2.6	2.6	0.0	0.3	100.0%	-5.6
16019	AT2G41570.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:17344815-17346071 FORWARD   Aliases: T32G6.9, T32G6_9	2.8	2.8	-0.0	-0.3	100.0%	-5.7
16020	AT2G33600.1   cinnamoyl-CoA reductase family, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Eucalyptus gunnii (GI:2058311)   chr2:14233842-14235787 FORWARD   Aliases: F4P9.37, F4P9_37	5.2	5.3	-0.1	-0.3	100.0%	-4.7
16021	AT5G39220.1   hydrolase, alpha/beta fold family protein, contains Pfam profile: PF00561 alpha/beta hydrolase fold   chr5:15723044-15725454 FORWARD   Aliases: K3K3.12, K3K3_12	2.5	2.6	-0.1	-0.3	100.0%	-5.1
16022	AT2G12550.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, low similarity to NUB1 (NEDD8-interacting protein) (Homo sapiens) GI:13383476; contains Pfam profile PF00627: UBA/TS-N domain	6.0	5.9	0.1	0.3	100.0%	-5.0
16023	AT2G30380.1   expressed protein, contains Pfam profile PF04859: Plant protein of unknown function (DUF641); expression supported by MPSS   chr2:12955361-12957650 FORWARD   Aliases: T9D9.19, T9D9_19	2.3	2.3	0.0	0.3	100.0%	-5.7
16024	AT2G42140.1   VQ motif-containing protein, contains PF05678: VQ motif   chr2:17575755-17576605 REVERSE   Aliases: T24P15.5, T24P15_5	2.6	2.7	-0.0	-0.3	100.0%	-5.7
16025	AT4G31250.1   leucine-rich repeat transmembrane protein kinase, putative, receptor kinase, Petunia inflata, Patchx:G498278   chr4:15178939-15181757 REVERSE   Aliases: F8F16.70, F8F16_70	3.8	3.9	-0.1	-0.3	100.0%	-4.6
16026	AT2G38240.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase (Citrus unshiu)(gi:4126403), leucoanthocyanidin dioxygenase (Daucus carota)(gi:5924383); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr2:16018360-16021831 REVERSE   Aliases: F16M14.17, F16M14_17	3.3	3.2	0.1	0.3	100.0%	-5.1
16027	AT5G67450.1   Symbol: AZF1   zinc finger (C2H2 type) protein 1 (AZF1), identical to Cys2/His2-type zinc finger protein 1 (Arabidopsis thaliana) gi:6009887:dbj:BAA85108   chr5:26936019-26937175 REVERSE   Aliases: ARABIDOPSIS ZINC FINGER PROTEIN 1, K8K14.19, K8K14_19	3.2	3.1	0.2	0.3	100.0%	-4.5
16028	AT1G28470.1   Symbol: ANAC010   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM protein GI:6066594 from (Petunia hybrida)   chr1:10010167-10012184 FORWARD   Aliases: ANAC010, F3M18.9, F3M18_9	3.3	3.2	0.1	0.3	100.0%	-4.9
16029	AT4G20420.1   tapetum-specific protein-related, similar to SaTAP 35 (Sinapis alba) GI:408108   chr4:11016981-11017634 FORWARD   Aliases: F9F13.70, F9F13_70	2.5	2.5	-0.0	-0.3	100.0%	-5.5
16030	AT1G35610.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr1:13143128-13144966 REVERSE   Aliases: F15O4.27	3.3	3.3	0.1	0.3	100.0%	-5.2
16031	AT2G30530.1   expressed protein   chr2:13015993-13018140 FORWARD   Aliases: T6B20.12, T6B20_12	6.8	6.7	0.1	0.3	100.0%	-4.9
16032	AT4G02270.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr4:992175-993031 REVERSE   Aliases: T2H3.4, T2H3_4	2.5	2.6	-0.1	-0.3	100.0%	-4.3
16033	AT2G32950.1   Symbol: COP1   COP1 regulatory protein, photomorphogenesis repressor; identical to COP1 regulatory protein/FUSCA protein FUS1 GI:402685 SP:P43254   chr2:13985019-13990608 FORWARD   Aliases: ATCOP1, CONSTITUTIVE PHOTOMORPHOGENIC 1, DET340, EMB168, EMBRYO DEFECTIVE 168, FUS1, FUSCA 1, T21L14.11, T21L14_11	6.1	6.2	-0.1	-0.3	100.0%	-4.8
16034	AT1G49180.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr1:18188322-18191197 REVERSE   Aliases: F27J15.5, F27J15_5	2.8	2.8	0.1	0.3	100.0%	-4.7
16035	AT5G48240.1   expressed protein, similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAX96070.1)   chr5:19576469-19578464 FORWARD   Aliases: MIF21.13, MIF21_13	8.6	8.8	-0.1	-0.3	100.0%	-4.6
16036	AT2G41970.1   protein kinase, putative, similar to Pto kinase interactor 1 (serine/threonine protein kinase) (Lycopersicon esculentum) gi:3668069:gb:AAC61805   chr2:17527595-17529722 REVERSE   Aliases: T6D20.14, T6D20_14	2.6	2.5	0.1	0.3	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16037	AT5G62810.1   Symbol: PEX14   peroxisomal protein (PEX14), identical to PEX14 (Arabidopsis thaliana) GI:11094252; contains Pfam profile PF04695: Peroxisomal membrane anchor protein (Pex14p) conserved region; supporting cDNA gi:11094253:dbj:AB037539.1:   chr5:25237391-25241015 FORWARD   Aliases: ATPEX14, MQB2.13, MQB2_13, PED2, PEROXISOME DEFECTIVE 2	7.3	7.4	-0.1	-0.3	100.0%	-5.0
16038	AT1G59610.1   Symbol: ADL3   dynamin-like protein, putative (ADL3), strong similarity to dynamin-like protein 6 (ADL6) (Arabidopsis thaliana) GI:6651399; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain, PF00169: PH domain; identical to cDNA dynamin-like protein ADL3, GI:4803835   chr1:21896886-21904750 FORWARD   Aliases: CF1, DYNAMIN LIKE 3, T30E16.17, T30E16_17	8.8	8.8	-0.1	-0.3	100.0%	-5.0
16039	AT4G00900.1   Symbol: ECA2   calcium-transporting ATPase 2, endoplasmic reticulum-type (ECA2), nearly identical to SP:O23087 Calcium-transporting ATPase 2, endoplasmic reticulum-type (EC 3.6.3.8) {Arabidopsis thaliana}; contains InterPro Accession IPR006069: Cation transporting ATPase	4.8	5.0	-0.2	-0.3	100.0%	-4.8
16040	AT5G53950.1   Symbol: CUC2   no apical meristem (NAM) family protein, identical to no apical meristem protein CUC2 (GI:1944132) (Arabidopsis thaliana); contains Pfam PF02365: No apical meristem (NAM) domain;   chr5:21919192-21921021 REVERSE   Aliases: ANAC098, CUP SHAPED COTYLEDON 2, K19P17.12, K19P17_12	2.6	2.6	0.1	0.3	100.0%	-5.2
16041	AT3G14340.1   expressed protein   chr3:4782764-4783144 FORWARD   Aliases: MLN21.13	5.1	5.2	-0.1	-0.3	100.0%	-4.4
16042	AT5G59060.1   expressed protein, ; expression supported by MPSS   chr5:23861620-23861952 REVERSE   Aliases: K18B18.6, K18B18_6	3.1	3.0	0.0	0.3	100.0%	-5.5
16043	AT5G59510.1   expressed protein   chr5:24007300-24007922 FORWARD   Aliases: F2O15.21, F2O15_21	2.2	2.3	-0.0	-0.3	100.0%	-5.7
16044	AT2G39100.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr2:16324516-16326465 FORWARD   Aliases: T7F6.27, T7F6_27	2.9	3.0	-0.0	-0.3	100.0%	-5.2
16045	AT1G61080.1   proline-rich family protein   chr1:22496859-22500684 REVERSE   Aliases: T7P1.21, T7P1_21	2.6	2.6	0.1	0.3	100.0%	-5.1
16046	AT5G56940.1   ribosomal protein S16 family protein, contains Pfam profile PF00886: ribosomal protein S16   chr5:23048027-23049637 FORWARD   Aliases: MHM17.5, MHM17_5	9.5	9.6	-0.1	-0.3	100.0%	-4.8
16047	AT1G53770.1   expressed protein   chr1:20074982-20077391 REVERSE   Aliases: T18A20.22, T18A20_22	5.1	5.1	0.1	0.3	100.0%	-5.1
16048	AT3G42110.1   expressed protein   chr3:14293271-14295692 REVERSE   Aliases: F4M19.70	2.4	2.4	0.0	0.3	100.0%	-5.4
16049	AT1G68360.1   zinc finger protein-related, similar to zinc finger protein GI:790683 from (Arabidopsis thaliana)   chr1:25625341-25626075 REVERSE   Aliases: T22E19.1, T22E19_1	7.3	7.4	-0.1	-0.3	100.0%	-4.4
16050	AT5G39650.1   expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679)   chr5:15892427-15893344 FORWARD   Aliases: MIJ24.15, MIJ24_15	2.3	2.3	0.0	0.3	100.0%	-5.7
16051	AT5G40100.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:16061157-16064583 FORWARD   Aliases: MUD12.7, MUD12_7	3.2	3.4	-0.2	-0.3	100.0%	-4.4
16052	AT1G72970.1   Symbol: HTH   glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:P52707); contains Pfam profile PF00732 GMC oxidoreductase   chr1:27456438-27459594 FORWARD   Aliases: ACE, ADHESION OF CALYX EDGES, F3N23.17, F3N23_17, HOTHEAD	3.0	2.9	0.0	0.3	100.0%	-5.2
16053	AT1G49260.1   expressed protein   chr1:18229996-18230445 FORWARD   Aliases: F13F21.29, F13F21_29	3.6	3.6	-0.0	-0.3	100.0%	-5.4
16054	AT5G46620.1   expressed protein, similar to unknown protein (pir::T05082)   chr5:18934886-18936647 REVERSE   Aliases: F10E10.1, F10E10_1	9.2	9.3	-0.1	-0.3	100.0%	-4.9
16055	AT1G77340.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:29073237-29074722 REVERSE   Aliases: F2P24.5, F2P24_5	2.8	2.8	-0.0	-0.3	100.0%	-5.6
16056	AT3G62500.1   expressed protein, hypothetical proteins - Arabidopsis thaliana; expression supported by MPSS   chr3:23131399-23133198 FORWARD   Aliases: T12C14.200	3.6	3.7	-0.0	-0.3	100.0%	-5.3
16057	AT5G05230.1   expressed protein   chr5:1551389-1553806 FORWARD   Aliases: K18I23.3, K18I23_3	3.5	3.5	0.1	0.3	100.0%	-5.0
16058	AT4G00660.2   DEAD/DEAH box helicase, putative, similar to ATP-dependent RNA helicases	4.7	4.9	-0.2	-0.3	100.0%	-4.8
16059	AT5G43160.1   expressed protein, contains Pfam profile: PF04484 family of unknown function (DUF566)   chr5:17345679-17347923 FORWARD   Aliases: MMG4.20, MMG4_20	3.5	3.4	0.1	0.3	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16060	AT3G21090.1   ABC transporter family protein, similar to ATP-binding cassette, sub-family G (WHITE), member 2 GB:NP_036050 from (Mus musculus)	3.2	3.1	0.1	0.3	100.0%	-5.0
16061	AT1G21050.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr1:7366764-7367667 FORWARD   Aliases: T22I11.13, T22I11_13	4.4	4.5	-0.1	-0.3	100.0%	-4.5
16062	AT5G19000.1   Symbol: ATBPM1	6.6	6.5	0.1	0.3	100.0%	-4.5
16063	AT1G14560.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:4980667-4983279 FORWARD   Aliases: T5E21.6, T5E21_6	5.2	5.1	0.1	0.3	100.0%	-4.8
16064	AT1G33110.2   similar to MATE efflux family protein [Arabidopsis thaliana] (TAIR:At1g33100.1); similar to MATE efflux family protein [Arabidopsis thaliana] (TAIR:At1g33090.1); similar to MATE efflux family protein [Arabidopsis thaliana] (TAIR:At1g33080.2); similar to MATE efflux family protein [Arabidopsis thaliana] (TAIR:At1g33080.1); similar to putative ripening regulated protein [Oryza sativa (japonica cultivar-group)] (GB:XP_482980.1); contains InterPro domain Multi antimicrobial extrusion protein MatE (InterPro:IPR002528)   chr1:12004907-12008798 FORWARD   Aliases: T9L6.1, T9L6_1	4.2	4.1	0.0	0.3	100.0%	-5.3
16065	AT3G11540.2   Symbol: SPY   gibberellin signal transduction protein (SPINDLY), identical to spindly GB:AAC49446 (GI:1589778) (Arabidopsis thaliana); contains Pfam profile PF00515 TPR Domain	4.6	4.5	0.1	0.3	100.0%	-4.9
16066	AT3G55020.1   RabGAP/TBC domain-containing protein, low similarity to SP:Q9BXI6 EBP50-PDZ interactor of 64 kDa (EPI64 protein) {Homo sapiens}; contains Pfam profile PF00566: TBC domain   chr3:20399846-20405888 REVERSE   Aliases: T15C9.20	2.5	2.5	-0.0	-0.3	100.0%	-5.5
16067	AT1G12280.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.1	3.1	-0.1	-0.3	100.0%	-5.1
16068	AT3G07270.2   GTP cyclohydrolase I, identical to GTP cyclohydrolase I GI:19909132 from (Arabidopsis thaliana); contains Pfam profile: PF01227 GTP cyclohydrolase I   chr3:2314004-2317194 FORWARD   Aliases: T1B9.6	5.0	5.2	-0.2	-0.3	100.0%	-4.8
16069	AT3G30230.1   myosin heavy chain-related, similar to Myosin heavy chain, non-muscle (Zipper protein) (Myosin II)(SP:Q99323) {Drosophila melanogaster}   chr3:11881714-11884267 REVERSE   Aliases: MIL15.12	2.2	2.2	-0.0	-0.3	100.0%	-5.8
16070	AT1G05280.1   fringe-related protein, Similar to hypothetical protein PID:e327464 (gb:Z97338) various hypothetical proteins from Arabidopsis thaliana strong similarity to unknown protein (pir::T13026) similarity to predicted proteins + similar to hypothetical protein GB:AAC23643 (Arabidopsis thaliana) + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr1:1535443-1537524 REVERSE   Aliases: YUP8H12.11, YUP8H12_11	2.1	2.1	0.0	0.3	100.0%	-6.0
16071	AT2G34160.1   expressed protein   chr2:14433282-14434462 FORWARD   Aliases: T14G11.28, T14G11_28	6.7	6.6	0.1	0.3	100.0%	-4.8
16072	AT2G33720.1   expressed protein   chr2:14270808-14272278 FORWARD   Aliases: T1B8.29, T1B8_29	2.5	2.5	0.0	0.3	100.0%	-5.5
16073	AT1G79850.1   Symbol: RPS17   30S ribosomal protein S17, chloroplast / CS17 (RPS17), identical to 30S ribosomal protein S17, chloroplast precursor GB:P16180 (Arabidopsis thaliana)   chr1:30046136-30046845 REVERSE   Aliases: CS17, F19K16.19, F19K16_19, ORE4, PRPS17	8.4	8.5	-0.1	-0.3	100.0%	-4.4
16074	AT5G41660.1   expressed protein, similar to unknown protein (emb:CAB86921.1)   chr5:16674244-16674876 FORWARD   Aliases: MBK23.19, MBK23_19	2.5	2.4	0.0	0.3	100.0%	-5.5
16075	AT2G32860.2   glycosyl hydrolase family 1 protein   chr2:13947264-13950878 FORWARD   Aliases: T21L14.20, T21L14_20	2.4	2.4	-0.0	-0.3	100.0%	-5.8
16076	AT2G20000.1   Symbol: HBT   cell division cycle family protein / CDC family protein, low similarity to SP:P30260:CC27_HUMAN Protein CDC27Hs (Cell division cycle protein 27 homolog) Homo sapiens; contains Pfam profile PF00515: TPR Domain   chr2:8639162-8644381 REVERSE   Aliases: HOBBIT, T2G17.20, T2G17_20	4.3	4.3	0.1	0.3	100.0%	-5.4
16077	AT5G54350.1   expressed protein, ; expression supported by MPSS   chr5:22087361-22088452 FORWARD   Aliases: MDK4.17, MDK4_17	3.0	2.9	0.1	0.3	100.0%	-5.1
16078	AT3G22350.1   F-box family protein, similar to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana); contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain   chr3:7901912-7903048 FORWARD   Aliases: MCB17.9	3.6	3.5	0.1	0.3	100.0%	-5.1
16079	AT5G65610.1   expressed protein, ; expression supported by MPSS   chr5:26236484-26238254 FORWARD   Aliases: K21L13.12, K21L13_12	3.7	3.7	0.1	0.3	100.0%	-4.9
16080	AT5G25400.1   phosphate translocator-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}   chr5:8823286-8824335 FORWARD   Aliases: F18G18.140, F18G18_140	3.1	3.0	0.1	0.3	100.0%	-5.3
16081	AT2G22030.1   kelch repeat-containing F-box family protein, low similarity to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:9379610-9380761 FORWARD   Aliases: T16B14.12, T16B14_12	3.9	4.0	-0.1	-0.3	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16082	AT2G16950.2   similar to importin beta-2, putative [Arabidopsis thaliana] (TAIR:At5g53480.1); similar to transportin 1 [Mus musculus] (GB:NP_848831.1); similar to Transportin 1 [Homo sapiens] (GB:AAH40340.1); similar to transportin [Homo sapiens] (GB:AAC50723.1); similar to PREDICTED: similar to transportin 1 [Rattus norvegicus] (GB:XP_219500.3); similar to MIP [Homo sapiens] (GB:AAB68948.1); contains InterPro domain Importin-beta, N-terminal (InterPro:IPR001494)   chr2:7360929-7368284 FORWARD   Aliases: F12A24.13, F12A24_13	5.3	5.2	0.1	0.3	100.0%	-4.6
16083	AT1G43630.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g18740.1); similar to OSJNBa0039K24.3 [Oryza sativa (japonica cultivar-group)] (GB:XP_474443.1); contains InterPro domain Protein of unknown function DUF793 (InterPro:IPR008511)   chr1:16438811-16440195 REVERSE   Aliases: T10P12.8, T10P12_8	3.3	3.4	-0.1	-0.3	100.0%	-5.1
16084	AT5G26660.1   Symbol: ATMYB4	2.7	2.6	0.1	0.3	100.0%	-5.0
16085	AT5G10420.1   ripening-responsive protein, putative, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr5:3273554-3276491 REVERSE   Aliases: F12B17.230, F12B17_230	3.0	3.0	-0.1	-0.3	100.0%	-5.4
16086	AT1G23980.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 zinc finger protein ATL4 (Arabidopsis thaliana) GI:4928399; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:8484692-8485991 REVERSE   Aliases: T23E23.15, T23E23_15	4.5	4.6	-0.1	-0.3	100.0%	-5.0
16087	AT3G03080.1   NADP-dependent oxidoreductase, putative, similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana; similar to allyl alcohol dehydrogenase (Nicotiana tabacum) GI:6692816   chr3:698537-700308 REVERSE   Aliases: T17B22.23, T17B22_23	3.7	3.6	0.0	0.3	100.0%	-5.4
16088	AT1G01300.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr1:116943-118764 FORWARD   Aliases: F6F3.10, F6F3_10	6.1	6.3	-0.2	-0.3	100.0%	-4.4
16089	AT4G20310.1   similar to PREDICTED: similar to Membrane-bound transcription factor site 2 protease (S2P endopeptidase) (Site-2 protease) (Sterol-regulatory element-binding proteins intramembrane protease) [Gallus gallus] (GB:XP_425566.1); similar to membrane-bound transcription factor protease, site 2 [Mus musculus] (GB:NP_758511.1); contains InterPro domain Mammalian sterol-regulatory element binding protein (SREBP) site 2 protease (InterPro:IPR001193)   chr4:10961624-10963958 FORWARD   Aliases: F1C12.220, F1C12_220	4.0	3.9	0.1	0.3	100.0%	-4.8
16090	AT3G04100.1   MADS-box family protein, contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)   chr3:1075306-1075929 FORWARD   Aliases: T6K12.28, T6K12_28	4.3	4.3	0.1	0.3	100.0%	-5.2
16091	AT1G31520.1   hypothetical protein   chr1:11278964-11279620 REVERSE   Aliases: F27M3.25, F27M3_25	2.7	2.8	-0.1	-0.3	100.0%	-5.0
16092	AT2G32500.1   expressed protein   chr2:13802337-13804259 REVERSE   Aliases: T26B15.6, T26B15_6	4.4	4.3	0.1	0.3	100.0%	-4.5
16093	AT2G28440.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; contains similarity to vegetative cell wall protein gp1 (Chlamydomonas reinhardtii) gi:12018147:gb:AAG45420; +   chr2:12168303-12169109 FORWARD   Aliases: T1B3.4, T1B3_4	2.4	2.3	0.0	0.3	100.0%	-5.4
16094	AT1G36510.1   hypothetical protein   chr1:13763138-13765477 FORWARD   Aliases: F28J9.5, F28J9_5	4.0	4.0	0.1	0.3	100.0%	-5.3
16095	AT4G17110.1   expressed protein, ; expression supported by MPSS   chr4:9613629-9615510 REVERSE   Aliases: DL4590C, FCAALL.359	5.4	5.6	-0.1	-0.3	100.0%	-4.6
16096	AT4G29090.1   reverse transcriptase, putative / RNA-dependent DNA polymerase, putative, similar to reverse transcriptase (Arabidopsis thaliana) GI:976278; contains Pfam profile PF00075: RNase H   chr4:14333534-14335261 FORWARD   Aliases: F19B15.120, F19B15_120	3.3	3.2	0.1	0.3	100.0%	-5.2
16097	AT5G29020.1   expressed protein   chr5:11041955-11046506 FORWARD   Aliases: F3F24.120, F3F24_120	3.3	3.3	0.0	0.3	100.0%	-5.2
16098	AT2G22690.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g37880.1); similar to hypothetical protein DDB0217500 [Dictyostelium discoideum] (GB:EAL70307.1); contains InterPro domain Zn-finger, RING (InterPro:IPR001841); contains InterPro domain CTLH, C-terminal to LisH motif (InterPro:IPR006595)   chr2:9656770-9658519 REVERSE   Aliases: T9I22.13, T9I22_13	4.9	5.0	-0.1	-0.3	100.0%	-4.8
16099	AT4G29200.1   expressed protein   chr4:14398060-14400204 REVERSE   Aliases: F17A13.20, F17A13_20	2.1	2.1	-0.0	-0.3	100.0%	-6.0
16100	AT1G47990.1   gibberellin 2-oxidase, putative / GA2-oxidase, putative, similar to GA2ox1 (GI:4678366); similar to dioxygenase GB:CAA70330 GI:1666096 from (Marah macrocarpus); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:17702324-17704503 FORWARD   Aliases: T2J15.10, T2J15_10	2.4	2.4	-0.0	-0.3	100.0%	-5.3
16101	AT5G39440.1   Snf1-related protein kinase, putative, similar to SNF1-related protein kinase KIN10 (EC 2.7.1.-) (AKIN10) (Arabidopsis thaliana) SWISS-PROT:Q38997   chr5:15799135-15801927 FORWARD   Aliases: MUL8.120, MUL8_120	2.8	2.9	-0.1	-0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16102	AT5G52160.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:21212270-21212984 FORWARD   Aliases: F17P19.6, F17P19_6	4.2	4.2	0.0	0.3	100.0%	-5.3
16103	AT3G27470.1   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr3:10164286-10168111 FORWARD   Aliases: K1G2.18	3.7	3.6	0.1	0.3	100.0%	-4.6
16104	AT5G15250.1   Symbol: FTSH6   encodes an FtsH protease that is localized to the chloroplast   chr5:4950414-4952780 REVERSE   Aliases: F8M21.140, F8M21_140, FTSH6	2.8	2.8	0.0	0.3	100.0%	-5.5
16105	AT1G32830.1   hypothetical protein, similar to At2g04970, At2g15200, At2g14140, At3g30450, At4g03990, At5g34895, At3g47270, At2g02200   chr1:11891161-11894800 REVERSE   Aliases: F9L11.3, F9L11_3	2.0	1.9	0.0	0.3	100.0%	-6.0
16106	AT4G32410.1   Symbol: CESA1   cellulose synthase, catalytic subunit, putative, similar to cellulose synthase-1 (gi:9622874) and -2 (gi:9622876) from Zea mays	6.5	6.6	-0.1	-0.3	100.0%	-5.1
16107	AT4G00450.1   Symbol: CRP   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_479342.1)   chr4:203471-211003 FORWARD   Aliases: A_IG005I10.24, A_IG005I10_24, CRYPTIC PRECOCIOUS, F5I10.24, F5I10_24	3.6	3.6	-0.1	-0.3	100.0%	-4.9
16108	AT3G03305.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.2	6.3	-0.1	-0.3	100.0%	-4.9
16109	AT3G49780.1   Symbol: ATPSK3	4.2	4.3	-0.1	-0.3	100.0%	-4.5
16110	AT5G14460.1   pseudouridylate synthase TruB family protein, similar to SP:P09171 tRNA pseudouridine synthase B (EC 4.2.1.70) (tRNA pseudouridine 55 synthase) (Pseudouridylate synthase) (Uracil hydrolyase) {Escherichia coli O157:H7}; contains Pfam profile PF01509: TruB family pseudouridylate synthase (N terminal domain)   chr5:4660242-4662546 REVERSE   Aliases: F18O22.250, F18O22_250	4.6	4.7	-0.1	-0.3	100.0%	-4.7
16111	AT1G53380.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g14870.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAV44148.1); contains InterPro domain Plant protein of unknown function DUF641 (InterPro:IPR006943)   chr1:19916747-19918680 REVERSE   Aliases: F12M16.27, F12M16_27	3.9	3.9	-0.1	-0.3	100.0%	-4.9
16112	AT4G17486.1   expressed protein   chr4:9749741-9751721 REVERSE   Aliases: FCAALL.234	7.8	7.6	0.2	0.3	100.0%	-4.6
16113	AT3G05710.2   Symbol: SYP43   syntaxin, putative, similar to syntaxin of plants 42 (Arabidopsis thaliana) GI:5059352   chr3:1685009-1687543 FORWARD   Aliases: ATSYP43, F18C1.2, F18C1_2	4.3	4.2	0.1	0.3	100.0%	-4.7
16114	AT2G23060.2   similar to N-acetyltransferase, putative / hookless1 (HLS1) [Arabidopsis thaliana] (TAIR:At4g37580.1); similar to putative acetyl transferase [Oryza sativa (japonica cultivar-group)] (GB:XP_469881.1); contains InterPro domain GCN5-related N-acetyltransferase (InterPro:IPR000182)   chr2:9819851-9821300 REVERSE   Aliases: F21P24.12, F21P24_12	3.7	3.8	-0.1	-0.3	100.0%	-5.0
16115	AT5G05700.1   Symbol: ATE1   arginine-tRNA-protein transferase 1 / arginyltransferase 1 / arginyl-tRNA-protein transferase 1 (ATE1), identical to SP:Q9ZT48 Arginine-tRNA-protein transferase 1 (EC 2.3.2.8) (R-transferase 1) (Arginyltransferase 1) (Arginyl-tRNA--protein transferase 1) {Arabidopsis thaliana}   chr5:1712671-1715700 REVERSE   Aliases: ARGININE TRNA PROTEIN TRANSFERASE 1, ATATE1, DELAYED LEAF SENESCENCE 1, DLS1, MJJ3.1, MJJ3_1	5.8	5.9	-0.1	-0.3	100.0%	-4.7
16116	AT5G46340.1   O-acetyltransferase-related, similar to O-acetyltransferase (Homo sapiens) GI:17016934   chr5:18813153-18817321 REVERSE   Aliases: MPL12.14, MPL12_14	4.4	4.3	0.1	0.3	100.0%	-4.7
16117	AT1G30010.1   intron maturase, type II family protein, similar to SP:Q57005 Group II intron-encoded protein ltrA {Lactococcus lactis subsp}; contains Pfam profiles PF01348: Type II intron maturase, PF00078: Reverse transcriptase (RNA-dependent DNA polymerase   chr1:10513178-10516369 FORWARD   Aliases: T1P2.4, T1P2_4	3.1	3.1	-0.0	-0.3	100.0%	-5.4
16118	AT5G06900.1   Symbol: CYP93D1   cytochrome P450 family protein   chr5:2136161-2137926 REVERSE   Aliases: MOJ9.6, MOJ9_6	3.0	3.0	0.0	0.3	100.0%	-5.5
16119	AT5G49500.1   signal recognition particle 54 kDa protein 2 / SRP54 (SRP-54B), identical to SP:P49966 Signal recognition particle 54 kDa protein 2 (SRP54) {Arabidopsis thaliana}   chr5:20094782-20097432 REVERSE   Aliases: K6M13.4, K6M13_4	5.7	5.6	0.1	0.3	100.0%	-4.8
16120	AT3G46400.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr3:17084181-17088313 FORWARD   Aliases: F18L15.120	2.6	2.6	0.0	0.3	100.0%	-5.7
16121	AT5G57140.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 Calcineurin-like phosphoesterase	3.4	3.5	-0.0	-0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16122	AT1G45332.1   mitochondrial elongation factor, putative, similar to mitochondrial elongation factor GI:3917 from ( <i>Saccharomyces cerevisiae</i> )   chr1:17174795-17179261 REVERSE   Aliases: AT1G45261, F2G19.2, F2G19_2	9.2	9.5	-0.2	-0.3	100.0%	-4.2
16123	AT2G45030.1   mitochondrial elongation factor, putative, similar to SP:P25039 Elongation factor G 1, mitochondrial precursor (mEF-G-1) { <i>Saccharomyces cerevisiae</i> }; contains Pfam profiles PF00009: Elongation factor Tu GTP binding domain, PF03764: Elongation factor G domain IV, PF00679: Elongation factor G C-terminus   chr2:18579486-18584045 FORWARD   Aliases: T14P1.16	9.2	9.5	-0.2	-0.3	100.0%	-4.2
16124	AT4G11740.1   Symbol: SAY1   ara4-interacting protein, putative (SAY1), similar to Ara4-interacting protein ( <i>Arabidopsis thaliana</i> ) GI:13160609; contains Pfam profiles PF00789: UBX domain, PF02809: Ubiquitin interaction motif   chr4:7071854-7075495 FORWARD   Aliases: T5C23.170, T5C23_170	7.0	6.9	0.1	0.3	100.0%	-4.9
16125	AT3G50820.1   Symbol: PSBO 2/PSBO2   Encodes a protein which is an extrinsic subunit of photosystem II and which has been proposed to play a central role in stabilization of the catalytic manganese cluster. In <i>Arabidopsis thaliana</i> the PsbO proteins are encoded by two genes: <i>psbO1</i> and <i>psbO2</i> . PsbO2 is the minor isoform in the wild-type.	6.3	6.2	0.1	0.3	100.0%	-4.6
16126	AT1G28220.1   Symbol: ATPUP3	4.2	4.3	-0.1	-0.3	100.0%	-5.0
16127	AT5G19670.1   exostosin family protein, contains Pfam domain, PF03016: Exostosin family   chr5:6646721-6649500 FORWARD   Aliases: T29J13.90, T29J13_90	3.9	3.8	0.1	0.3	100.0%	-5.2
16128	AT1G67290.1   glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor ( <i>Phanerochaete chrysosporium</i> ) gi:1050302:gb:AAA87594   chr1:25194684-25196900 REVERSE   Aliases: F1N21.11	3.0	2.9	0.1	0.3	100.0%	-5.1
16129	AT5G19590.1   expressed protein, contains Pfam profile PF04398: Protein of unknown function, DUF538   chr5:6611616-6612105 REVERSE   Aliases: T29J13.10, T29J13_10	7.9	7.7	0.2	0.3	100.0%	-4.6
16130	AT1G19230.1   respiratory burst oxidase protein E (RbohE) / NADPH oxidase, nearly identical to respiratory burst oxidase protein E GI:3242787 (gi:3242787) from ( <i>Arabidopsis thaliana</i> )	2.8	2.9	-0.1	-0.3	100.0%	-4.5
16131	AT5G58600.2   expressed protein, various predicted proteins, <i>Arabidopsis thaliana</i> and <i>Oryza sativa</i>   chr5:23701017-23702941 REVERSE   Aliases: MZN1.6, MZN1_6	5.4	5.3	0.1	0.3	100.0%	-4.5
16132	AT3G13810.1   zinc finger (C2H2 type) family protein, similar to finger protein pcp1 GB:S48856 from ( <i>Solanum tuberosum</i> ) contains Pfam domain, PF00096: Zinc finger, C2H2 type	3.0	2.9	0.1	0.3	100.0%	-5.2
16133	AT1G02670.1   DNA repair protein, putative, similar to SP:P79051 DNA repair protein rhp16 (RAD16 homolog) { <i>Schizosaccharomyces pombe</i> }; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr1:576046-580299 FORWARD   Aliases: T14P4.5, T14P4_5	3.6	3.7	-0.1	-0.3	100.0%	-5.2
16134	AT5G28600.1   hypothetical protein   chr5:10597813-10603454 FORWARD   Aliases: T10I18.60, T10I18_60	3.2	3.2	0.1	0.3	100.0%	-5.3
16135	AT5G46310.1   WRKY family transcription factor, identical to WRKY transcription factor 8 GI:15384212 from ( <i>Arabidopsis thaliana</i> )   chr5:18802899-18804183 FORWARD   Aliases: MPL12.9, MPL12_9	3.9	4.0	-0.1	-0.3	100.0%	-5.2
16136	AT3G17800.1   expressed protein   chr3:6090467-6093157 REVERSE   Aliases: MEB5.2	8.3	8.2	0.1	0.3	100.0%	-5.1
16137	AT5G47460.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:19269690-19271420 REVERSE   Aliases: MNJ7.5, MNJ7_5	4.7	4.8	-0.1	-0.3	100.0%	-5.0
16138	AT1G05030.1   hexose transporter, putative, similar to hexose transporters from <i>Nicotiana tabacum</i> (GI:8347244), <i>Solanum tuberosum</i> (GI:8347246), <i>Arabidopsis thaliana</i> (GI:8347250); contains Pfam profile PF00083: major facilitator superfamily protein   chr1:1438151-1441416 REVERSE   Aliases: T7A14.10, T7A14_10	5.6	5.7	-0.1	-0.3	100.0%	-4.9
16139	AT3G05820.1   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase ( <i>Daucus carota</i> ) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr3:1732997-1735632 REVERSE   Aliases: F10A16.11, F10A16_11	3.0	3.0	0.0	0.3	100.0%	-5.6
16140	AT3G62310.1   RNA helicase, putative, similar to SP:P53131 Pre-mRNA splicing factor RNA helicase PRP43 (Helicase JA1) { <i>Saccharomyces cerevisiae</i> }; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr3:23068221-23071665 REVERSE   Aliases: T12C14.10	7.3	7.5	-0.1	-0.3	100.0%	-4.9
16141	AT1G79270.1   expressed protein, contains Pfam profile PF04146: YT521-B-like family   chr1:29820399-29824585 FORWARD   Aliases: YUP8H12R.13, YUP8H12R_13	6.4	6.2	0.1	0.3	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16142	AT2G44210.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g55360.1); similar to putative DD1A protein [Oryza sativa (japonica cultivar-group)] (GB:XP_477068.1); contains InterPro domain Protein of unknown function DUF239 (InterPro:IPR004314)   chr2:18287699-18289952 FORWARD   Aliases: F4I1.2	5.0	5.1	-0.1	-0.3	100.0%	-4.6
16143	AT5G56900.2   Cwfj-like family protein / zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar), PF04677: Protein similar to Cwfj C-terminus 1, PF04676: Protein similar to Cwfj C-terminus 2   chr5:23036554-23039896 REVERSE   Aliases: MHM17.1, MHM17_1	3.7	3.7	0.0	0.3	100.0%	-5.4
16144	AT5G66690.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:26642306-26644019 FORWARD   Aliases: MSN2.8, MSN2_8	5.6	5.4	0.1	0.3	100.0%	-4.5
16145	AT1G34670.1   myb family transcription factor, similar to myb-related protein mixta GI:485867 from (Antirrhinum majus)	2.7	2.8	-0.1	-0.3	100.0%	-4.9
16146	AT1G25460.1   oxidoreductase family protein, similar to dihydroflavonol 4-reductase GI:1332411 from (Rosa hybrida), cinnamoyl CoA reductase from Pinus taeda (gi:17978649), Eucalyptus gunnii (gi:2058311)   chr1:8942798-8944231 FORWARD   Aliases: F2J7.17, F2J7_17	2.5	2.5	-0.1	-0.3	100.0%	-5.1
16147	AT4G01050.1   hydroxyproline-rich glycoprotein family protein, contains a rhodanese homology domain.   chr4:455768-458510 FORWARD   Aliases: F2N1.31, F2N1_31	6.0	6.2	-0.2	-0.3	100.0%	-4.6
16148	AT3G23130.1   Symbol: SUP   superman protein (SUP) / zinc finger (C2H2 type) family protein, identical to superman protein GB:S60325 from (Arabidopsis thaliana); contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:8242309-8243379 FORWARD   Aliases: FLO10, FLORAL DEFECTIVE 10, FLORAL ORGAN NUMBER1, FON1, K14B15.18, SUPERMAN	2.5	2.5	-0.0	-0.3	100.0%	-5.5
16149	AT1G64910.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	3.3	3.3	0.0	0.3	100.0%	-5.8
16150	AT5G07640.1   zinc finger (C3HC4-type RING finger) family protein, contains a zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518 and a IBR domain, Pfam:PF01485	2.8	2.7	0.0	0.3	100.0%	-5.7
16151	AT5G57920.1   plastocyanin-like domain-containing protein   chr5:23470825-23471623 FORWARD   Aliases: MTI20.18, MTI20_18	6.5	6.4	0.1	0.3	100.0%	-5.1
16152	AT5G25810.1   Symbol: TNY   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family (TINY). The protein contains one AP2 domain. There are 17 members in this subfamily including TINY. Ectopic or overexpression of this gene in a Ds tagged line has reduced cell expansion. The expression of this gene is induced by ethylene and light and appears to stimulate cytokinin biosynthesis.   chr5:8986774-8987790 REVERSE   Aliases: F18A17.60, F18A17_60, TINY, TNY	2.6	2.5	0.1	0.3	100.0%	-4.1
16153	AT2G24080.1   F-box family protein-related, similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)   chr2:10244684-10245859 REVERSE   Aliases: T29E15.28, T29E15_28	3.1	3.1	-0.0	-0.3	100.0%	-5.5
16154	AT1G08620.1   transcription factor jumonji (jnj) family protein / zinc finger (C5HC2 type) family protein, contains Pfam domains, PF02375: jmjN domain, PF02373: jmjC domain and PF02928: C5HC2 zinc finger   chr1:2737557-2743673 FORWARD   Aliases: F22O13.10, F22O13_10	4.9	5.1	-0.2	-0.3	100.0%	-4.8
16155	AT5G55800.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.2	-0.1	-0.3	100.0%	-5.3
16156	AT1G32350.1   alternative oxidase, putative, similar to Alternative oxidase 1a, mitochondrial precursor from Arabidopsis thaliana (SP:Q39219), alternative oxidase 2, mitochondrial precursor from Nicotiana tabacum (SP:Q40578); contains Pfam profile PF01786 Alternative oxidase   chr1:11666957-11668670 REVERSE   Aliases: F27G20.12	3.7	3.8	-0.1	-0.3	100.0%	-5.1
16157	AT1G60570.1   kelch repeat-containing F-box family protein, low similarity to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr1:22315501-22316646 FORWARD   Aliases: F8A5.11, F8A5_11	4.7	4.6	0.1	0.3	100.0%	-5.0
16158	AT1G01450.1   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr1:164105-165517 REVERSE   Aliases: F22L4.1, F22L4_1	2.4	2.5	-0.0	-0.3	100.0%	-5.7
16159	AT1G32480.1   isocitrate/isopropylmalate dehydrogenase family protein, similar to NAD+ dependent isocitrate dehydrogenase subunit 2 (Arabidopsis thaliana) GI:1766048; contains Pfam profile PF00180 dehydrogenase, isocitrate/isopropylmalate family   chr1:11741063-11741970 FORWARD   Aliases: F5D14.26, F5D14_26	2.7	2.7	-0.0	-0.3	100.0%	-5.5
16160	AT5G42950.1   GYF domain-containing protein, contains Pfam profile: PF02213 GYF domain	6.6	6.7	-0.1	-0.3	100.0%	-4.7
16161	AT5G27710.1   expressed protein   chr5:9812992-9815424 FORWARD   Aliases: T1G16.40, T1G16_40	5.1	5.2	-0.1	-0.3	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16162	AT1G79860.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr1:30046992-30049068 REVERSE   Aliases: F19K16.18, F19K16_18, KINASE PARTNER PROTEIN LIKE, KPP LIKE	2.4	2.5	-0.1	-0.3	100.0%	-4.5
16163	AT1G70430.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:26549252-26552419 FORWARD   Aliases: F17O7.3, F17O7_3	2.7	2.7	-0.0	-0.3	100.0%	-5.6
16164	AT1G73270.1   Symbol: SCPL6   serine carboxypeptidase S10 family protein, similar to serine carboxypeptidase I precursor (SP:P07519) (Hordeum vulgare), glucose acyltransferase GB:AAD01263 (Solanum berthaultii); contains Pfam profile: PF00450 Serine carboxypeptidase;   chr1:27553067-27556178 REVERSE   Aliases: SCPL6, T18K17.6, T18K17_6	2.8	2.8	0.1	0.3	100.0%	-5.0
16165	AT5G36220.1   Symbol: CYP81D1   cytochrome P450 81D1 (CYP81D1) (CYP91A1), Identical to Cytochrome P450 (SP:Q9FG65) (Arabidopsis thaliana);   chr5:14270995-14273263 REVERSE   Aliases: CYP91A1, CYTOCHROME P450 91A1, CYTOCHROME P450 MONOOXYGENASE, T30G6.3, T30G6_3	3.6	3.6	-0.1	-0.3	100.0%	-4.9
16166	AT1G32310.1   expressed protein   chr1:11653544-11654771 FORWARD   Aliases: F27G20.14	7.8	7.9	-0.1	-0.3	100.0%	-4.5
16167	AT2G04032.1   metal transporter, putative (ZIP7), identical to putative metal transporter ZIP7 (Arabidopsis thaliana) gi:17385788:gb:AAL38434; similar to iron-regulated transporter 1 (Lycopersicon esculentum) gi:9716481:gb:AAF97509; similar to root iron transporter protein (Pisum sativum) gi:3153889:gb:AAC17441; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563   chr2:1289941-1291248 FORWARD   Aliases: F3L12.21	3.8	3.8	0.1	0.3	100.0%	-5.0
16168	AT3G23030.1   Symbol: IAA2   auxin-responsive protein / indoleacetic acid-induced protein 2 (IAA2), identical to SP:P49678 Auxin-responsive protein IAA2 (Indoleacetic acid-induced protein 2) {Arabidopsis thaliana}	4.2	4.1	0.1	0.3	100.0%	-4.9
16169	AT1G10890.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.9	2.9	0.0	0.3	100.0%	-5.4
16170	AT5G17600.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:5799907-5801149 REVERSE   Aliases: K10A8.80, K10A8_80	3.1	3.2	-0.1	-0.3	100.0%	-4.6
16171	AT3G02220.1   expressed protein   chr3:412090-413611 REVERSE   Aliases: F14P3.13, F14P3_13	8.0	7.9	0.1	0.3	100.0%	-4.7
16172	AT2G18760.1   SNF2 domain-containing protein / helicase domain-containing protein, similar to SP:Q03468 Excision repair protein ERCC-6 (Cockayne syndrome protein CSB) {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr2:8136236-8140584 FORWARD   Aliases: MSF3.14, MSF3_14	2.9	2.9	0.0	0.3	100.0%	-5.6
16173	AT3G25855.1   expressed protein   chr3:9460658-9461532 REVERSE   Aliases: None	2.4	2.4	-0.0	-0.3	100.0%	-5.7
16174	AT3G13440.1   expressed protein   chr3:4377104-4379582 FORWARD   Aliases: MRP15.19	7.3	7.4	-0.1	-0.3	100.0%	-4.7
16175	AT2G47620.1   Symbol: ATSWI3A   SWIRM domain-containing protein / DNA-binding family protein, contains similarity to SWI/SNF complex 170 KDa subunit (Homo sapiens) gi:1549241:gb:AAC50694; contains Pfam domains PF04433: SWIRM domain, PF00249: Myb-like DNA-binding domain	4.7	4.8	-0.1	-0.3	100.0%	-5.1
16176	AT5G14850.2   mannosyltransferase, putative, similar to PIGB from Homo sapiens (gi:1552169), Mus musculus (gi:7634741)	5.0	4.9	0.1	0.3	100.0%	-5.1
16177	AT1G19390.1   wall-associated kinase, putative, similar to GB:CAB42872 from (Arabidopsis thaliana) (Plant Mol. Biol. 39 (6), 1189-1196 (1999))	3.0	3.1	-0.1	-0.3	100.0%	-4.9
16178	AT4G01410.1   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 ( GI:1619321) (Nicotiana tabacum)	2.5	2.5	0.0	0.3	100.0%	-5.2
16179	AT5G14260.3   SET domain-containing protein, low similarity to ribulose-1,5-bisphosphate carboxylase/oxygenase small subunit N-methyltransferase I (Spinacia oleracea) GI:3403236; contains Pfam profile PF00856: SET domain   chr5:4600999-4604450 FORWARD   Aliases: F18O22.50, F18O22_50	6.7	6.6	0.1	0.3	100.0%	-4.8
16180	AT4G37050.1   patatin, putative, similar to patatin-like latex allergen (Hevea brasiliensis)(PMID:10589016); contains patatin domain PF01734   chr4:17457129-17459613 REVERSE   Aliases: AP22.16, AP22_16	3.8	3.9	-0.1	-0.3	100.0%	-4.4
16181	AT3G30650.1   expressed protein   chr3:12203280-12204656 FORWARD   Aliases: MQP15.6	2.2	2.3	-0.0	-0.3	100.0%	-5.7
16182	AT5G07720.1   galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)	4.4	4.5	-0.1	-0.3	100.0%	-4.3
16183	AT1G27330.1   expressed protein, similar to EST gb:AA650671 and gb:T20610   chr1:9492965-9494051 FORWARD   Aliases: F17L21.12, F17L21_12	10.9	10.9	-0.1	-0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16184	AT1G27350.1   expressed protein, contains 1 transmembrane domain; similar to ribosome associated membrane protein RAMP4 GI:4585827 (Rattus norvegicus); similar to ESTs gb:T20610 and gb:AA586199   chr1:9498138-9499412 REVERSE   Aliases: F17L21.31	10.9	10.9	-0.1	-0.3	100.0%	-5.3
16185	AT1G32240.1   myb family transcription factor (KAN2), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA GARP-like putative transcription factor KANADI2 (KAN2) GI:15723594   chr1:11625680-11630606 REVERSE   Aliases: F27G20.7, F27G20_7	2.6	2.7	-0.0	-0.3	100.0%	-5.6
16186	AT2G36650.1   expressed protein   chr2:15366994-15368407 FORWARD   Aliases: F13K3.5, F13K3_5	3.7	3.6	0.1	0.3	100.0%	-4.5
16187	AT4G20470.1   expressed protein   chr4:11032343-11032765 REVERSE   Aliases: F9F13.120, F9F13_120	3.5	3.6	-0.1	-0.3	100.0%	-5.0
16188	AT1G65990.1   type 2 peroxiredoxin-related / thiol specific antioxidant / mal allergen family protein, similar to type 2 peroxiredoxin (Brassica rapa subsp. pekinensis) GI:4928472; contains Pfam profiles PF00646: F-box domain, PF00578: AhpC/TSA family   chr1:24575266-24577134 REVERSE   Aliases: F12P19.16, F12P19_16	2.7	2.7	-0.1	-0.3	100.0%	-5.2
16189	AT1G69510.3   expressed protein   chr1:26130049-26131596 FORWARD   Aliases: F10D13.16, F10D13_16	11.3	11.2	0.1	0.3	100.0%	-5.4
16190	AT1G22400.1   Symbol: UGT85A1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:7903649-7906662 REVERSE   Aliases: F12K8.26, F12K8_26, UGT85A1	3.4	3.3	0.1	0.3	100.0%	-4.8
16191	AT2G42340.1   expressed protein   chr2:17642385-17644700 REVERSE   Aliases: MHK10.6, MHK10_6	2.8	2.9	-0.0	-0.3	100.0%	-5.4
16192	AT1G72340.1   eukaryotic translation initiation factor 2B family protein / eIF-2B family protein, similar to SP:Q64270 Translation initiation factor eIF-2B alpha subunit {Rattus norvegicus}; contains Pfam profile PF01008: Initiation factor 2 subunit family   chr1:27240543-27242274 FORWARD   Aliases: T10D10.19, T10D10_19	8.9	9.0	-0.1	-0.3	100.0%	-4.7
16193	AT2G48140.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:19693479-19694734 FORWARD   Aliases: F11L15.4	3.1	3.2	-0.2	-0.3	100.0%	-4.1
16194	AT1G72490.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g17400.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD36146.1)   chr1:27292570-27294702 REVERSE   Aliases: T10D10.4, T10D10_4	2.8	2.8	-0.0	-0.3	100.0%	-5.3
16195	AT2G27280.1   expressed protein   chr2:11680904-11682691 REVERSE   Aliases: F12K2.14, F12K2_14	3.2	3.3	-0.1	-0.3	100.0%	-5.2
16196	AT1G49920.1   zinc finger protein-related, weak similarity to mudrA (Zea mays) GI:540581, MURAZC (Zea mays) GI:1857256; contains Pfam profiles PF03108: MuDR family transposase, PF04434: SWIM zinc finger   chr1:18485466-18487901 REVERSE   Aliases: T18C15.1, T18C15_1	2.6	2.6	-0.0	-0.3	100.0%	-5.4
16197	AT3G03520.1   phosphoesterase family protein, low similarity to SP:P95246 Phospholipase C 2 precursor (EC 3.1.4.3) {Mycobacterium tuberculosis}; contains Pfam profile PF04185: Phosphoesterase family	3.9	4.0	-0.1	-0.3	100.0%	-4.7
16198	AT1G77470.1   replication factor C 36 kDa, putative, similar to SWISS-PROT:P40937 activator 1 36 kDa subunit (Replication factor C 36 kDa subunit, A1 36 kDa subunit, RF-C 36 kDa subunit, RFC36) (Homo sapiens)   chr1:29116842-29119329 REVERSE   Aliases: T5M16.6, T5M16_6	5.8	5.8	-0.1	-0.3	100.0%	-4.9
16199	AT5G46660.1   CHP-rich zinc finger protein, putative, contains similarity to CHP-rich zinc finger protein   chr5:18949408-18950325 FORWARD   Aliases: MZA15.6, MZA15_6	2.3	2.3	0.0	0.3	100.0%	-5.8
16200	AT5G01440.1   insulin-degrading enzyme-related, contains weak similarity to Swiss-Prot:P14735 insulin-degrading enzyme (Insulysin) (Insulinase) (Insulin protease) (Homo sapiens)   chr5:179821-181320 FORWARD   Aliases: T10O8.150, T10O8_150	2.3	2.3	-0.0	-0.3	100.0%	-6.0
16201	AT1G65620.1   Symbol: AS2   LOB domain protein 6 / lateral organ boundaries domain protein 6 (LBD6) / asymmetric leaves2 (AS2), identical to SP:O04479 LOB domain protein 6 (ASYMMETRIC LEAVES2) {Arabidopsis thaliana}   chr1:24402914-24404632 FORWARD   Aliases: ASYMMETRIC LEAVES 2, F5I14.15, F5I14_15	3.4	3.3	0.0	0.3	100.0%	-5.3
16202	AT5G54480.1   expressed protein   chr5:22135230-22137392 FORWARD   Aliases: F24B18.10, F24B18_10	2.9	2.9	0.0	0.3	100.0%	-5.6
16203	AT5G64620.1   Symbol: C/VIF2	4.8	4.7	0.1	0.3	100.0%	-4.6
16204	AT3G44610.1   protein kinase family protein, similar to viroid symptom modulation protein (protein kinase)(Lycopersicon esculentum) gi:7672777:gb:AAF66637; contains protein kinase domain, Pfam:PF00069   chr3:16199116-16203162 REVERSE   Aliases: T18B22.10	3.6	3.7	-0.1	-0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16205	AT5G23670.2   Symbol: LCB2   similar to serine C-palmitoyltransferase, putative [Arabidopsis thaliana] (TAIR:At3g48780.1); similar to putative serine palmitoyltransferase [Oryza sativa (japonica cultivar-group)] (GB:NP_914892.1); similar to putative serine palmitoyltransferase [Oryza sativa (japonica cultivar-group)] (GB:NP_914893.1); similar to serine palmitoyltransferase [Lotus corniculatus var. japonicus] (GB:BAC55228.1); similar to putative serine palmitoyltransferase [Oryza sativa (japonica cultivar-group)] (GB:NP_914891.1); similar to putative serine palmitoyltransferase [Oryza sativa (japonica cultivar-group)] (GB:BAD88168.1); contains InterPro domain Aminotransferase, class I and II (InterPro:IPR004839)   chr5:7981660-7985401 FORWARD   Aliases: ATLCB2, MQM1.6, MQM1_6, SERINE PALMITOYLTRANSFERASE	6.8	6.7	0.1	0.3	100.0%	-4.7
16206	AT4G26800.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:13489846-13492060 FORWARD   Aliases: F10M23.140, F10M23_140	2.7	2.7	-0.0	-0.3	100.0%	-5.7
16207	AT5G52260.1   myb family transcription factor (MYB19), contains PFAM profile: Myb DNA binding domain PF00249   chr5:21237391-21238506 FORWARD   Aliases: F17P19.16, F17P19_16	2.5	2.5	-0.1	-0.3	100.0%	-5.1
16208	AT2G23310.2   Symbol: ATRER1C   RER1C protein, identical to SP:Q9ZWI7 RER1C protein (AtRER1C) {Arabidopsis thaliana}   chr2:9924600-9926298 FORWARD   Aliases: ATRER1C, T20D16.6, T20D16_6	4.3	4.3	0.1	0.3	100.0%	-5.2
16209	AT3G26680.3   Symbol: SNM1   similar to sterile alpha motif (SAM) domain-containing protein [Arabidopsis thaliana] (TAIR:At2g45700.1); similar to Snm1 [Oryza sativa (japonica cultivar-group)] (GB:BAD82911.1)   chr3:9802451-9805029 FORWARD   Aliases: MLJ15.7, SENSITIVE TO NITROGEN MUSTARD 1	4.9	4.9	-0.1	-0.3	100.0%	-5.0
16210	AT1G32950.1   subtilase family protein, contains similarity to SBT1 GI:1771160 from (Lycopersicon esculentum)   chr1:11941418-11944740 FORWARD   Aliases: F9L11.12, F9L11_12	2.5	2.5	0.0	0.3	100.0%	-5.5
16211	AT1G24190.1   paired amphipathic helix repeat-containing protein, similar to transcription co-repressor Sin3 (Xenopus laevis) GI:4960210; contains Pfam profile PF02671: Paired amphipathic helix repeat   chr1:8563547-8569985 REVERSE   Aliases: F3I6.12, F3I6_12	3.4	3.5	-0.1	-0.3	100.0%	-5.0
16212	AT5G61120.1   expressed protein   chr5:24599529-24601312 REVERSE   Aliases: MAF19.12, MAF19_12	2.4	2.5	-0.0	-0.3	100.0%	-5.2
16213	AT4G21865.1   expressed protein   chr4:11601917-11603287 FORWARD   Aliases: None	5.6	5.8	-0.2	-0.3	100.0%	-4.1
16214	AT5G64390.2   Symbol: HEN4   KH domain-containing RNA-binding protein (HEN4), contains similarity to RNA-binding protein; identical to cDNA HEN4 isoform 2 (HEN4) GI:28261404; contains Pfam domain PF00013: KH domain; identical to cDNA HEN4 (HEN4) GI:28261402   chr5:25760570-25764774 FORWARD   Aliases: HUA ENHANCER 4, MSJ1.23, MSJ1_23	4.1	4.0	0.1	0.3	100.0%	-5.0
16215	AT1G51580.1   KH domain-containing protein   chr1:19129251-19131827 FORWARD   Aliases: F5D21.23, F5D21_23	6.4	6.5	-0.1	-0.3	100.0%	-4.7
16216	AT4G13420.1   Symbol: HAK5   potassium transporter (HAK5), identical to K+ transporter HAK5 (Arabidopsis thaliana) gi:7108597:gb:AAF36490; similar to high-affinity potassium transporter AtKUP1p (Arabidopsis thaliana) gi:2688979:gb:AAB88901; KUP/HAK/KT Transporter family member, PMID:11500563   chr4:7796846-7802247 REVERSE   Aliases: T9E8.160, T9E8_160	2.7	2.7	0.1	0.3	100.0%	-4.6
16217	AT1G15890.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.3	3.4	-0.1	-0.3	100.0%	-4.9
16218	AT1G27435.1   expressed protein   chr1:9527561-9528865 REVERSE   Aliases: None	11.0	10.9	0.1	0.3	100.0%	-4.8
16219	AT1G60540.1   dynamin family protein, similar to SP:Q91192 Interferon-induced GTP-binding protein Mx {Oncorhynchus mykiss}; contains Pfam profiles PF01031: Dynamin central region, PF00350: Dynamin family, PF02212: Dynamin GTPase effector domain   chr1:22306151-22308650 REVERSE   Aliases: F8A5.8, F8A5_8	2.8	2.7	0.0	0.3	100.0%	-5.3
16220	AT1G22460.1   expressed protein, similar to axi 1 (Nicotiana tabacum) GI:559921; contains Pfam profile PF03138: Plant protein family   chr1:7927417-7930646 REVERSE   Aliases: F12K8.19, F12K8_19	2.9	3.0	-0.1	-0.3	100.0%	-5.3
16221	AT3G12730.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:4047079-4048621 REVERSE   Aliases: MBK21.11	2.2	2.2	0.0	0.3	100.0%	-5.4
16222	AT3G25060.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:9128523-9130328 FORWARD   Aliases: K3G3.8	2.9	2.9	-0.0	-0.3	100.0%	-5.3
16223	AT3G60720.1   receptor-like protein kinase-related, contains Pfam PF01657: Domain of unknown function, duplicated in 33kDa secretory proteins; weak similarity to receptor-like protein kinase homolog RK20-1 (GI:4530126) (Phaseolus vulgaris)   chr3:22452746-22454746 FORWARD   Aliases: T4C21.130	4.6	4.5	0.1	0.3	100.0%	-5.0
16224	AT1G02800.1   Symbol: ATCEL2	4.7	4.7	0.1	0.3	100.0%	-4.6
16225	AT1G27000.1   bZIP family transcription factor	7.2	7.0	0.2	0.3	100.0%	-4.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16226	AT1G33480.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:12147403-12150101 REVERSE   Aliases: F10C21.23, F10C21_23	3.9	4.0	-0.1	-0.3	100.0%	-5.1
16227	AT1G36340.1   ubiquitin-conjugating enzyme family protein, similar to Ubiquitin-conjugating enzyme E2-16 kDa (EC 6.3.2.19) (Ubiquitin-protein ligase) (Ubiquitin carrier protein) from {Schizosaccharomyces pombe} SP:P46595, {Caenorhabditis elegans} SP:P35129; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme	3.4	3.3	0.1	0.3	100.0%	-4.9
16228	AT1G74650.1   myb family transcription factor (cY13), similar to myb protein cY13 GI:928930 from (Arabidopsis thaliana); contains Pfam profile: PF00249 myb DNA-binding domain; identical to cDNA cY13 gene GI:928929   chr1:28044852-28046656 FORWARD   Aliases: F1M20.33, F1M20_33	2.3	2.4	-0.0	-0.3	100.0%	-5.6
16229	AT5G16690.1   similar to origin recognition complex subunit 3 [Zea mays] (GB:AAL10454.1)   chr5:5474397-5479954 FORWARD   Aliases: F5E19.30, F5E19_30	2.5	2.5	-0.0	-0.3	100.0%	-5.7
16230	AT3G62350.1   expressed protein   chr3:23082055-23082741 REVERSE   Aliases: T12C14.50	2.8	2.9	-0.0	-0.3	100.0%	-5.5
16231	AT3G23350.1   expressed protein, ; expression supported by MPSS   chr3:8354111-8355208 FORWARD   Aliases: MLM24.8	2.0	2.1	-0.0	-0.3	100.0%	-6.0
16232	AT3G44630.3   disease resistance protein RPP1-WsB-like (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein., closest Col-0 homolog to RPP1-WsB   chr3:16206971-16211582 FORWARD   Aliases: T18B22.30	2.8	2.8	0.0	0.3	100.0%	-5.3
16233	AT3G29210.1   hypothetical protein, similar to At1g32840, At4g04010, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At5g34900, At2g02210, At3g32900   chr3:11178527-11181209 FORWARD   Aliases: MXO21.6	3.1	3.2	-0.1	-0.3	100.0%	-4.6
16234	AT4G00170.1   vesicle-associated membrane family protein / VAMP family protein, similar to VAP27 GI:6688926 (Nicotiana plumbaginifolia)   chr4:70491-72196 REVERSE   Aliases: F6N15.21, F6N15_21	5.0	4.9	0.1	0.3	100.0%	-5.0
16235	AT5G18950.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:6328521-6329972 REVERSE   Aliases: F17K4.200, F17K4_200	6.1	6.2	-0.1	-0.3	100.0%	-5.0
16236	AT2G35770.1   Symbol: SCPL28	2.1	2.2	-0.1	-0.3	100.0%	-4.7
16237	AT2G22320.1   hypothetical protein   chr2:9487185-9487520 FORWARD   Aliases: T26C19.2, T26C19_2	2.5	2.4	0.0	0.3	100.0%	-6.1
16238	AT2G43080.1   Symbol: AT P4H 1   Encodes a prolyl-4 hydroxylase that can hydroxylate poly(L-proline),the collagen model peptide (Pro-Pro-Gly)10 and other proline rich peptides.   chr2:17922642-17925831 FORWARD   Aliases: A. THALIANA P4H ISOFORM 1, AT P4H 1, MFL8.6, PROLYL 4 HYDROXYLASE	7.6	7.7	-0.1	-0.3	100.0%	-4.9
16239	AT2G34555.1   Symbol: ATGA2OX3   gibberellin 2-oxidase / GA2-oxidase (GA2OX3), identical to ga2ox3 (GI:4678370)   chr2:14564067-14565776 FORWARD   Aliases: ATGA2OX3	2.7	2.7	-0.1	-0.3	100.0%	-5.4
16240	AT1G07190.1   hypothetical protein   chr1:2208012-2208176 FORWARD   Aliases: F10K1.10, F10K1_10	2.4	2.4	0.0	0.3	100.0%	-6.1
16241	AT4G26540.1   protein kinase family protein, Three false introns were added with non-consensus splice sites to circumvent frameshifts likely due to sequencing errors; this is extremely unusual and is under investigation.	2.3	2.3	-0.0	-0.3	100.0%	-5.8
16242	AT3G05960.1   sugar transporter, putative, similar to hexose transporter GI:5734440 GB:CAB52689 (Lycopersicon esculentum), Sugar carrier protein C (Ricinus communis) SP:Q41144, monosaccharide transporter (Nicotiana tabacum) GI:19885; contains Pfam profile PF00083: major facilitator superfamily protein	2.8	2.8	0.0	0.3	100.0%	-5.3
16243	AT5G52350.1   exocyst subunit EXO70 family protein, strong similarity to unknown protein (emb:CAB83315.1); contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr5:21272137-21274844 FORWARD   Aliases: K24M7.8, K24M7_8	2.2	2.2	-0.0	-0.3	100.0%	-6.0
16244	AT1G01540.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	6.6	6.5	0.1	0.3	100.0%	-5.1
16245	AT3G29791.1   expressed protein   chr3:11698235-11699250 FORWARD   Aliases: K17E7.5	2.9	3.0	-0.0	-0.3	100.0%	-5.6
16246	AT5G60900.1   Symbol: RLK1   lectin protein kinase family protein, contains Pfam domains, PF01453: Lectin (probable mannose binding) and PF00069: Protein kinase domain   chr5:24515693-24518720 REVERSE   Aliases: RECEPTOR LIKE PROTEIN KINASE 1	2.5	2.5	-0.1	-0.3	100.0%	-5.5
16247	AT3G17680.2   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g48405.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_468573.1)   chr3:6042953-6044075 REVERSE   Aliases: MKP6.26	3.4	3.5	-0.1	-0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16248	AT4G35910.1   expressed protein   chr4:17008584-17011454 REVERSE   Aliases: T19K4.40	6.4	6.3	0.1	0.3	100.0%	-4.7
16249	AT2G45750.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr2:18849613-18852541 FORWARD   Aliases: F4I18.27	3.8	3.9	-0.1	-0.3	100.0%	-4.4
16250	AT2G01970.1   endomembrane protein 70, putative   chr2:451870-454884 REVERSE   Aliases: F14H20.4, F14H20_4	5.7	5.4	0.3	0.3	100.0%	-4.5
16251	AT5G27270.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:9605653-9609790 FORWARD   Aliases: F21A20.6	4.6	4.7	-0.1	-0.3	100.0%	-5.1
16252	AT1G11680.1   Symbol: CYP51G1   obtusifoliol 14-demethylase (CYP51), identical to obtusifoliol 14-demethylase (GI:14624983) (Arabidopsis thaliana)   chr1:3938522-3940754 FORWARD   Aliases: CYP51, CYP51A2, CYTOCHROME P450 51, EMB1738, EMBRYO DEFECTIVE 1738, F25C20.17, F25C20_17	7.2	7.0	0.2	0.3	100.0%	-4.8
16253	AT1G17970.1   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:6184897-6187465 FORWARD   Aliases: F2H15.19, F2H15_19	2.8	2.7	0.1	0.3	100.0%	-4.8
16254	AT3G02130.1   leucine-rich repeat transmembrane protein kinase, putative, contains Pfam profile: Eukaryotic protein kinase domain   chr3:381226-384449 FORWARD   Aliases: F1C9.8, F1C9_8	4.5	4.5	0.1	0.3	100.0%	-5.1
16255	AT1G56360.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.3	2.3	-0.0	-0.3	100.0%	-5.7
16256	AT3G17210.1   stable protein 1-related, similar to stable protein 1 (GI:13445204) (Populus tremula) PMID:12376651; similar to pop3 peptide GB:AAC26526 from (Populus balsamifera subsp. trichocarpa X Populus deltoides)   chr3:5882290-5883206 FORWARD   Aliases: MGD8.2	9.2	9.3	-0.1	-0.3	100.0%	-5.0
16257	AT1G31580.1   Symbol: ECS1   expressed protein, identical to ORF1 (Arabidopsis thaliana) gi:457716:emb:CAA50905   chr1:11311154-11311970 FORWARD   Aliases: CXC750, F27M3.20, F27M3_20	2.3	2.3	0.0	0.3	100.0%	-5.6
16258	AT1G11570.1   nuclear transport factor 2 (NTF2), putative, similar to Swiss-Prot:P33331 nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10) (Saccharomyces cerevisiae)   chr1:3883280-3883663 FORWARD   Aliases: T23J18.32, T23J18_32	2.1	2.1	0.0	0.3	100.0%	-5.3
16259	AT3G27240.1   cytochrome c1, putative, cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III) (Solanum tuberosum) SWISS-PROT:P25076   chr3:10057026-10059953 REVERSE   Aliases: K17E12.6	8.9	9.2	-0.3	-0.3	100.0%	-4.6
16260	AT3G05160.1   sugar transporter, putative, similar to sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:1453112-1457155 REVERSE   Aliases: T12H1.12	6.9	6.9	0.1	0.3	100.0%	-4.8
16261	AT3G05165.3   similar to sugar-porter family protein 2 (SFP2) [Arabidopsis thaliana] (TAIR:At5g27360.1); similar to sugar transporter, putative [Arabidopsis thaliana] (TAIR:At3g05160.1); similar to sugar-porter family protein 1 (SFP1) [Arabidopsis thaliana] (TAIR:At5g27350.1); similar to putative integral membrane protein [Oryza sativa (japonica cultivar-group)] (GB:AAU10669.1); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sugar transporter (InterPro:IPR003663)   chr3:1458142-1462922 REVERSE   Aliases: None	6.9	6.9	0.1	0.3	100.0%	-4.8
16262	AT3G09140.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g43240.1); similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g01150.1); similar to OSJNBa0006A01.16 [Oryza sativa (japonica cultivar-group)] (GB:CAD41561.3); contains InterPro domain Protein of unknown function DUF674 (InterPro:IPR007750)   chr3:2800858-2802800 REVERSE   Aliases: MZB10.17	2.4	2.4	0.0	0.3	100.0%	-5.7
16263	AT4G24460.1   expressed protein   chr4:12642898-12645438 FORWARD   Aliases: T22A6.290, T22A6_290	4.6	4.7	-0.1	-0.3	100.0%	-5.1
16264	ATCG00510.1   Symbol: PSAI   PSI I protein   chrC:59247-59360 FORWARD   Aliases: PSAI	8.2	8.6	-0.4	-0.3	100.0%	-4.8
16265	AT2G40070.1   expressed protein   chr2:16735272-16738664 REVERSE   Aliases: T28M21.23, T28M21_23	4.4	4.4	-0.1	-0.3	100.0%	-4.8
16266	AT2G24000.1   Symbol: SCPL22	2.8	2.8	0.0	0.3	100.0%	-5.5
16267	AT4G38120.1   expressed protein   chr4:17894166-17896101 REVERSE   Aliases: F20D10.240, F20D10_240	2.3	2.3	-0.0	-0.3	100.0%	-5.7
16268	AT1G60600.1   Symbol: ABC4   Encodes a protein similar to 1,4-dihydroxy-2-naphthoic acid phytyltransferase involved in phylloquinone and plastoquinone biosynthesis. Mutants are pale green and heterotrophic with defects in photosynthetic electron transport.   chr1:22328370-22330953 REVERSE   Aliases: 1,4 DIHYDROXY 2 NAPHTHOIC ACID PHYTYLTRANSFERASE, ABC4, ABERRANT CHLORPLAST DEVELOPMENT4, F8A5.36, F8A5_36	3.1	3.1	-0.1	-0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16269	AT5G17440.1   LUC7 N_terminus domain-containing protein, contains Pfam domain PF03194: Protein of unknown function, DUF259   chr5:5749764-5753644 FORWARD   Aliases: K3M16.10, K3M16_10	5.6	5.4	0.1	0.3	100.0%	-4.8
16270	AT5G38260.1   serine/threonine protein kinase, putative, similar to receptor serine/threonine kinase PR55K gi:1235680:gb:AAC49208; contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290   chr5:15300922-15303067 REVERSE   Aliases: MXA21.150, MXA21_150	3.0	3.0	-0.0	-0.3	100.0%	-5.9
16271	AT5G13150.1   exocyst subunit EXO70 family protein, leucine zipper-containing protein - Lycopersicon esculentum, EMBL:Z12127 contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr5:4172972-4174933 REVERSE   Aliases: T19L5.110, T19L5_110	4.0	3.9	0.1	0.3	100.0%	-4.6
16272	AT1G35160.1   Symbol: GRF4   14-3-3 protein GF14 phi (GRF4), identical to GF14 protein phi chain GI:1493805, SP:P46077 from (Arabidopsis thaliana)   chr1:12867159-12868771 FORWARD   Aliases: GF14 PHI, GF14 PROTEIN PHI CHAIN, GRF4, T32G9.30, T32G9_30	11.5	11.2	0.3	0.3	100.0%	-4.5
16273	AT4G09000.1   Symbol: GRF1   14-3-3-like protein GF14 chi / general regulatory factor 1 (GRF1), identical to 14-3-3 protein GF14 chi chain GI:1702986, SP:P42643 from (Arabidopsis thaliana)	11.5	11.2	0.3	0.3	100.0%	-4.5
16274	AT4G10060.1   expressed protein, contains Pfam domain PF04685: Protein of unknown function, DUF608   chr4:6288850-6295398 FORWARD   Aliases: F28M11.3	4.1	4.0	0.1	0.3	100.0%	-4.9
16275	AT5G37180.1   sucrose synthase, putative / sucrose-UDP glucosyltransferase, putative, similar to sucrose synthase GI:6682841 from (Citrus unshiu)   chr5:14735468-14740143 FORWARD   Aliases: MJG14.14, MJG14_14	4.0	3.9	0.1	0.3	100.0%	-4.4
16276	AT1G03490.1   Symbol: ANAC006   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr1:871875-872730 FORWARD   Aliases: ANAC006, F21B7.11	2.7	2.7	-0.1	-0.3	100.0%	-5.2
16277	AT4G34980.1   Symbol: SLP2   subtilase family protein, similar to SBT1, a subtilase from tomato plants GI:1771160 from (Lycopersicon esculentum)   chr4:16656696-16659344 REVERSE   Aliases: M4E13.40, M4E13_40	6.6	6.7	-0.1	-0.3	100.0%	-4.7
16278	AT2G14800.1   expressed protein   chr2:6362264-6364061 FORWARD   Aliases: F26C24.6, F26C24_6	5.4	5.5	-0.2	-0.3	100.0%	-4.4
16279	AT3G03680.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr3:907507-910814 FORWARD   Aliases: T12J13.4, T12J13_4	3.9	4.0	-0.1	-0.3	100.0%	-4.7
16280	AT5G54490.1   Symbol: PBP1   calcium-binding EF-hand protein, putative, similar to EF-hand Ca2+-binding protein CCD1 (Triticum aestivum) GI:9255753; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:22138630-22139157 FORWARD   Aliases: F24B18.11, F24B18_11, PID BINDING PROTEIN 1, PINOID BINDING PROTEIN 1	3.5	3.6	-0.1	-0.3	100.0%	-4.6
16281	AT3G56960.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr3:21091936-21094864 FORWARD   Aliases: T8M16.6	4.4	4.3	0.1	0.3	100.0%	-4.6
16282	AT1G03370.1   C2 domain-containing protein / GRAM domain-containing protein, contains Pfam profiles PF00168: C2 domain; contains PF02893: GRAM domain; similar to Chain A, Crystal Structure Of Synaptotagmin Iii C2aC2B Length(GI:6980525); similar to Synaptotagmin III (SytIII) (Swiss-Prot:P40748) (Rattus norvegicus)   chr1:827182-835361 FORWARD   Aliases: F15K9.2, F15K9_2	4.5	4.6	-0.1	-0.3	100.0%	-4.6
16283	AT2G13680.1   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr2:5702206-5713216 FORWARD   Aliases: None	3.0	3.0	-0.0	-0.3	100.0%	-5.7
16284	AT1G23030.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:8156635-8159050 FORWARD   Aliases: F19G10.3, F19G10_3	4.4	4.3	0.1	0.3	100.0%	-5.1
16285	AT1G52000.1   jacalin lectin family protein, similar to myrosinase binding protein (Brassica napus) GI:1711296, myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile: PF01419 jacalin-like lectin domain   chr1:19336828-19339782 REVERSE   Aliases: F5F19.6, F5F19_6	2.7	2.7	-0.0	-0.3	100.0%	-5.6
16286	AT5G41900.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-7-methylocta-2,4-dienoate hydrolase (Pseudomonas putida) GI:2822275; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:16786181-16788924 FORWARD   Aliases: K16L22.19, K16L22_19	2.7	2.7	0.0	0.3	100.0%	-5.4
16287	AT2G03340.1   Symbol: WRKY3   WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain   chr2:1014347-1017012 REVERSE   Aliases: T4M8.23, T4M8_23	4.2	4.1	0.1	0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16288	AT4G27760.1   Symbol: FEY   similar to oxidoreductase, putative [Arabidopsis thaliana] (TAIR:At5g53090.1); similar to forever young oxidoreductase [Solanum bulbocastanum] (GB:AAL60069.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)   chr4:13844086-13846752 FORWARD   Aliases: FEY3, FOREVER YOUNG, FOREVER YOUNG 3, T27E11.1	3.6	3.6	0.0	0.3	100.0%	-5.3
16289	AT5G02170.1   amino acid transporter family protein, belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II	3.1	3.1	0.1	0.3	100.0%	-5.2
16290	AT4G05140.1   equilibrative nucleoside transporter family protein, contains similarity to SWISS-PROT:P31381 nucleoside transporter FUN26 (Saccharomyces cerevisiae)   chr4:2651013-2653206 REVERSE   Aliases: C17L7.60, C17L7_60	3.4	3.4	-0.1	-0.3	100.0%	-5.3
16291	AT2G01440.1   ATP-dependent DNA helicase, putative   chr2:194093-199055 REVERSE   Aliases: F2I9.6, F2I9_6	2.9	2.9	0.1	0.3	100.0%	-5.2
16292	AT4G03110.2   RNA-binding protein, putative, similar to Etr-1 (Danio rerio) GI:7670536, BRUNO-like 6 RNA-binding protein (Homo sapiens) GI:15341327, CUG-BP and ETR-3 like factor 3 (Homo sapiens) GI:12746392; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr4:1376306-1379398 REVERSE   Aliases: F4C21.3	4.2	4.0	0.1	0.3	100.0%	-4.7
16293	AT3G24100.1   four F5 family protein / 4F5 family protein, contains Pfam PF04419: 4F5 protein family   chr3:8703613-8704235 FORWARD   Aliases: MUJ8.7	7.9	7.9	-0.1	-0.3	100.0%	-4.7
16294	AT1G24110.1   peroxidase, putative, similar to peroxidase ATP26a, GB:CAA72487   chr1:8527827-8528807 FORWARD   Aliases: F3I6.3, F3I6_3	3.6	3.6	-0.0	-0.3	100.0%	-5.3
16295	AT4G15340.1   Symbol: ATPEN1	2.3	2.2	0.1	0.3	100.0%	-4.6
16296	AT4G38570.1   CDP-diacylglycerol--inositol 3-phosphatidyltransferase, putative / phosphatidylinositol synthase, putative, similar to phosphatidylinositol synthase (PIS1) - Arabidopsis thaliana, PID:e1313354 (gi:3367632)   chr4:18030852-18033534 REVERSE   Aliases: F20M13.130, F20M13_130	6.2	6.1	0.1	0.3	100.0%	-5.0
16297	AT4G31880.1   expressed protein   chr4:15419410-15424189 REVERSE   Aliases: F11C18.80, F11C18_80	5.5	5.5	0.1	0.3	100.0%	-4.8
16298	AT3G15420.1   expressed protein   chr3:5207711-5208296 REVERSE   Aliases: MJK13.8	4.3	4.2	0.1	0.3	100.0%	-4.6
16299	AT3G18840.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:6496204-6498946 FORWARD   Aliases: MCB22.1	3.6	3.7	-0.1	-0.3	100.0%	-5.1
16300	AT3G53680.1   PHD finger transcription factor, putative, predicted proteins, Arabidopsis thaliana   chr3:19903841-19908390 REVERSE   Aliases: F4P12.380	4.2	4.2	-0.0	-0.3	100.0%	-5.2
16301	AT3G22050.1   receptor-like protein kinase-related, contains Pfam profile: PF01657 Domain of unknown function; weak similarity to receptor-like protein kinase homolog RK20-1 (GI:4530126) (Phaseolus vulgaris)   chr3:7764138-7765150 FORWARD   Aliases: MZN24.23	2.3	2.3	-0.0	-0.3	100.0%	-5.9
16302	AT1G27670.1   expressed protein   chr1:9627559-9628483 REVERSE   Aliases: T22C5.12, T22C5_12	2.8	2.7	0.0	0.3	100.0%	-5.2
16303	AT5G10880.1   tRNA synthetase-related / tRNA ligase-related, similar to SP:P07814 Bifunctional aminoacyl-tRNA synthetase (Includes: Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase)) {Homo sapiens}; contains Pfam profile PF03129: Anticodon binding domain   chr5:3432694-3433868 FORWARD   Aliases: T30N20.150, T30N20_150	2.9	2.9	-0.1	-0.3	100.0%	-5.3
16304	AT2G32480.2   membrane-associated zinc metalloprotease, putative, similar to Hypothetical zinc metalloprotease AII3971 (SP:Q8YQ64) (strain PCC 7120) {Anabaena sp.} Pfam PF00595: PDZ domain (Also known as DHR or GLGF); contains TIGRFAM TIGR00054: membrane-associated zinc metalloprotease, putative   chr2:13795594-13797150 REVERSE   Aliases: T26B15.4, T26B15_4	9.1	9.0	0.1	0.3	100.0%	-4.7
16305	AT2G17580.1   polynucleotide adenylyltransferase family protein, similar to SP:P13685 Poly(A) polymerase (EC 2.7.7.19) {Escherichia coli O157:H7}; contains Pfam profile PF01743: polyA polymerase family protein   chr2:7653545-7657402 FORWARD   Aliases: MJB20.14, MJB20_14	2.8	2.8	0.0	0.3	100.0%	-5.4
16306	AT3G13682.1   amine oxidase family protein / SWIRM domain-containing protein, similar to polyamine oxidase isoform-1 (Homo sapiens) GI:14860862; contains Pfam profile:PF01593	3.5	3.6	-0.1	-0.3	100.0%	-5.0
16307	AT3G26320.1   Symbol: CYP71B36   cytochrome P450 71B36, putative (CYP71B36), identical to Cytochrome P450 71B36 (SP:Q9LIP4) (Arabidopsis thaliana); contains Pfam profile: PF00067 cytochrome P450   chr3:9645620-9647301 REVERSE   Aliases: F20C19.4	2.9	2.9	0.0	0.3	100.0%	-5.6
16308	AT4G16680.1   RNA helicase, putative, similar to SP:Q14562 ATP-dependent helicase DDX8 (RNA helicase HRH1) (DEAH-box protein 8) {Homo sapiens}; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain   chr4:9388093-9390796 REVERSE   Aliases: DL4365C, FCAALL.3	2.6	2.7	-0.1	-0.3	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16309	AT4G33870.1   peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781334:emb:CAA71494   chr4:16234675-16236497 REVERSE   Aliases: F17I5.60, F17I5_60	3.1	3.1	0.0	0.3	100.0%	-5.2
16310	AT4G39000.1   glycosyl hydrolase family 9 protein, endo-1,4-beta-glucanase precursor - Fragaria x ananassa, PID:g3549291   chr4:18171716-18173791 REVERSE   Aliases: F19H22.100, F19H22_100	2.7	2.7	-0.1	-0.3	100.0%	-5.1
16311	AT3G56670.1   expressed protein, hypothetical proteins - Arabidopsis thaliana   chr3:21000014-21000974 REVERSE   Aliases: T5P19.320	2.2	2.2	0.0	0.3	100.0%	-5.9
16312	AT1G19890.1   histone H3, putative, similar to histone H3 from Chlamydomonas reinhardtii GI:571470, Volvox carteri SP:P08437, histone H3.2 minor from Lolium temulentum SP:P11105; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4   chr1:6905025-6906009 FORWARD   Aliases: F6F9.5, F6F9_5	2.3	2.3	-0.0	-0.3	100.0%	-5.7
16313	AT2G45670.2   calcineurin B subunit-related, contains Pfam PF00036: EF hand domain and Prosite PS00018: EF-hand calcium-binding domain; contains Pfam profile PF01553: Acyltransferase; weak similarity to Calcineurin B subunit isoform 2 (Protein phosphatase 2B regulatory subunit 2) (Protein phosphatase 3 regulatory subunit B alpha isoform 2) (Swiss-Prot:Q63811) (Mus musculus)   chr2:18821783-18825525 REVERSE   Aliases: F17K2.20	2.8	2.8	-0.0	-0.3	100.0%	-5.2
16314	AT4G20860.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr4:11172633-11174478 FORWARD   Aliases: T13K14.20, T13K14_20	4.3	4.5	-0.2	-0.3	100.0%	-4.5
16315	AT1G64280.1   Symbol: NPR1   regulatory protein (NPR1), identical to regulatory protein NPR1 (nonexpresser of PR genes 1, NPR1; noninducible immunity 1, Nim1; salicylic acid insensitive 1, Sai1) (Arabidopsis thaliana) SWISS-PROT:P93002   chr1:23856411-23859229 REVERSE   Aliases: F15H21.6, F15H21_6, NIM1, NON INDUCIBLE IMMUNITY 1, NONEXPRESSER OF PR GENES 1, NPR1, REGULATORY PROTEIN NPR1, SAI1, SALICYLIC ACID INSENSITIVE 1	5.1	5.0	0.1	0.3	100.0%	-4.5
16316	AT2G28180.1   Symbol: ATCHX8	2.4	2.4	0.0	0.3	100.0%	-5.9
16317	AT4G10500.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to hyoscyamine 6 beta-hydroxylase (Atropa belladonna)(GI:4996123); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr4:6491085-6492442 FORWARD   Aliases: F7L13.80, F7L13_80	2.7	2.7	-0.0	-0.3	100.0%	-5.5
16318	AT4G25940.1   epsin N-terminal homology (ENTH) domain-containing protein, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to Chain B, Crystal Structure Of N-Terminal Domain Of Drosophila Ap180 (GP:13399617) (Drosophila melanogaster); supporting cDNA gi:20465326:gb:AY096427.1:   chr4:13169650-13172842 REVERSE   Aliases: F20B18.50, F20B18_50	2.4	2.5	-0.1	-0.3	100.0%	-5.2
16319	AT1G76740.1   expressed protein, weak similarity to fimbriae-associated protein Fap1 (GI:3929312) (Streptococcus parasanguinis); weak similarity to 1MDa_1 protein (GI:24620455) (Caenorhabditis elegans)   chr1:28810129-28815451 FORWARD   Aliases: F28O16.11, F28O16_11	3.2	3.2	0.0	0.3	100.0%	-5.5
16320	AT1G55630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:20795344-20797226 REVERSE   Aliases: F20N2.6	4.3	4.3	-0.1	-0.3	100.0%	-4.7
16321	AT1G33610.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr1:12188890-12192829 FORWARD   Aliases: T1E4.10, T1E4_10	3.2	3.2	-0.0	-0.3	100.0%	-5.2
16322	AT3G02710.1   nuclear associated protein-related / NAP-related, similar to Nuclear associated protein (NAP) (NYD-SP19) (Swiss-Prot:Q8WYA6) (Homo sapiens)   chr3:583120-585955 FORWARD   Aliases: F16B3.34, F16B3_34	3.9	4.0	-0.1	-0.3	100.0%	-5.0
16323	AT5G43900.1   Symbol: MYA2   myosin heavy chain (MYA2), nearly identical to PIR:S51824 myosin heavy chain MYA2 (Arabidopsis thaliana)	5.0	5.1	-0.1	-0.3	100.0%	-4.8
16324	AT5G19790.1   Symbol: RAP2.11   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family (RAP2.11). The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.	4.2	4.3	-0.1	-0.3	100.0%	-4.5
16325	AT3G10470.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:3260356-3261849 FORWARD   Aliases: F13M14.25	3.2	3.2	0.1	0.3	100.0%	-5.0
16326	AT5G41490.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr5:16617673-16618836 FORWARD   Aliases: MYC6.19, MYC6_19	2.3	2.3	-0.0	-0.3	100.0%	-5.8
16327	AT5G07850.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:2508918-2510504 FORWARD   Aliases: F13G24.50, F13G24_50	2.8	2.7	0.0	0.3	100.0%	-5.5
16328	AT3G24620.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315); expression supported by MPSS   chr3:8980702-8982800 REVERSE   Aliases: KINASE PARTNER PROTEIN LIKE, KPP LIKE, MOB24.21	2.9	2.9	0.1	0.3	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16329	AT4G01090.1   extra-large G-protein-related, contains weak similarity to extra-large G-protein (Arabidopsis thaliana) gi:3201682:gb:AAC19353   chr4:470526-473792 REVERSE   Aliases: F2N1.13, F2N1_13	4.0	3.9	0.0	0.3	100.0%	-5.3
16330	AT4G29420.1   F-box family protein, contains F-box Pfam:PF00646 ; similar to SKIP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr4:14470465-14472238 REVERSE   Aliases: F17A13.240, F17A13_240	2.5	2.5	0.0	0.3	100.0%	-5.9
16331	AT3G30450.1   hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At4g03990, At5g34895, At3g47270, At2g02200   chr3:12086105-12089910 FORWARD   Aliases: MSJ3.6	1.9	1.9	0.0	0.3	100.0%	-6.2
16332	AT3G53720.1   Symbol: ATCHX20   cation/hydrogen exchanger, putative (CHX20), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr3:19916656-19921090 REVERSE   Aliases: CHX20, F5K20.20	3.1	3.1	0.1	0.3	100.0%	-5.3
16333	AT4G00680.1   actin-depolymerizing factor, putative, strong similarity to SP:P30175 Actin-depolymerizing factor (ADF) {Lilium longiflorum}; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein   chr4:279603-280699 REVERSE   Aliases: F6N23.12, F6N23_12	5.8	5.7	0.1	0.3	100.0%	-4.6
16334	AT1G35730.1   pumilio/Puf RNA-binding domain-containing protein   chr1:13228536-13231008 REVERSE   Aliases: F14D7.3, F14D7_3	2.6	2.5	0.0	0.3	100.0%	-5.5
16335	AT1G28160.1   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.	2.5	2.5	-0.0	-0.3	100.0%	-5.8
16336	AT2G26720.1   plastocyanin-like domain-containing protein / mavicyanin, putative, similar to mavicyanin SP:P80728 from (Cucurbita pepo)   chr2:11391860-11392480 FORWARD   Aliases: F18A8.9, F18A8_9	2.2	2.2	-0.0	-0.3	100.0%	-5.8
16337	AT1G33320.1   cystathionine gamma-synthase, chloroplast, putative / O-succinylhomoserine (Thiol)-lyase, putative, strong similarity to SP:P55217 Cystathionine gamma-synthase, chloroplast precursor (EC 4.2.99.9) (CGS) (O-succinylhomoserine (Thiol)-lyase) {Arabidopsis thaliana}; contains Pfam profile PF01053: Cys/Met metabolism PLP-dependent enzyme   chr1:12080989-12083442 FORWARD   Aliases: F10C21.1	3.1	3.2	-0.1	-0.3	100.0%	-4.3
16338	AT3G02450.1   cell division protein ftsH, putative, similar to SWISS-PROT:P46469 cell division protein ftsH homolog (Lactococcus lactis); contains Pfam domain, PF00004: ATPase, AAA family ('ATPases 'A'associated with diverse cellular 'A'activities)   chr3:502714-505237 REVERSE   Aliases: F16B3.8, F16B3_8	5.1	5.1	0.1	0.3	100.0%	-4.9
16339	AT1G74670.1   gibberellin-responsive protein, putative, similar to SP:P46690 Gibberellin-regulated protein 4 precursor {Arabidopsis thaliana} GASA4; contains Pfam profile PF02704: Gibberellin regulated protein   chr1:28056960-28057810 FORWARD   Aliases: F1M20.35, F1M20_35	2.8	2.8	-0.0	-0.3	100.0%	-5.7
16340	AT1G16030.1   Symbol: HSP70B	5.6	5.7	-0.1	-0.3	100.0%	-4.9
16341	AT2G22300.1   ethylene-responsive calmodulin-binding protein, putative (SR1), identical to partial sequence of ethylene-induced calmodulin-binding protein GI:11545505 from (Arabidopsis thaliana); contains Pfam profiles PF03859: CG-1 domain, PF00612: IQ calmodulin-binding motif, and PF00023: Ankyrin repeat   chr2:9478472-9484147 FORWARD   Aliases: T26C19.4, T26C19_4	6.2	6.1	0.1	0.3	100.0%	-4.8
16342	AT1G65380.1   Symbol: CLV2   receptor-like protein CLAVATA2 (CLV2), identical to receptor-like protein CLAVATA2 (Arabidopsis thaliana) gi:6049566:gb:AAF02654 contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611;   chr1:24290489-24292912 FORWARD   Aliases: CLAVATA 2, T8F5.16, T8F5_16	4.4	4.5	-0.1	-0.3	100.0%	-5.3
16343	AT3G52860.1   expressed protein   chr3:19602826-19603743 REVERSE   Aliases: F8J2.30	4.0	3.9	0.1	0.3	100.0%	-4.9
16344	AT5G11940.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr5:3849284-3852418 FORWARD   Aliases: F14F18.110, F14F18_110	1.9	1.9	0.0	0.3	100.0%	-6.2
16345	AT3G25570.1   adenosylmethionine decarboxylase family protein, contains Pfam profile: PF01536 adenosylmethionine decarboxylase	3.3	3.4	-0.1	-0.3	100.0%	-4.8
16346	AT2G36830.1   Symbol: GAMMA TIP   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr2:15452505-15453653 FORWARD   Aliases: GAMMA TIP1, GAMMA TONOPLAST INTRINSIC PROTEIN, T1J8.1, T1J8_1, TIP1;1	9.0	9.1	-0.1	-0.3	100.0%	-4.6
16347	AT4G31390.2   similar to ABC1 family protein [Arabidopsis thaliana] (TAIR:At1g79600.1); similar to COG0661: Predicted unusual protein kinase [Nostoc punctiforme PCC 73102] (GB:ZP_00110959.1); similar to all0592 [Nostoc sp. PCC 7120] (GB:BA72550.1); contains InterPro domain ABC1 protein (InterPro:IPR004147)   chr4:15233080-15237115 FORWARD   Aliases: F3L17.6	5.2	5.1	0.1	0.3	100.0%	-4.8
16348	AT1G30480.1   Symbol: DRT111	7.2	7.3	-0.1	-0.3	100.0%	-4.7
16349	AT5G28420.1   hypothetical protein, predicted proteins - Arabidopsis thaliana   chr5:10364838-10365293 FORWARD   Aliases: F21B23.80, F21B23_80	2.6	2.6	0.1	0.3	100.0%	-5.2
16350	AT4G13520.1   expressed protein   chr4:7864390-7864920 FORWARD   Aliases: T6G15.70, T6G15_70	11.0	10.9	0.1	0.3	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16351	AT2G20400.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:8806268-8809054 FORWARD   Aliases: F11A3.5, F11A3_5	3.8	3.8	-0.0	-0.3	100.0%	-5.0
16352	AT4G25520.1   transcriptional co-regulator family protein, contains similarity to GP:18033922:gb:AAL57277 SEUSS transcriptional co-regulator (Arabidopsis thaliana)   chr4:13032246-13035935 REVERSE   Aliases: M7J2.110, M7J2_110	3.1	3.0	0.1	0.3	100.0%	-5.0
16353	AT4G02780.1   Symbol: GA1   copalyl diphosphate synthase / CPS / ent-kaurene synthetase A (GA1), identical to GI:571330 (PMID: 7994182); formerly called ent-kaurene synthetase A   chr4:1237767-1244813 REVERSE   Aliases: ABC33, ENT KAURENE SYNTHETASE A, GA REQUIRING 1, T5J8.9, T5J8_9	2.6	2.7	-0.0	-0.3	100.0%	-5.5
16354	AT5G07710.1   exonuclease family protein, contains exonuclease domain, Pfam:PF00929   chr5:2453136-2455547 FORWARD   Aliases: MBK20.17, MBK20_17	5.4	5.3	0.1	0.3	100.0%	-4.9
16355	AT2G28820.1   similar to alanine aminotransferase, putative [Arabidopsis thaliana] (TAIR:At1g72330.1); similar to ribosomal protein L16 [Vigna angularis] (GB:AAN04889.1); contains InterPro domain Ribosomal protein L16 (InterPro:IPR000114)	3.1	3.0	0.1	0.3	100.0%	-5.0
16356	AT3G58730.1   vacuolar ATP synthase subunit D (VATD) / V-ATPase D subunit / vacuolar proton pump D subunit (VATPD), identical to Vacuolar ATP synthase subunit D (EC 3.6.3.14) (V-ATPase D subunit) (Vacuolar proton pump D subunit) (Swiss-Prot:Q9XGM1) (Arabidopsis thaliana)   chr3:21729234-21730925 REVERSE   Aliases: T20N10.80	8.5	8.2	0.3	0.3	100.0%	-4.5
16357	AT4G32160.1   phox (PX) domain-containing protein, contains Pfam profile PF00787: PX domain   chr4:15528811-15533106 FORWARD   Aliases: F10N7.30, F10N7_30	4.5	4.4	0.1	0.3	100.0%	-4.8
16358	AT3G42390.1   hypothetical protein   chr3:14529007-14529453 REVERSE   Aliases: T14K23.100	3.4	3.3	0.1	0.3	100.0%	-5.2
16359	AT4G35890.1   La domain-containing protein, contains Pfam PF05383: La domain   chr4:16997142-17000836 FORWARD   Aliases: T19K4.20	7.0	7.1	-0.1	-0.3	100.0%	-5.1
16360	AT3G03450.1   Symbol: RGL2   gibberellin response modulator, putative / gibberellin-responsive modulator, putative, similar to GAI (GI:2569938), RGA1 (GB:AAC67333) and RGA2 (GI:2339980) (Arabidopsis thaliana); possible involvement in nitrogen metabolism   chr3:819344-821413 REVERSE   Aliases: RGA LIKE 2, RGA1 LIKE, T21P5.13, T21P5_13	2.5	2.5	-0.0	-0.3	100.0%	-5.6
16361	AT1G35860.1   chloroplast outer membrane protein-related, similar to chloroplastic outer envelope membrane protein (OEP75) (Pisum sativum) GI:633607   chr1:13333259-13335262 REVERSE   Aliases: F10O5.4, F10O5_4	2.7	2.8	-0.0	-0.3	100.0%	-5.5
16362	AT3G26870.1   self-incompatibility protein-related, low similarity to self-incompatibility (Papaver nudicaule) GI:3097262   chr3:9904525-9904917 REVERSE   Aliases: MDJ14.21	2.3	2.3	-0.0	-0.3	100.0%	-5.8
16363	AT4G25630.1   Symbol: FIB2   fibrillar protein 2 (FIB2), identical to fibrillar protein 2 GI:9965655 from (Arabidopsis thaliana)   chr4:13074142-13076432 FORWARD   Aliases: ATFIB2, FIBRILLARIN 2, L73G19.10, L73G19_10	8.0	8.1	-0.1	-0.3	100.0%	-4.7
16364	AT3G28080.2   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr3:10452778-10456466 FORWARD   Aliases: MMG15.13	2.4	2.3	0.0	0.3	100.0%	-5.6
16365	AT3G52660.2   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At4g00830.1); similar to putative RNA-binding protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52145.1); contains InterPro domain RNA-binding region RNP-1	9.5	9.4	0.1	0.3	100.0%	-5.7
16366	AT5G28390.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:10342028-10343001 REVERSE   Aliases: F21B23.40, F21B23_40	9.5	9.4	0.1	0.3	100.0%	-5.7
16367	AT4G16143.1   importin alpha-2, putative (IMPA-2), similar to importin alpha 2 (Capsicum annuum) GI:13752562; contains Pfam profiles PF01749: Importin beta binding domain, PF00514: Armadillo/beta-catenin-like repeat; non-consensus GG donor splice site at exon 1 and 6; CT acceptor splice site at exon 2	3.2	3.2	-0.0	-0.3	100.0%	-5.9
16368	AT3G48990.1   AMP-dependent synthetase and ligase family protein, similar to peroxisomal-coenzyme A synthetase (FAT2) (gi:586339) from Saccharomyces cerevisiae; contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA; identical to cDNA adenosine monophosphate binding protein 3 AMPBP3 (AMPBP3)GI:20799714   chr3:18169732-18172334 REVERSE   Aliases: T2J13.170	11.2	11.2	0.1	0.3	100.0%	-5.3
16369	AT1G22870.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:8089490-8094162 FORWARD   Aliases: F19G10.17, F19G10_17	4.1	4.0	0.1	0.3	100.0%	-5.0
16370	AT3G47770.1   Symbol: ATATH5	2.8	2.8	0.1	0.3	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16371	AT4G13220.1   expressed protein   chr4:7674295-7675303 REVERSE   Aliases: F17N18.110, F17N18_110	5.3	5.3	-0.1	-0.3	100.0%	-4.6
16372	AT1G77680.1   ribonuclease II family protein, weak similarity to SP:P37202 Mitotic control protein dis3 {Schizosaccharomyces pombe}; contains Pfam profile PF00773: RNB-like protein   chr1:29197082-29200857 REVERSE   Aliases: T32E8.1	4.3	4.2	0.1	0.3	100.0%	-4.8
16373	AT4G18710.1   Symbol: BIN2   shaggy-related protein kinase eta / ASK-eta (ASK7), identical to shaggy-related protein kinase eta (ASK-eta) (Arabidopsis thaliana) SWISS-PROT:Q39011   chr4:10296284-10299373 FORWARD   Aliases: BRASSINOSTEROID INSENSITIVE 2, DWF12, F28A21.120, F28A21_120, UCU1, ULTRACURVATA1	5.6	5.4	0.2	0.3	100.0%	-4.7
16374	AT3G04130.2   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At3g22670.1); similar to putative reverse transcriptase [Oryza sativa (japonica cultivar-group)] (GB:XP_469720.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr3:1083981-1086392 FORWARD   Aliases: T6K12.25, T6K12_25	3.5	3.5	0.0	0.3	100.0%	-5.3
16375	AT4G00980.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr4:422478-424588 REVERSE   Aliases: A_TM018A10.1, A_TM018A10_1, T18A10.10, T18A10_10	3.6	3.7	-0.1	-0.3	100.0%	-5.0
16376	AT4G14750.1   calmodulin-binding family protein, contains Pfam profile PF00612: IQ calmodulin-binding motif   chr4:8470376-8472182 FORWARD   Aliases: DL3415W, FCAALL.303	2.9	2.9	-0.0	-0.3	100.0%	-5.2
16377	AT3G27510.1   similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At3g45530.1); similar to DC1 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g42840.1); contains InterPro domain DC1 domain (InterPro:IPR004146)	2.3	2.2	0.0	0.3	100.0%	-5.9
16378	AT3G06970.1   RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr3:2199659-2201156 REVERSE   Aliases: F17A9.12	2.1	2.1	0.0	0.3	100.0%	-6.1
16379	AT1G19930.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr1:6917011-6918129 FORWARD   Aliases: F6F9.32, F6F9_32	3.9	3.8	0.1	0.3	100.0%	-4.9
16380	AT2G04160.1   Symbol: AIR3   subtilisin-like protease (AIR3), almost identical to subtilisin-like protease AIR3 GI:4218991 from (Arabidopsis thaliana), missing 200 aa at N-terminus   chr2:1401447-1407691 REVERSE   Aliases: T16B23.1	2.9	3.0	-0.0	-0.3	100.0%	-5.3
16381	AT2G39180.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:16351245-16353686 REVERSE   Aliases: T16B24.18, T16B24_18	4.0	4.1	-0.1	-0.3	100.0%	-5.1
16382	AT2G41660.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr2:17374900-17376267 FORWARD   Aliases: T32G6.18, T32G6_18	3.5	3.7	-0.2	-0.3	100.0%	-4.3
16383	AT2G07280.1   expressed protein   chr2:3026395-3029071 FORWARD   Aliases: T13E11.5, T13E11_5	2.2	2.2	0.0	0.3	100.0%	-6.1
16384	AT3G07250.1   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein, contains Pfam profiles PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain), PF02136: Nuclear transport factor 2 (NTF2) domain   chr3:2300585-2308311 REVERSE   Aliases: T1B9.8	3.2	3.3	-0.0	-0.3	100.0%	-5.9
16385	AT4G11940.1   hypothetical protein, predicted proteins Arabidopsis thaliana   chr4:7168167-7168961 FORWARD   Aliases: F16J13.10, F16J13_10	2.6	2.5	0.0	0.3	100.0%	-5.4
16386	AT5G48655.3   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:19748399-19750251 REVERSE   Aliases: None	7.0	6.9	0.2	0.3	100.0%	-4.6
16387	AT1G28560.1   snRNA activating complex family protein, similar to snRNA activating protein complex 50 kDa subunit (SNAPc 50 kDa subunit) (Proximal sequence element-binding transcription factor beta subunit) (PSE-binding factor beta subunit) (PTF beta subunit) (Swiss-Prot:Q92966) (Homo sapiens)	4.2	4.1	0.1	0.3	100.0%	-5.0
16388	AT1G02320.1   expressed protein   chr1:461828-461974 FORWARD   Aliases: T6A9.30	2.4	2.5	-0.0	-0.3	100.0%	-5.7
16389	AT1G27770.2   Symbol: ACA1   calcium-transporting ATPase 1, plasma membrane-type / Ca(2+)-ATPase isoform 1 (ACA1) / plastid envelope ATPase 1 (PEA1), identical to SP:Q37145 Calcium-transporting ATPase 1, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 1) (Plastid envelope ATPase 1) {Arabidopsis thaliana}; identical to cDNA envelope Ca2+-ATPase (PEA1) chloroplast gene encoding chloroplast protein GI:509809   chr1:9671625-9676144 REVERSE   Aliases: CA2+ ATPASE, PEA1, T22C5.23, T22C5_23	7.1	7.0	0.1	0.3	100.0%	-4.9
16390	AT5G40690.1   expressed protein   chr5:16307939-16308811 FORWARD   Aliases: MNF13.25, MNF13_25	3.3	3.4	-0.1	-0.3	100.0%	-4.4
16391	AT1G43810.1   hypothetical protein   chr1:16582887-16583240 REVERSE   Aliases: F28H19.20, F28H19_20	2.8	2.7	0.0	0.3	100.0%	-5.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16392	AT3G45720.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:16796031-16797930 FORWARD   Aliases: T6D9.50	2.8	2.8	0.1	0.3	100.0%	-5.3
16393	AT4G27330.1   Symbol: SPL   sporocyteless (SPL), identical to sporocyteless SPL (MADS-box related protein) (Arabidopsis thaliana) gi:5566240:gb:AAD45344   chr4:13682084-13683544 REVERSE   Aliases: F27G19.11, NOZZLE, NZZ, SPOROCTELESS	2.9	3.0	-0.1	-0.3	100.0%	-5.1
16394	AT5G23520.1   expressed protein   chr5:7929594-7931299 REVERSE   Aliases: MQM1.22, MQM1_22	3.9	3.8	0.1	0.3	100.0%	-4.9
16395	AT4G11050.1   endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-beta-1,4-glucanase Gl:4972236 from (Fragaria x ananassa)   chr4:6747463-6751307 REVERSE   Aliases: T22B4.30, T22B4_30	3.0	3.0	-0.0	-0.3	100.0%	-5.6
16396	AT3G13270.1   expressed protein, contains similarity to replication protein A1	2.8	2.8	0.0	0.3	100.0%	-5.5
16397	AT2G01880.1   purple acid phosphatase (PAP7), identical to purple acid phosphatase (PAP7) Gl:20257476 from (Arabidopsis thaliana); contains Pfam profile: PF00149 calcineurin-like phosphoesterase   chr2:391422-393999 REVERSE   Aliases: T23K3.7, T23K3_7	2.8	2.9	-0.1	-0.3	100.0%	-4.6
16398	AT4G27730.1   Symbol: ATOPT6	3.6	3.5	0.1	0.3	100.0%	-4.9
16399	AT5G65650.1   expressed protein   chr5:26256728-26258741 FORWARD   Aliases: K21L13.17, K21L13_17	5.4	5.5	-0.1	-0.3	100.0%	-4.8
16400	AT2G03210.1   Symbol: FUT2   xyloglucan fucosyltransferase, putative (FUT2), identical to SP:O81053 Probable fucosyltransferase 2 (EC 2.4.1.-) (AtFUT2) {Arabidopsis thaliana}; similar to xyloglucan fucosyltransferase Gl:5231145 from (Arabidopsis thaliana)   chr2:968332-970015 REVERSE   Aliases: ATFUT2, T18E12.12, T18E12_12	3.1	3.2	-0.1	-0.3	100.0%	-5.2
16401	AT4G19620.1   expressed protein   chr4:10682443-10682854 REVERSE   Aliases: F24J7.170, F24J7_170	3.0	3.0	0.0	0.3	100.0%	-5.2
16402	AT5G42010.1   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP: Q9UGP9) (Homo sapiens)   chr5:16819508-16822241 FORWARD   Aliases: MJC20.11, MJC20_11	3.7	3.8	-0.1	-0.3	100.0%	-4.9
16403	AT5G44420.1   Symbol: PDF1.2	3.1	3.0	0.0	0.3	100.0%	-5.1
16404	AT2G45890.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr2:18890546-18892639 FORWARD   Aliases: F4I18.13, KINASE PARTNER PROTEIN LIKE, KPP LIKE	1.8	1.7	0.0	0.3	100.0%	-5.2
16405	AT3G16160.1   similar to tesmin/TSO1-like CXC domain-containing protein [Arabidopsis thaliana] (TAIR:At4g29000.1); similar to transcription factor-like [Oryza sativa (japonica cultivar-group)] (GB:XP_482017.1); contains InterPro domain Tesmin/TSO1-like CXC domain (InterPro:IPR005172)   chr3:5473372-5475096 REVERSE   Aliases: MSL1.20	3.1	3.2	-0.1	-0.3	100.0%	-5.2
16406	AT5G61750.1   cupin family protein, similar to germin-like protein from Mesembryanthemum crystallinum, PIR:T12426 (SP:P45852), rhicadhesin receptor precursor (Germin-like protein) from Pisum sativum (SP:Q9S8P4); contains Pfam profile PF00190: Cupin   chr5:24830030-24830662 REVERSE   Aliases: MAC9.10, MAC9_10	3.2	3.2	0.1	0.3	100.0%	-5.3
16407	AT4G09020.1   Symbol: ATISA3/ISA3   isoamylase, putative / starch debranching enzyme, putative, similar to isoamylase isoform 3 (Solanum tuberosum) Gl:27728149, isoamylase (Oryza sativa) Gl:3252794; contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain   chr4:5784073-5788997 FORWARD   Aliases: ATISA3, F23J3.50, F23J3_50, ISA3	7.3	7.2	0.1	0.3	100.0%	-4.7
16408	AT2G23990.2   plastocyanin-like domain-containing protein   chr2:10213915-10214991 REVERSE   Aliases: T29E15.19, T29E15_19	2.8	2.8	0.0	0.3	100.0%	-5.3
16409	AT2G44800.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase SP:Q96330 {Arabidopsis thaliana}, SP:Q07512 {Petunia hybrida}; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr2:18473895-18475626 FORWARD   Aliases: F16B22.29	2.3	2.3	-0.0	-0.3	100.0%	-5.5
16410	AT4G17710.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to HD-Zip homeo domain OCL4 protein (Gl:8920425) (Zea mays); contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain   chr4:9856309-9859301 REVERSE   Aliases: DL4890C, FCAALL.102	3.4	3.4	0.1	0.3	100.0%	-5.3
16411	AT1G73250.1   Symbol: ATFX/GER1   encodes a bifunctional 3, 5-epimerase-4-reductase in L-fucose synthesis and converts GDP-D-mannose to GDP-L-fucose in vitro along with MUR1 (GDP-D-mannose 4,6-dehydratase). It is expressed in all tissues examined, but most abundantly in roots and flowers.   chr1:27548667-27550085 REVERSE   Aliases: ATFX, GDP 4 KETO 6 DEOXY D MANNOSE 3,5 EPIMERASE 4 REDUCTASE, GER1, T18K17.8, T18K17_8	6.2	6.1	0.1	0.3	100.0%	-5.1
16412	AT3G12940.1   expressed protein   chr3:4130014-4132474 REVERSE   Aliases: MGH6.5	2.8	2.8	0.0	0.3	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16413	AT5G17080.1   cathepsin-related, contains weak similarity to Cathepsin L (EC 3.4.22.15) (Progesterone-dependent protein) (PDP) (Fragment) (Swiss-Prot:P25773) (Felis silvestris catus)	2.6	2.6	-0.0	-0.3	100.0%	-5.5
16414	AT4G19530.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:10651754-10657292 FORWARD   Aliases: F24J7.90, F24J7_90	3.1	3.0	0.1	0.3	100.0%	-5.2
16415	AT4G26080.1   Symbol: ABI1   protein phosphatase 2C ABI1 / PP2C ABI1 / abscisic acid-insensitive 1 (ABI1), nearly identical to SP:P49597 Protein phosphatase 2C ABI1 (EC 3.1.3.16) (PP2C) (Abscisic acid- insensitive 1) {Arabidopsis thaliana}   chr4:13219970-13222293 REVERSE   Aliases: ABA INSENSITIVE 1, ABSCISIC ACID INSENSITIVE 1, F20B18.190, F20B18_190, PROTEIN PHOSPHATASE 2C ABI1	6.8	6.7	0.1	0.2	100.0%	-4.9
16416	AT5G60490.1   Symbol: FLA12   fasciclin-like arabinogalactan-protein (FLA12)   chr5:24342953-24343928 REVERSE   Aliases: MUF9.12, MUF9_12	3.6	3.7	-0.1	-0.2	100.0%	-5.0
16417	AT4G15370.1   pentacyclic triterpene synthase, putative, similar to pentacyclic triterpene synthase (gi:6650208) (PMID:11247608)   chr4:8773786-8779685 REVERSE   Aliases: DL3730C, FCAALL.279	3.4	3.4	0.1	0.2	100.0%	-5.2
16418	AT4G32620.1   expressed protein, predicted protein T10M13.8, Arabidopsis thaliana   chr4:15731679-15737278 FORWARD   Aliases: F4D11.180, F4D11_180	5.9	5.9	-0.1	-0.2	100.0%	-5.0
16419	AT4G20300.2   expressed protein   chr4:10955448-10959223 FORWARD   Aliases: F1C12.211, F1C12_211	4.3	4.6	-0.2	-0.2	100.0%	-4.7
16420	AT2G04750.1   fimbrin-like protein, putative, similar to fimbrin-like protein (ATFIM1) (Arabidopsis thaliana) GI:2905893; contains Pfam profile PF00307: Calponin homology (CH) domain	2.5	2.4	0.0	0.2	100.0%	-5.8
16421	AT4G04500.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:2238409-2240863 FORWARD   Aliases: T26N6.11, T26N6_11	2.7	2.7	0.0	0.2	100.0%	-5.4
16422	AT5G16280.1   expressed protein   chr5:5323178-5331348 REVERSE   Aliases: T21H19.200, T21H19_200	4.3	4.2	0.1	0.2	100.0%	-5.0
16423	AT5G39360.1   circadian clock coupling factor-related, similar to circadian clock coupling factor ZGT (Nicotiana tabacum) GI:14210079   chr5:15770220-15771290 REVERSE   Aliases: MUL8.4, MUL8_4	4.3	4.4	-0.0	-0.2	100.0%	-5.2
16424	AT2G31850.1   expressed protein   chr2:13547276-13547617 FORWARD   Aliases: F20M17.11, F20M17_11	3.1	3.1	-0.0	-0.2	100.0%	-5.4
16425	AT5G45950.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386) and EXL1 (GI:15054382) (Arabidopsis thaliana), anther-specific proline-rich protein APG (Arabidopsis thaliana) GI:22599; contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:18651361-18653926 FORWARD   Aliases: K15I22.15, K15I22_15	2.3	2.4	-0.0	-0.2	100.0%	-5.6
16426	AT3G10150.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.9	2.9	0.0	0.2	100.0%	-5.2
16427	AT5G64790.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr5:25919939-25921785 FORWARD   Aliases: MXK3.1, MXK3_1	3.0	3.1	-0.1	-0.2	100.0%	-5.1
16428	AT2G32260.1   cholinephosphate cytidyltransferase, putative / phosphorylcholine transferase, putative / CTP:phosphocholine cytidyltransferase, putative, strong similarity to CTP:phosphocholine cytidyltransferase (Brassica napus) GI:1418125; contains Pfam profile PF01467: Cytidylyltransferase   chr2:13704593-13707718 FORWARD   Aliases: T32F6.22, T32F6_22	7.7	7.8	-0.1	-0.2	100.0%	-5.1
16429	AT5G65830.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to receptor protein kinase-like protein   chr5:26359342-26360547 REVERSE   Aliases: K22J17.4, K22J17_4	2.6	2.5	0.0	0.2	100.0%	-5.4
16430	AT3G56750.1   expressed protein   chr3:21029068-21031410 REVERSE   Aliases: T8M16.80	3.1	3.1	-0.1	-0.2	100.0%	-5.1
16431	AT5G39670.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr5:15900407-15901295 FORWARD   Aliases: MIJ24.17, MIJ24_17	3.0	2.9	0.1	0.2	100.0%	-4.9
16432	AT5G57120.1   expressed protein, weak similarity to SP:Q14978 Nucleolar phosphoprotein p130 {Homo sapiens}   chr5:23139766-23141739 REVERSE   Aliases: MUL3.6, MUL3_6	9.8	9.7	0.1	0.2	100.0%	-5.1
16433	AT2G04020.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL6 (GI:15054390), EXL1 (GI:15054382) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr2:1274424-1275521 FORWARD   Aliases: F3C11.13, F3C11_13	3.6	3.6	-0.1	-0.2	100.0%	-5.3
16434	AT1G36050.1   expressed protein   chr1:13451416-13454454 FORWARD   Aliases: F5J5.4, F5J5_4	8.7	8.6	0.1	0.2	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16435	AT4G15400.1   transferase family protein, similar to deacetylindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034), benzylalcohol acetyltransferase (Clarkia breweri)(GI:6166336)(PMID:10588064)   chr4:8811928-8813478 REVERSE   Aliases: DL3745C, FCAALL.284	2.6	2.7	-0.1	-0.2	100.0%	-4.4
16436	AT4G18980.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr4:10398929-10399523 FORWARD   Aliases: F13C5.150, F13C5_150	2.4	2.4	0.0	0.2	100.0%	-5.8
16437	AT3G47260.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g32840, At4g04010, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At5g34900, At3g29210, At2g02210, At3g32900   chr3:17414114-17418812 FORWARD   Aliases: T21L8.10	2.1	2.1	0.0	0.2	100.0%	-6.1
16438	AT5G23030.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr5:7726791-7727712 FORWARD   Aliases: MYJ24.2, MYJ24_2	2.2	2.3	-0.1	-0.2	100.0%	-4.7
16439	AT3G02330.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr3:473888-476599 REVERSE   Aliases: F11A12.2, F11A12_2	3.3	3.3	0.0	0.2	100.0%	-5.3
16440	AT4G29430.1   Symbol: RPS15AE   40S ribosomal protein S15A (RPS15aE), ribosomal protein S15a - Brassica napus,PIR2:S20945   chr4:14472408-14473627 FORWARD   Aliases: F17A13.250, F17A13_250, RPS15AE	7.4	7.4	0.1	0.2	100.0%	-4.7
16441	AT5G20360.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein, contains Pfam profiles PF00564: PB1 domain, PF00515: TPR Domain   chr5:6882123-6884632 REVERSE   Aliases: F5O24.250, F5O24_250	3.4	3.4	0.0	0.2	100.0%	-5.2
16442	AT1G55200.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr1:20592868-20595730 REVERSE   Aliases: F7A10.8, F7A10_8	2.6	2.6	0.0	0.2	100.0%	-5.8
16443	AT5G43140.1   peroxisomal membrane 22 kDa family protein, contains Mpv17 / PMP22 family domain, Pfam:PF04117   chr5:17338773-17340633 FORWARD   Aliases: MMG4.17, MMG4_17	5.4	5.3	0.1	0.2	100.0%	-4.7
16444	AT1G52810.1   2-oxoglutarate-dependent dioxygenase-related, similar to AOP1.2 (Arabidopsis thaliana) GI:16118887   chr1:19670795-19671905 FORWARD   Aliases: F14G24.8, F14G24_8	2.7	2.7	0.0	0.2	100.0%	-5.2
16445	AT3G04420.1   Symbol: ANAC048   no apical meristem (NAM) family protein, similar to NAC1 (GI:7716952) {Medicago truncatula}; contains Pfam PF02365 : No apical meristem (NAM) protein   chr3:1172752-1174473 FORWARD   Aliases: ANAC048, T27C4.6, T27C4_6	3.6	3.6	0.1	0.2	100.0%	-4.7
16446	AT5G19620.1   Symbol: OEP80   outer membrane OMP85 family protein, weak similarity to chloroplastic outer envelope membrane protein (OEP75) (Pisum sativum) GI:633607; contains Pfam profile PF01103: outer membrane protein, OMP85 family   chr5:6623206-6627811 FORWARD   Aliases: ARABIDOPSIS THALIANA OUTER ENVELOPE PROTEIN OF 80 KDA, ATOEP80, T29J13.40, T29J13_40	5.9	6.0	-0.1	-0.2	100.0%	-4.8
16447	AT2G28540.2   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At5g60170.1)   chr2:12228248-12230905 FORWARD   Aliases: T17D12.10, T17D12_10	4.0	4.0	0.0	0.2	100.0%	-5.6
16448	AT5G01520.2   zinc finger (C3HC4-type RING finger) family protein, similar to MTD2 (Medicago truncatula) GI:9294812; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:206431-208610 FORWARD   Aliases: F7A7.40, F7A7_40	4.5	4.4	0.1	0.2	100.0%	-4.5
16449	AT3G09130.1   hypothetical protein   chr3:2799317-2800510 FORWARD   Aliases: MZB10.16	2.4	2.4	-0.0	-0.2	100.0%	-5.5
16450	AT4G09630.1   expressed protein, contains Pfam profile: PF04765 protein of unknown function (DUF616)   chr4:6083710-6088131 FORWARD   Aliases: T25P22.70, T25P22_70	4.7	4.6	0.1	0.2	100.0%	-4.8
16451	AT1G80960.3   F-box protein-related, contains weak hit to Pfam PF00646: F-box domain   chr1:30420729-30423183 FORWARD   Aliases: F23A5.32, F23A5_32	6.3	6.1	0.1	0.2	100.0%	-4.9
16452	AT1G24100.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:8525424-8527076 REVERSE   Aliases: F3I6.2, F3I6_2	7.2	7.3	-0.1	-0.2	100.0%	-5.0
16453	AT5G17910.1   expressed protein   chr5:5927404-5932724 FORWARD   Aliases: MPI7.8, MPI7_8	5.4	5.2	0.2	0.2	100.0%	-4.5
16454	AT3G31430.1   expressed protein, low similarity to zinc finger protein (Arabidopsis thaliana) GI:976277   chr3:12798340-12799350 REVERSE   Aliases: T22C2.102	2.3	2.2	0.0	0.2	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16455	AT2G28400.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr2:12155381-12156129 REVERSE   Aliases: T1B3.8, T1B3_8	4.0	3.9	0.1	0.2	100.0%	-4.6
16456	AT5G28530.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr5:10525082-10527304 REVERSE   Aliases: T26D3.9, T26D3_9	3.1	3.2	-0.0	-0.2	100.0%	-5.3
16457	AT3G48480.1   expressed protein   chr3:17968311-17970047 REVERSE   Aliases: T29H11.250	3.7	3.7	0.0	0.2	100.0%	-5.2
16458	AT2G37730.1   fringe-related protein, similarity to predicted proteins + similar to hypothetical protein GB:AAC23643 (Arabidopsis thaliana) + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.   chr2:15829264-15831616 REVERSE   Aliases: F13M22.23	2.2	2.3	-0.0	-0.2	100.0%	-5.9
16459	NA	10.6	10.4	0.2	0.2	100.0%	-5.0
16460	AT4G04530.1   Ulp1 protease family protein (snoR29), contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; snoR29 gene for small nucleolar RNA GI:15706258	2.6	2.6	0.0	0.2	100.0%	-5.7
16461	AT1G11200.1   expressed protein, contains Pfam profile PF03619: Domain of unknown function   chr1:3753365-3755638 FORWARD   Aliases: T28P6.25	5.7	5.8	-0.1	-0.2	100.0%	-4.9
16462	AT3G12680.1   Symbol: HUA1   floral homeotic protein (HUA1), identical to floral homeotic protein HUA1 (Arabidopsis thaliana) gi:16797661:gb:AAK01470	5.8	5.8	-0.1	-0.2	100.0%	-5.3
16463	AT1G34580.1   monosaccharide transporter, putative, similar to monosaccharide transporter 3 (Oryza sativa) GI:11991114, monosaccharide transporter (Nicotiana tabacum) GI:19885, monosaccharide transporter 1 (Oryza sativa) GI:11991110; contains Pfam profile PF00083: major facilitator superfamily protein	3.6	3.7	-0.1	-0.2	100.0%	-5.1
16464	AT4G19580.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QYI4 DnaJ homolog subfamily B member 12 {Mus musculus}; contains Pfam profile PF00226: DnaJ domain   chr4:10668410-10669462 FORWARD   Aliases: F24J7.140, F24J7_140	2.3	2.3	0.0	0.2	100.0%	-5.8
16465	AT3G13460.4   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g55500.1); similar to putative RNA-binding protein [Oryza sativa] (GB:XP_469739.1); contains InterPro domain YT521-B-like protein (InterPro:IPR007275)   chr3:4384721-4388484 REVERSE   Aliases: MRP15.12	5.0	4.8	0.1	0.2	100.0%	-4.6
16466	AT3G51700.1   expressed protein   chr3:19190245-19192168 REVERSE   Aliases: T18N14.80	2.8	2.7	0.0	0.2	100.0%	-5.7
16467	AT5G52120.1   Symbol: ATPP2 A14   F-box family protein / SKP1 interacting partner 3-related, contains Pfam profile PF00646: F-box domain   chr5:21193659-21197536 REVERSE   Aliases: ATPP2 A14, MSG15.5, MSG15_5	4.8	4.9	-0.1	-0.2	100.0%	-4.9
16468	AT2G37600.1   60S ribosomal protein L36 (RPL36A)   chr2:15781323-15782420 REVERSE   Aliases: F13M22.10, F13M22_10	6.1	6.2	-0.1	-0.2	100.0%	-4.8
16469	AT5G15900.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr5:5189494-5192073 REVERSE   Aliases: F1N13.40, F1N13_40	2.2	2.3	-0.0	-0.2	100.0%	-5.4
16470	AT5G56670.1   40S ribosomal protein S30 (RPS30C)   chr5:22952639-22953207 REVERSE   Aliases: MIK19.12	11.5	11.5	-0.1	-0.2	100.0%	-5.4
16471	AT3G45950.1   splicing factor-related, similar to step II splicing factor SLU7 (Homo sapiens) GI:4249705   chr3:16900446-16901603 REVERSE   Aliases: F16L2.160	2.8	2.8	-0.0	-0.2	100.0%	-5.4
16472	AT3G43980.1   40S ribosomal protein S29 (RPS29A), ribosomal protein S29, rat, PIR:S30298   chr3:15789389-15790298 REVERSE   Aliases: T15B3.120, T15B3_120	13.1	13.0	0.1	0.2	100.0%	-6.1
16473	AT3G44010.1   40S ribosomal protein S29 (RPS29B), ribosomal protein S29, rat, PIR:S30298   chr3:15810918-15812187 REVERSE   Aliases: T15B3.150	13.1	13.0	0.1	0.2	100.0%	-6.1
16474	AT5G14380.1   hydroxyproline-rich glycoprotein family protein, identical to gi:4775268:emb:CAB42531   chr5:4635800-4636679 REVERSE   Aliases: F18O22.170, F18O22_170	3.3	3.4	-0.0	-0.2	100.0%	-5.2
16475	AT3G26950.1   expressed protein   chr3:9942375-9944648 REVERSE   Aliases: MOJ10.3	8.4	8.5	-0.1	-0.2	100.0%	-5.1
16476	AT4G18720.1   transcription elongation factor-related, contains weak similarity to transcription elongation factors   chr4:10299956-10301239 FORWARD   Aliases: F28A21.130, F28A21_130	3.9	3.8	0.0	0.2	100.0%	-5.3
16477	AT1G03310.2   Symbol: ATISA2/DBE1/ISA2   isoamylase, putative / starch debranching enzyme, putative, similar to isoamylase isoform 2 (Solanum tuberosum) GI:27728147, isoamylase from (Triticum aestivum) GI:17932898, (Hordeum vulgare) GI:21314275, (Oryza sativa) GI:3252794; contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain; ESTs gb:H36690, gb:AA712462, gb:AA651230 and gb:N95932 come from this gene   chr1:813493-816749 FORWARD   Aliases: ATISA2, DBE1, DEBRANCHING ENZYME 1, F15K9.9, F15K9_9, ISA2	7.5	7.6	-0.1	-0.2	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16478	AT5G46840.1   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:19022828-19024993 FORWARD   Aliases: MZA15.26	8.4	8.6	-0.1	-0.2	100.0%	-4.7
16479	AT2G03120.1   signal peptide peptidase family protein, contains Pfam domain PF04258: Membrane protein of unknown function (DUF435)   chr2:937419-940310 FORWARD   Aliases: T18E12.21, T18E12_21	7.9	8.1	-0.2	-0.2	100.0%	-4.7
16480	AT4G30210.2   Symbol: ATR2   NADPH-cytochrome p450 reductase, putative / NADPH-ferrihemoprotein reductase, putative, similar to NADPH-cytochrome P450 oxydoreductase from (Populus balsamifera subsp. trichocarpa x Populus deltoides) Gl:13183564, Gl:13183566   chr4:14796770-14800927 FORWARD   Aliases: ARABIDOPSIS P450 REDUCTASE 2, F9N11.60, F9N11_60	5.4	5.2	0.1	0.2	100.0%	-4.9
16481	AT4G23660.2   Symbol: ATPPT1	4.3	4.4	-0.1	-0.2	100.0%	-4.6
16482	AT4G26250.1   galactinol synthase, putative, similar to galactinol synthase, isoform GolS-1 (Ajuga reptans) Gl:5608497; contains Pfam profile: PF01501 glycosyl transferase family 8   chr4:13289650-13291093 FORWARD   Aliases: T25K17.60, T25K17_60	2.4	2.4	-0.0	-0.2	100.0%	-5.7
16483	AT1G22015.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr1:7750991-7753508 REVERSE   Aliases: None	3.0	3.1	-0.1	-0.2	100.0%	-5.1
16484	AT5G58550.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515 TPR Domain   chr5:23682538-23685700 REVERSE   Aliases: MZN1.1	3.4	3.4	-0.0	-0.2	100.0%	-5.4
16485	AT2G17950.1   Symbol: WUS   homeodomain transcription factor (WUSCHEL), 99.4% identical to WUSCHELL (Gl:4090200) (Arabidopsis thaliana)   chr2:7815959-7817877 REVERSE   Aliases: PGA6, T27K22.18, T27K22_18, WUSCHEL	2.2	2.2	0.0	0.2	100.0%	-6.0
16486	AT5G24690.1   expressed protein   chr5:8455460-8458741 REVERSE   Aliases: MXC17.8, MXC17_8	4.3	4.2	0.1	0.2	100.0%	-5.0
16487	AT4G03240.1   frataxin protein-related, contains weak similarity to Frataxin, mitochondrial precursor (Friedreich's ataxia protein) (Fxn) (Swiss-Prot:Q16595) (Homo sapiens)   chr4:1423445-1424759 REVERSE   Aliases: F4C21.17, F4C21_17	6.8	6.7	0.1	0.2	100.0%	-4.7
16488	AT5G47635.1   expressed protein   chr5:19324280-19325121 REVERSE   Aliases: None	3.0	3.1	-0.1	-0.2	100.0%	-4.6
16489	AT3G47240.1   expressed protein   chr3:17404846-17405973 REVERSE   Aliases: F13I12.290	2.1	2.1	-0.0	-0.2	100.0%	-6.0
16490	AT3G13200.1   Cwf15 / Cwc15 cell cycle control family protein, contains Pfam profile PF04889: Cwf15/Cwc15 cell cycle control protein; similar to Cell cycle control protein cwf15 (Swiss-Prot:P78794) (Schizosaccharomyces pombe)   chr3:4242132-4244140 FORWARD   Aliases: MJG19.16	9.3	9.2	0.1	0.2	100.0%	-4.5
16491	AT3G30750.1   expressed protein   chr3:12423035-12423472 FORWARD   Aliases: MIF6.12	2.1	2.1	-0.0	-0.2	100.0%	-6.1
16492	AT1G29700.1   expressed protein   chr1:10384967-10387427 REVERSE   Aliases: F15D2.25	4.2	4.1	0.1	0.2	100.0%	-5.0
16493	AT5G62900.1   expressed protein   chr5:25266023-25267103 FORWARD   Aliases: MQB2.22, MQB2_22	5.5	5.4	0.1	0.2	100.0%	-4.6
16494	AT3G25420.1   Symbol: SCPL21	3.2	3.2	0.1	0.2	100.0%	-4.9
16495	AT3G48170.1   Symbol: ALDH10A9   betaine-aldehyde dehydrogenase, putative, similar to betaine-aldehyde dehydrogenase, chloroplast precursor (BADH) (Arabidopsis thaliana) SWISS-PROT:Q9S795   chr3:17797129-17800967 REVERSE   Aliases: T24C20.50	11.6	11.5	0.1	0.2	100.0%	-5.5
16496	AT5G40020.1   pathogenesis-related thaumatin family protein, similar to SP:P50699 Thaumatin-like protein precursor {Arabidopsis thaliana}, pathogenesis-related group 5 protein (Brassica rapa) Gl:2749943; contains Pfam profile PF00314: Thaumatin family   chr5:16039990-16041544 REVERSE   Aliases: MYH19.180, MYH19_180	3.7	3.9	-0.1	-0.2	100.0%	-4.1
16497	AT2G36210.1   auxin-responsive family protein, similar to auxin-induced protein SAUR-AC1 (Gl:546362) (PIR:T06084) (Arabidopsis thaliana)   chr2:15193119-15193883 REVERSE   Aliases: F2H17.18, F2H17_18	3.2	3.3	-0.1	-0.2	100.0%	-4.7
16498	AT5G26180.2   NOL1/NOP2/sun family protein, similar to NOL1R (Homo sapiens) Gl:16226071; contains Pfam profile PF01189: NOL1/NOP2/sun family   chr5:9149230-9153505 FORWARD   Aliases: T19G15.30, T19G15_30	4.9	5.0	-0.1	-0.2	100.0%	-4.8
16499	AT5G53980.1   homeobox-leucine zipper family protein, contains Pfam PF00046: Homeobox domain; similar to homeobox protein PpHB5 (Gl:7415622) (Physcomitrella patens)   chr5:21931271-21931965 FORWARD   Aliases: K19P17.15, K19P17_15	2.7	2.7	0.1	0.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16500	AT5G12400.1   PHD finger transcription factor, putative, similarity to predicted proteins, Arabidopsis thaliana   chr5:4013814-4020910 FORWARD   Aliases: None	2.9	3.0	-0.1	-0.2	100.0%	-5.1
16501	AT3G12590.1   expressed protein   chr3:3995729-4003664 REVERSE   Aliases: T2E22.10	2.5	2.4	0.0	0.2	100.0%	-5.5
16502	AT2G37880.1   expressed protein, contains Pfam profile PF04759: Protein of unknown function, DUF617   chr2:15867711-15868696 FORWARD   Aliases: T8P21.21, T8P21_21	3.5	3.6	-0.1	-0.2	100.0%	-5.2
16503	AT5G25830.1   zinc finger (GATA type) family protein, GATA transcription factor, Arabidopsis thaliana, PIR:T05288   chr5:9004401-9005505 REVERSE   Aliases: F18A17.80, F18A17_80	5.5	5.5	0.1	0.2	100.0%	-5.0
16504	AT1G15460.1   anion exchange family protein, member of the PF:00955 Anion exchanger family   chr1:5309996-5313424 REVERSE   Aliases: F9L1.41, F9L1_41	2.3	2.4	-0.0	-0.2	100.0%	-5.4
16505	AT5G46050.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:18692262-18696373 REVERSE   Aliases: MCL19.10, MCL19_10	2.8	2.9	-0.1	-0.2	100.0%	-4.6
16506	AT1G02420.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile: PF01535 PPR repeat   chr1:493683-495158 FORWARD   Aliases: T6A9.11, T6A9_11	4.5	4.4	0.1	0.2	100.0%	-4.9
16507	AT2G39250.1   Symbol: SNZ   similar to AP2 domain-containing transcription factor, putative [Arabidopsis thaliana] (TAIR:At3g54990.1); similar to APETALA2-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470121.1); similar to putative transcription factor AP2 family protein, 3'-partial [Oryza sativa (japonica cultivar-group)] (GB:AAO60032.1); contains InterPro domain Proline-rich region (InterPro:IPR000694); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr2:16395964-16398151 REVERSE   Aliases: SCHNARCHZAPFEN, T16B24.11, T16B24_11	2.3	2.3	0.0	0.2	100.0%	-5.3
16508	AT4G25420.1   Symbol: GA5   gibberellin 20-oxidase, identical to GI:1109695   chr4:12990894-12992449 REVERSE   Aliases: AT2301, ATGA20OX1, GA REQUIRING 5, GA20OX1, GIBBERELLIN 20 OXIDASE, T30C3.90, T30C3_90	2.3	2.3	-0.0	-0.2	100.0%	-5.6
16509	AT5G41100.2   expressed protein   chr5:16464450-16468109 FORWARD   Aliases: MEE6.17, MEE6_17	4.4	4.3	0.1	0.2	100.0%	-4.8
16510	AT5G36230.1   eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein, low similarity to SP:Q13144 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) {Homo sapiens}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon   chr5:14290614-14294232 FORWARD   Aliases: T30G6.9, T30G6_9	8.6	8.6	-0.1	-0.2	100.0%	-5.1
16511	AT2G39360.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:16444550-16447232 REVERSE   Aliases: F12L6.2, F12L6_2	4.4	4.5	-0.1	-0.2	100.0%	-4.4
16512	AT1G11740.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam domain PF00023   chr1:3963277-3966824 REVERSE   Aliases: F25C20.11, F25C20_11	3.8	3.7	0.1	0.2	100.0%	-4.6
16513	AT1G35410.1   expressed protein   chr1:13024139-13024919 FORWARD   Aliases: F12A4.5, F12A4_5	3.4	3.4	-0.1	-0.2	100.0%	-5.0
16514	AT2G19190.1   light-responsive receptor protein kinase / senescence-responsive receptor-like serine/threonine kinase, putative (SIRK), similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains Pfam profiles PF00069: Protein kinase domain and PF00560: Leucine Rich Repeat   chr2:8333131-8337026 REVERSE   Aliases: T20K24.21, T20K24_21	3.2	3.2	-0.1	-0.2	100.0%	-5.1
16515	AT5G38370.1   hypothetical protein   chr5:15357623-15357925 REVERSE   Aliases: MXI10.4, MXI10_4	2.6	2.6	0.0	0.2	100.0%	-5.7
16516	AT4G37090.2   expressed protein, similar to hypothetical protein DDB0205993 [Dictyostelium discoideum] (GB:EAL67624.1)	7.3	7.4	-0.1	-0.2	100.0%	-4.6
16517	AT4G19170.1   Symbol: NCED4   9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, similar to 9-cis-epoxycarotenoid dioxygenase (Phaseolus vulgaris)(GI:6715257); neoxanthin cleavage enzyme, Lycopersicon esculentum, PATX:E325797   chr4:10481797-10483868 FORWARD   Aliases: NINE CIS EPOXYCAROTENOID DIOXYGENASE 4, T18B16.140, T18B16_140	3.7	3.6	0.1	0.2	100.0%	-4.9
16518	AT5G52520.1   tRNA synthetase class II (G, H, P and S) family protein, similar to SP:P07814 Bifunctional aminoacyl-tRNA synthetase (Includes: Glutamyl-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase); Prolyl-tRNA synthetase (EC 6.1.1.15) (Proline--tRNA ligase)) {Homo sapiens}; contains Pfam profiles PF00587: tRNA synthetase class II core domain (G, H, P, S and T), PF03129: Anticodon binding domain	8.1	8.0	0.1	0.2	100.0%	-4.5
16519	AT3G19870.1   expressed protein   chr3:6907487-6911239 FORWARD   Aliases: MPN9.11	5.0	5.1	-0.1	-0.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16520	AT1G69030.1   similar to BSD domain-containing protein [Arabidopsis thaliana] (TAIR:At1g26300.1); contains InterPro domain BSD domain (InterPro:IPR005607)   chr1:25950928-25952925 REVERSE   Aliases: T6L1.21, T6L1_21	8.1	8.0	0.1	0.2	100.0%	-4.9
16521	AT1G15340.1   Symbol: MBD10   methyl-CpG-binding domain-containing protein, contains Pfam profile PF01429: Methyl-CpG binding domain   chr1:5275672-5277657 REVERSE   Aliases: F9L1.28, F9L1_28	9.7	9.8	-0.1	-0.2	100.0%	-5.3
16522	AT1G22885.1   expressed protein   chr1:8101554-8102364 FORWARD   Aliases: None	5.8	5.9	-0.2	-0.2	100.0%	-4.6
16523	AT2G29110.1   Symbol: ATGLR2.8   glutamate receptor family protein (GLR2.8) (GLUR9), plant glutamate receptor family, PMID:11379626   chr2:12513957-12517629 REVERSE   Aliases: GLR2.8, T9I4.19, T9I4_19	2.3	2.4	-0.0	-0.2	100.0%	-5.7
16524	AT1G26420.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:9141554-9143291 REVERSE   Aliases: T1K7.20, T1K7_20	2.4	2.4	-0.0	-0.2	100.0%	-5.5
16525	AT3G17611.2   rhomboid family protein / zinc finger protein-related, contains Pfam profiles PF01694: Rhomboid family, PF00641: Zn-finger in Ran binding protein and others   chr3:6024919-6026449 FORWARD   Aliases: None	5.3	5.2	0.1	0.2	100.0%	-4.8
16526	AT1G72370.2   Symbol: P40   similar to 40S ribosomal protein SA (RPSaB) [Arabidopsis thaliana] (TAIR:At3g04770.2); similar to RSSA_DAUCA 40S ribosomal protein SA (p40) (GB:O80377); contains InterPro domain Ribosomal protein S2, eukaryotic and archaeal form (InterPro:IPR005707); contains InterPro domain Ribosomal protein S2 (InterPro:IPR001865)   chr1:27246607-27248589 REVERSE   Aliases: AP40, P40, RP40, RPSAA, T10D10.16, T10D10_16	10.7	10.6	0.2	0.2	100.0%	-4.8
16527	AT1G79550.2   Symbol: PGK   phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase   chr1:29928916-29931431 REVERSE   Aliases: PHOSPHOGLYCERATE KINASE, T8K14.3, T8K14_3	11.8	11.9	-0.1	-0.2	100.0%	-4.9
16528	AT3G03710.1   polyribonucleotide nucleotidyltransferase, putative, similar to polynucleotide phosphorylase GB:AAC50039 (Pisum sativum), identical to putative polynucleotide phosphorylase GB:AAF00646 (Arabidopsis thaliana)   chr3:919549-925345 FORWARD   Aliases: F20H23.26	4.6	4.5	0.1	0.2	100.0%	-4.9
16529	AT5G28820.1   hypothetical protein   chr5:10831803-10832536 FORWARD   Aliases: T32B20.110, T32B20_110	2.6	2.7	-0.0	-0.2	100.0%	-5.6
16530	AT5G52860.1   ABC transporter family protein   chr5:21437002-21438793 REVERSE   Aliases: MXC20.8, MXC20_8	2.7	2.7	0.0	0.2	100.0%	-5.3
16531	AT3G51040.2   expressed protein, contains Pfam PF05608: Protein of unknown function (DUF778)   chr3:18963125-18964661 REVERSE   Aliases: F24M12.80	7.3	7.2	0.1	0.2	100.0%	-5.2
16532	AT2G16870.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr2:7315159-7318768 REVERSE   Aliases: F12A24.5, F12A24_5	3.0	3.0	-0.1	-0.2	100.0%	-5.0
16533	AT2G29480.1   Symbol: ATGSTU2   glutathione S-transferase, putative, similar to Glutathione S-Transferase (Arabidopsis thaliana) gi:940381:16226389:gb:AF428387.   chr2:12637459-12638309 REVERSE   Aliases: F16P2.14, F16P2_14, GLUTATHIONE S TRANSFERASE 20, GST20	4.5	4.5	-0.1	-0.2	100.0%	-4.7
16534	AT1G19360.1   expressed protein   chr1:6690447-6692461 REVERSE   Aliases: F18O14.8, F18O14_8	7.5	7.7	-0.2	-0.2	100.0%	-4.6
16535	AT3G18970.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:6543324-6545438 REVERSE   Aliases: K13E13.8	2.6	2.6	0.0	0.2	100.0%	-5.6
16536	AT1G71530.2   protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108   chr1:26943229-26946614 FORWARD   Aliases: F26A9.10	3.8	3.7	0.1	0.2	100.0%	-4.7
16537	AT3G43880.1   hypothetical protein, p97 homologous protein, Canis familiaris, EMBL:CFA388531   chr3:15749160-15749603 REVERSE   Aliases: T15B3.20	2.8	2.9	-0.1	-0.2	100.0%	-5.3
16538	AT4G01530.1   hypothetical protein   chr4:663408-665102 FORWARD   Aliases: F11O4.8, F11O4_8	2.6	2.7	-0.0	-0.2	100.0%	-5.5
16539	AT3G63120.1   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr3:23333931-23335222 REVERSE   Aliases: T20O10.220	4.8	4.9	-0.1	-0.2	100.0%	-4.8
16540	AT1G33960.1   Symbol: AIG1   avirulence-responsive protein / avirulence induced gene (AIG1), identical to AIG1 (exhibits RPS2- and avrRpt2-dependent induction early after infection with Pseudomonas SP:U40856 (Arabidopsis thaliana) (Plant Cell 8 (2), 241-249 (1996))   chr1:12346229-12348464 FORWARD   Aliases: AIG1, AVRRPT2 INDUCED GENE 1, F12G12.27	2.4	2.4	-0.0	-0.2	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16541	AT1G14580.1   zinc finger (C2H2 type) family protein, similar to zinc finger protein ID1 GB:AAC18941 GI:3170601 from (Zea mays) contains Pfam domain, PF00096: Zinc finger, C2H2 type	3.4	3.3	0.0	0.2	100.0%	-5.1
16542	AT1G05490.1   C protein immunoglobulin-A-binding beta antigen-related, contains weak similarity to C protein immunoglobulin-A-binding beta antigen (Streptococcus agalactiae) gi:18028989:gb:AAL56250   chr1:1620999-1623450 REVERSE   Aliases: T25N20.14	2.4	2.3	0.0	0.2	100.0%	-5.6
16543	AT1G30490.1   Symbol: PHV   homeobox-leucine zipper transcription factor (HB-9), identical to HD-Zip protein GB:CAA71854 GI:2145358 from (Arabidopsis thaliana)   chr1:10796117-10800885 REVERSE   Aliases: ATHB9, F26G16.11, F26G16_11, PHAVOLUTA	6.8	7.0	-0.2	-0.2	100.0%	-4.6
16544	AT3G53060.1   Symbol: ASK6   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At6), putative, E3 ubiquitin ligase; similar to Skp1 GI:4959710 from (Medicago sativa)   chr3:19681144-19681401 FORWARD   Aliases: ARABIDOPSIS SKP1 LIKE 6, ASK6, F8J2.230	2.5	2.5	-0.0	-0.2	100.0%	-6.0
16545	AT5G44270.1   expressed protein   chr5:17850863-17852967 FORWARD   Aliases: K9L2.2, K9L2_2	2.4	2.5	-0.0	-0.2	100.0%	-5.7
16546	AT1G07410.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB11C GI:1370146 from (Lotus japonicus)   chr1:2276267-2277151 FORWARD   Aliases: F22G5.24, F22G5_24	3.8	3.8	-0.1	-0.2	100.0%	-5.0
16547	AT2G07260.1   hypothetical protein   chr2:3019653-3021695 REVERSE   Aliases: T13E11.3, T13E11_3	2.2	2.1	0.0	0.2	100.0%	-5.7
16548	AT4G20200.1   terpene synthase/cyclase family protein, 5-epi-aristolochene synthase, Nicotiana tabacum, PATX:G505588   chr4:10908682-10911161 REVERSE   Aliases: F1C12.120, F1C12_120	2.6	2.5	0.0	0.2	100.0%	-5.5
16549	AT3G28950.1   avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related, similar to SP:P54121 AIG2 protein {Arabidopsis thaliana}   chr3:10977345-10978729 REVERSE   Aliases: K5K13.15	5.7	5.7	0.0	0.2	100.0%	-5.2
16550	AT2G27520.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr2:11769139-11770182 FORWARD   Aliases: F10A12.29	3.1	3.1	-0.1	-0.2	100.0%	-5.2
16551	AT4G19860.1   lecithin:cholesterol acyltransferase family protein / LACT family protein, similar to lysosomal phospholipase A2 (Mus musculus) GI:18699602; contains Pfam profile PF02450: Lecithin:cholesterol acyltransferase (phosphatidylcholine-sterol acyltransferase)   chr4:10777522-10780373 REVERSE   Aliases: T16H5.220, T16H5_220	8.8	8.9	-0.1	-0.2	100.0%	-4.8
16552	AT2G34670.1   proline-rich family protein, contains proline-rich region, INTERPRO:IPR000694   chr2:14619665-14622812 REVERSE   Aliases: T29F13.12, T29F13_12	4.2	4.2	0.1	0.2	100.0%	-5.0
16553	AT5G62280.1   expressed protein   chr5:25034308-25035472 FORWARD   Aliases: MMI9.11, MMI9_11	3.7	3.6	0.1	0.2	100.0%	-5.0
16554	AT3G02870.2   similar to inositol monophosphatase family protein [Arabidopsis thaliana] (TAIR:At1g31190.1); similar to L-galactose-1-phosphate phosphatase [Malus x domestica] (GB:AAV49507.1); contains InterPro domain Inositol monophosphatase (InterPro:IPR000760)	10.0	10.1	-0.1	-0.2	100.0%	-5.0
16555	AT5G64940.2   Symbol: ATATH13   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr5:25966199-25971048 FORWARD   Aliases: MXK3.17, MXK3_17	5.4	5.6	-0.2	-0.2	100.0%	-4.3
16556	AT3G25740.1   Symbol: MAP1B   metalloproteinase M24 family protein, similar to SP:O33343 Methionine aminopeptidase (EC 3.4.11.18) (Peptidase M) {Mycobacterium tuberculosis}; contains Pfam profile PF00557: metalloproteinase family M24   chr3:9399023-9400999 FORWARD   Aliases: K13N2.17, MAP1C, METHIONINE AMINOPEPTIDASE 1C	4.6	4.7	-0.1	-0.2	100.0%	-5.0
16557	AT4G18700.1   Symbol: CIPK12	8.5	8.5	-0.1	-0.2	100.0%	-5.3
16558	AT1G78150.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g35780.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466380.1)   chr1:29409541-29411645 FORWARD   Aliases: T11I11.9, T11I11_9	7.0	6.8	0.2	0.2	100.0%	-4.6
16559	AT1G21630.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain; ESTs gb:T44428 and gb:AA395440 come from this gene   chr1:7581141-7588140 FORWARD   Aliases: F8K7.4, F8K7_4	4.4	4.5	-0.1	-0.2	100.0%	-4.9
16560	AT4G17370.1   oxidoreductase family protein, weak similarity to SP:P26935 Myo-inositol 2-dehydrogenase (EC 1.1.1.18). {Bacillus subtilis}; contains Pfam profiles PF01408: Oxidoreductase family NAD-binding Rossmann fold, PF02894: Oxidoreductase family C-terminal alpha/beta domain   chr4:9706070-9708273 FORWARD   Aliases: DL4720W, FCAALL.420	8.2	8.1	0.1	0.2	100.0%	-5.0
16561	AT1G15130.1   hydroxyproline-rich glycoprotein family protein   chr1:5205997-5209910 REVERSE   Aliases: F9L1.7, F9L1_7	4.1	4.2	-0.1	-0.2	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16562	AT5G45350.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr5:18399064-18400926 REVERSE   Aliases: MFC19.1, MFC19_1	9.1	9.0	0.1	0.2	100.0%	-4.5
16563	AT4G03490.1   similar to ankyrin repeat family protein [Arabidopsis thaliana] (TAIR:At4g03500.1); similar to ankyrin repeat protein family-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_478489.1); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr4:1549616-1552782 REVERSE   Aliases: F9H3.12, F9H3_12	3.1	3.1	0.0	0.2	100.0%	-5.3
16564	AT4G22130.1   similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g14350.2); similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g53730.1); similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g14350.1); similar to Putative leucine-rich repeat transmembrane protein kinase 1 [Oryza sativa] (GB:XP_470566.1); similar to putative leucine-rich repeat transmembrane protein kinase [Oryza sativa (japonica cultivar-group)] (GB:AAO72637.1); similar to leucine-rich repeat transmembrane protein kinase 2 [Zea mays] (GB:AAC27895.1); similar to leucine-rich repeat transmembrane protein kinase 1 [Zea mays] (GB:AAC27894.1); similar to putative leucine-rich repeat transmembrane protein kinase 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD37979.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr4:11723637-11727685 FORWARD   Aliases: F1N20.230, F1N20_230	3.9	4.0	-0.1	-0.2	100.0%	-5.0
16565	AT2G36885.2   expressed protein   chr2:15489090-15490785 REVERSE   Aliases: None	7.1	7.3	-0.1	-0.2	100.0%	-4.7
16566	AT3G16930.1   hypothetical protein   chr3:5778882-5779369 FORWARD   Aliases: K14A17.28	2.6	2.6	0.0	0.2	100.0%	-5.2
16567	AT3G25940.1   transcription factor S-II (TFIIS) domain-containing protein, similar to SP:O94703 DNA-directed RNA polymerase I 13.1 kDa polypeptide (EC 2.7.7.6) {Schizosaccharomyces pombe}; contains Pfam profile PF01096: Transcription factor S-II (TFIIS)   chr3:9495934-9497329 FORWARD   Aliases: MPE11.11	7.6	7.5	0.1	0.2	100.0%	-4.7
16568	AT4G23230.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:12157579-12160280 REVERSE   Aliases: F21P8.120, F21P8_120	2.5	2.5	0.0	0.2	100.0%	-5.6
16569	AT1G03540.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:883782-885611 FORWARD   Aliases: F21B7.16	3.8	3.8	-0.1	-0.2	100.0%	-5.1
16570	AT1G13100.1   Symbol: CYP71B29   cytochrome P450 71B29, putative (CYP71B29), strong similarity to gb:X97864 cytochrome P450 and identical to Cytochrome P450 71B29 (SP:Q9SAE4)(Arabidopsis thaliana);PF:00067 Cytochrome P450 family   chr1:4463922-4465536 FORWARD   Aliases: F3F19.12, F3F19_12	2.7	2.8	-0.1	-0.2	100.0%	-4.5
16571	AT5G41860.1   expressed protein   chr5:16775179-16775757 FORWARD   Aliases: K16L22.15, K16L22_15	2.5	2.5	-0.0	-0.2	100.0%	-5.7
16572	AT1G60470.1   galactinol synthase, putative, similar to galactinol synthase GI:5608497 from (Ajuga reptans)   chr1:22282642-22284251 REVERSE   Aliases: F8A5.2, F8A5_2	3.2	3.2	-0.0	-0.2	100.0%	-5.2
16573	AT2G24620.1   S-locus glycoprotein family protein, contains Pfam profile: PF00954 S-locus glycoprotein family   chr2:10470155-10470628 REVERSE   Aliases: F25P17.8, F25P17_8	2.8	2.7	0.0	0.2	100.0%	-5.7
16574	AT1G03660.1   expressed protein, contains 2 predicted transmembrane domains; expression supported by MPSS   chr1:911435-911758 REVERSE   Aliases: F21B7.26, F21B7_26	3.9	3.8	0.1	0.2	100.0%	-4.5
16575	AT3G51150.1   kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain   chr3:19011835-19017748 FORWARD   Aliases: F24M12.190	2.9	2.9	0.0	0.2	100.0%	-5.5
16576	AT3G22430.1   expressed protein   chr3:7953267-7954490 FORWARD   Aliases: MCB17.18	5.1	5.0	0.1	0.2	100.0%	-4.9
16577	AT3G46710.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.2	3.2	0.1	0.2	100.0%	-5.0
16578	AT3G15355.1   ubiquitin-conjugating enzyme-related, similar to ubiquitin-conjugating enzyme (GI:3319990) (Mus musculus); similar to Baculoviral IAP repeat-containing protein 6 (Ubiquitin-conjugating BIR-domain enzyme apollon) (Swiss-Prot:Q9NR09) (Homo sapiens);   chr3:5183865-5186871 FORWARD   Aliases: MJK13.1	2.6	2.7	-0.0	-0.2	100.0%	-5.5
16579	AT2G24130.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:10265228-10268300 FORWARD   Aliases: F27D4.4, F27D4_4	3.1	3.1	0.0	0.2	100.0%	-5.5
16580	AT5G38800.1   bZIP transcription factor family protein, similar to bZIP transcription factor GI:1769891 from (Arabidopsis thaliana); contains PFAM profile: bZIP transcription factor PF00170   chr5:15555427-15556032 REVERSE   Aliases: K15E6.1	2.3	2.3	-0.0	-0.2	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16581	AT2G34960.1   Symbol: CAT5   amino acid permease family protein, similar to cationic amino acid transporter 3 (Rattus norvegicus) GI:2116552; contains Pfam profile PF00324: Amino acid permease   chr2:14751116-14753040 REVERSE   Aliases: CATIONIC AMINO ACID TRANSPORTER 5, F19I3.19, F19I3_19	3.2	3.1	0.1	0.2	100.0%	-5.2
16582	AT2G44810.1   Symbol: DAD1   defective in anther dehiscence1 (DAD1), identical to DEFECTIVE IN ANOTHER DEHISCENCE1 (Arabidopsis thaliana) GI:16215706; contains Pfam profile PF01764: Lipase   chr2:18486128-18487268 FORWARD   Aliases: DEFECTIVE ANOTHER DEHISCENCE 1, F16B22.45	2.7	2.8	-0.1	-0.2	100.0%	-5.1
16583	AT2G39790.1   mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	2.4	2.4	-0.0	-0.2	100.0%	-5.6
16584	AT4G10890.1   expressed protein   chr4:6688829-6693754 FORWARD   Aliases: None	4.2	4.2	-0.1	-0.2	100.0%	-5.0
16585	AT1G27450.2   Symbol: APT1   adenine phosphoribosyltransferase 1 (APT1), nearly identical to SP:P31166 Adenine phosphoribosyltransferase 1 (EC 2.4.2.7) (APRT) {Arabidopsis thaliana}	9.7	9.4	0.2	0.2	100.0%	-4.4
16586	AT3G13910.1   expressed protein   chr3:4590926-4591490 REVERSE   Aliases: MDC16.3	6.8	6.7	0.1	0.2	100.0%	-4.7
16587	AT4G02340.1   epoxide hydrolase, putative, similar to epoxide hydrolases from Glycine max GI:2764806, Solanum tuberosum GI:407938; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:1035683-1037615 FORWARD   Aliases: T14P8.15, T14P8_15	7.9	7.7	0.2	0.2	100.0%	-4.5
16588	AT4G35070.1   expressed protein   chr4:16694175-16695699 FORWARD   Aliases: T12J5.5	3.2	3.1	0.1	0.2	100.0%	-5.2
16589	AT2G47120.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to 3-beta-hydroxysteroiddehydrogenase GI:15983819 from (Digitalis lanata)   chr2:19354429-19355308 REVERSE   Aliases: F14M4.5	2.6	2.6	0.0	0.2	100.0%	-5.3
16590	AT5G08290.1   Symbol: YLS8   yellow-leaf-specific protein 8 (YLS8) / mitosis protein DIM1, putative, contains Pfam domain PF02966: Mitosis protein DIM1; identical to cDNA YLS8 mRNA for Dim1 homolog GI:13122293   chr5:2665977-2667156 FORWARD   Aliases: F8L15.20, F8L15_20	12.1	12.0	0.1	0.2	100.0%	-5.8
16591	AT4G24300.1   hypothetical protein, hypothetical protein - Arabidopsis thaliana, PIR2:T05128   chr4:12598990-12600223 REVERSE   Aliases: T22A6.130, T22A6_130	3.5	3.6	-0.1	-0.2	100.0%	-5.2
16592	AT4G26280.1   sulfotransferase family protein, similar to steroid sulfotransferase 3 (Brassica napus) GI:3420008; contains Pfam profile PF00685: Sulfotransferase domain   chr4:13304730-13305731 REVERSE   Aliases: T25K17.90, T25K17_90	3.5	3.6	-0.1	-0.2	100.0%	-5.3
16593	AT4G26680.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:13454859-13456424 FORWARD   Aliases: F10M23.20, F10M23_20	3.8	3.9	-0.1	-0.2	100.0%	-4.9
16594	AT4G26420.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to caffeine synthase (Camellia sinensis)(GI:9967143), defense-related protein cjs1 (Brassica carinata)(GI:14009292), S-adenosyl-L-methionine:salicylic acid carboxyl methyltransferase (Clarkia breweri)(GI:6002712)   chr4:13349147-13352566 REVERSE   Aliases: M3E9.150, M3E9_150	2.4	2.3	0.0	0.2	100.0%	-5.4
16595	AT1G26600.1   Symbol: CLE9   CLE9, putative, CLAVATA3/ESR-Related 9 (CLE9); similar to hypothetical protein GB:AAF67770 GI:7705091 from (Arabidopsis thaliana)   chr1:9191594-9192388 FORWARD   Aliases: CLAVATA3/ESR RELATED 9, T1K7.3, T1K7_3	2.1	2.1	0.0	0.2	100.0%	-6.0
16596	AT2G25600.1   Symbol: SPIK   potassium channel protein, putative, similar to potassium channel (Lycopersicon esculentum) GI:8980432; member of the 1 pore, 6 transmembrane (1P/6TM- Shaker-type) K+ channel family, PMID:11500563; Shaker Pollen Inward K+ Channel (SPIK) PMID:11825875   chr2:10901681-10905447 FORWARD   Aliases: AKT6, F3N11.5, F3N11_5, SHAKER FAMILY K+ CHANNEL	2.4	2.4	0.0	0.2	100.0%	-5.6
16597	AT5G17950.1   hypothetical protein   chr5:5944555-5944961 REVERSE   Aliases: MCM23.2, MCM23_2	2.8	2.8	-0.1	-0.2	100.0%	-5.2
16598	AT1G77330.1   1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative, similar to 1-aminocyclopropane-1-carboxylate oxidase GI:3386565 from (Sorghum bicolor)   chr1:29067884-29069431 REVERSE   Aliases: F2P24.4, F2P24_4	6.0	6.1	-0.1	-0.2	100.0%	-4.5
16599	AT5G06440.3   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g11720.1)   chr5:1964469-1966956 REVERSE   Aliases: MHF15.4, MHF15_4	5.3	5.4	-0.1	-0.2	100.0%	-5.0
16600	AT2G20420.1   succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial, putative / succinyl-CoA synthetase, beta chain, putative / SCS-beta, putative, identical to SP:O82662 Succinyl-CoA ligase (GDP-forming) beta-chain, mitochondrial precursor (EC 6.2.1.4) (Succinyl-CoA synthetase, beta chain) (SCS- beta) {Arabidopsis thaliana}; similar to SP:O97580 Succinyl-CoA ligase (ADP-forming) beta-chain, mitochondrial precursor (EC 6.2.1.5) {Sus scrofa}; contains Pfam profiles PF00549: CoA-ligase, PF02222: ATP-grasp domain   chr2:8812537-8815187 FORWARD   Aliases: F11A3.3, F11A3_3	9.5	9.7	-0.2	-0.2	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16601	AT5G56470.1   FAD-dependent oxidoreductase family protein, contains TIGRfam TIGR01677: plant-specific FAD-dependent oxidoreductase   chr5:22886286-22887184 FORWARD   Aliases: MCD7.24, MCD7_24	3.3	3.3	0.0	0.2	100.0%	-5.4
16602	AT2G22450.1   riboflavin biosynthesis protein, putative, similar to SP:P50855 Riboflavin biosynthesis protein ribA (Includes: GTP cyclohydrolase II (EC 3.5.4.25); 3,4-dihydroxy-2-butanone 4-phosphate synthase (DHBP synthase)) {Actinobacillus pleuropneumoniae}; contains Pfam profiles PF00925: GTP cyclohydrolase II, PF00926: 3,4-dihydroxy-2-butanone 4-phosphate synthase   chr2:9537627-9539990 FORWARD   Aliases: F14M13.15, F14M13_15	6.5	6.6	-0.1	-0.2	100.0%	-4.5
16603	AT5G15460.2   expressed protein   chr5:5018774-5020656 REVERSE   Aliases: T20K14.70, T20K14_70	9.1	9.3	-0.1	-0.2	100.0%	-5.2
16604	AT1G80580.1   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.	3.2	3.1	0.1	0.2	100.0%	-5.3
16605	AT1G04710.1   acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative, similar to 3-ketoacyl-CoA thiolase (E.C. 2.3.1.16) from (Arabidopsis thaliana) GI:2981616, (Cucumis sativus) GI:393707, (Cucurbita cv. Kurokawa Amakuri) GI:1694621; contains InterPro accession IPR002155: Thiolase	8.1	8.0	0.1	0.2	100.0%	-4.2
16606	AT4G29800.1   patatin-related, low similarity to patatin precursor (Solanum brevidens)(GI:563125); contains Patatin domain PF01743   chr4:14590837-14592542 REVERSE   Aliases: F27B13.40, F27B13_40	4.8	5.0	-0.1	-0.2	100.0%	-4.2
16607	AT5G59260.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:23925127-23927151 REVERSE   Aliases: MNC17.17, MNC17_17	3.3	3.2	0.1	0.2	100.0%	-4.4
16608	AT2G43390.1   expressed protein   chr2:18027427-18027938 REVERSE   Aliases: T1O24.13	2.9	3.0	-0.1	-0.2	100.0%	-4.9
16609	AT3G50400.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr3:18715746-18717551 FORWARD   Aliases: F11C1.240	2.1	2.3	-0.1	-0.2	100.0%	-4.3
16610	AT3G22640.1   cupin family protein, contains similarity to vicilin-like protein precursor (Juglans regia) GI:6580762, vicilin precursor (Theobroma cacao) PIR:S22477, vicilin precursor (Macadamia integrifolia) GI:5852872   chr3:8011733-8013909 REVERSE   Aliases: MWI23.1	2.6	2.6	-0.0	-0.2	100.0%	-5.8
16611	AT5G52320.1   Symbol: CYP96A4   cytochrome P450, putative   chr5:21262204-21263908 REVERSE   Aliases: K24M7.5, K24M7_5	2.5	2.5	-0.0	-0.2	100.0%	-5.7
16612	AT3G23710.1   chloroplast inner membrane import protein Tic22, putative, similar to Tic22 (Pisum sativum) gi:3769671:gb:AAC64606; contains Pfam domain PF04278: Tic22-like family   chr3:8534039-8536381 FORWARD   Aliases: MYM9.5	5.9	5.8	0.1	0.2	100.0%	-4.6
16613	AT1G25360.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:8894415-8896787 FORWARD   Aliases: F4F7.25, F4F7_25	4.3	4.3	-0.1	-0.2	100.0%	-5.1
16614	AT1G77700.1   pathogenesis-related thaumatin family protein, similar to thaumatin-like protein (Arabidopsis thaliana) GI:2435406; contains Pfam profile PF00314: Thaumatin family   chr1:29209641-29211111 FORWARD   Aliases: T32E8.3, T32E8_3	2.4	2.4	-0.1	-0.2	100.0%	-5.0
16615	AT5G12240.1   expressed protein   chr5:3959121-3960778 REVERSE   Aliases: MXC9.20, MXC9_20	3.6	3.5	0.0	0.2	100.0%	-5.2
16616	AT4G33140.1   expressed protein   chr4:15981408-15984354 FORWARD   Aliases: F4I10.70, F4I10_70	5.3	5.4	-0.1	-0.2	100.0%	-4.9
16617	AT2G36710.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:15396545-15398328 REVERSE   Aliases: F13K3.11, F13K3_11	3.1	3.0	0.0	0.2	100.0%	-5.3
16618	AT5G44450.1   expressed protein, contains Pfam profile PF05891: Eukaryotic protein of unknown function (DUF858)   chr5:17931258-17933232 REVERSE   Aliases: MFC16.11, MFC16_11	3.1	3.0	0.1	0.2	100.0%	-5.3
16619	AT2G46130.2   Symbol: WRKY43	2.3	2.4	-0.1	-0.2	100.0%	-5.2
16620	AT5G20090.1   expressed protein, contains Pfam domain, PF03650: Uncharacterized protein family (UPF0041)   chr5:6787004-6788656 REVERSE   Aliases: F28I16.240, F28I16_240	11.7	11.7	0.1	0.2	100.0%	-5.3
16621	AT5G49830.1   expressed protein   chr5:20267712-20272215 REVERSE   Aliases: K21G20.4, K21G20_4	4.0	4.1	-0.1	-0.2	100.0%	-5.0
16622	AT1G10800.1   expressed protein   chr1:3598159-3598592 REVERSE   Aliases: T16B5.6	5.1	5.0	0.1	0.2	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16623	AT5G46180.1   Symbol: delta OAT   ornithine aminotransferase, putative / ornithine--oxo-acid aminotransferase, putative, similar to SP:Q92413 Ornithine aminotransferase (EC 2.6.1.13) (Ornithine--oxo-acid aminotransferase) (Aspergillus nidulans) {Emericella nidulans}; contains Pfam profile PF00202: aminotransferase, class III   chr5:18735702-18738498 REVERSE   Aliases: MCL19.24, MCL19_24	8.6	8.4	0.1	0.2	100.0%	-4.8
16624	AT2G45180.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to 14 kDa polypeptide (Catharanthus roseus) Gl:407410; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:18633413-18633951 FORWARD   Aliases: F4L23.31	3.2	3.2	0.0	0.2	100.0%	-5.2
16625	AT3G47480.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr3:17507339-17507932 REVERSE   Aliases: F1P2.30	3.0	3.0	0.1	0.2	100.0%	-5.4
16626	AT1G70450.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:26556239-26558100 FORWARD   Aliases: F24J13.2, F24J13_2	3.8	3.6	0.2	0.2	100.0%	-4.4
16627	AT1G35750.1   pumilio/Puf RNA-binding domain-containing protein   chr1:13254610-13256782 REVERSE   Aliases: F14D7.5, F14D7_5	2.7	2.7	0.0	0.2	100.0%	-5.5
16628	AT1G03750.1   helicase, putative, similar to SP:Q03468 Excision repair protein ERCC-6 (Cockayne syndrome protein CSB) {Homo sapiens}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF02810: SEC-C motif   chr1:937919-941067 FORWARD   Aliases: F21M11.34, F21M11_34	6.0	6.1	-0.2	-0.2	100.0%	-5.1
16629	AT1G65640.1   DegP protease, putative, contains similarity to DegP2 protease Gl:13172275 from (Arabidopsis thaliana)   chr1:24414514-24417190 REVERSE   Aliases: F1E22.2	2.4	2.5	-0.0	-0.2	100.0%	-5.6
16630	AT4G08270.1   hypothetical protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr4:5218102-5218401 FORWARD   Aliases: T12G13.110, T12G13_110	3.0	3.1	-0.1	-0.2	100.0%	-5.2
16631	AT1G57550.1   hydrophobic protein, putative / low temperature and salt responsive protein, putative, similar to SP:Q9ARD5 Low-temperature induced protein It101.2 {Hordeum vulgare}, SP:Q9ZNP7 Hydrophobic protein RCI2A (Low temperature and salt responsive protein LTI6A) {Arabidopsis thaliana}; contains Pfam profile PF01679: Uncharacterized protein family   chr1:21316206-21316474 REVERSE   Aliases: F25P12.2, F25P12_2	4.2	4.2	-0.1	-0.2	100.0%	-5.3
16632	AT4G27860.1   integral membrane family protein, contains Pfam PF01988: Integral membrane protein   chr4:13873803-13876532 FORWARD   Aliases: T27E11.100, T27E11_100	2.5	2.6	-0.0	-0.2	100.0%	-5.0
16633	AT5G50880.1   expressed protein   chr5:20718592-20718870 REVERSE   Aliases: K3K7.2, K3K7_2	2.9	2.9	-0.0	-0.2	100.0%	-5.8
16634	AT1G13000.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g26440.1); similar to P0456E05.23 [Oryza sativa (japonica cultivar-group)] (GB:XP_463604.1); contains InterPro domain Protein of unknown function DUF707 (InterPro:IPR007877)   chr1:4436103-4439457 REVERSE   Aliases: F3F19.3, F3F19_3	4.7	4.6	0.1	0.2	100.0%	-4.6
16635	AT4G19865.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:10780966-10782375 REVERSE   Aliases: None	4.3	4.4	-0.1	-0.2	100.0%	-4.9
16636	AT2G29070.2   ubiquitin fusion degradation UFD1 family protein, similar to SP:P70362 Ubiquitin fusion degradation protein 1 homolog (UB fusion protein 1) {Mus musculus}; contains Pfam profile PF03152: Ubiquitin fusion degradation protein UFD1   chr2:12494358-12496457 FORWARD   Aliases: T9I4.15, T9I4_15	4.0	4.1	-0.1	-0.2	100.0%	-4.9
16637	AT5G16950.1   expressed protein   chr5:5572579-5573073 FORWARD   Aliases: F2K13.100, F2K13_100	7.6	7.7	-0.1	-0.2	100.0%	-4.9
16638	AT2G45220.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:18651160-18653521 REVERSE   Aliases: F4L23.27	3.7	3.5	0.2	0.2	100.0%	-4.4
16639	AT3G20740.1   Symbol: FIE   fertilization-independent endosperm protein (FIE), contains 6 WD-40 repeats (PF00400); identical to fertilization-independent endosperm protein (Gl:4567095) (Arabidopsis thaliana)   chr3:7248815-7252458 REVERSE   Aliases: FERTILIZATION INDEPENDENT ENDOSPERM, FERTILIZATION INDEPENDENT ENDOSPERM 1, FIE1, FIS3, MOE17.5	5.2	5.3	-0.0	-0.2	100.0%	-5.3
16640	AT3G09520.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr3:2923749-2925635 FORWARD   Aliases: F11F8.10	3.0	2.9	0.1	0.2	100.0%	-5.0
16641	AT3G49370.1   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium/calmodulin-dependent protein kinase CaMK1 (Nicotiana tabacum) gi:16904222:gb:AAL30818   chr3:18315727-18318891 REVERSE   Aliases: F2K15.230	3.1	3.1	-0.1	-0.2	100.0%	-4.7
16642	AT1G23210.1   glycosyl hydrolase family 9 protein, similar to endo-1,4-beta-glucanase GB:CAA67157 Gl:2440035 from (Arabidopsis thaliana)   chr1:8240163-8242118 FORWARD   Aliases: F26F24.6, F26F24_6	2.3	2.3	0.0	0.2	100.0%	-5.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16643	AT4G04670.1   Met-10+ like family protein / kelch repeat-containing protein, contains Pfam profiles PF01344: Kelch motif, PF02475: Met-10+ like-protein   chr4:2367564-2372209 FORWARD   Aliases: T19J18.2, T19J18_2	3.9	3.9	-0.1	-0.2	100.0%	-4.8
16644	AT2G03260.1   EXS family protein / ERD1/XPR1/SYG1 family protein, similar to PHO1 protein (Arabidopsis thaliana) GI:20069032; contains Pfam profiles PF03105: SPX domain, PF03124: EXS family   chr2:987931-992329 REVERSE   Aliases: T18E12.7, T18E12_7	4.3	4.4	-0.1	-0.2	100.0%	-4.7
16645	AT3G51860.1   Symbol: CAX3   cation exchanger, putative (CAX3), similar to high affinity calcium antiporter CAX1 (Arabidopsis thaliana) gi:9256741:gb:AAB05913; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563; non-consensus AT-acceptor splice site at intron 1   chr3:19250404-19253856 FORWARD   Aliases: ATCAX3, ATEM1.11, ATHCX1, CALCIUM/PROTON EXCHANGER CAX1 LIKE PROTEIN, CAX1 LIKE, CAX3	3.7	3.8	-0.1	-0.2	100.0%	-4.7
16646	AT3G62510.1   protein disulfide isomerase-related, contains weak similarity tot Swiss-Prot:P80284 protein disulfide isomerase precursor (PDI) (Endosperm protein E-1) (Hordeum vulgare)   chr3:23134374-23134750 FORWARD   Aliases: T12C14.210	3.5	3.6	-0.1	-0.2	100.0%	-5.0
16647	AT1G73150.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr1:27507773-27509773 REVERSE   Aliases: F3N23.35, F3N23_35	3.4	3.4	-0.0	-0.2	100.0%	-5.3
16648	AT2G35310.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr2:14871935-14873677 FORWARD   Aliases: T4C15.2, T4C15_2	2.9	2.9	0.1	0.2	100.0%	-5.3
16649	AT5G38450.1   Symbol: CYP735A1   cytochrome P450 family protein, similar to cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus)   chr5:15410984-15414509 REVERSE   Aliases: MXI10.18, MXI10_18	3.3	3.3	-0.0	-0.2	100.0%	-5.3
16650	AT2G43230.1   serine/threonine protein kinase, putative, similar to Pto kinase interactor 1 (Pti1)(Lycopersicon esculentum) gi:3668069:gb:AAC61805   chr2:17973384-17976133 FORWARD   Aliases: F14B2.17	2.6	2.5	0.0	0.2	100.0%	-5.3
16651	AT2G31955.2   Symbol: CNX2   similar to MGC84142 protein [Xenopus laevis] (GB:AAH74319.1); contains InterPro domain Elongator protein 3/MiaB/NifB (InterPro:IPR006638); contains InterPro domain MoaA/nifB/pqqE family (InterPro:IPR000385); contains InterPro domain Radical SAM (InterPro:IPR007197)   chr2:13591216-13593777 REVERSE   Aliases: AT2G31950, COFACTOR OF NITRATE REDUCTASE AND XANTHINE DEHYDROGENASE 2, F22D22.30, F22D22_30	6.5	6.4	0.1	0.2	100.0%	-5.0
16652	AT3G19920.1   expressed protein   chr3:6929717-6931812 REVERSE   Aliases: MPN9.17	3.4	3.3	0.0	0.2	100.0%	-5.5
16653	AT4G04210.1   Symbol: pux4   UBX domain-containing protein, similar to XY40 protein (Rattus norvegicus) GI:2547025; contains Pfam profile PF00789: UBX domain	7.4	7.3	0.1	0.2	100.0%	-5.1
16654	AT3G10380.1   Symbol: SEC8   exocyst complex component-related, identical to Probable exocyst complex component Sec8 (Swiss-Prot:Q93YU5) (Arabidopsis thaliana); weak similarity to Exocyst complex component Sec8 (rSec8) (Swiss-Prot:Q62824) (Rattus norvegicus)   chr3:3219528-3228863 REVERSE   Aliases: F14P13.2	4.8	5.0	-0.2	-0.2	100.0%	-4.8
16655	AT3G46560.1   Symbol: TIM9   mitochondrial import inner membrane translocase (TIM9), identical to mitochondrial import inner membrane translocase subunit Tim9 (Arabidopsis thaliana) Swiss-Prot:Q9XGX9; contains Pfam domain, PF02953: Tim10/DDP family zinc finger   chr3:17149572-17150473 FORWARD   Aliases: EMB2474, EMBRYO DEFECTIVE 2474, F12A12.80	10.1	10.2	-0.1	-0.2	100.0%	-4.5
16656	AT4G36980.1   expressed protein   chr4:17433639-17437057 REVERSE   Aliases: AP22.35, AP22_35	6.6	6.5	0.1	0.2	100.0%	-4.8
16657	AT2G19650.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.9	-0.0	-0.2	100.0%	-5.5
16658	AT5G47720.5   similar to acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana] (TAIR:At5g48230.2); similar to acetyl-CoA C-acyltransferase, putative / 3-ketoacyl-CoA thiolase, putative [Arabidopsis thaliana] (TAIR:At5g48230.1); similar to cytosolic acetoacetyl-coenzyme A thiolase [Nicotiana tabacum] (GB:AAU95618.1); similar to peroxisomal acetoacetyl-coenzyme A thiolase [Nicotiana tabacum] (GB:AAU95619.1); contains InterPro domain Thiolase (InterPro:IPR002155)   chr5:19348883-19352038 FORWARD   Aliases: MCA23.4, MCA23_4	9.3	9.2	0.1	0.2	100.0%	-5.1
16659	AT1G70760.1   inorganic carbon transport protein-related, contains weak similarity to Swiss-Prot:P27372 inorganic carbon transport protein (Synechocystis sp.)	1.9	2.0	-0.0	-0.2	100.0%	-6.2
16660	AT5G55770.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.5	0.0	0.2	100.0%	-5.5
16661	AT2G03050.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr2:899689-900945 REVERSE   Aliases: T17M13.22, T17M13_22	4.0	4.1	-0.1	-0.2	100.0%	-4.8
16662	AT5G35920.1   Symbol: CYP79A4P   cytochrome P450, putative, similar to cytochrome P450 (Sinapis alba) gi:3283433:gb:AAD03415   chr5:14073667-14074134 FORWARD   Aliases: F14A1.7, F14A1_7	2.3	2.3	0.0	0.2	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16663	AT3G01300.1   protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548   chr3:90605-93592 REVERSE   Aliases: T22N4.7, T22N4_7	2.5	2.6	-0.1	-0.2	100.0%	-5.0
16664	AT5G15080.1   protein kinase, putative, similar to protein kinase APK1A (Arabidopsis thaliana) Swiss-Prot:Q06548   chr5:4886131-4888791 FORWARD   Aliases: F2G14.200, F2G14_200	2.5	2.6	-0.1	-0.2	100.0%	-5.0
16665	AT2G24540.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 4 (Arabidopsis thaliana) GI:10716953; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:10433422-10434674 FORWARD   Aliases: F25P17.16, F25P17_16	5.5	5.4	0.1	0.2	100.0%	-4.9
16666	AT4G25090.1   respiratory burst oxidase, putative / NADPH oxidase, putative, similar to respiratory burst oxidase protein A from Arabidopsis thaliana, gb:AF055353 (gi:3242781), protein D (gi:3242789); contains Pfam profile PF01794 Ferric reductase like transmembrane component   chr4:12878785-12883609 REVERSE   Aliases: F24A6.3	3.2	3.3	-0.1	-0.2	100.0%	-4.7
16667	AT2G39260.1   similar to hUPF2 [Homo sapiens] (GB:AAG48509.1); similar to OTTHUMP00000045025 [Homo sapiens] (GB:CAI16755.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAF92436.1); similar to KIAA1408 protein [Homo sapiens] (GB:BAA92646.1); contains InterPro domain Up-frameshift suppressor 2 (InterPro:IPR007193); contains InterPro domain Initiation factor eIF-4 gamma, middle (InterPro:IPR003890)   chr2:16399125-16406758 REVERSE   Aliases: T16B24.10, T16B24_10	6.2	6.3	-0.1	-0.2	100.0%	-4.7
16668	AT4G11530.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:6985617-6989593 FORWARD   Aliases: F25E4.150, F25E4_150	3.0	3.0	-0.1	-0.2	100.0%	-4.8
16669	AT2G04038.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr2:1331916-1332416 FORWARD   Aliases: F3L12.14, F3L12_14	2.5	2.5	-0.0	-0.2	100.0%	-5.9
16670	AT4G16090.1   hypothetical protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr4:9103090-9103968 FORWARD   Aliases: DL4085W, FCAALL.276	3.6	3.5	0.0	0.2	100.0%	-5.2
16671	AT3G44820.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr3:16372851-16375396 REVERSE   Aliases: F28D10.10	3.2	3.1	0.0	0.2	100.0%	-5.6
16672	AT5G65890.1   Symbol: ACR1   ACT domain-containing protein (ACR1), contains Pfam profile ACT domain PF01842   chr5:26372135-26375092 FORWARD   Aliases: K14B20.6, K14B20_6	5.0	4.9	0.1	0.2	100.0%	-4.7
16673	AT3G49100.1   signal recognition particle 9 kDa protein, putative / SRP9, putative, similar to SP:P49458 Signal recognition particle 9 kDa protein (SRP9) {Homo sapiens}; contains Pfam PF05486: Signal recognition particle 9 kDa protein (SRP9)   chr3:18207828-18209432 FORWARD   Aliases: T2J13.60	6.2	6.1	0.1	0.2	100.0%	-4.6
16674	AT4G35335.1   nucleotide-sugar transporter family protein, similar to SP:O77592 UDP N-acetylglucosamine transporter (Golgi UDP-GlcNAc transporter) {Canis familiaris}, SP:P78382 CMP-sialic acid transporter {Homo sapiens}; contains Pfam profile PF04142: Nucleotide-sugar transporter   chr4:16807270-16809828 FORWARD   Aliases: AT4G35330, AT4G35340	4.5	4.5	0.0	0.2	100.0%	-5.3
16675	AT2G24400.1   auxin-responsive protein, putative / small auxin up RNA (SAUR_D), similar to SAUR-AC-like protein (small auxin up RNA) (GI:4455308) from (Arabidopsis thaliana); auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesnerian)	2.6	2.6	-0.0	-0.2	100.0%	-5.6
16676	AT2G43450.1   expressed protein, ; expression supported by MPSS   chr2:18050311-18051302 REVERSE   Aliases: T1O24.19	2.4	2.3	0.0	0.2	100.0%	-5.9
16677	AT5G26990.1   drought-responsive family protein, non-consensus AT donor splice site at exon 3, AC acceptor splice site at exon 4; similar to drought-induced mRNA, Di19 (Arabidopsis thaliana) gi:469110:emb:CAA55321   chr5:9491369-9493642 FORWARD   Aliases: F2P16.10, F2P16_10	6.6	6.5	0.1	0.2	100.0%	-4.7
16678	AT3G18700.1   expressed protein   chr3:6431728-6432911 REVERSE   Aliases: MVE11.6	2.4	2.4	0.0	0.2	100.0%	-5.7
16679	AT1G21430.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenases YUCCA (gi:16555352), YUCCA2 (gi:16555354), and YUCCA3 (gi:16555356) from Arabidopsis thaliana   chr1:7500834-7502175 FORWARD   Aliases: F24J8.6, F24J8_6	3.1	3.2	-0.1	-0.2	100.0%	-5.2
16680	AT3G47440.1   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr3:17493010-17494364 FORWARD   Aliases: T21L8.190	3.4	3.4	-0.1	-0.2	100.0%	-5.2
16681	AT2G35700.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr2:15012284-15012868 FORWARD   Aliases: T20F21.11, T20F21_11	2.8	2.7	0.0	0.2	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16682	AT1G31220.1   phosphoribosylglycinamide formyltransferase, similar to phosphoribosylglycinamide formyltransferase, chloroplast precursor (Arabidopsis thaliana) SWISS-PROT:P52422   chr1:11156783-11158664 FORWARD   Aliases: F28K20.18, F28K20_18	5.6	5.6	0.0	0.2	100.0%	-5.0
16683	AT4G35900.1   Symbol: FD   DNA-binding protein-related, weak similarity to DNA-binding factor gmlip15 (Zea mays) GI:14289167   chr4:17004598-17006253 FORWARD   Aliases: FD, FD 1, T19K4.30	2.1	2.1	0.0	0.2	100.0%	-5.9
16684	AT3G63260.2   Symbol: ATMRK1	5.7	5.8	-0.1	-0.2	100.0%	-4.9
16685	AT2G41070.3   Symbol: EEL   basic leucine zipper transcription factor (BZIP12), nearly identical to basic leucine zipper transcription factor (Arabidopsis thaliana) GI:21694632; contains a bZIP transcription factor basic domain signature (PDOC00036)   chr2:17137899-17139423 FORWARD   Aliases: ATBZIP12, ENHANCED EM LEVEL, T3K9.16, T3K9_16	2.9	3.0	-0.1	-0.2	100.0%	-4.9
16686	AT5G37910.1   seven in absentia (SINA) family protein, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr5:15113440-15114548 REVERSE   Aliases: K18L3.11, K18L3_11	2.1	2.0	0.0	0.2	100.0%	-5.8
16687	AT4G18860.1   expressed protein, ; expression supported by MPSS   chr4:10344698-10345599 FORWARD   Aliases: F13C5.30, F13C5_30	2.3	2.3	0.0	0.2	100.0%	-5.9
16688	AT5G57840.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from Dianthus caryophyllus (gi:2239091)   chr5:23450030-23452458 REVERSE   Aliases: MTI20.9, MTI20_9	4.7	4.8	-0.1	-0.2	100.0%	-4.8
16689	AT4G26910.3   2-oxoacid dehydrogenase family protein, similar to SP:P36957 Dihydrolipoamide succinyltransferase component of 2-oxoglutarate dehydrogenase complex, mitochondrial precursor (EC 2.3.1.61) {Homo sapiens}; contains Pfam profiles PF00198: 2-oxo acid dehydrogenases acyltransferase (catalytic domain), PF00364: Biotin-requiring enzyme   chr4:13519817-13522448 REVERSE   Aliases: F10M23.250, F10M23_250	8.3	8.4	-0.1	-0.2	100.0%	-5.0
16690	AT1G53660.1   phosphate translocator-related, low similarity to SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275; contains 8 predicted transmembrane domains   chr1:20036950-20039614 FORWARD   Aliases: F22G10.26, F22G10_26	3.0	2.9	0.0	0.2	100.0%	-5.1
16691	AT2G27740.1   expressed protein, contains Pfam profile PF04949: Family of unknown function (DUF662)   chr2:11829855-11830808 FORWARD   Aliases: F15K20.16, F15K20_16	3.7	3.6	0.1	0.2	100.0%	-4.7
16692	AT5G38770.1   hypothetical protein   chr5:15543344-15543637 FORWARD   Aliases: MKD10.70, MKD10_70	2.7	2.7	0.0	0.2	100.0%	-5.2
16693	AT2G01790.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr2:341321-342479 REVERSE   Aliases: T8O11.4, T8O11_4	3.5	3.6	-0.1	-0.2	100.0%	-5.1
16694	AT2G29020.1   Rab5-interacting family protein, similar to Protein C20orf24 (Rab5-interacting protein) (RIP5) (PNAS-11) (Swiss-Prot:Q9BUV8) (Homo sapiens); contains transmembrane domains   chr2:12476806-12478742 FORWARD   Aliases: T9I4.10, T9I4_10	9.4	9.3	0.0	0.2	100.0%	-5.2
16695	AT4G19840.1   Symbol: ATPP2 A1   lectin-related, similar to PP2 lectin polypeptide (Cucurbita maxima) GI:410437   chr4:10774286-10775911 FORWARD   Aliases: T16H5.200, T16H5_200	4.4	4.3	0.1	0.2	100.0%	-4.7
16696	AT5G22630.1   prephenate dehydratase family protein, contains Pfam profile PF00800: prephenate dehydratase   chr5:7524345-7526163 FORWARD   Aliases: MDJ22.5, MDJ22_5	9.3	9.1	0.2	0.2	100.0%	-4.7
16697	AT1G08990.1   glycogenin glucosyltransferase (glycogenin)-related, low similarity to glycogenin-1 from Mus musculus (SP:Q9R062), Rattus norvegicus (SP:O08730), Oryctolagus cuniculus (SP:P13280)   chr1:2888927-2890962 FORWARD   Aliases: F7G19.14, F7G19_14	2.3	2.4	-0.1	-0.2	100.0%	-4.3
16698	AT3G45190.1   SIT4 phosphatase-associated family protein, contains Pfam profile: PF04499 SIT4 phosphatase-associated protein   chr3:16552979-16559146 REVERSE   Aliases: T14D3.130	3.0	2.9	0.0	0.2	100.0%	-5.3
16699	AT2G25580.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At4g32450.1); similar to putative selenium-binding protein [Oryza sativa (japonica cultivar-group)] (GB:NP_916013.1); contains InterPro domain PPR repeat (InterPro:IPR002885)	3.6	3.7	-0.0	-0.2	100.0%	-5.2
16700	AT3G01730.1   expressed protein   chr3:266565-266994 FORWARD   Aliases: F4P13.28	3.2	3.1	0.1	0.2	100.0%	-4.7
16701	AT5G46140.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g46130.1); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR005174)   chr5:18722241-18723935 REVERSE   Aliases: MCL19.20, MCL19_20	2.4	2.4	0.0	0.2	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16702	AT2G11520.1   Symbol: CRCK3   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:4625743-4628658 FORWARD   Aliases: F14P14.15, F14P14_15	5.7	5.8	-0.1	-0.2	100.0%	-5.0
16703	AT5G59270.1   lectin protein kinase family protein, contains Pfam domains PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr5:23928377-23930461 REVERSE   Aliases: MNC17.20, MNC17_20	3.4	3.4	-0.0	-0.2	100.0%	-5.6
16704	AT1G06320.1   expressed protein   chr1:1930601-1931448 FORWARD   Aliases: T2D23.15, T2D23_15	2.3	2.3	0.0	0.2	100.0%	-5.9
16705	AT2G40435.1   expressed protein   chr2:16893902-16895716 FORWARD   Aliases: T2P4.23	2.3	2.3	-0.0	-0.2	100.0%	-6.1
16706	AT5G13820.1   Symbol: TBP1   telomeric DNA-binding protein 1 (TBP1), identical to telomeric DNA-binding protein 1 (Arabidopsis thaliana) gi:13641340:gb:AAK31590   chr5:4460918-4464669 FORWARD   Aliases: ATBP 1, ATBP1, ATTBP1, H PROTEIN PROMOTER BINDING FACTOR 1, HPPBF 1, MAC12.23, MAC12_23, TELOMERIC DNA BINDING PROTEIN 1	4.4	4.4	-0.0	-0.2	100.0%	-5.2
16707	AT3G56940.1   Symbol: AT103   dicarboxylate diiron protein, putative (Crd1), similar to leucine-containing zipper protein At103 GP:6911864; contains Pfam profile PF05447: Copper response defect 1 (CRD1)   chr3:21087524-21089571 FORWARD   Aliases: CHL27, CRD1, DICARBOXYLATE DIIRON 1, T8M16.1	6.2	6.1	0.1	0.2	100.0%	-4.6
16708	AT1G74100.1   sulfotransferase family protein, similar to SP:P52837 Flavonol 4'-sulfotransferase (EC 2.8.2.-) (F4-ST) {Flaveria chloraefolia}; contains Pfam profile PF00685: Sulfotransferase domain   chr1:27868006-27869355 REVERSE   Aliases: F2P9.3, F2P9_3	6.5	6.6	-0.1	-0.2	100.0%	-4.7
16709	AT1G72020.1   expressed protein   chr1:27112954-27114093 REVERSE   Aliases: F28P5.9, F28P5_9	10.4	10.5	-0.1	-0.2	100.0%	-4.8
16710	AT1G72850.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr1:27417632-27418996 FORWARD   Aliases: F3N23.5, F3N23_5	3.3	3.2	0.1	0.2	100.0%	-4.6
16711	AT5G16600.1   Symbol: MYB43   myb family transcription factor (MYB43), contains PFAM profile: myb DNA binding domain PF00249   chr5:5438294-5440248 FORWARD   Aliases: MTG13.12, MTG13_12	3.1	3.2	-0.2	-0.2	100.0%	-4.7
16712	AT3G45310.2   similar to cysteine proteinase, putative / AALP protein (AALP) [Arabidopsis thaliana] (TAIR:At5g60360.1); similar to cysteine protease [Prunus armeniaca] (GB:AAB97142.1); contains InterPro domain Papain cysteine protease (C1) (InterPro:IPR000668); contains InterPro domain Eukaryotic thiol (cysteine) protease (InterPro:IPR000169)   chr3:16639369-16641506 REVERSE   Aliases: F18N11.70	8.7	8.5	0.2	0.2	100.0%	-4.6
16713	AT3G56700.1   male sterility protein, putative, similar to SP:Q08891 Male sterility protein 2 {Arabidopsis thaliana}; contains Pfam profile PF03015: Male sterility protein   chr3:21010710-21013037 REVERSE   Aliases: T8M16.30	2.8	2.8	0.0	0.2	100.0%	-5.7
16714	AT5G52630.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:21367601-21369367 FORWARD   Aliases: F6N7.12, F6N7_12	4.7	4.6	0.1	0.2	100.0%	-4.7
16715	AT2G03720.1   universal stress protein (USP) family protein, contains Pfam profile PF00582: universal stress protein family   chr2:1132167-1133376 FORWARD   Aliases: F19B11.17, F19B11_17	3.0	2.9	0.1	0.2	100.0%	-4.2
16716	AT4G35370.1   transducin family protein / WD-40 repeat family protein, contains 4 (3 significant) WD-40 repeats; similar to periodic tryptophan protein 1 homolog (Keratinocyte protein IEF SSP 9502) (PWP1)(SP:Q13610) (PIR2:I39360) (Homo sapiens)   chr4:16815143-16817291 FORWARD   Aliases: F23E12.70, F23E12_70	4.3	4.3	0.1	0.2	100.0%	-4.9
16717	AT5G48100.1   laccase family protein / diphenol oxidase family protein, similar to laccase (Pinus taeda)(GI:13661197)	2.5	2.4	0.0	0.2	100.0%	-5.7
16718	AT3G04880.1   Symbol: DRT102	6.5	6.4	0.1	0.2	100.0%	-4.9
16719	AT1G55460.1   Kin17 DNA-binding protein-related, contains similarity to zinc finger protein rts2 GB:U16133 GI:563244 from (Saccharomyces cerevisiae)   chr1:20711144-20712690 FORWARD   Aliases: T5A14.13, T5A14_13	8.4	8.6	-0.2	-0.2	100.0%	-4.5
16720	AT2G42660.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:17774127-17775367 REVERSE   Aliases: F14N22.7, F14N22_7	2.7	2.7	0.0	0.2	100.0%	-5.1
16721	AT3G20950.1   Symbol: CYP705A32   cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) (Glycine max);   chr3:7342681-7344750 FORWARD   Aliases: MFD22.9	2.7	2.7	-0.0	-0.2	100.0%	-5.6
16722	AT1G69810.1   Symbol: WRKY36	3.3	3.1	0.1	0.2	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16723	AT2G40600.1   appr-1-p processing enzyme family protein, contains Pfam domain PF01661: Appr-1-p processing enzyme family   chr2:16953948-16955615 REVERSE   Aliases: T2P4.5, T2P4_5	8.7	8.8	-0.1	-0.2	100.0%	-4.9
16724	AT1G55550.1   kinesin motor protein-related, Similar to Kinesin proteins; Contains kinesin motor domain protein motif and kinesin heavy chain signature motif   chr1:20752581-20756528 FORWARD   Aliases: T5A14.3, T5A14_3	3.1	3.1	0.1	0.2	100.0%	-5.3
16725	AT3G06590.2   expressed protein   chr3:2052699-2055413 REVERSE   Aliases: F5E6.8, F5E6_8	3.9	4.0	-0.1	-0.2	100.0%	-4.7
16726	AT4G17810.1   similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At2g37740.1); similar to OSJNBa0086006.19 [Oryza sativa (japonica cultivar-group)] (GB:XP_473719.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087)   chr4:9906861-9907670 FORWARD   Aliases: DL4940W, FCAALL.130	2.6	2.5	0.0	0.2	100.0%	-5.3
16727	AT5G40510.1   expressed protein   chr5:16246416-16248326 FORWARD   Aliases: MNF13.5, MNF13_5	3.8	3.7	0.1	0.2	100.0%	-4.4
16728	AT2G23290.1   myb family transcription factor   chr2:9911867-9913000 REVERSE   Aliases: T20D16.8, T20D16_8	6.0	6.2	-0.2	-0.2	100.0%	-5.0
16729	AT1G20550.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'axi 1 protein -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr1:7115475-7118151 REVERSE   Aliases: F5M15.13	4.7	4.8	-0.1	-0.2	100.0%	-5.2
16730	AT2G38790.1   expressed protein   chr2:16221269-16222342 REVERSE   Aliases: F13I13.2	4.0	3.9	0.1	0.2	100.0%	-4.8
16731	AT1G74890.1   Symbol: ARR15   two-component responsive regulator / response regulator 15 (ARR15), identical to response regulator 15 GI:11870065 from (Arabidopsis thaliana); contains Pfam profile: PF00072 response regulator receiver domain   chr1:28135251-28136371 REVERSE   Aliases: F25A4.14, F25A4_14, RESPONSE REGULATOR 15	3.6	3.6	0.0	0.2	100.0%	-5.3
16732	AT1G11080.1   Symbol: SCPL31	2.6	2.5	0.1	0.2	100.0%	-4.6
16733	AT3G57190.1   peptide chain release factor, putative, similar to SP:P07012 Peptide chain release factor 2 (RF-2) {Escherichia coli}; contains Pfam profile PF03462: PCRF domain   chr3:21177382-21179355 FORWARD   Aliases: F28O9.40	3.9	4.0	-0.1	-0.2	100.0%	-4.8
16734	AT4G00300.1   fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	7.1	6.9	0.2	0.2	100.0%	-4.7
16735	AT5G08250.1   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr5:2653581-2655727 REVERSE   Aliases: F8L15.12	2.3	2.4	-0.1	-0.2	100.0%	-5.2
16736	AT2G14290.1   F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.8	0.1	0.2	100.0%	-4.9
16737	AT1G20130.1   family II extracellular lipase, putative, contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase; similar to EXL3 (PMID:11431566)	3.2	3.2	0.0	0.2	100.0%	-5.5
16738	AT1G53840.1   Symbol: ATPME1	5.3	5.4	-0.1	-0.2	100.0%	-4.4
16739	AT1G17840.1   ABC transporter family protein, similar to ABC transporter GI:10280532 from (Homo sapiens)   chr1:6142603-6146514 FORWARD   Aliases: F2H15.7, F2H15_7	2.8	2.7	0.0	0.2	100.0%	-5.5
16740	AT1G13570.1   F-box family protein, contains F-box domain Pfam:PF00646 ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:4642343-4644419 REVERSE   Aliases: F13B4.6, F13B4_6	5.1	5.0	0.1	0.2	100.0%	-4.9
16741	AT5G13580.1   ABC transporter family protein   chr5:4370695-4373204 FORWARD   Aliases: T6I14.7	3.4	3.5	-0.1	-0.2	100.0%	-4.6
16742	AT1G13900.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	7.1	7.2	-0.1	-0.2	100.0%	-5.1
16743	AT3G04510.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr3:1215818-1216423 REVERSE   Aliases: T27C4.16, T27C4_16	2.5	2.4	0.0	0.2	100.0%	-5.1
16744	AT5G10310.1   expressed protein   chr5:3241519-3242128 REVERSE   Aliases: F18D22.80, F18D22_80	2.2	2.3	-0.0	-0.2	100.0%	-5.9
16745	AT5G39730.1   avirulence-responsive protein-related / avirulence induced gene (AIG) protein-related, similar to SP:P54121 AIG2 protein {Arabidopsis thaliana}   chr5:15918907-15920057 FORWARD   Aliases: MKM21.20, MKM21_20	7.8	7.6	0.2	0.2	100.0%	-4.6
16746	AT2G29190.1   pumilio/Puf RNA-binding domain-containing protein   chr2:12550889-12555567 REVERSE   Aliases: F16P2.43, F16P2_43	3.3	3.2	0.0	0.2	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16747	AT5G24980.1   expressed protein   chr5:8609084-8609531 FORWARD   Aliases: F6A4.190, F6A4_190	8.8	8.7	0.2	0.2	100.0%	-4.6
16748	AT3G30843.1   expressed protein   chr3:12609750-12610729 REVERSE   Aliases: MJ16.4	3.2	3.2	0.0	0.2	100.0%	-5.3
16749	AT1G01660.1   U-box domain-containing protein   chr1:240057-242608 REVERSE   Aliases: T1N6.4, T1N6_4	2.8	2.9	-0.1	-0.2	100.0%	-4.6
16750	AT5G27210.1   expressed protein, weak similarity to seven transmembrane domain orphan receptor (Mus musculus) GI:4321619   chr5:9572103-9574138 REVERSE   Aliases: T21B4.120, T21B4_120	4.0	3.9	0.1	0.2	100.0%	-5.1
16751	AT1G73380.2   expressed protein   chr1:27592693-27594540 FORWARD   Aliases: T9L24.41, T9L24_41	6.3	6.2	0.1	0.2	100.0%	-4.9
16752	AT1G31060.1   expressed protein, similar to EST gb:T43267   chr1:11078801-11079160 REVERSE   Aliases: F17F8.2	2.5	2.4	0.1	0.2	100.0%	-5.2
16753	AT2G19110.1   Symbol: HMA4   ATPase E1-E2 type family protein / haloacid dehalogenase-like hydrolase family protein / heavy-metal-associated domain-containing protein, similar to cadmium efflux pump protein from Geobacillus stearothermophilus (GI:16753175), cadmium resistance protein B from Staphylococcus aureus (GI:14020985); T20K24.13 has been merged with T20K24.12 per suggestion of Dr. Kristian Axelsen (axe@biobase.dk)   chr2:8285965-8293527 FORWARD   Aliases: T20K24.12, T20K24_12	8.0	7.9	0.1	0.2	100.0%	-5.1
16754	AT5G05500.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr5:1629668-1630397 FORWARD   Aliases: MOP10.4, MOP10_4	2.5	2.7	-0.1	-0.2	100.0%	-4.5
16755	AT1G05990.1   calcium-binding protein, putative, strong similarity to calcium-binding protein (Lotus japonicus) GI:18413495; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:1818446-1819039 FORWARD   Aliases: T21E18.4, T21E18_4	4.1	4.2	-0.1	-0.2	100.0%	-5.0
16756	AT3G14930.3   uroporphyrinogen decarboxylase, putative / UPD, putative, similar to uroporphyrinogen decarboxylase (chloroplast) from Nicotiana tabacum (SP:Q42967), Hordeum vulgare (SP:Q42855), Zea mays (SP:O81220); contains Pfam domain uroporphyrinogen decarboxylase (URO-D) PF01208   chr3:5020598-5022966 FORWARD   Aliases: K15M2.7	4.7	4.6	0.1	0.2	100.0%	-4.8
16757	AT2G32170.1   expressed protein, ;supported by cDNA GI:20259498   chr2:13673533-13678181 FORWARD   Aliases: F22D22.8, F22D22_8	7.8	7.9	-0.2	-0.2	100.0%	-4.6
16758	AT5G07420.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:2349456-2351509 FORWARD   Aliases: T21I.130, T21I_130	2.4	2.4	-0.0	-0.2	100.0%	-5.7
16759	AT2G34530.2   expressed protein   chr2:14556168-14557320 REVERSE   Aliases: T31E10.13, T31E10_13	2.7	2.7	-0.0	-0.2	100.0%	-5.4
16760	AT5G59160.3   Symbol: TOPP2   similar to serine/threonine protein phosphatase PP1 isozyme 5 (TOPP5) / phosphoprotein phosphatase 1 [Arabidopsis thaliana] (TAIR:At3g46820.1); similar to protein phosphatase type 1 [Nicotiana tabacum] (GB:CAB07804.1); contains InterPro domain Metallo-phosphoesterase (InterPro:IPR004843); contains InterPro domain Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetrakisphosphate (InterPro:IPR006186)   chr5:23896563-23898855 FORWARD   Aliases: MNC17.9, MNC17_9, PPO	9.3	9.4	-0.1	-0.2	100.0%	-5.0
16761	NA	2.8	2.8	0.0	0.2	100.0%	-5.5
16762	AT1G05880.1   similar to IBR domain-containing protein / ARIADNE-like protein ARI7 (ARI7) [Arabidopsis thaliana] (TAIR:At2g31510.1); similar to putative ariadne [Oryza sativa (japonica cultivar-group)] (GB:XP_483571.1); contains InterPro domain Zn-finger, cysteine-rich C6HC (InterPro:IPR002867)   chr1:1775642-1778552 FORWARD   Aliases: T20M3.15, T20M3_15	2.8	2.7	0.0	0.2	100.0%	-5.4
16763	AT5G48450.1   Symbol: SKS3   multi-copper oxidase type I family protein, contains Pfam profile: PF00394 Multicopper oxidase; also similar to l-ascorbate oxidase and pollen-specific protein   chr5:19650521-19652838 REVERSE   Aliases: MJE7.8, MJE7_8, SKS3	4.1	4.2	-0.1	-0.2	100.0%	-5.0
16764	AT1G08060.2   Symbol: MOM   MOM1, identical to MOM1 (mutation in a 'Morpheus molecule') (Arabidopsis thaliana) gi:8132770:gb:AAF73381.1:   chr1:2501739-2510526 REVERSE   Aliases: MAINTENANCE OF METHYLATION, MOM, MOM1, MORPHEUS MOLECULE, T6D22.14, T6D22_14	4.1	4.1	-0.1	-0.2	100.0%	-5.4
16765	AT1G49110.1   expressed protein   chr1:18175263-18176118 FORWARD   Aliases: F27J15.12, F27J15_12	4.6	4.5	0.1	0.2	100.0%	-4.8
16766	AT5G09370.2   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to lipid transfer protein - Hordeum vulgare, EMBL:AF109195; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	2.9	3.0	-0.1	-0.2	100.0%	-5.3
16767	AT4G29500.1   prolidase-related, contains similarity to prolidase GI:3114966 from (Suberites domuncula)   chr4:14490217-14491495 FORWARD   Aliases: T16L4.10, T16L4_10	7.8	7.8	0.1	0.2	100.0%	-5.3
16768	AT1G31690.1   copper amine oxidase, putative, similar to copper amine oxidase (Lens culinaris) gi:15451834:gb:AAB34918	2.5	2.5	0.0	0.2	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16769	AT5G08415.1   lipoic acid synthase family protein, similar to lipoic acid synthase from Arabidopsis thaliana (gi:3928758), from Mus musculus (gi:14669826) Pfam profile PF04055: radical SAM domain protein   chr5:2710820-2713133 REVERSE   Aliases: None	7.8	7.7	0.1	0.2	100.0%	-4.7
16770	AT5G65760.1   serine carboxypeptidase S28 family protein, similar to SP:P42785 Lysosomal Pro-X carboxypeptidase precursor (EC 3.4.16.2) (Prolylcarboxypeptidase) (PRCP) (Proline carboxypeptidase) {Homo sapiens}; contains Pfam profile PF05577: Serine carboxypeptidase S28	10.3	10.4	-0.1	-0.2	100.0%	-5.0
16771	AT1G05680.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:1703091-1704688 REVERSE   Aliases: F3F20.13, F3F20_13	3.0	3.0	-0.0	-0.2	100.0%	-5.4
16772	AT1G54955.1   expressed protein   chr1:20497787-20498401 FORWARD   Aliases: F14C21.48, F14C21_48	2.9	2.8	0.1	0.2	100.0%	-5.2
16773	AT5G55910.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr5:22657070-22659528 REVERSE   Aliases: MYN21.2, MYN21_2	5.4	5.3	0.1	0.2	100.0%	-4.8
16774	AT1G48900.1   signal recognition particle 54 kDa protein 3 / SRP54 (SRP-54C), identical to SP:P49967 Signal recognition particle 54 kDa protein 3 (SRP54) {Arabidopsis thaliana}   chr1:18088450-18091547 REVERSE   Aliases: F27K7.8, F27K7_8	10.7	10.8	-0.1	-0.2	100.0%	-5.0
16775	AT4G37230.1   oxygen-evolving enhancer protein, chloroplast, putative / 33 kDa subunit of oxygen evolving system of photosystem II, putative, similar to Oxygen-evolving enhancer protein 1, chloroplast precursor (OEE1) (33 kDa subunit of oxygen evolving system of photosystem II) (OEC 33 kDa subunit) (33 kDa thylakoid membrane protein) (SP:P14226) {Pisum sativum}   chr4:17516418-17517581 FORWARD   Aliases: AP22.76, AP22_76	3.2	3.1	0.1	0.2	100.0%	-5.0
16776	AT4G24430.1   expressed protein   chr4:12630729-12633085 FORWARD   Aliases: T22A6.260, T22A6_260	2.7	2.6	0.1	0.2	100.0%	-5.3
16777	AT2G19320.1   expressed protein   chr2:8377946-8378179 REVERSE   Aliases: F27F23.12, F27F23_12	2.7	2.7	-0.0	-0.2	100.0%	-5.6
16778	AT5G48060.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr5:19492522-19496228 FORWARD   Aliases: MDN11.14, MDN11_14	3.0	3.1	-0.1	-0.2	100.0%	-4.8
16779	AT1G19520.1   expressed protein   chr1:6759956-6761224 FORWARD   Aliases: F18O14.40	4.3	4.4	-0.1	-0.2	100.0%	-5.1
16780	AT4G14090.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase ;similar to UDP-glucose:anthocyanin 5-O-glucosyltransferase GI:4115563 from (Verbena x hybrida)   chr4:8122185-8123830 REVERSE   Aliases: DL3090C, FCAALL.84	5.1	5.0	0.1	0.2	100.0%	-4.9
16781	AT1G03840.2   similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At5g44160.1); similar to zinc finger protein-like [Oryza sativa (japonica cultivar-group)] (GB:NP_913610.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087)   chr1:967520-970057 REVERSE   Aliases: F21M11.25, F21M11_25	2.6	2.5	0.0	0.2	100.0%	-5.2
16782	AT1G79100.1   arginine/serine-rich protein-related, similar to arginine/serine-rich protein (Arabidopsis thaliana) GI:6601502   chr1:29758541-29759281 FORWARD   Aliases: YUP8H12R.28, YUP8H12R_28	3.3	3.3	0.0	0.2	100.0%	-5.3
16783	AT4G34250.1   fatty acid elongase, putative, similar to fatty acid elongase 1 (Fae1), Arabidopsis thaliana, U29142 (GI:881615)	2.8	2.8	0.0	0.2	100.0%	-5.5
16784	AT3G20650.2   mRNA capping enzyme family protein, contains Pfam PF03291: mRNA capping enzyme, large subunit   chr3:7220887-7224034 REVERSE   Aliases: F3H11.3	3.7	3.7	-0.1	-0.2	100.0%	-5.1
16785	AT1G06225.1   Symbol: CLE3   Clavata3 / ESR-Related-3 (CLE3), CLAVATA3/ESR-Related 3 (CLE3)   chr1:1905974-1906225 FORWARD   Aliases: CLAVATA3/ESR RELATED 3	3.2	3.2	0.0	0.2	100.0%	-5.6
16786	AT1G11930.2   alanine racemase family protein, contains Pfam domain, PF01168: Alanine racemase, N-terminal domain   chr1:4028733-4030537 FORWARD   Aliases: F12F1.20, F12F1_20	7.8	7.7	0.1	0.2	100.0%	-4.9
16787	AT4G03680.1   expressed protein   chr4:1628883-1629934 FORWARD   Aliases: T5L23.18, T5L23_18	2.8	2.8	0.0	0.2	100.0%	-5.7
16788	AT1G60130.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.2	3.1	0.1	0.2	100.0%	-5.3
16789	AT5G23310.1   Symbol: FSD3   superoxide dismutase (Fe) / iron superoxide dismutase 3 (FSD3), identical to iron superoxide dismutase 3 (Arabidopsis thaliana) gi:3273757:gb:AAC24834   chr5:7850550-7852535 FORWARD   Aliases: FE SUPEROXIDE DISMUTASE 3, MKD15.17, MKD15_17	6.2	6.1	0.1	0.2	100.0%	-4.4
16790	AT1G31240.1   expressed protein, identical to hypothetical protein GB:AAD21690 GI:4512621 from (Arabidopsis thaliana)   chr1:11163839-11164909 REVERSE   Aliases: F28K20.20, F28K20_20	3.6	3.6	0.1	0.2	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16791	AT3G53500.2   Symbol: RSZ32   zinc knuckle (CCHC-type) family protein, contains Pfam domain PF00098: Zinc knuckle   chr3:19845324-19847976 REVERSE   Aliases: F4P12.200, RSZ32	8.6	8.5	0.1	0.2	100.0%	-4.7
16792	AT3G63410.1   Symbol: APG1   chloroplast inner envelope membrane protein, putative (APG1), similar to SP:P23525 37 kDa inner envelope membrane protein, chloroplast precursor (E37) {Spinacia oleracea}; contains Pfam profile PF01209: methyltransferase, UbiE/COQ5 family   chr3:23426190-23428093 REVERSE   Aliases: ALBINO OR PALE GREEN MUTANT 1, MAA21.40, VITAMIN E DEFECTIVE, VTE3	10.3	10.4	-0.1	-0.2	100.0%	-4.4
16793	AT5G28760.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr5:10786312-10788953 FORWARD   Aliases: T32B20.3, T32B20_3	3.0	3.0	-0.1	-0.2	100.0%	-5.4
16794	AT1G11290.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3791454-3793883 REVERSE   Aliases: T28P6.20, T28P6_20	3.6	3.7	-0.0	-0.2	100.0%	-5.2
16795	AT4G27700.1   rhodanese-like domain-containing protein, contains rhodanese-like domain PF00581	6.1	6.0	0.1	0.2	100.0%	-4.8
16796	AT2G21930.1   F-box family protein, contains F-box domain Pfam:PF00646	3.0	3.1	-0.1	-0.2	100.0%	-5.2
16797	AT1G08640.1   expressed protein   chr1:2748430-2751281 REVERSE   Aliases: F22O13.12, F22O13_12	6.6	6.5	0.1	0.2	100.0%	-4.5
16798	AT1G78400.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to exopolygalacturonase GI:311962 from (Arabidopsis thaliana); contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:29503174-29504575 REVERSE   Aliases: F3F9.9, F3F9_9	2.4	2.3	0.0	0.2	100.0%	-5.8
16799	AT3G16110.1   Symbol: ATPDIL1 6   Encodes a protein disulfide isomerase-like (PDIL) protein, a member of a multigene family within the thioredoxin (TRX) superfamily.	4.9	4.9	0.0	0.2	100.0%	-5.1
16800	NA	3.2	3.1	0.0	0.2	100.0%	-5.4
16801	AT1G18485.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:6363165-6366226 FORWARD   Aliases: None	3.5	3.6	-0.1	-0.2	100.0%	-5.0
16802	AT4G13450.2   expressed protein   chr4:7815035-7816000 REVERSE   Aliases: T9E8.190, T9E8_190	2.2	2.2	0.0	0.2	100.0%	-5.6
16803	AT1G67020.1   hypothetical protein   chr1:25014671-25016650 REVERSE   Aliases: F1O19.7, F1O19_7	3.5	3.4	0.0	0.2	100.0%	-5.3
16804	AT3G16080.1   60S ribosomal protein L37 (RPL37C), similar to ribosomal protein L37 GB:BAA04888 from (Homo sapiens)   chr3:5454824-5455933 FORWARD   Aliases: MSL1.12	12.5	12.5	-0.1	-0.2	100.0%	-5.4
16805	AT1G17800.1   plastocyanin-like domain-containing protein, contains plastocyanin-like domain Pfam:PF02298; similar to basic blue protein GI:6688810 from (Medicago sativa)   chr1:6128816-6129497 FORWARD   Aliases: F2H15.3, F2H15_3	3.1	3.0	0.0	0.2	100.0%	-5.4
16806	AT5G38950.1   germin-like protein-related, contains some similarity to germin-like protein GI:5869975 from (Triticum aestivum)	2.5	2.5	-0.0	-0.2	100.0%	-5.7
16807	AT2G39640.1   glycosyl hydrolase family 17 protein   chr2:16532164-16534090 REVERSE   Aliases: F12L6.1	2.6	2.5	0.1	0.2	100.0%	-5.0
16808	AT5G55970.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:22684612-22686771 FORWARD   Aliases: MDA7.1, MDA7_1	3.8	3.7	0.1	0.2	100.0%	-4.5
16809	AT2G41020.2   WW domain-containing protein, contains Pfam domain PF00397: WW domain   chr2:17124412-17128166 FORWARD   Aliases: AT2G41030, T3K9.21, T3K9_21	3.9	3.9	0.0	0.2	100.0%	-5.4
16810	AT2G43280.1   far-red impaired responsive family protein / FAR1 family protein, weak similarity to far-red impaired response protein (Arabidopsis thaliana) GI:5764395; contains Pfam profile PF03101: FAR1 family   chr2:17996775-17998099 FORWARD   Aliases: F14B2.32	5.5	5.5	0.1	0.2	100.0%	-5.0
16811	AT1G79420.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr1:29876351-29879208 FORWARD   Aliases: T8K14.16, T8K14_16	2.5	2.5	-0.0	-0.2	100.0%	-5.4
16812	AT1G42980.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains Pfam profile PF02181: Formin Homology 2 Domain   chr1:16135726-16138026 FORWARD   Aliases: F13A11.4, F13A11_4	3.2	3.2	0.1	0.2	100.0%	-5.0
16813	AT3G47860.1   apolipoprotein D-related, contains weak similarity to Apolipoprotein D precursor (ApoD) (Swiss-Prot:P51910) (Mus musculus)   chr3:17667682-17669273 REVERSE   Aliases: T23J7.190	9.4	9.5	-0.1	-0.2	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16814	AT5G15420.1   expressed protein   chr5:5007829-5008967 REVERSE   Aliases: T20K14.30, T20K14_30	2.2	2.3	-0.0	-0.2	100.0%	-5.8
16815	AT5G03780.1   Symbol: TRFL10	4.4	4.5	-0.1	-0.2	100.0%	-4.8
16816	AT3G28220.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:10525641-10527965 FORWARD   Aliases: T19D11.1	2.8	2.8	0.0	0.2	100.0%	-5.4
16817	AT3G49950.1   scarecrow transcription factor family protein, lateral suppressor protein - Lycopersicon esculentum, EMBL:AF098674   chr3:18533555-18534787 FORWARD   Aliases: F3A4.30	3.1	3.1	0.0	0.2	100.0%	-5.7
16818	AT1G67640.1   lysine and histidine specific transporter, putative, similar to lysine and histidine specific transporter GB:AAC49885 GI:2576361 (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:25355791-25357571 REVERSE   Aliases: F12B7.20, F12B7_20	3.3	3.2	0.0	0.2	100.0%	-5.3
16819	AT1G49820.1   5-methylthioribose kinase family, contains TIGRfam TIGR01767: 5-methylthioribose kinase profile   chr1:18446600-18448766 FORWARD   Aliases: F10F5.1, F10F5_1	9.6	9.7	-0.2	-0.2	100.0%	-5.1
16820	AT3G04550.1   expressed protein   chr3:1225928-1227442 FORWARD   Aliases: F7O18.2, F7O18_2	9.7	9.6	0.1	0.2	100.0%	-5.0
16821	AT4G25360.2   similar to leaf senescence protein-related (YLS7 ) [Arabidopsis thaliana] (TAIR:At5g51640.1); similar to leaf senescence protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD68439.1); contains InterPro domain Protein of unknown function DUF231 (InterPro:IPR004253)	6.2	6.2	0.1	0.2	100.0%	-5.1
16822	AT1G69910.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:26333777-26335929 FORWARD   Aliases: T17F3.6, T17F3_6	4.8	4.9	-0.1	-0.2	100.0%	-5.0
16823	AT4G38900.3   similar to bZIP family transcription factor [Arabidopsis thaliana] (TAIR:At2g21230.1); similar to vsf-1 [Lycopersicon esculentum] (GB:CAA52015.1); similar to vsf-1 protein - tomato (GB:S52203); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)	4.9	5.0	-0.1	-0.2	100.0%	-4.6
16824	AT5G17020.1   Symbol: XPO1A   exportin1 (XPO1), nearly identical to Exportin1 (XPO1) protein (Arabidopsis thaliana) GI:7671510   chr5:5594739-5602958 FORWARD   Aliases: ATCRM1, ATXPO1, F2K13.170, F2K13_170, XPO1	3.4	3.5	-0.1	-0.2	100.0%	-5.1
16825	ATMG00660.1   Symbol: ORF149	9.2	8.9	0.3	0.2	100.0%	-4.9
16826	AT1G52470.1   expressed protein   chr1:19558382-19559026 FORWARD   Aliases: F6D8.31, F6D8_31	3.4	3.4	-0.1	-0.2	100.0%	-5.2
16827	AT5G43730.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.8	3.0	-0.2	-0.2	100.0%	-5.0
16828	AT1G61380.1   S-locus protein kinase, putative, similar to KI domain interacting kinase 1 (Zea mays) gi:2735017:gb:AAB93834; contains S-locus glycoprotein family domain, Pfam:PF00954	4.5	4.4	0.1	0.2	100.0%	-4.9
16829	AT3G20970.2   Symbol: NFU4   similar to nitrogen fixation NifU-like family protein [Arabidopsis thaliana] (TAIR:At1g51390.1); similar to hypothetical protein UM04972.1 [Ustilago maydis 521] (GB:EAK85802.1); contains InterPro domain Nitrogen-fixing NifU, C-terminal (InterPro:IPR001075)	4.6	4.7	-0.1	-0.2	100.0%	-5.1
16830	AT4G39880.1   ribosomal protein L23 family protein, contains Pfam profile PF00276: ribosomal protein L23   chr4:18504531-18505332 FORWARD   Aliases: T5J17.50, T5J17_50	6.6	6.7	-0.1	-0.2	100.0%	-4.6
16831	AT5G53100.1   oxidoreductase, putative, similar to forever young oxidoreductase (FEY3) GI:12004621 from (Arabidopsis thaliana)	3.5	3.6	-0.0	-0.2	100.0%	-5.3
16832	AT4G28703.1   expressed protein   chr4:14166275-14166928 FORWARD   Aliases: None	3.5	3.4	0.1	0.2	100.0%	-5.1
16833	AT1G01050.1   inorganic pyrophosphatase, putative (soluble) / pyrophosphate phospho-hydrolase, putative / PPase, putative, strong similarity to SP:Q43187 Soluble inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho- hydrolase) (PPase) {Solanum tuberosum}; contains Pfam profile PF00719: inorganic pyrophosphatase   chr1:31181-33148 REVERSE   Aliases: T25K16.5, T25K16_5	10.5	10.6	-0.1	-0.2	100.0%	-4.9
16834	AT4G11140.1   encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	2.7	2.6	0.0	0.2	100.0%	-5.5
16835	AT4G37540.1   LOB domain protein 39 / lateral organ boundaries domain protein 39 (LBD39), identical to SP:Q9SZE8 LOB domain protein 39 {Arabidopsis thaliana}   chr4:17639527-17640651 REVERSE   Aliases: F19F18.30, F19F18_30	4.7	4.8	-0.2	-0.2	100.0%	-4.6
16836	AT5G10030.1   Symbol: TGA4   bZIP family transcription factor	4.6	4.5	0.1	0.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16837	AT2G02450.2   Symbol: ANAC034/ANAC035   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain   chr2:648043-650813 FORWARD   Aliases: ANAC034, ANAC035	2.7	2.7	-0.0	-0.2	100.0%	-5.9
16838	AT3G56680.1   expressed protein   chr3:21002259-21004646 FORWARD   Aliases: T8M16.10	9.4	9.3	0.1	0.2	100.0%	-4.7
16839	AT5G60740.1   ABC transporter family protein, similar to ATP-binding cassette, sub-family G, member 2 (Placenta-specific ATP-binding cassette transporter) (Breast cancer resistance protein) SP:Q9UNQ0 from (Homo sapiens)   chr5:24443298-24447495 REVERSE   Aliases: MUP24.11, MUP24_11	3.0	3.0	0.0	0.2	100.0%	-5.4
16840	AT3G30360.1   hypothetical protein   chr3:11967002-11967542 FORWARD   Aliases: T6J22.15	3.2	3.3	-0.0	-0.2	100.0%	-5.6
16841	AT3G43540.2   expressed protein, hypothetical protein slr1699 - Synechocystis sp. (strain PCC 6803), PIR:S75306   chr3:15441747-15444175 FORWARD   Aliases: T18D12.110	6.4	6.3	0.1	0.2	100.0%	-4.6
16842	AT2G43910.1   thiol methyltransferase, putative, similar to thiol methyltransferase 1 GI:14583119 from (Brassica oleracea)   chr2:18191557-18194101 REVERSE   Aliases: F6E13.4	8.0	8.2	-0.2	-0.2	100.0%	-4.6
16843	AT2G43920.1   thiol methyltransferase, putative, similar to thiol methyltransferase 1 GI:14583119 from (Brassica oleracea)   chr2:18196128-18198324 REVERSE   Aliases: F6E13.5	8.0	8.2	-0.2	-0.2	100.0%	-4.6
16844	AT3G57650.1   Symbol: LPAT2   acyl-CoA:1-acylglycerol-3-phosphate acyltransferase, putative, similar to acyl-CoA:1-acylglycerol-3-phosphate acyltransferase GI:4583544 from (Brassica napus)   chr3:21360491-21364151 FORWARD   Aliases: F15B8.160	10.2	10.2	0.1	0.2	100.0%	-5.1
16845	AT5G60660.1   Symbol: PIP2;4/PIP2F   major intrinsic family protein / MIP family protein, similar to mipC protein GI:1657948 from (Mesembryanthemum crystallinum)   chr5:24392686-24394215 REVERSE   Aliases: MUP24.9, MUP24_9, PIP2;4, PIP2F	3.6	3.7	-0.1	-0.2	100.0%	-4.3
16846	AT3G05540.1   translationally controlled tumor family protein, similar to translationally controlled tumor protein GB:AAD10032 from (Hevea brasiliensis)   chr3:1606493-1608036 REVERSE   Aliases: F18C1.20, F18C1_20	2.8	2.8	-0.0	-0.2	100.0%	-5.4
16847	AT5G40070.1   hypothetical protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr5:16056407-16056975 FORWARD   Aliases: MUD12.50, MUD12_50	2.3	2.2	0.0	0.2	100.0%	-6.0
16848	AT1G47720.1   expressed protein, contains Pfam PF05329: Protein of unknown function (DUF731)   chr1:17563795-17565323 REVERSE   Aliases: T2E6.21	5.6	5.5	0.1	0.2	100.0%	-4.7
16849	AT4G22980.1   expressed protein, ; expression supported by MPSS   chr4:12043985-12045664 REVERSE   Aliases: F7H19.160, F7H19_160	2.8	2.8	-0.0	-0.2	100.0%	-5.5
16850	AT4G00690.1   Ulp1 protease family protein, similar to SUMO-1/Smt3-specific isopeptidase 2 (Mus musculus) GI:16118473, sentrin/SUMO-specific protease (Homo sapiens) GI:6906859; contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr4:281645-283129 FORWARD   Aliases: F6N23.7, F6N23_7	2.9	3.0	-0.0	-0.2	100.0%	-5.4
16851	AT3G04710.2   similar to stress-inducible protein, putative [Arabidopsis thaliana] (TAIR:At4g12400.1); similar to stress-inducible protein, putative [Arabidopsis thaliana] (TAIR:At1g62740.1); similar to ankyrin-like protein [Solanum tuberosum] (GB:BAC23047.1); contains InterPro domain TPR repeat (InterPro:IPR001440); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr3:1278090-1281124 FORWARD   Aliases: F7O18.18, F7O18_18	5.7	5.8	-0.1	-0.2	100.0%	-4.6
16852	AT4G10130.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to SP:Q9QY17 DnaJ homolog subfamily B member 8 Mus musculus, SP:P50025 Chaperone protein dnaJ Legionella pneumophila; contains Pfam profile PF00226 DnaJ domain   chr4:6320630-6321639 REVERSE   Aliases: F28M11.50, F28M11_50	4.8	4.7	0.0	0.2	100.0%	-5.5
16853	AT5G36930.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:14584881-14589845 REVERSE   Aliases: MLF18.50, MLF18_50	2.2	2.2	-0.0	-0.2	100.0%	-5.9
16854	AT3G45360.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr3:16652604-16652984 FORWARD   Aliases: F18N11.120	2.6	2.7	-0.0	-0.2	100.0%	-5.9
16855	AT5G07080.1   transferase family protein, similar to 10-deacetylbaecatin III-10-O-acetyl transferase - Taxus cuspidata, AF193765, EMBL:AF193765; contains Pfam transferase family domain PF00248   chr5:2200333-2202111 FORWARD   Aliases: T28J14.20, T28J14_20	3.0	3.2	-0.2	-0.2	100.0%	-4.4
16856	AT1G13650.2   expressed protein   chr1:4680434-4682094 REVERSE   Aliases: F21F23.9, F21F23_9	2.4	2.4	-0.0	-0.2	100.0%	-5.5
16857	AT5G45620.2   26S proteasome regulatory subunit, putative (RPN9), contains similarity to 26S proteasome subunit p40.5 GI:3618343 from (Homo sapiens)   chr5:18518772-18521344 FORWARD   Aliases: MRA19.2, MRA19_2	7.7	7.9	-0.3	-0.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16858	AT5G47000.1   peroxidase, putative   chr5:19086171-19087560 REVERSE   Aliases: MQD22.14, MQD22_14	2.2	2.2	0.0	0.2	100.0%	-5.7
16859	AT2G07040.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:2916535-2918939 FORWARD   Aliases: T4E14.15, T4E14_15	3.0	3.1	-0.0	-0.2	100.0%	-5.4
16860	AT5G64190.1   expressed protein   chr5:25696658-25698379 FORWARD   Aliases: MSJ1.3, MSJ1_3	2.6	2.6	-0.0	-0.2	100.0%	-5.5
16861	AT3G26140.1   glycosyl hydrolase family 5 protein / cellulase family protein, contains Pfam profile: PF00150 cellulase (glycosyl hydrolase family 5)   chr3:9560919-9564307 REVERSE   Aliases: MTC11.4	2.0	2.0	-0.0	-0.2	100.0%	-6.0
16862	AT3G44490.1   histone deacetylase-related / HD-related, similar to SP:O09106 Histone deacetylase 1 (HD1) {Mus musculus}   chr3:16108466-16109373 FORWARD   Aliases: F14L2.40	6.3	6.3	0.0	0.2	100.0%	-5.1
16863	AT2G33130.1   Symbol: RALFL18   rapid alkalization factor (RALF) family protein   chr2:14053598-14053909 REVERSE   Aliases: F25I18.13, F25I18_13, RALF LIKE 18	3.1	3.1	0.0	0.2	100.0%	-5.6
16864	AT1G78300.1   Symbol: GRF2   14-3-3 protein GF14 omega (GRF2), identical to GF14omega isoform GI:487791 from (Arabidopsis thaliana)   chr1:29466564-29468278 FORWARD   Aliases: F3F9.16, F3F9_16, GF14 OMEGA	7.3	7.6	-0.3	-0.2	100.0%	-4.4
16865	AT3G01150.1   Symbol: PTB   polypyrimidine tract-binding protein, putative / heterogeneous nuclear ribonucleoprotein, putative, similar to Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear ribonucleoprotein I) (hnRNP I) from {Sus scrofa} SP:Q29099, {Mus musculus} SP:P17225; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:51644-54513 FORWARD   Aliases: POLYPYRIMIDINE TRACT BINDING, T4P13.16, T4P13_16	4.7	4.8	-0.1	-0.2	100.0%	-4.7
16866	AT1G20730.1   expressed protein, contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.7	2.6	0.1	0.2	100.0%	-5.2
16867	AT1G07510.1   Symbol: FTSH10	8.7	8.8	-0.1	-0.2	100.0%	-5.0
16868	AT2G43870.1   polygalacturonase, putative / pectinase, putative, similar to SP:P48979 Polygalacturonase precursor (EC 3.2.1.15) (PG) (Pectinase) {Prunus persica}; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr2:18173692-18175341 REVERSE   Aliases: F18O19.2	2.6	2.6	0.0	0.2	100.0%	-5.4
16869	AT4G30040.1   aspartyl protease family, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr4:14685608-14686891 FORWARD   Aliases: F6G3.70, F6G3_70	2.6	2.7	-0.0	-0.2	100.0%	-5.5
16870	AT3G02940.1   Symbol: MYB107	1.9	1.9	-0.0	-0.2	100.0%	-6.3
16871	AT5G26060.1   S1 self-incompatibility protein-related, contains weak similarity to S1 self-incompatibility protein (GI:452430) (Papaver rhoeas)   chr5:9104854-9105527 REVERSE   Aliases: T1N24.103, T1N24_103	2.7	2.7	0.0	0.2	100.0%	-5.7
16872	AT1G62010.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr1:22919410-22920995 FORWARD   Aliases: F8K4.20, F8K4_20	3.8	3.8	-0.1	-0.2	100.0%	-4.8
16873	AT1G64470.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr1:23948448-23949435 REVERSE   Aliases: F1N19.30, F1N19_30	3.3	3.2	0.1	0.2	100.0%	-5.1
16874	AT1G65870.1   disease resistance-responsive family protein, similar to dirigent protein (Forsythia x intermedia) gi:6694693:gb:AAF25357; similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669   chr1:24507287-24507856 FORWARD   Aliases: F12P19.3, F12P19_3	2.8	2.7	0.1	0.2	100.0%	-5.1
16875	AT4G31470.1   pathogenesis-related protein, putative, similar to pathogenesis related protein-1 from Zea mays GI:3290004; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:15261752-15262309 REVERSE   Aliases: F3L17.40, F3L17_40	2.9	2.9	-0.0	-0.2	100.0%	-5.0
16876	AT3G16750.1   expressed protein, ; expression supported by MPSS   chr3:5701151-5702019 REVERSE   Aliases: MGL6.22	2.8	2.8	-0.1	-0.2	100.0%	-5.2
16877	AT4G29285.1   Symbol: LCR24   Encodes a member of a family of small,secreted, cysteine rich protein with sequence similarity to the PCP (pollen coat protein) gene family.   chr4:14431532-14432294 FORWARD   Aliases: LCR24, Low molecular weight cysteine rich 24	2.4	2.3	0.0	0.2	100.0%	-5.5
16878	AT5G52880.1   F-box family protein, ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr5:21449063-21450938 REVERSE   Aliases: MXC20.10, MXC20_10	6.0	5.9	0.1	0.2	100.0%	-4.6
16879	AT1G67270.1   expressed protein   chr1:25187032-25189456 REVERSE   Aliases: F1N21.9	3.8	3.9	-0.0	-0.2	100.0%	-5.7
16880	AT5G03010.1   kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (1 repeat)   chr5:704682-705437 FORWARD   Aliases: F15A17.40, F15A17_40	3.4	3.5	-0.1	-0.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16881	AT2G40860.1   protein kinase family protein / protein phosphatase 2C ( PP2C) family protein, contains Pfam PF00481: Protein phosphatase 2C domain; contains Pfam PF00069: Protein kinase domain; similar to partner of PIX 1 (GI:21702695) (Homo sapiens)   chr2:17060703-17064205 REVERSE   Aliases: T20B5.6, T20B5_6	2.7	2.7	0.0	0.2	100.0%	-5.5
16882	AT3G62800.2   double-stranded RNA-binding domain (DsRBD)-containing protein, weak similarity to SP:P19525 Interferon-induced, double-stranded RNA-activated protein kinase (EC 2.7.1.-) {Homo sapiens}; contains Pfam profile PF00035: Double-stranded RNA binding motif   chr3:23236567-23238487 REVERSE   Aliases: F26K9.230	6.4	6.5	-0.1	-0.2	100.0%	-5.1
16883	AT1G04870.2   protein arginine N-methyltransferase family protein, similar to SP:Q96LA8 Protein arginine N-methyltransferase 6 (EC 2.1.1.-) {Homo sapiens}   chr1:1373233-1375741 REVERSE   Aliases: F13M7.14, F13M7_14	8.8	8.9	-0.1	-0.2	100.0%	-4.6
16884	AT4G11780.1   expressed protein   chr4:7085964-7088206 FORWARD   Aliases: T5C23.210, T5C23_210	2.6	2.5	0.0	0.2	100.0%	-5.7
16885	AT5G65230.1   myb family transcription factor (MYB53), contains PFAM profile: myb DNA binding domain PF00249   chr5:26085516-26086878 FORWARD   Aliases: MQN23.17, MQN23_17	2.7	2.7	-0.0	-0.2	100.0%	-5.5
16886	AT5G42330.1   expressed protein   chr5:16943887-16944716 FORWARD   Aliases: MDH9.2, MDH9_2	7.1	7.3	-0.1	-0.2	100.0%	-4.1
16887	AT1G54110.1   cation exchanger, putative (CAX10), Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563   chr1:20203086-20205363 FORWARD   Aliases: F15I1.20	5.5	5.6	-0.1	-0.2	100.0%	-4.7
16888	AT3G05600.1   epoxide hydrolase, putative, similar to epoxide hydrolase from (Glycine max) GI:2764806, (Arabidopsis thaliana) GI:1109600; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr3:1623397-1624768 REVERSE   Aliases: F18C1.13, F18C1_13	2.7	2.6	0.0	0.2	100.0%	-5.3
16889	AT3G24840.1   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, similar to phosphatidylinositol transfer-like protein IV (GI:14486707) (Lotus japonicus); similar to SEC14 CYTOSOLIC FACTOR (PHOSPHATIDYLINOSITOL/ PHOSPHATIDYLCHOLINE TRANSFER PROTEIN) GB:P46250 from (Candida albicans) (Yeast (1996) 12(11), 1097-1105); contains Pfam PF00650 : CRAL/TRIO domain; contains Pfam PF03765 : CRAL/TRIO, N-terminus   chr3:9067269-9070633 FORWARD   Aliases: K7P8.31	3.3	3.3	-0.0	-0.2	100.0%	-5.6
16890	NA	2.7	2.6	0.0	0.2	100.0%	-5.4
16891	AT1G62260.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:23001491-23003461 REVERSE   Aliases: F19K23.18, F19K23_18	3.0	2.9	0.1	0.2	100.0%	-5.4
16892	AT4G19670.1   zinc finger (C3HC4-type RING finger) family protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature and Pfam domain PF01485: IBR domain   chr4:10699251-10701462 REVERSE   Aliases: T16H5.30, T16H5_30	6.0	6.1	-0.1	-0.2	100.0%	-4.5
16893	AT4G26120.1   ankyrin repeat family protein / BTB/POZ domain-containing protein, contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain   chr4:13236457-13238496 FORWARD   Aliases: F20B18.230, F20B18_230	2.4	2.3	0.0	0.2	100.0%	-5.6
16894	AT2G39210.1   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr2:16373235-16375353 REVERSE   Aliases: T16B24.15, T16B24_15	5.2	5.0	0.1	0.2	100.0%	-4.6
16895	AT2G14580.1   Symbol: ATPRB1	3.3	3.4	-0.0	-0.2	100.0%	-5.6
16896	AT1G34040.1   alliinase family protein, contains Pfam profiles: PF04864 alliinase C-terminal domain, PF04863 alliinase EGF-like domain   chr1:12374413-12376159 FORWARD   Aliases: F12G12.14, F12G12_14	2.6	2.5	0.1	0.2	100.0%	-4.3
16897	AT1G34060.1   alliinase family protein, contains Pfam profiles: PF04864 alliinase C-terminal domain, PF04863 alliinase EGF-like domain   chr1:12396399-12398348 REVERSE   Aliases: F12G12.12, F12G12_12	2.6	2.5	0.1	0.2	100.0%	-4.3
16898	AT2G42010.1   Symbol: PLDBETA1   phospholipase D beta 1 / PLD beta 1 (PLDBETA1), identical to SP:P93733 Phospholipase D beta 1 (EC 3.1.4.4) (AtPLDbeta1) (PLD beta 1) (PLDbeta) {Arabidopsis thaliana}; contains Pfam profiles: PF00614 phospholipase D.active site motif, PF00168 C2 domain   chr2:17539891-17545476 REVERSE   Aliases: PHOSPHOLIPASE D, PHOSPHOLIPASE D BETA 1, PLDBETA, T6D20.10, T6D20_10	5.2	5.1	0.0	0.2	100.0%	-5.1
16899	AT5G28070.1   hypothetical protein   chr5:10083174-10083523 FORWARD   Aliases: T24G3.1	2.5	2.5	0.0	0.2	100.0%	-5.9
16900	AT4G26490.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g56050.1); similar to P0456E05.10 [Oryza sativa (japonica cultivar-group)] (GB:XP_463593.1)   chr4:13380580-13381446 FORWARD   Aliases: M3E9.80, M3E9_80	4.5	4.6	-0.1	-0.2	100.0%	-4.5



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16901	AT5G67040.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr5:26775122-26775701 REVERSE   Aliases: K8A10.11, K8A10_11	3.1	3.1	0.0	0.2	100.0%	-5.5
16902	AT2G29450.1   Symbol: ATGSTU5   glutathione S-transferase (103-1A), identical to Swiss-Prot:P46421 glutathione S-transferase 103-1A (Arabidopsis thaliana)   chr2:12631663-12632711 REVERSE   Aliases: AT103_1A, ATGSTU1, F16P2.17, F16P2_17, GLUTATHIONE S TRANSFERASE	6.0	6.1	-0.1	-0.2	100.0%	-4.6
16903	AT1G56710.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase PG1 GI:5669846, PG2 GI:5669848 from (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:21261673-21263598 REVERSE   Aliases: F25P12.85, F25P12_85	2.7	2.7	-0.0	-0.2	100.0%	-5.9
16904	AT2G35120.1   glycine cleavage system H protein, mitochondrial, putative, similar to SP:Q39732 Glycine cleavage system H protein, mitochondrial precursor {Flaveria anomala}; contains Pfam profile PF01597: Glycine cleavage H-protein   chr2:14812718-14814415 REVERSE   Aliases: T4C15.21, T4C15_21	9.5	9.7	-0.2	-0.2	100.0%	-4.6
16905	AT4G23570.3   Symbol: SGT1A   similar to phosphatase-related [Arabidopsis thaliana] (TAIR:At4g11260.1); similar to SGT1-like protein [Brassica oleracea] (GB:CAF06581.1); contains InterPro domain SGS (InterPro:IPR007699); contains InterPro domain TPR repeat (InterPro:IPR001440); contains InterPro domain CS domain (InterPro:IPR007052)   chr4:12299973-12302729 FORWARD   Aliases: F9D16.40, F9D16_40, SGT1B	5.5	5.5	0.1	0.2	100.0%	-4.8
16906	AT4G23930.2   expressed protein, hin1 protein homolog, Oryza sativa, PIR:T02662   chr4:12435956-12436722 REVERSE   Aliases: T32A16.100, T32A16_100	4.0	4.1	-0.1	-0.2	100.0%	-4.8
16907	AT3G52460.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:19457948-19458850 FORWARD   Aliases: F22O6.160	5.1	5.1	0.1	0.2	100.0%	-5.1
16908	AT1G75850.1   similar to vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein [Arabidopsis thaliana] (TAIR:At3g51310.1); similar to vacuolar protein sorting-associated protein 35 family protein / VPS35 family protein [Arabidopsis thaliana] (TAIR:At2g17790.1); similar to novel protein similar to human and mouse vacuolar protein sorting 35 (yeast) (VPS35) [Danio rerio] (GB:CAE49237.1); contains InterPro domain Vacuolar protein sorting-associated protein 35 (InterPro:IPR005378)	4.8	4.7	0.1	0.2	100.0%	-4.7
16909	AT5G42060.1   expressed protein   chr5:16835616-16836183 REVERSE   Aliases: MJC20.17, MJC20_17	6.3	6.3	0.1	0.2	100.0%	-4.6
16910	AT2G18200.1   expressed protein   chr2:7931349-7931741 REVERSE   Aliases: F8D23.12	2.6	2.7	-0.0	-0.2	100.0%	-5.5
16911	AT2G48090.1   expressed protein, weak similarity to protein kinase   chr2:19676180-19676834 REVERSE   Aliases: T9J23.24	2.7	2.7	0.0	0.2	100.0%	-5.3
16912	AT5G11700.1   glycine-rich protein, predicted protein, Arabidopsis thaliana   chr5:3762467-3771124 REVERSE   Aliases: T22P22.90, T22P22_90	3.6	3.6	-0.1	-0.2	100.0%	-4.9
16913	AT4G02420.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr4:1064363-1066372 REVERSE   Aliases: T14P8.4, T14P8_4	5.1	5.1	0.1	0.2	100.0%	-4.8
16914	AT3G18980.1   F-box family protein, contains Pfam:PF00646 F-box domain ; contains TIGRFAM TIGR01640: F-box protein interaction domain ; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:6546469-6548068 FORWARD   Aliases: K13E13.9	4.9	5.0	-0.1	-0.2	100.0%	-4.7
16915	AT2G40170.1   Symbol: ATEM6   Em-like protein GEA6 (EM6), identical to SP:Q02973 Em-like protein GEA6 {Arabidopsis thaliana}; contains Pfam profile PF00477: Small hydrophilic plant seed protein   chr2:16786704-16787326 REVERSE   Aliases: ARABIDOPSIS EARLY METHIONINE LABELLED 6, ATEM6, GEA6, T7M7.23	3.6	3.5	0.1	0.2	100.0%	-5.2
16916	AT5G63370.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:25401132-25404450 REVERSE   Aliases: K9H21.10, K9H21_10	5.7	5.7	-0.1	-0.2	100.0%	-4.8
16917	AT2G43350.1   Symbol: ATGPX3	6.5	6.4	0.1	0.2	100.0%	-5.1
16918	AT1G68440.1   expressed protein   chr1:25661696-25662936 FORWARD   Aliases: T2E12.1, T2E12_1	4.4	4.3	0.1	0.2	100.0%	-4.5
16919	AT1G56030.1   MIF4G domain-containing protein / U-box domain-containing protein, low similarity to intermediate filament filarin (Hirudo medicinalis) GI:4761082; contains Pfam profiles PF02854: MIF4G domain, PF04564: U-box domain   chr1:20960763-20962215 REVERSE   Aliases: T6H22.25, T6H22_25	2.6	2.6	-0.0	-0.2	100.0%	-5.7
16920	AT1G49890.1   expressed protein, contains Pfam domain, PF04484: Family of unknown function (DUF566)   chr1:18473743-18477491 FORWARD   Aliases: F10F5.10, F10F5_10	3.3	3.4	-0.0	-0.2	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16921	AT3G53760.1   tubulin family protein, similar to SP:Q9SC88 Gamma-tubulin complex component 4 homolog {Medicago truncatula}, SP:Q9UGJ1:GCP4_HUMAN Gamma-tubulin complex component 4 {Homo sapiens}; contains Pfam profile PF04130: Spc97 / Spc98 family	3.3	3.3	-0.1	-0.2	100.0%	-5.1
16922	AT3G27070.1   Symbol: TOM20 1   mitochondrial import receptor subunit TOM20-1 / translocase of outer membrane 20 kDa subunit 1 (TOM20-1), identical to mitochondrial import receptor subunit TOM20-1 SP:P82872 from (Arabidopsis thaliana)   chr3:9984241-9985981 REVERSE   Aliases: MOJ10.21, TRANSLOCASE OUTER MEMBRANE 20 1	5.0	4.9	0.1	0.2	100.0%	-4.9
16923	AT1G17330.1   metal-dependent phosphohydrolase HD domain-containing protein-related   chr1:5929959-5931588 FORWARD   Aliases: T13M22.1	2.5	2.5	0.0	0.2	100.0%	-5.6
16924	AT5G58930.1   expressed protein, contains Pfam PF05340: Protein of unknown function (DUF740)   chr5:23811541-23813687 REVERSE   Aliases: K19M22.12, K19M22_12	9.8	9.9	-0.0	-0.2	100.0%	-5.2
16925	AT1G01740.1   protein kinase family protein, low similarity to protein kinase (Arabidopsis thaliana) GI:2852449; contains Pfam profile: PF00069 Protein kinase domain   chr1:272111-274239 REVERSE   Aliases: T1N6.15, T1N6_15	4.1	4.2	-0.1	-0.2	100.0%	-5.1
16926	AT1G71680.1   lysine and histidine specific transporter, putative, similar to lysine and histidine specific transporter GB: AAC49885 GI:2576361 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:26948536-26950258 FORWARD   Aliases: F14O23.2, F14O23_2	3.4	3.3	0.1	0.2	100.0%	-5.0
16927	AT1G02060.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:360918-363094 REVERSE   Aliases: T7I23.14, T7I23_14	2.9	3.0	-0.0	-0.2	100.0%	-5.6
16928	AT3G05910.1   pectinacetyltransferase, putative, similar to pectinacetyltransferase precursor GI:1431629 from (Vigna radiata)   chr3:1764301-1767581 REVERSE   Aliases: F2O10.13	8.1	8.2	-0.1	-0.2	100.0%	-4.8
16929	AT3G07630.2   prephenate dehydratase family protein, similar to P-protein: chorismate mutase, prephenate dehydratase GB:P43900 (Haemophilus influenzae)   chr3:2435456-2437971 FORWARD   Aliases: MLP3.8	6.3	6.2	0.1	0.2	100.0%	-4.7
16930	AT3G02000.1   Symbol: ROXY1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)   chr3:332282-332992 REVERSE   Aliases: F1C9.22	4.4	4.5	-0.1	-0.2	100.0%	-4.9
16931	AT2G34910.1   expressed protein   chr2:14733979-14735126 FORWARD   Aliases: F19I3.14, F19I3_14	3.3	3.4	-0.1	-0.2	100.0%	-4.1
16932	AT5G01560.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr5:218137-220529 REVERSE   Aliases: F7A7.80, F7A7_80	2.1	2.1	0.0	0.2	100.0%	-5.3
16933	AT5G54790.1   expressed protein   chr5:22272356-22272715 REVERSE   Aliases: MBG8.5, MBG8_5	2.7	2.8	-0.0	-0.2	100.0%	-5.2
16934	AT2G29320.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12599225-12600763 FORWARD   Aliases: F16P2.30, F16P2_30	3.5	3.6	-0.1	-0.2	100.0%	-4.7
16935	AT4G11180.1   disease resistance-responsive family protein / dirigent family protein, similar to dirigent protein (Thuja plicata) gi:6694699:gb:AAF25360; similar to pathogenesis-related protein (Pisum sativum) gi:4585273:gb:AAD25355   chr4:6820029-6820743 FORWARD   Aliases: T22B4.160, T22B4_160	2.8	2.8	0.0	0.2	100.0%	-5.3
16936	AT1G62380.1   Symbol: ACO2   1-aminocyclopropane-1-carboxylate oxidase, putative / ACC oxidase, putative, nearly identical to ACC oxidase (ACC ox1) GI:587086 from (Brassica oleracea)   chr1:23085927-23087918 FORWARD   Aliases: ACC OXIDASE, ACC OXIDASE 2, ATACO2, F24O1.40, F24O1_40	8.8	8.7	0.1	0.2	100.0%	-4.8
16937	AT1G51880.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19273862-19277737 REVERSE   Aliases: T14L22.9, T14L22_9	3.0	3.1	-0.1	-0.2	100.0%	-4.5
16938	AT1G78320.1   Symbol: ATGSTU23   glutathione S-transferase, putative, similar to glutathione transferase GI:2853219 from (Carica papaya)   chr1:29472333-29473267 REVERSE   Aliases: F3F9.14, F3F9_14	3.4	3.3	0.1	0.2	100.0%	-4.7
16939	AT4G04840.1   methionine sulfoxide reductase domain-containing protein / SelR domain-containing protein, low similarity to pilin-like transcription factor (Homo sapiens) GI:5059062; contains Pfam profile PF01641: SelR domain   chr4:2449558-2451587 FORWARD   Aliases: T4B21.4, T4B21_4	3.5	3.5	0.1	0.2	100.0%	-4.9
16940	AT2G46710.1   rac GTPase activating protein, putative, similar to rac GTPase activating protein 2 (Lotus japonicus) GI:3695061; contains Pfam profiles PF00620: RhoGAP domain, PF00786: P21-Rho-binding domain	5.6	5.7	-0.1	-0.2	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16941	AT5G37300.1   expressed protein   chr5:14784729-14787479 FORWARD   Aliases: MNJ8.9, MNJ8_9	3.3	3.2	0.0	0.2	100.0%	-5.8
16942	AT5G24360.1   protein kinase family protein / Ire1 homolog-1 (IRE1-1), identical to Ire1 homolog-1 (Arabidopsis thaliana) GI:15277137; cDNA Ire1 homolog-1 GI:15277136;   chr5:8316446-8319980 FORWARD   Aliases: K16H17.7, K16H17_7	6.7	6.7	0.0	0.2	100.0%	-5.1
16943	AT5G52970.1   thylakoid lumen 15.0 kDa protein, SP:Q9LVV5; similar to unknown protein (pir :S77462)   chr5:21496835-21498452 FORWARD   Aliases: MNB8.3, MNB8_3	8.0	7.9	0.1	0.2	100.0%	-4.3
16944	AT5G15880.1   expressed protein   chr5:5185791-5188050 FORWARD   Aliases: F1N13.20, F1N13_20	6.9	6.9	-0.1	-0.2	100.0%	-5.1
16945	AT2G23640.1   reticulon family protein (RTNLB13), weak similarity to Nogo-C protein (Rattus norvegicus) GI:6822251; contains Pfam profile PF02453: Reticulon   chr2:10064634-10066188 FORWARD   Aliases: F26B6.29	3.6	3.5	0.1	0.2	100.0%	-4.9
16946	AT5G07300.1   Symbol: BON2   copine, putative, strong similarity to BONZAI1 (Arabidopsis thaliana) GI:15487382; contains Pfam profile PF00168: C2 domain   chr5:2299962-2303269 FORWARD   Aliases: BONZAI 2, T2I1.10, T2I1_10	4.8	4.9	-0.1	-0.2	100.0%	-5.0
16947	AT1G77240.1   AMP-binding protein, putative, strong similarity to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501   chr1:29022852-29024683 REVERSE   Aliases: T14N5.10, T14N5_10	3.0	3.0	0.0	0.2	100.0%	-5.4
16948	AT1G16740.1   ribosomal protein L20 family protein, similar to ribosomal protein L20 GI:3603025 from (Guillardia theta)   chr1:5727683-5729072 FORWARD   Aliases: F19K19.15	11.0	11.1	-0.1	-0.2	100.0%	-5.1
16949	AT2G26490.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); related to En/Spm transposon family of maize   chr2:11275020-11276701 FORWARD   Aliases: T9J22.16, T9J22_16	2.7	2.7	-0.0	-0.2	100.0%	-5.4
16950	AT4G04920.1   expressed protein   chr4:2497929-2504798 FORWARD   Aliases: T1J1.2, T1J1_2	3.9	4.0	-0.0	-0.2	100.0%	-5.3
16951	AT5G25350.1   Symbol: EBF2   F-box family protein, contains Pfam PF00646: F-box domain and Pfam PF00560: Leucine Rich Repeat (6 copies); similar to F-box protein FBL6 (GI:4432860) (Homo sapiens)   chr5:8794845-8797015 REVERSE   Aliases: EIN3 BINDING F BOX PROTEIN 2, F18G18.90, F18G18_90	3.1	3.2	-0.1	-0.2	100.0%	-4.4
16952	AT3G56810.1   expressed protein   chr3:21047739-21049926 REVERSE   Aliases: T8M16.140	3.7	3.8	-0.1	-0.2	100.0%	-5.0
16953	AT4G31820.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr4:15390656-15394436 REVERSE   Aliases: F11C18.20, F11C18_20	6.6	6.5	0.1	0.2	100.0%	-4.4
16954	AT4G36250.1   Symbol: ALDH3F1   aldehyde dehydrogenase family protein, contains aldehyde dehydrogenase (NADP) family protein domain, Pfam:PF00171   chr4:17150941-17153581 FORWARD   Aliases: F23E13.140, F23E13_140	2.5	2.5	-0.0	-0.2	100.0%	-5.5
16955	AT1G79820.3   similar to hexose transporter, putative [Arabidopsis thaliana] (TAIR:At1g67300.1); similar to putative sugar transporter [Oryza sativa (japonica cultivar-group)] (GB:XP_464929.1); contains InterPro domain Sugar transporter superfamily (InterPro:IPR005829); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sugar transporter (InterPro:IPR003663)	7.2	7.1	0.1	0.2	100.0%	-4.9
16956	AT5G48420.1   expressed protein   chr5:19643588-19644016 REVERSE   Aliases: MJE7.5, MJE7_5	3.1	3.1	0.0	0.2	100.0%	-5.5
16957	AT3G48640.1   expressed protein   chr3:18032635-18033309 REVERSE   Aliases: T8P19.150	3.0	3.0	-0.0	-0.2	100.0%	-5.5
16958	AT5G59860.1   RNA recognition motif (RRM)-containing protein, similar to SP:Q14011 Cold-inducible RNA-binding protein (Glycine-rich RNA-binding protein CIRP) {Homo sapiens}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:24130688-24131675 FORWARD   Aliases: MMN10.9, MMN10_9	2.7	2.7	0.0	0.2	100.0%	-5.2
16959	AT1G71190.1   Symbol: SAG18   expressed protein   chr1:26837072-26838689 REVERSE   Aliases: F23N20.18, F23N20_18, TTN4	6.7	6.6	0.1	0.2	100.0%	-4.9
16960	AT1G54360.4   similar to TATA box-binding protein-associated factor (TAF) family protein [Arabidopsis thaliana] (TAIR:At1g04950.1); similar to TATA box-binding protein-associated factor (TAF) family protein [Arabidopsis thaliana] (TAIR:At1g04950.2); similar to SPCC16C4.18c [Schizosaccharomyces pombe] (GB:CAA20756.1); contains InterPro domain Histone-fold/TFIID-TAF/NF-Y (InterPro:IPR007124); contains InterPro domain TATA box binding protein associated factor (TAF) (InterPro:IPR004823)   chr1:20294267-20296991 FORWARD   Aliases: F20D21.18, F20D21_18	9.2	9.3	-0.0	-0.2	100.0%	-5.2
16961	AT1G04790.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:1345035-1348436 FORWARD   Aliases: F13M7.22, F13M7_22	4.3	4.3	0.0	0.2	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16962	AT3G16320.1   similar to cell division cycle family protein / CDC family protein [Arabidopsis thaliana] (TAIR:At2g20000.1); similar to PREDICTED: similar to Cell division cycle protein 27 homolog (CDC27Hs) (H-NUC) [Rattus norvegicus] (GB:XP_340922.2); contains InterPro domain TPR repeat (InterPro:IPR001440)   chr3:5529368-5534471 FORWARD   Aliases: MYA6.15	3.0	2.9	0.0	0.2	100.0%	-5.4
16963	AT2G43070.1   protease-associated (PA) domain-containing protein, contains protease associated (PA) domain, Pfam:PF02225   chr2:17918015-17921928 REVERSE   Aliases: None	5.2	5.0	0.2	0.2	100.0%	-4.6
16964	AT1G13310.1   expressed protein   chr1:4561067-4562295 REVERSE   Aliases: T6J4.7, T6J4_7	2.6	2.6	-0.0	-0.2	100.0%	-5.4
16965	AT3G22670.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:8017778-8019466 REVERSE   Aliases: MWI23.4	5.2	5.3	-0.1	-0.2	100.0%	-4.7
16966	AT1G01430.1   expressed protein, similar to hypothetical protein GB:CAB80917 GI:7267605 from (Arabidopsis thaliana)   chr1:156801-158655 REVERSE   Aliases: F6F3.23, F6F3_23	4.2	4.3	-0.0	-0.2	100.0%	-5.0
16967	AT4G14570.1   acylaminoacyl-peptidase-related, similar to Acylamino-acid-releasing enzyme (EC 3.4.19.1) (Acyl-peptide hydrolase) (APH) (Acylaminoacyl-peptidase) (Swiss-Prot:P13676) (Rattus norvegicus); annotated with nonconsensus TT and CT acceptor splice sites.	3.1	3.2	-0.0	-0.2	100.0%	-5.1
16968	AT1G65090.1   similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At5g36100.1); similar to glutamic acid-rich protein cNBL1700 [Trichinella spiralis] (GB:AAM19760.1)	3.6	3.5	0.0	0.2	100.0%	-5.1
16969	AT1G49880.1   Erv1/Alr family protein, similar to SP:Q63042 Augmenter of liver regeneration {Rattus norvegicus}; contains Pfam profile PF04777: Erv1 / Alr family   chr1:18467685-18469745 FORWARD   Aliases: F10F5.3, F10F5_3	3.3	3.3	0.0	0.2	100.0%	-5.5
16970	AT5G58630.1   expressed protein   chr5:23712906-23714678 REVERSE   Aliases: MZN1.24, MZN1_24	2.9	2.9	0.0	0.2	100.0%	-5.4
16971	AT5G24520.3   Symbol: TTG1   transparent testa glabra 1 protein (TTG1), identical to transparent testa glabra 1 (Ttg1) protein (GI:10177852) {Arabidopsis thaliana}; contains Pfam PF00400: WD domain, G-beta repeat (4 copies,1 weak);   chr5:8370709-8372850 REVERSE   Aliases: K18P6.4, K18P6_4, TRANSPARENT TESTA GLABRA 1, TTG	4.2	4.1	0.1	0.2	100.0%	-4.7
16972	AT1G78040.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr1:29350732-29352001 FORWARD   Aliases: F28K19.26, F28K19_26	11.5	11.5	-0.1	-0.2	100.0%	-5.2
16973	AT1G66110.1   expressed protein, contains Pfam profile PF04510: Family of unknown function (DUF577)   chr1:24612757-24613895 REVERSE   Aliases: F15E12.15, F15E12_15	3.7	3.7	0.1	0.2	100.0%	-5.1
16974	AT3G42850.1   galactokinase, putative, contains some similarity to galactokinase (Pasteurella multocida) SWISS-PROT:P57899   chr3:14951102-14956279 REVERSE   Aliases: F18P9.10	4.0	3.9	0.0	0.2	100.0%	-5.3
16975	AT5G53400.1   nuclear movement family protein, contains Pfam profile: PF03593 nuclear movement protein	10.0	9.9	0.1	0.2	100.0%	-4.6
16976	AT1G56170.1   Symbol: HAP5B   transcription factor, putative, similar to Transcription factor GB:CAA74053 GI:2398533 from (Arabidopsis thaliana) similarity to transcription factor Hap5a similar to transcription factor Hap5a (Arabidopsis thaliana)(GI:6523090)   chr1:21028429-21029548 FORWARD   Aliases: ATHAP5B, F14G9.21	6.5	6.6	-0.2	-0.2	100.0%	-4.3
16977	AT3G61850.2   Symbol: DAG1   Dof zinc finger protein DAG1 / Dof affecting germination 1 (DAG1) / transcription factor BBFa (BBFA), identical to SP:Q43385 DOF zinc finger protein DAG1 (Dof affecting germination 1) (Transcription factor BBFa) (AtBBFa) (rolB domain B factor a) {Arabidopsis thaliana}   chr3:22906494-22908533 FORWARD   Aliases: BBFA, DOF AFFECTING GERMINATION 1, F21F14.20	3.0	3.0	0.0	0.2	100.0%	-5.4
16978	AT1G64310.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:23869716-23871374 FORWARD   Aliases: F15H21.19, F15H21_19	3.1	3.2	-0.0	-0.2	100.0%	-5.5
16979	AT3G27410.1   expressed protein   chr3:10146481-10146879 REVERSE   Aliases: K1G2.12	2.2	2.2	0.0	0.2	100.0%	-5.6
16980	AT4G26590.1   Symbol: ATOPT5	4.5	4.5	0.1	0.2	100.0%	-5.1
16981	AT4G39210.1   Symbol: APL3   glucose-1-phosphate adenylyltransferase large subunit 3 (APL3) / ADP-glucose pyrophosphorylase, identical to SP:P55231   chr4:18259603-18263411 FORWARD   Aliases: T22F8.110, T22F8_110	6.2	6.3	-0.1	-0.2	100.0%	-4.2
16982	AT4G17480.1   palmitoyl protein thioesterase family protein   chr4:9745018-9746978 REVERSE   Aliases: DL4775C, FCAALL.380	3.6	3.7	-0.1	-0.2	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
16983	AT1G12140.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase ( <i>Cavia porcellus</i> ) GI:191259; contains Pfam profile PF00743: Flavin-binding monooxygenase-like   chr1:4121367-4123540 FORWARD   Aliases: T28K15.12, T28K15_12	7.3	7.5	-0.1	-0.2	100.0%	-5.0
16984	AT5G01480.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.1	0.1	0.2	100.0%	-5.0
16985	AT3G22120.1   Symbol: CWLP   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to SP:Q00451:PRF1_LYCES 36.4 kDa proline-rich protein <i>Lycopersicon esculentum</i> , proline-rich cell wall protein ( <i>Medicago sativa</i> ) GI:3818416; contains Pfam profile PF00234 Protease inhibitor/seed storage/LTP family   chr3:7794964-7796317 REVERSE   Aliases: CELL WALL PLASMA MEMBRANE LINKER PROTEIN, MKA23.6	2.6	2.5	0.1	0.2	100.0%	-4.9
16986	AT1G05575.1   expressed protein   chr1:1661690-1662186 REVERSE   Aliases: None	2.5	2.3	0.1	0.2	100.0%	-4.8
16987	AT1G75300.1   isoflavone reductase, putative, identical to SP:P52577 Isoflavone reductase homolog P3 (EC 1.3.1.-) { <i>Arabidopsis thaliana</i> }; contains Pfam profile PF02716: Isoflavone reductase   chr1:28259156-28260701 FORWARD   Aliases: F22H5.16, F22H5_16	3.3	3.4	-0.0	-0.2	100.0%	-5.2
16988	AT1G20680.1   expressed protein, contains Pfam profile PF05742: Protein of unknown function (DUF833)   chr1:7168301-7173330 FORWARD   Aliases: F2D10.17, F2D10_17	2.9	2.8	0.0	0.2	100.0%	-5.3
16989	AT1G64480.1   Symbol: CBL8   calcineurin B-like protein 8 (CBL8), identical to calcineurin B-like protein 8 (GI:15866276) ( <i>Arabidopsis thaliana</i> ); similar to CALCINEURIN B SUBUNIT GB:P25296 from ( <i>Saccharomyces cerevisiae</i> )   chr1:23951691-23953414 REVERSE   Aliases: CALCINEURIN B LIKE PROTEIN 5, CBL8, F1N19.5, F1N19_5	2.4	2.5	-0.1	-0.2	100.0%	-4.3
16990	AT2G43270.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.7	3.8	-0.1	-0.2	100.0%	-5.2
16991	AT1G15820.1   Symbol: LHCB6   chlorophyll A-B binding protein, chloroplast (LHCB6), nearly identical to Lhcb6 protein ( <i>Arabidopsis thaliana</i> ) GI:4741960; contains Pfam profile PF00504: Chlorophyll A-B binding protein   chr1:5446123-5447776 REVERSE   Aliases: CP24, F7H2.16, F7H2_16, LHCB6	9.8	9.7	0.1	0.2	100.0%	-4.4
16992	AT4G05470.1   F-box family protein (FBL21), contains similarity to N7 protein GI:3273101 from ( <i>Medicago truncatula</i> )   chr4:2763253-2767954 REVERSE   Aliases: None	2.5	2.5	0.0	0.2	100.0%	-5.8
16993	AT1G51805.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase ( <i>Arabidopsis thaliana</i> ) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19224646-19229358 REVERSE   Aliases: F19C24.2, F19C24_2	2.6	2.6	-0.0	-0.2	100.0%	-5.9
16994	AT2G20760.1   expressed protein   chr2:8949844-8952304 REVERSE   Aliases: F5H14.27, F5H14_27	7.1	7.2	-0.1	-0.2	100.0%	-4.6
16995	AT2G30420.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:12968014-12968992 REVERSE   Aliases: T9D9.23, T9D9_23	2.7	2.8	-0.1	-0.2	100.0%	-5.0
16996	AT1G20693.2   Symbol: HMGB2   similar to high mobility group protein beta2 (HMGBeta2) / HMG protein beta2 [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g20696.1); similar to high mobility group protein [ <i>Solanum tuberosum</i> ] (GB:CAA05365.1); contains InterPro domain HMG1/2 (high mobility group) box (InterPro:IPR000910); contains InterPro domain High mobility group proteins HMG1 and HMG2 (InterPro:IPR000135)   chr1:7176765-7178810 FORWARD   Aliases: HIGH MOBILITY GROUP B 2, HMG BETA 1, NFD02, NFD2	6.7	6.9	-0.2	-0.2	100.0%	-4.7
16997	AT1G35614.1   expressed protein   chr1:13148570-13149537 FORWARD   Aliases: F15O4.23	3.2	3.2	-0.0	-0.2	100.0%	-5.7
16998	AT5G06400.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:1955960-1959052 FORWARD   Aliases: MHF15.8, MHF15_8	3.0	3.1	-0.0	-0.2	100.0%	-5.5
16999	AT3G54120.1   reticulon family protein (RTNLB12), contains Pfam profile PF02453: Reticulon   chr3:20051974-20053318 REVERSE   Aliases: F24B22.80	6.8	6.7	0.1	0.2	100.0%	-4.4
17000	AT2G38050.1   Symbol: DET2   3-oxo-5-alpha-steroid 4-dehydrogenase, putative / steroid 5-alpha-reductase, putative, identical to gi:1280611; contains a steroid 5-alpha reductase, C-terminal domain   chr2:15928019-15929391 REVERSE   Aliases: DE ETIOLATED 2, DWARF 6, DWF6, STEROID REDUCTASE DET2, T8P21.4, T8P21_4	7.8	7.9	-0.1	-0.2	100.0%	-5.3
17001	AT1G51360.1   expressed protein   chr1:19047852-19048568 FORWARD   Aliases: F11M15.22, F11M15_22	3.2	3.2	0.0	0.2	100.0%	-5.3
17002	AT5G47810.1   phosphofructokinase family protein, similar to phosphofructokinase ( <i>Amycolatopsis methanolica</i> ) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase   chr5:19373582-19375351 REVERSE   Aliases: MCA23.13, MCA23_13	9.8	9.7	0.1	0.2	100.0%	-4.8
17003	AT2G43950.3   expressed protein   chr2:18207400-18209746 REVERSE   Aliases: F6E13.8	4.9	5.0	-0.1	-0.2	100.0%	-5.3
17004	AT3G04790.1   ribose 5-phosphate isomerase-related, similar to ribose-5-phosphate isomerase GI:18654317 from ( <i>Spinacia oleracea</i> )   chr3:1313324-1314369 FORWARD   Aliases: F7O18.28, F7O18_28	9.3	9.4	-0.1	-0.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17005	AT4G34320.1   expressed protein, similar to At14a, GI:11994571 and GI:11994573 (Arabidopsis thaliana)   chr4:16422170-16423949 FORWARD   Aliases: F10M10.90, F10M10_90	3.0	3.0	0.0	0.2	100.0%	-5.3
17006	AT1G23300.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:8263816-8266037 REVERSE   Aliases: F26F24.14, F26F24_14	3.7	3.6	0.1	0.2	100.0%	-4.9
17007	AT3G11470.3   similar to COP1-interacting protein-related [Arabidopsis thaliana] (TAIR:At2g02770.1); similar to MtaA [Stigmatella aurantiaca] (GB:AAF19809.1); contains InterPro domain 4'-phosphopantetheinyl transferase (InterPro:IPR008278)   chr3:3610153-3612376 REVERSE   Aliases: F24K9.14	3.3	3.3	0.1	0.2	100.0%	-5.0
17008	AT2G15680.1   calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced SP:P25070 from (Arabidopsis thaliana)   chr2:6838106-6838669 FORWARD   Aliases: F9O13.23	4.3	4.3	0.1	0.2	100.0%	-4.9
17009	AT5G08160.2   Symbol: ATPK3   serine/threonine protein kinase, putative, identical to serine/threonine protein kinase (Arabidopsis thaliana) gi:2109293:gb:AAB69123   chr5:2625560-2628111 REVERSE   Aliases: None	6.8	6.6	0.1	0.2	100.0%	-5.1
17010	AT5G24940.1   protein phosphatase 2C, putative / PP2C, putative, protein phosphatase type 2C - Lotus japonicus, EMBL:AF092432   chr5:8591410-8593604 REVERSE   Aliases: F6A4.150, F6A4_150	2.5	2.5	0.0	0.2	100.0%	-5.7
17011	AT4G33380.1   expressed protein   chr4:16071895-16074876 FORWARD   Aliases: F17M5.140, F17M5_140	7.9	7.8	0.1	0.2	100.0%	-4.9
17012	AT3G42460.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr3:14601277-14602206 REVERSE   Aliases: T32A11.30	2.7	2.7	-0.0	-0.2	100.0%	-5.6
17013	AT1G18190.1   expressed protein, similar to golgin-84 {Homo sapiens} (GI:4191344)   chr1:6257844-6261443 REVERSE   Aliases: T10F20.19	4.8	4.8	-0.1	-0.2	100.0%	-4.6
17014	AT4G18350.1   Symbol: NCED2   9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, neoxanthin cleavage enzyme, Lycopersicon esculentum, PATCHX:E325797; and viviparous-14, Zea mays, PATCHX:G2232017; similar to 9-cis-epoxycarotenoid dioxygenase (Phaseolus vulgaris)(GI:6715257)   chr4:10142683-10144434 FORWARD   Aliases: ATNCED2, F28J12.10, F28J12_10	3.6	3.6	-0.0	-0.2	100.0%	-5.3
17015	AT1G09960.1   Symbol: SUT4   sucrose transporter / sucrose-proton symporter (SUT4), nearly identical to sucrose transporter SUT4 (Arabidopsis thaliana) GI:9957053   chr1:3244215-3247202 FORWARD   Aliases: ATSUT4, F21M12.35, F21M12_35, SUCROSE TRANSPORTER 4, SUT4	3.8	3.7	0.1	0.2	100.0%	-4.9
17016	AT4G20360.1   elongation factor Tu / EF-Tu (TUFA), identical to SWISS-PROT:P17745 elongation factor Tu, chloroplast precursor (EF-Tu) (Arabidopsis thaliana)   chr4:10989963-10991720 FORWARD   Aliases: F9F13.10, F9F13_10	10.1	10.2	-0.1	-0.2	100.0%	-4.7
17017	AT2G32780.1   ubiquitin-specific protease 1, putative (UBP1), similar to GI:11993461   chr2:13905508-13908947 REVERSE   Aliases: F24L7.8, F24L7_8	2.4	2.3	0.0	0.2	100.0%	-5.8
17018	AT4G18950.1   ankyrin protein kinase, putative, similar to ankyrin-kinase (Medicago truncatula) gi:18700701:gb:AAL78674   chr4:10375375-10378400 FORWARD   Aliases: F13C5.120, F13C5_120	3.6	3.5	0.1	0.2	100.0%	-4.9
17019	AT2G46940.1   expressed protein   chr2:19293846-19294650 REVERSE   Aliases: F14M4.23	3.4	3.3	0.1	0.2	100.0%	-4.6
17020	AT3G54220.1   Symbol: SCR   scarecrow transcription factor, putative, nearly identical to SCARECROW (Arabidopsis thaliana) GI:1497987	3.3	3.4	-0.1	-0.2	100.0%	-4.5
17021	AT3G51370.2   protein phosphatase 2C, putative / PP2C, putative, similar to Ser/Thr protein phosphatase 2C (PP2C6) (GI:15020818) (Arabidopsis thaliana); similar to protein phosphatase 2C (GI:3608412) (Mesembryanthemum crystallinum); contains Pfam PF00481 : Protein phosphatase 2C domain	8.4	8.5	-0.1	-0.2	100.0%	-4.8
17022	AT1G21920.1   MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profile PF02493: MORN repeat   chr1:7704244-7706129 REVERSE   Aliases: T26F17.15, T26F17_15	8.5	8.4	0.1	0.2	100.0%	-4.9
17023	AT5G45960.1   GDSL-motif lipase/hydrolase family protein   chr5:18654250-18657585 REVERSE   Aliases: K15I22.16, K15I22_16	2.4	2.4	0.0	0.2	100.0%	-5.8
17024	AT1G72060.1   expressed protein   chr1:27122109-27122673 FORWARD   Aliases: F28P5.12, F28P5_12	3.4	3.5	-0.0	-0.2	100.0%	-5.2
17025	AT3G14670.1   expressed protein   chr3:4927854-4928875 FORWARD   Aliases: MIE1.17	2.8	2.8	0.0	0.2	100.0%	-5.6
17026	AT3G11920.1   glutaredoxin-related, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)   chr3:3772317-3774893 FORWARD   Aliases: F26K24.21	2.2	2.2	-0.0	-0.2	100.0%	-5.9
17027	AT1G12845.1   expressed protein   chr1:4378937-4379514 REVERSE   Aliases: None	3.3	3.2	0.1	0.2	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17028	AT1G72140.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:27145530-27148152 FORWARD   Aliases: T9N14.16, T9N14_16	2.4	2.4	-0.0	-0.2	100.0%	-5.5
17029	AT3G13750.1   Symbol: BGAL1   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase precursor SP:P48980 from (Lycopersicon esculentum)   chr3:4510985-4516305 FORWARD   Aliases: MMM17.1	5.8	6.0	-0.2	-0.2	100.0%	-4.6
17030	AT5G37560.1   zinc finger protein-related, contains weak similarity to zinc fingers and Pfam:PF01485 IBR domain   chr5:14939216-14941020 FORWARD   Aliases: K12B20.10, K12B20_10	2.4	2.4	-0.0	-0.2	100.0%	-5.9
17031	AT3G01510.1   5'-AMP-activated protein kinase beta-1 subunit-related, contains similarity to Swiss-Prot:P80387 5'-AMP-activated protein kinase, beta-1 subunit (AMPK beta-1 chain) (AMPKb) (40 kDa subunit) (Sus scrofa)   chr3:198686-201749 REVERSE   Aliases: F4P13.6, F4P13_6	3.3	3.2	0.1	0.2	100.0%	-5.2
17032	AT1G76110.1   high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein, low similarity to high mobility group protein (Plasmodium falciparum) GI:790198; contains Pfam profiles PF00505: HMG (high mobility group) box, PF01388: ARID/BRIGHT DNA binding domain	2.4	2.4	-0.0	-0.2	100.0%	-6.0
17033	AT4G14440.1   enoyl-CoA hydratase/isomerase family protein, low similarity to PhaB (Pseudomonas putida) GI:3253198, SP:P31551 Carnitine racemase {Escherichia coli}; contains Pfam profile PF00378 enoyl-CoA hydratase/isomerase family protein   chr4:8306741-8307749 REVERSE   Aliases: DL3260C, FCAALL.212	3.9	4.0	-0.1	-0.2	100.0%	-4.4
17034	AT2G25890.1   glycine-rich protein / oleosin   chr2:11044458-11045204 FORWARD   Aliases: F17H15.8, F17H15_8	2.2	2.2	-0.0	-0.2	100.0%	-5.8
17035	AT5G18560.1   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.	3.3	3.2	0.1	0.2	100.0%	-4.7
17036	AT4G14130.1   Symbol: XTR7   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative (XTR7), almost identical to xyloglucan endotransglycosylase-related protein XTR7 GI:1244760 from (Arabidopsis thaliana), one amino acid difference   chr4:8137047-8138276 REVERSE   Aliases: DL3105C, FCAALL.173, XYLOGLUCAN ENDOTRANSGLYCOSYLASE 7	5.8	5.9	-0.1	-0.2	100.0%	-4.8
17037	AT5G49720.1   Symbol: KOR1   endo-1,4-beta-glucanase KORRIGAN (KOR) / cellulase (OR16pep), identical to endo-1,4-beta-D-glucanase KORRIGAN (Arabidopsis thaliana) GI:3978258; similar to endo-1,4-beta-D-glucanase; cellulase GI:5689613 from (Brassica napus); identical to cDNA cellulase (OR16pep)	7.7	7.5	0.1	0.2	100.0%	-4.9
17038	AT4G04370.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr4:2134058-2136247 REVERSE   Aliases: T19B17.9, T19B17_9	3.0	3.0	0.1	0.2	100.0%	-5.6
17039	AT1G53830.1   Symbol: ATPME2	3.4	3.3	0.0	0.2	100.0%	-5.0
17040	AT3G49510.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	2.8	2.8	-0.0	-0.2	100.0%	-5.5
17041	AT2G03200.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr2:966448-967915 REVERSE   Aliases: T18E12.13, T18E12_13	2.1	2.2	-0.1	-0.2	100.0%	-4.5
17042	AT4G35720.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr4:16927977-16929175 FORWARD   Aliases: F8D20.230, F8D20_230	3.6	3.5	0.1	0.2	100.0%	-5.2
17043	AT1G20520.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr1:7106912-7107607 REVERSE   Aliases: F5M15.16, F5M15_16	3.2	3.2	-0.0	-0.2	100.0%	-5.3
17044	AT1G19940.1   glycosyl hydrolase family 9 protein, similar to endo-beta-1,4-D-glucanase GI:4165132 from (Lycopersicon esculentum)   chr1:6918182-6920368 REVERSE   Aliases: F6F9.1, F6F9_1	2.7	2.8	-0.0	-0.2	100.0%	-5.7
17045	AT2G15300.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:6656712-6659092 FORWARD   Aliases: F27O10.5, F27O10_5	3.0	3.0	-0.0	-0.2	100.0%	-5.2
17046	AT5G53860.3   Symbol: EMB2737   expressed protein   chr5:21882494-21886068 FORWARD   Aliases: EMB2737, EMBRYO DEFECTIVE 2737, K6O8.3	6.8	6.9	-0.1	-0.2	100.0%	-4.6
17047	AT2G16160.1   hypothetical protein, includes At2g06610, At5g28266, At3g42620, At4g07696, At2g06690, At2g16160, At2g05480, At2g12140, At1g45080, At2g16330   chr2:7019652-7020548 FORWARD   Aliases: F7H1.18, F7H1_18	2.6	2.7	-0.0	-0.2	100.0%	-5.3
17048	AT5G51020.1   expressed protein, similar to unknown protein (pir::S76207)   chr5:20762680-20764472 REVERSE   Aliases: K3K7.20, K3K7_20	8.5	8.4	0.1	0.2	100.0%	-5.1
17049	AT2G04540.1   3-oxoacyl-(acyl-carrier-protein) synthase II, putative, similar to Swiss-Prot:P56902 3-oxoacyl-(acyl-carrier-protein) synthase II (EC 2.3.1.41) (Beta-ketoacyl-ACP synthase II) (KAS II) (Rhizobium meliloti)   chr2:1581413-1584685 REVERSE   Aliases: T1O3.5, T1O3_5	6.7	6.6	0.1	0.2	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17050	AT3G46440.2   Symbol: UXS5   similar to NAD-dependent epimerase/dehydratase family protein [Arabidopsis thaliana] (TAIR:At2g28760.2); similar to NAD-dependent epimerase/dehydratase family protein [Arabidopsis thaliana] (TAIR:At2g28760.1); similar to UDP-glucuronic acid decarboxylase (UXS3) [Arabidopsis thaliana] (TAIR:At5g59290.1); similar to UDP-D-glucuronate carboxy-lyase [Pisum sativum] (GB:BAB40967.1); contains InterPro domain NAD-dependent epimerase/dehydratase (InterPro:IPR001509)   chr3:17100030-17102811 REVERSE   Aliases: F18L15.160	11.1	10.9	0.2	0.2	100.0%	-4.7
17051	AT4G13950.1   Symbol: RALFL31   rapid alkalization factor (RALF) family protein, similar to RALF precursor (Nicotiana tabacum) GI:16566316   chr4:8058067-8058670 REVERSE   Aliases: DL3015C, FCAALL.121, RALF LIKE 31	6.6	6.7	-0.1	-0.2	100.0%	-4.5
17052	AT3G27130.1   expressed protein   chr3:10003896-10005518 REVERSE   Aliases: MOJ10.23	3.1	3.1	0.0	0.2	100.0%	-5.5
17053	AT5G54700.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr5:22240322-22242735 REVERSE   Aliases: K5F14.4, K5F14_4	3.0	2.9	0.1	0.2	100.0%	-4.5
17054	AT5G54230.1   Symbol: MYB49   myb family transcription factor (MYB49), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:22033476-22035159 REVERSE   Aliases: MDK4.5, MDK4_5	2.0	2.2	-0.2	-0.2	100.0%	-4.2
17055	AT5G46470.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18859928-18866968 FORWARD   Aliases: K11I1.6, K11I1_6	3.3	3.3	0.0	0.2	100.0%	-5.8
17056	AT4G27940.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr4:13904480-13907249 FORWARD   Aliases: T13J8.50, T13J8_50	6.5	6.4	0.1	0.2	100.0%	-4.7
17057	AT4G11760.1   Symbol: LCR17   Encodes a member of a family of small, secreted, cysteine rich protein with sequence similarity to the PCP (pollen coat protein) gene family.   chr4:7079310-7080439 FORWARD   Aliases: LCR17, Low molecular weight cysteine rich 17, T5C23.190, T5C23_190	3.3	3.2	0.0	0.2	100.0%	-5.5
17058	AT3G50770.1   calmodulin-related protein, putative, similar to regulator of gene silencing calmodulin-related protein GI:12963415 from (Nicotiana tabacum)   chr3:18884939-18885761 FORWARD   Aliases: F18B3.50, F18B3_50	2.3	2.3	0.0	0.2	100.0%	-5.6
17059	AT1G33900.1   avirulence-responsive protein, putative / avirulence induced gene protein, putative / AIG protein, putative, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}; contains Pfam profile PF04548: AIG1 family   chr1:12311498-12313498 REVERSE   Aliases: T3M13.8, T3M13_8	2.6	2.6	-0.0	-0.2	100.0%	-5.3
17060	AT2G29340.2   short-chain dehydrogenase/reductase (SDR) family protein, similar to tropinone reductase-I GI:424160 from (Datura stramonium)   chr2:12604194-12605496 FORWARD   Aliases: F16P2.28, F16P2_28	3.2	3.3	-0.1	-0.2	100.0%	-4.8
17061	AT3G53280.1   Symbol: CYP71B5   cytochrome P450 71B5 (CYP71B5), identical to Cytochrome P450 71B5 (SP:O65784) (Arabidopsis thaliana)   chr3:19766682-19768583 FORWARD   Aliases: CYTOCHROME P450 71B5, T4D2.200	2.9	2.9	0.1	0.2	100.0%	-4.9
17062	AT1G20840.1   transporter-related, low similarity to D-xylose proton-symporter (Lactobacillus brevis) GI:2895856; contains Pfam profile PF00083: major facilitator superfamily protein	4.2	4.3	-0.0	-0.2	100.0%	-5.0
17063	AT5G51670.1   expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668)   chr5:21010786-21012322 FORWARD   Aliases: K10D11.2, K10D11_2	3.4	3.5	-0.1	-0.2	100.0%	-4.5
17064	AT5G47850.1   protein kinase, putative, contains similarity to cytokinin-regulated kinase 1 (Nicotiana tabacum) gi:10998537:gb:AAG25966; contains protein kinase domain, Pfam:PF00069   chr5:19395927-19398308 REVERSE   Aliases: MCA23.19, MCA23_19	2.8	2.8	-0.0	-0.2	100.0%	-5.5
17065	AT4G15360.1   Symbol: CYP705A3   cytochrome P450 family protein   chr4:8770223-8771899 FORWARD   Aliases: DL3725W, FCAALL.277	2.8	2.8	-0.0	-0.2	100.0%	-5.5
17066	AT2G36050.1   ovate protein-related, contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568   chr2:15142651-15143828 REVERSE   Aliases: F11F19.32, F11F19_32	3.1	3.2	-0.1	-0.2	100.0%	-5.1
17067	AT4G36070.1   Symbol: CPK18   calcium-dependent protein kinase family protein / CDPK family protein, contains Pfam domains, PF00069: Protein kinase domain and PF00036: EF hand   chr4:17056910-17059598 REVERSE   Aliases: T19K4.200, T19K4_200	2.4	2.4	0.0	0.2	100.0%	-5.9
17068	AT2G46820.2   Symbol: TMP14   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g52220.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54812.1)   chr2:19250565-19252206 FORWARD   Aliases: F19D11.10, THYLAKOID MEMBRANE PHOSPHOPROTEIN OF 14 KDA	8.2	8.1	0.1	0.2	100.0%	-4.7
17069	AT2G05430.1   expressed protein   chr2:1985993-1987263 FORWARD   Aliases: F16J10.2, F16J10_2	2.7	2.7	0.0	0.2	100.0%	-5.7
17070	AT5G02630.1   expressed protein   chr5:591769-593185 FORWARD   Aliases: T22P11.220, T22P11_220	4.2	4.2	0.0	0.2	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17071	AT5G58910.1   laccase, putative / diphenol oxidase, putative, similar to diphenol oxidase (Nicotiana tabacum)(GI:1685087)   chr5:23806748-23808907 REVERSE   Aliases: K19M22.11, K19M22_11	2.4	2.5	-0.0	-0.2	100.0%	-5.3
17072	AT2G45860.1   expressed protein   chr2:18881834-18882649 REVERSE   Aliases: F4I18.16	6.9	6.9	0.1	0.2	100.0%	-4.6
17073	AT3G49630.1   2-oxoacid-dependent oxidase, putative, strong similarity to partial cds of 2-oxoacid-dependent oxidase (din11) from GI:10834554 (Arabidopsis thaliana)   chr3:18408744-18411240 FORWARD   Aliases: T9C5.220	3.2	3.3	-0.1	-0.2	100.0%	-5.1
17074	AT3G25080.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At1g24370.1); contains InterPro domain Arabidopsis paralogous family (InterPro:IPR006462)   chr3:9136638-9138059 FORWARD   Aliases: MJL12.2	3.5	3.4	0.0	0.2	100.0%	-5.4
17075	AT3G15800.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr3:5345058-5346995 FORWARD   Aliases: MSJ11.20	2.4	2.3	0.0	0.2	100.0%	-5.2
17076	AT1G45545.1   expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827)   chr1:17183055-17185397 REVERSE   Aliases: F2G19.5, F2G19_5	3.1	3.0	0.1	0.2	100.0%	-4.2
17077	AT2G47640.3   small nuclear ribonucleoprotein D2, putative / snRNP core protein D2, putative / Sm protein D2, putative, similar to small nuclear ribonucleoprotein Sm D2 (snRNP core protein D2) (Sm-D2) (Mus musculus) SWISS-PROT:P43330   chr2:19544275-19545669 FORWARD   Aliases: F17A22.3	10.2	10.2	-0.1	-0.2	100.0%	-5.0
17078	AT5G03320.1   protein kinase, putative, similar to serine/threonine-protein kinase NAK (Arabidopsis thaliana) SWISS-PROT:P43293   chr5:802055-804397 FORWARD   Aliases: F12E4.50, F12E4_50	4.9	5.0	-0.1	-0.2	100.0%	-4.9
17079	AT5G52410.2   expressed protein   chr5:21293182-21296669 FORWARD   Aliases: K24M7.15, K24M7_15	4.1	4.3	-0.1	-0.2	100.0%	-4.7
17080	AT1G65410.1   Symbol: ATNAP11   ABC transporter family protein, contains similarity to toluene tolerance protein Ttg2A GI:4336798 from (Pseudomonas putida)   chr1:24298836-24301258 FORWARD   Aliases: T8F5.19, T8F5_19	5.8	5.7	0.1	0.2	100.0%	-5.1
17081	AT5G44300.1   dormancy/auxin associated family protein, contains Pfam profile: PF05564 dormancy/auxin associated protein   chr5:17862398-17863421 REVERSE   Aliases: K9L2.6, K9L2_6	3.2	3.2	0.0	0.2	100.0%	-5.2
17082	AT3G45330.1   lectin protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, Prosite:PS00108; contains Pfam profiles PF00069: Protein kinase domain, PF00139: Legume lectins beta domain, PF00138: Legume lectins alpha domain	2.7	2.8	-0.1	-0.2	100.0%	-4.6
17083	AT2G33100.1   Symbol: ATCSLD1   cellulose synthase family protein, similar to gi:2827143 from Arabidopsis thaliana (Ath-B)   chr2:14043396-14047121 REVERSE   Aliases: CSLD1, F25I18.16, F25I18_16	2.6	2.6	0.0	0.2	100.0%	-5.6
17084	AT2G44440.1   emsy N terminus domain-containing protein / ENT domain-containing protein, contains Pfam profile PF03735: ENT domain   chr2:18343484-18346266 REVERSE   Aliases: F4I1.25	3.6	3.6	-0.0	-0.2	100.0%	-5.5
17085	AT4G01380.1   plastocyanin-like domain-containing protein   chr4:569148-570076 REVERSE   Aliases: F2N1.2, F2N1_2	2.2	2.2	0.0	0.2	100.0%	-5.7
17086	AT5G58780.1   dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076   chr5:23752855-23754561 REVERSE   Aliases: MZN1.33	2.9	3.0	-0.1	-0.2	100.0%	-4.3
17087	NA	3.0	3.0	0.0	0.2	100.0%	-6.1
17088	AT4G15280.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr4:8719182-8720618 FORWARD   Aliases: DL3685W, FCAALL.255	3.8	3.8	0.0	0.2	100.0%	-5.4
17089	AT1G49780.1   U-box domain-containing protein, similar to immediate-early fungal elicitor protein CMPG1 (Petroselinum crispum) GI:14582200; contains Pfam profile PF04564: U-box domain   chr1:18432574-18433987 REVERSE   Aliases: F14J22.1, F14J22_1	3.9	3.8	0.1	0.2	100.0%	-4.9
17090	AT3G10560.1   Symbol: CYP77A7   cytochrome P450, putative, similar to cytochrome P450 77A3 GB:O48928 (Glycine max)   chr3:3299898-3301709 FORWARD   Aliases: F13M14.16	3.1	3.1	0.1	0.2	100.0%	-5.4
17091	AT2G30260.1   Symbol: U2B"   small nuclear ribonucleoprotein U2B, putative / spliceosomal protein, putative, similar to spliceosomal protein (Solanum tuberosum) GI:169589   chr2:12912482-12914586 REVERSE   Aliases: T9D9.7, T9D9_7, U2B"	7.2	7.1	0.1	0.2	100.0%	-4.8
17092	AT2G29040.1   exostosin family protein, contains Pfam profile: PF03016	2.4	2.4	-0.0	-0.2	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17093	AT2G37260.1   Symbol: TTG2   WRKY family transcription factor (TTG2), contains Pfam profile: PF03106 WRKY DNA -binding domain	2.6	2.6	0.0	0.2	100.0%	-5.6
17094	AT3G50430.1   expressed protein   chr3:18724678-18728654 FORWARD   Aliases: T20E23.30	4.5	4.5	-0.1	-0.2	100.0%	-4.9
17095	AT2G46570.1   laccase family protein / diphenol oxidase family protein, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)   chr2:19133944-19136141 FORWARD   Aliases: F13A10.10	3.2	3.3	-0.0	-0.2	100.0%	-5.1
17096	AT3G23850.1   hypothetical protein   chr3:8615571-8616540 FORWARD   Aliases: F14O13.31	3.1	3.1	0.0	0.2	100.0%	-5.4
17097	AT2G45970.1   Symbol: CYP86A8   Encodes a member of the CYP86A subfamily of cytochrome p450 genes.   chr2:18919333-18921812 REVERSE   Aliases: CYP86A6, F4I18.5, LACERATA, LCR	2.8	2.8	0.0	0.2	100.0%	-5.1
17098	AT3G03090.1   sugar transporter family protein, similar to xylose permease (Bacillus megaterium) GI:1924928; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:700463-704724 REVERSE   Aliases: T17B22.22, T17B22_22	3.8	3.8	-0.1	-0.2	100.0%	-5.0
17099	AT4G14650.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g22795.1); similar to mature parasite-infected erythrocyte surface antigen [Plasmodium falciparum] (GB:AAC13303.1); similar to GH09355p [Drosophila melanogaster] (GB:AAL68190.1); contains domain GLU_RICH (PS50313)   chr4:8400569-8402906 REVERSE   Aliases: DL3365C, FCAALL.281	2.5	2.6	-0.1	-0.2	100.0%	-4.6
17100	AT2G39130.1   amino acid transporter family protein, belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II	3.3	3.3	-0.0	-0.2	100.0%	-5.2
17101	AT2G35790.1   expressed protein   chr2:15047758-15049201 FORWARD   Aliases: T20F21.20	7.0	6.9	0.1	0.2	100.0%	-4.7
17102	AT4G10210.1   hypothetical protein, IB1C3-1 protein, Arabidopsis thaliana, AJ011845 contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr4:6357214-6360252 FORWARD   Aliases: F24G24.10, F24G24_10	2.9	2.8	0.0	0.2	100.0%	-5.3
17103	AT5G04520.1   expressed protein, ; expression supported by MPSS   chr5:1290013-1291064 REVERSE   Aliases: T32M21.120, T32M21_120	5.6	5.5	0.1	0.2	100.0%	-5.1
17104	AT1G35660.1   expressed protein   chr1:13192721-13197262 FORWARD   Aliases: F15O4.11	2.4	2.5	-0.0	-0.2	100.0%	-5.9
17105	AT2G07320.1   SWIM zinc finger family protein, contains Pfam profile PF04434: SWIM zinc finger	2.9	2.9	0.0	0.2	100.0%	-5.5
17106	AT3G32400.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, common family members: At2g43800, At3g25500, At5g48360, At4g15200, At3g05470, At3g07540, At5g07780, At5g07650 (Arabidopsis thaliana);   chr3:13360708-13364285 REVERSE   Aliases: F1D9.13	2.8	2.8	-0.0	-0.2	100.0%	-5.0
17107	AT2G13600.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:5678575-5680668 FORWARD   Aliases: T10F5.14, T10F5_14	4.1	4.2	-0.0	-0.2	100.0%	-5.2
17108	AT2G24765.1   ADP-ribosylation factor 3 (ARF3), identical to GP:453191 ADP-ribosylation factor 3 {Arabidopsis thaliana}; contains domain PF00025: ADP-ribosylation factor family   chr2:10569805-10572274 FORWARD   Aliases: F27A10.8	11.2	11.2	0.1	0.2	100.0%	-5.1
17109	AT1G27510.1   expressed protein   chr1:9554932-9558280 REVERSE   Aliases: T17H3.1	3.9	3.9	0.0	0.2	100.0%	-5.0
17110	AT5G03970.2   similar to F-box family protein [Arabidopsis thaliana] (TAIR:At5g07610.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52196.1); similar to putative F-Box protein [Solanum demissum] (GB:AAT38719.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain F-box protein interaction domain (InterPro:IPR006527)   chr5:1071568-1073395 REVERSE   Aliases: F8F6.180, F8F6_180	7.1	7.1	0.1	0.2	100.0%	-4.5
17111	AT3G49160.1   pyruvate kinase family protein, similar to SP:Q92122 Pyruvate kinase, muscle isozyme (EC 2.7.1.40) (Cytosolic thyroid hormone binding protein) (CTHBP) {Xenopus laevis}; contains Pfam profile PF00224: Pyruvate kinase, barrel domain   chr3:18232979-18235870 REVERSE   Aliases: F2K15.20	5.3	5.4	-0.1	-0.2	100.0%	-4.5
17112	AT1G62920.1   expressed protein, ; expression supported by MPSS   chr1:23307978-23310039 FORWARD   Aliases: F16P17.25, F16P17_25	3.0	3.0	0.0	0.2	100.0%	-5.2
17113	AT4G36110.1   auxin-responsive protein, putative, similar to auxin-induced protein TGSAUR22 (GP:10185820) {Tulipa gesneriana}; auxin-induced protein 15A (PIR2:JQ1096) (Glycine max)   chr4:17089952-17090828 FORWARD   Aliases: T19K4.240, T19K4_240	2.8	2.8	0.0	0.2	100.0%	-5.4
17114	AT4G35410.2   clathrin adaptor complex small chain family protein, contains Pfam profile: PF01217 clathrin adaptor complex small chain	4.7	4.8	-0.1	-0.2	100.0%	-5.0
17115	AT2G13150.1   expressed protein, contains a bZIP transcription factor basic domain signature (PDOC00036)   chr2:5444138-5445541 FORWARD   Aliases: T17A11.14, T17A11_14	2.4	2.4	-0.0	-0.2	100.0%	-5.9
17116	AT1G05070.1   expressed protein   chr1:1457067-1458742 REVERSE   Aliases: T7A14.6, T7A14_6	8.1	8.2	-0.1	-0.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17117	AT3G30710.1   expressed protein, similar to Arginine-tRNA-protein transferase 1 (EC 2.3.2.8)(R-transferase 1) (Arginyltransferase 1) (Arginyl-tRNA--protein transferase 1)(SP:Q9Z2A5) {Mus musculus}; similar to MRP homologs in mycobacteria (SP:P53382), which belong to the MR?/NBP35 family of ATP-binding proteins.   chr3:12294291-12296616 REVERSE   Aliases: F21A17.3	4.1	4.1	0.1	0.2	100.0%	-5.0
17118	AT2G21530.1   forkhead-associated domain-containing protein / FHA domain-containing protein   chr2:9226404-9227666 FORWARD   Aliases: F3K23.29, F3K23_29	5.0	5.1	-0.1	-0.2	100.0%	-4.2
17119	AT1G33680.1   KH domain-containing protein, similar to FUSE binding protein 2 GB:AAC50892 GI:1575607 from (Homo sapiens)   chr1:12203925-12209088 FORWARD   Aliases: F14M2.18, F14M2_18	3.4	3.5	-0.0	-0.2	100.0%	-5.6
17120	AT2G21280.1   Symbol: GC1   expressed protein, similar to YfhF (GI:2804536) (Bacillus subtilis)   chr2:9117394-9119776 REVERSE   Aliases: GIANT CHLOROPLAST 1	7.0	6.9	0.1	0.2	100.0%	-4.4
17121	AT4G26880.1   stigma-specific Stig1 family protein, similar to stigma-specific protein STIG1 (Nicotiana tabacum) GI:496647; contains Pfam profile PF04885: Stigma-specific protein, Stig1   chr4:13508271-13508729 REVERSE   Aliases: F10M23.220, F10M23_220	2.5	2.5	0.0	0.2	100.0%	-5.4
17122	AT4G03430.1   pre-mRNA splicing factor-related, similar to pre-mRNA splicing factor pre-mRNA splicing factor prp1 (SP:Q12381) (Fission yeast)   chr4:1517132-1520561 REVERSE   Aliases: F9H3.5, F9H3_5	4.7	4.8	-0.1	-0.2	100.0%	-5.0
17123	AT1G08310.1   esterase/lipase/thioesterase family protein, contains Interpro entry IPR000379   chr1:2618683-2620408 FORWARD   Aliases: T23G18.18, T23G18_18	3.5	3.6	-0.1	-0.2	100.0%	-4.5
17124	AT3G24790.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:9052989-9054538 FORWARD   Aliases: K7P8.12	2.7	2.7	0.0	0.2	100.0%	-5.8
17125	AT1G33060.2   Symbol: ANAC014   no apical meristem (NAM) family protein, similar to NAC1 GB:AAF68626 GI:7716952 from (Medicago truncatula)   chr1:11975322-11978501 REVERSE   Aliases: ANAC014, T9L6.13, T9L6_13	4.9	5.0	-0.1	-0.2	100.0%	-4.9
17126	AT1G04410.1   malate dehydrogenase, cytosolic, putative, strong similarity to malate dehydrogenase from Mesembryanthemum crystallinum (SP:O24047), Medicago sativa (SP:O48905), Prunus persica (GI:15982948); contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr1:1189077-1191411 REVERSE   Aliases: F19P19.13, F19P19_13	12.3	12.4	-0.1	-0.2	100.0%	-5.1
17127	AT5G07700.1   Symbol: MYB76   myb family transcription factor (MYB76), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:2450326-2451579 FORWARD   Aliases: MBK20.16, MBK20_16	2.3	2.4	-0.0	-0.2	100.0%	-5.7
17128	AT5G49610.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640: F-box protein interaction domain; similar to unknown protein (gb:AAF30317.1)   chr5:20148500-20149955 REVERSE   Aliases: K6M13.17, K6M13_17	4.5	4.4	0.1	0.2	100.0%	-4.9
17129	AT3G01090.2   Symbol: AKIN10	5.5	5.4	0.1	0.2	100.0%	-4.8
17130	AT5G12230.1   expressed protein   chr5:3953149-3956186 REVERSE   Aliases: MXC9.19, MXC9_19	6.5	6.7	-0.2	-0.2	100.0%	-4.8
17131	AT1G78980.1   similar to leucine-rich repeat transmembrane protein kinase, putative [Arabidopsis thaliana] (TAIR:At3g13065.1); similar to Putative leucine-rich repeat transmembrane protein kinase 1 [Oryza sativa] (GB:XP_470566.1); similar to putative leucine-rich repeat transmembrane protein kinase [Oryza sativa (japonica cultivar-group)] (GB:AAO72637.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Leucine-rich repeat, typical subtype (InterPro:IPR003591); contains InterPro domain Leucine-rich repeat, plant specific (InterPro:IPR007090); contains InterPro domain Leucine-rich repeat (InterPro:IPR001611)   chr1:29712580-29716314 REVERSE   Aliases: YUP8H12R.40, YUP8H12R_40	2.2	2.2	-0.0	-0.2	100.0%	-6.0
17132	AT2G34440.1   MADS-box family protein, similar to SP:Q9XGJ4 MADS box protein GGM13 {Gnetum gnemon}; contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)	2.4	2.4	-0.0	-0.2	100.0%	-5.6
17133	AT3G19780.1   expressed protein   chr3:6870205-6874856 FORWARD   Aliases: MMB12.5	2.9	3.0	-0.0	-0.2	100.0%	-6.0
17134	AT2G17890.1   Symbol: CPK16   calcium-dependent protein kinase family protein / CDPK family protein, contains Pfam domains, PF00069: Protein kinase domain and PF00036: EF hand   chr2:7776967-7779709 REVERSE   Aliases: T13L16.9, T13L16_9	2.7	2.6	0.0	0.2	100.0%	-5.2
17135	AT2G20100.1   ethylene-responsive family protein, similar to Ethylene-regulated ER33 protein (GI:5669656) (Lycopersicon esculentum); PMID: 12679534; putative bHLH133 transcription factor   chr2:8685163-8689167 FORWARD   Aliases: T2G17.10, T2G17_10	4.3	4.3	0.0	0.2	100.0%	-5.2
17136	AT3G50570.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich protein domains, INTERPRO:IPR000694   chr3:18777730-18778510 REVERSE   Aliases: T20E23.170	2.8	2.8	-0.0	-0.2	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17137	AT2G26890.1   Symbol: GRV2   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226: DnaJ domain	6.6	6.7	-0.1	-0.2	100.0%	-5.0
17138	AT1G73560.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to GI:2627141 from (Picea abies) (Plant Mol. Biol. 42 (3), 461-478 (2000)); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234	2.2	2.2	0.0	0.2	100.0%	-5.8
17139	AT4G13060.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr4:7619932-7620939 REVERSE   Aliases: F25G13.150, F25G13_150	2.8	2.9	-0.0	-0.2	100.0%	-5.3
17140	AT4G11160.1   translation initiation factor IF-2, mitochondrial, putative, similar to SP:P46198:IF2M_BOVIN Translation initiation factor IF-2, mitochondrial precursor (IF-2Mt) (IF-2(Mt)) {Bos taurus}   chr4:6803615-6806871 FORWARD   Aliases: T22B4.140, T22B4_140	6.9	6.8	0.1	0.2	100.0%	-5.1
17141	AT3G44730.1   kinesin motor protein-related, similar to 4 other kinesin-like proteins of A. thaliana: F02P16.12 (PID:g2191180), katA (D11371), katB (D21137), and katC (D21138); contains non-consensus AT-AC splice sites at intron 10   chr3:16296875-16301839 FORWARD   Aliases: T32N15.10	3.1	3.0	0.0	0.2	100.0%	-5.0
17142	AT5G41640.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626); expression supported by MPSS   chr5:16670565-16671863 REVERSE   Aliases: MBK23.16, MBK23_16	2.9	2.9	0.0	0.2	100.0%	-5.2
17143	AT1G01630.1   SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative, contains Pfam PF00650 : CRAL/TRIO domain and PF03765 : CRAL/TRIO, N-terminus; similar to polyphosphoinositide binding protein Ssh2p GB:AAB94599 GI:2739046 from (Glycine max)   chr1:229057-230917 FORWARD   Aliases: T1N6.1, T1N6_1	9.7	9.7	0.1	0.2	100.0%	-4.9
17144	AT2G34610.1   expressed protein   chr2:14582471-14583596 FORWARD   Aliases: T31E10.5, T31E10_5	3.8	3.8	-0.0	-0.2	100.0%	-5.2
17145	AT1G73110.1   ribulose bisphosphate carboxylase/oxygenase activase, putative / RuBisCO activase, putative, similar to ribulose bisphosphate carboxylase/oxygenase activase, chloroplast precursor (RuBisCO activase, RA) (Oryza sativa) SWISS-PROT:P93431   chr1:27497901-27500539 REVERSE   Aliases: F3N23.32, F3N23_32	6.1	6.0	0.1	0.2	100.0%	-4.5
17146	AT2G07110.1   hypothetical protein   chr2:2952607-2953205 REVERSE   Aliases: T25N22.7, T25N22_7	3.0	3.0	0.0	0.2	100.0%	-5.3
17147	AT1G51280.2   similar to Toll-Interleukin-Resistance (TIR) domain-containing protein [Arabidopsis thaliana] (TAIR:At5g45000.1); similar to R 1 protein [Glycine max] (GB:AAO23076.1); contains InterPro domain TIR domain (InterPro:IPR000157)	3.5	3.4	0.1	0.2	100.0%	-4.9
17148	AT3G26360.1   ribosomal protein-related, similar to SP:Q9Z354 30S ribosomal protein S21 {Rhizobium meliloti}   chr3:9656519-9657610 REVERSE   Aliases: F20C19.8	7.4	7.4	-0.1	-0.2	100.0%	-4.7
17149	AT4G11280.1   Symbol: ACS6   1-aminocyclopropane-1-carboxylate synthase 6 / ACC synthase 6 (ACS6), identical to GI:3746125   chr4:6864093-6866112 FORWARD   Aliases: 1 AMINOCYCLOPROPANE 1 CARBOXYLIC ACID (ACC) SYNTHASE 6, F8L21.70, F8L21_70	6.6	6.6	-0.1	-0.2	100.0%	-4.8
17150	AT4G26610.1   protein kinase, putative, similar to protein kinase G11A (Oryza sativa) SWISS-PROT:P47997   chr4:13424614-13427324 FORWARD   Aliases: T15N24.60, T15N24_60	5.8	5.9	-0.1	-0.2	100.0%	-4.7
17151	AT4G39820.1   expressed protein   chr4:18476001-18477937 REVERSE   Aliases: T5J17.8	5.7	5.6	0.1	0.2	100.0%	-4.9
17152	AT5G38350.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr5:15345889-15348758 FORWARD   Aliases: MXI10.1, MXI10_1	2.1	2.2	-0.1	-0.2	100.0%	-4.9
17153	AT5G20690.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase PRK1, tomato, PIR:T07865   chr5:7002455-7004553 FORWARD   Aliases: T1M15.90, T1M15_90	2.4	2.4	0.0	0.2	100.0%	-5.7
17154	AT5G60890.1   Symbol: ATR1   receptor-like protein kinase (ATR1) (MYB34), identical to receptor-like protein kinase(ATR1) GI:3150037 from (Arabidopsis thaliana); contains PFAM profile: myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB34) mRNA, partial cds GI:3941443	3.1	3.2	-0.1	-0.2	100.0%	-4.4
17155	AT3G60340.2   palmitoyl protein thioesterase family protein, palmitoyl-protein thioesterase precursor, Mus musculus, EMBL:AF071025   chr3:22315148-22317899 FORWARD   Aliases: T8B10.2	9.1	9.1	0.1	0.2	100.0%	-4.9
17156	AT1G75620.1   glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594   chr1:28398440-28400257 REVERSE   Aliases: F10A5.18, F10A5_18	2.8	2.8	0.1	0.2	100.0%	-4.8
17157	AT4G30990.1   expressed protein, ; expression supported by MPSS   chr4:15084691-15095956 FORWARD   Aliases: F6I18.5	2.9	2.8	0.0	0.2	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17158	AT2G25900.1   Symbol: ATCTH   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:11048796-11050249 FORWARD   Aliases: F17H15.7, F17H15_7, PUTATIVE CYS3HIS ZINC FINGER PROTEIN	3.6	3.6	0.1	0.2	100.0%	-4.9
17159	AT5G28930.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr5:10968251-10972491 FORWARD   Aliases: F3F24.30, F3F24_30	2.6	2.6	0.0	0.2	100.0%	-5.6
17160	AT1G36060.1   encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.   chr1:13455930-13456906 REVERSE   Aliases: F5J5.5, F5J5_5	4.0	4.1	-0.0	-0.2	100.0%	-5.0
17161	AT1G04500.1   zinc finger CONSTANS-related, similar to Zinc finger protein constans-like 15 (SP:Q9FHH8) {Arabidopsis thaliana}	2.1	2.1	-0.0	-0.2	100.0%	-6.0
17162	AT3G06310.1   NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8) family protein, contains Pfam profile PF05850: NADH-ubiquinone oxidoreductase 19 kDa subunit (NDUFA8); similar to NADH-ubiquinone oxidoreductase 19 kDa subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-19KD) (CI-19KD) (Complex I-PGIV) (CI-PGIV) (Swiss-Prot:P51970) (Homo sapiens)   chr3:1912978-1914387 REVERSE   Aliases: F24P17.23, F24P17_23	10.0	10.0	0.1	0.2	100.0%	-4.9
17163	AT3G61110.1   Symbol: ARS27A	11.4	11.3	0.1	0.2	100.0%	-5.4
17164	AT3G20920.2   similar to translocation protein sec62, putative [Plasmodium berghei] (GB:CAH98034.1); contains InterPro domain Translocation protein Sec62 (InterPro:IPR004728)	8.2	8.2	-0.1	-0.2	100.0%	-5.0
17165	AT5G41580.1   similar to zinc finger (MIZ type) family protein [Arabidopsis thaliana] (TAIR:At1g08910.1); similar to putative transcription factor [Oryza sativa (japonica cultivar-group)] (GB:BAD67847.1); contains InterPro domain Zn-finger, MIZ type (InterPro:IPR004181)	2.8	2.8	-0.0	-0.2	100.0%	-5.5
17166	AT1G53260.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g15000.1); similar to proline-rich protein 15 - rat (GB:B39066); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr1:19862935-19864644 REVERSE   Aliases: F12M16.16, F12M16_16	2.9	2.9	-0.0	-0.2	100.0%	-5.3
17167	AT2G44650.1   Symbol: CHL CPN10   chloroplast chaperonin 10 (cpn10), identical to chloroplast chaperonin 10 GI:14041813 from (Arabidopsis thaliana)   chr2:18426478-18428186 REVERSE   Aliases: CHLOROPLAST CHAPERONIN 10, CPN10, F16B22.14	8.3	8.4	-0.1	-0.2	100.0%	-4.9
17168	AT4G26150.1   zinc finger (GATA type) family protein, Arabidopsis thaliana mRNA for GATA transcription factor 3, PID:e1254739   chr4:13253219-13254913 FORWARD   Aliases: F20B18.260, F20B18_260	2.4	2.4	0.0	0.2	100.0%	-5.7
17169	AT4G23520.1   cysteine proteinase, putative, contains similarity to cysteine proteinase (thiol protease) RD21A GI:435619, SP:P43297 from (Arabidopsis thaliana)   chr4:12274467-12276229 REVERSE   Aliases: F16G20.220, F16G20_220	2.8	2.8	0.0	0.2	100.0%	-5.2
17170	AT5G61605.1   expressed protein   chr5:24785608-24786192 REVERSE   Aliases: None	3.1	3.2	-0.0	-0.2	100.0%	-5.6
17171	AT5G41090.1   Symbol: ANAC095   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to unknown protein (emb:CAB88055.1)   chr5:16462992-16463765 FORWARD   Aliases: ANAC095, MEE6.16, MEE6_16	2.4	2.4	-0.0	-0.2	100.0%	-5.7
17172	AT4G27840.1   expressed protein   chr4:13865051-13866293 REVERSE   Aliases: T27E11.80, T27E11_80	3.7	3.7	0.1	0.2	100.0%	-5.1
17173	AT3G60450.1   expressed protein   chr3:22351940-22353285 FORWARD   Aliases: T8B10.110	9.8	9.7	0.1	0.2	100.0%	-4.6
17174	AT2G01890.2   Symbol: PAP8   purple acid phosphatase, putative, contains Pfam profile: PF00149 calcineurin-like phosphoesterase; identical to purple acid phosphatase (GI:20257479) (Arabidopsis thaliana);   chr2:396808-399190 REVERSE   Aliases: PAP8, PURPLE ACID PHOSPHATASE PRECURSOR, T23K3.8, T23K3_8	3.3	3.2	0.1	0.2	100.0%	-4.3
17175	AT1G50160.1   hypothetical protein, similar to putative non-LTR retroelement reverse transcriptase GB:AAD25836 GI:4587608 from (Arabidopsis thaliana)	2.6	2.5	0.0	0.2	100.0%	-5.8
17176	AT1G09410.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:3035445-3037562 FORWARD   Aliases: F14J9.7, F14J9_7	2.7	2.6	0.0	0.2	100.0%	-5.4
17177	AT2G18030.2   peptide methionine sulfoxide reductase family protein, similar to SP:P08761 Ecdysone-induced protein 28/29 kDa {Drosophila melanogaster}; contains Pfam profile PF01625: Peptide methionine sulfoxide reductase   chr2:7847149-7848736 FORWARD   Aliases: T27K22.10, T27K22_10	6.3	6.4	-0.1	-0.2	100.0%	-4.6
17178	AT1G24430.1   transferase family protein, similar to deacetylindoline 4-O-acetyltransferase from Catharanthus roseus GI:4091808 GB:AAC99311, acetyl CoA: benzylalcohol acetyltransferase Clarkia breweri GI:3170250, acetyl-CoA:benzylalcohol acetyltransferase Clarkia concinna GI:6166328; contains Pfam profile PF02458 transferase family   chr1:8657992-8659494 REVERSE   Aliases: F21J9.9	3.9	3.9	-0.0	-0.2	100.0%	-5.1
17179	AT1G50350.1   expressed protein   chr1:18652424-18652895 FORWARD   Aliases: F14I3.23, F14I3_23	2.6	2.7	-0.0	-0.2	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17180	AT4G13150.1   expressed protein   chr4:7651532-7652585 REVERSE   Aliases: F17N18.40, F17N18_40	3.0	3.0	-0.0	-0.2	100.0%	-5.9
17181	ATMG00650.1   Symbol: NAD4L   Encodes NADH dehydrogenase subunit 4L.   chrM:188929-189231 REVERSE   Aliases: NAD4L	4.2	4.4	-0.2	-0.2	100.0%	-4.8
17182	AT4G17690.1   peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781336:emb:CAA71495   chr4:9846140-9847120 FORWARD   Aliases: DL4880W, FCAALL.96	3.0	3.0	-0.0	-0.2	100.0%	-5.4
17183	AT5G06490.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 finger protein ATL6 (Arabidopsis thaliana) GI:4928403; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:1977997-1978590 REVERSE   Aliases: F15M7.2, F15M7_2	2.9	2.8	0.0	0.2	100.0%	-5.4
17184	AT3G12710.1   methyladenine glycosylase family protein, similar to SP:P05100 DNA-3-methyladenine glycosylase I (EC 3.2.2.20) (3-methyladenine-DNA glycosylase I, constitutive) {Escherichia coli}; contains Pfam profile PF03352: Methyladenine glycosylase   chr3:4040331-4041989 REVERSE   Aliases: MBK21.9	2.9	2.9	0.0	0.2	100.0%	-5.4
17185	AT1G09170.1   kinesin motor protein-related, similar to GB:AAB61066   chr1:2956591-2962209 REVERSE   Aliases: T12M4.14, T12M4_14	2.7	2.7	0.1	0.2	100.0%	-4.6
17186	AT3G29630.1   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	3.4	3.3	0.1	0.2	100.0%	-4.3
17187	AT3G15550.1   expressed protein, ; expression supported by MPSS   chr3:5267358-5268228 FORWARD   Aliases: MJK13.21	3.1	3.2	-0.0	-0.2	100.0%	-5.8
17188	AT2G43750.1   Symbol: OASB   cysteine synthase, chloroplast / O-acetylserine (thiol)-lyase / O-acetylserine sulfhydrylase / cpACS1 (OASB), identical to SP:P47999 Cysteine synthase, chloroplast precursor (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) (cpACS1) {Arabidopsis thaliana}; identical to cDNA O-acetylserine lyase (At.OAS.7-4) GI:6983575   chr2:18136488-18139629 REVERSE   Aliases: ACS1, ATCS B, CPACS1, CSASE B, CYSTEINE SYNTHASE, CYSTEINE SYNTHASE 1, F18O19.14	9.8	9.7	0.1	0.2	100.0%	-5.1
17189	AT5G41610.2   Symbol: ATCHX18   cation/hydrogen exchanger, putative (CHX18), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr5:16655598-16658485 REVERSE   Aliases: CHX18, MBK23.12, MBK23_12	6.7	6.6	0.1	0.2	100.0%	-4.2
17190	AT2G20520.1   Symbol: FLA6   fasciclin-like arabinogalactan-protein (FLA6), identical to gi:13377780_gb_AAK20859   chr2:8847744-8848542 FORWARD   Aliases: T13C7.11, T13C7_11, fasciclin like arabinogalactan protein 6	3.0	3.1	-0.1	-0.2	100.0%	-4.7
17191	AT1G54350.1   ABC transporter family protein, similar to hypothetical ABC transporter ATP-binding protein GI:9955395 from (Microcystis aeruginosa)   chr1:20290549-20294068 FORWARD   Aliases: F20D21.17, F20D21_17	6.2	6.3	-0.1	-0.2	100.0%	-5.1
17192	AT1G05700.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase, gi:2129635; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:1709795-1713244 FORWARD   Aliases: F3F20.15, F3F20_15	2.8	2.7	0.1	0.2	100.0%	-4.2
17193	AT4G35120.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:16716811-16718022 FORWARD   Aliases: T12J5.7	3.2	3.2	0.0	0.2	100.0%	-5.2
17194	AT1G01260.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	4.6	4.7	-0.1	-0.2	100.0%	-4.9
17195	AT2G18890.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At5g57670.1); similar to putative benzothiadiazole-induced somatic embryogenesis receptor kinase 1 [Oryza sativa (japonica cultivar-group)] (GB:BAD53863.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr2:8190992-8193878 FORWARD   Aliases: F19F24.9, F19F24_9	2.6	2.7	-0.0	-0.2	100.0%	-5.3
17196	AT1G19920.1   Symbol: APS2   sulfate adenylyltransferase 2 / ATP-sulfurylase 2 (ASA1) (MET3-1) (APS2), identical to ATP sulfurylase (APS2) (Arabidopsis thaliana) GI:1575324   chr1:6914604-6916745 REVERSE   Aliases: ASA1, ATP SULFURYLASE PRECURSOR, F6F9.2, F6F9_2	9.2	9.4	-0.2	-0.2	100.0%	-4.8
17197	AT4G36910.1   CBS domain-containing protein, contains Pfam profile PF00571: CBS domain	9.1	9.0	0.1	0.2	100.0%	-4.2
17198	AT5G13540.2   expressed protein, HERC2 - Homo sapiens, EMBL:AF071172; isoform contains non-consensus GG acceptor splice site at intron 6   chr5:4351396-4354684 FORWARD   Aliases: T6I14.70, T6I14_70	4.1	4.0	0.1	0.2	100.0%	-5.2
17199	AT5G39210.1   expressed protein   chr5:15720421-15721328 FORWARD   Aliases: K3K3.10, K3K3_10	2.7	2.7	-0.0	-0.2	100.0%	-5.5
17200	AT5G48200.1   expressed protein   chr5:19562481-19564496 FORWARD   Aliases: MIF21.9, MIF21_9	3.3	3.3	-0.0	-0.2	100.0%	-5.1
17201	AT5G17290.1   autophagy protein Apg5 family, contains Pfam profile: PF04106 autophagy protein Apg5   chr5:5686947-5689878 REVERSE   Aliases: MKP11.20, MKP11_20	6.5	6.6	-0.1	-0.2	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17202	AT2G01940.2   similar to zinc finger (C2H2 type) family protein [Arabidopsis thaliana] (TAIR:At1g68130.1); similar to putative zinc finger protein ID1 [Oryza sativa (japonica cultivar-group)] (GB:BAD37964.1); contains InterPro domain Zn-finger, C2H2 type (InterPro:IPR007087)   chr2:432274-435076 FORWARD   Aliases: F14H20.1, F14H20_1	4.5	4.4	0.1	0.2	100.0%	-4.6
17203	AT1G78420.1   expressed protein   chr1:29509426-29512379 FORWARD   Aliases: F3F9.7, F3F9_7	6.1	6.2	-0.1	-0.2	100.0%	-4.6
17204	AT5G39310.1   Symbol: ATEXPA24   expansin, putative (EXP24), similar to expansin - Prunus armeniaca, EMBL:U93167; alpha-expansin gene family, PMID:11641069   chr5:15756508-15757742 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A24, ATEXP24, ATHEXP ALPHA 1.19, EXP24, K3K3.160, K3K3_160	2.5	2.5	-0.0	-0.2	100.0%	-5.6
17205	AT5G49980.1   transport inhibitor response protein, putative, E3 ubiquitin ligase SCF complex F-box subunit; similar to F-box containing protein TIR1 GI:13249030 from (Populus tremula x Populus tremuloides)	4.1	4.2	-0.1	-0.2	100.0%	-4.7
17206	AT2G42160.1   zinc finger (ubiquitin-hydrolase) domain-containing protein, similar to BRCA1-associated protein 2 (Homo sapiens) GI:3252872; contains Pfam profile PF02148: Zn-finger in ubiquitin-hydrolases and other protein	5.0	5.2	-0.1	-0.2	100.0%	-4.5
17207	AT5G51180.2   expressed protein   chr5:20814243-20817440 FORWARD   Aliases: MWD22.12, MWD22_12	6.3	6.2	0.1	0.2	100.0%	-4.9
17208	AT1G51520.2   expressed protein, contains a weak hit to PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr1:19110355-19113255 FORWARD   Aliases: F5D21.15, F5D21_15	3.1	3.0	0.0	0.2	100.0%	-5.5
17209	AT2G24920.1   expressed protein   chr2:10608939-10609529 FORWARD   Aliases: F27C12.16, F27C12_16	3.8	3.9	-0.1	-0.2	100.0%	-4.7
17210	AT2G34180.1   Symbol: CIPK13	2.8	2.7	0.0	0.2	100.0%	-4.9
17211	AT4G09690.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.5	0.0	0.2	100.0%	-5.5
17212	AT1G07830.1   ribosomal protein L29 family protein, similar to GB:CAA83057 from (Saccharomyces cerevisiae)   chr1:2422295-2423650 FORWARD   Aliases: F24B9.7, F24B9_7	7.9	7.8	0.1	0.2	100.0%	-4.7
17213	AT2G31460.1   hypothetical protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)	3.1	3.1	0.0	0.2	100.0%	-5.6
17214	AT5G50320.1   radical SAM domain-containing protein / GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profiles PF00583: acetyltransferase, GNAT family, PF04055: Radical SAM superfamily	5.8	5.7	0.1	0.2	100.0%	-5.0
17215	AT4G36140.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:17098959-17104482 REVERSE   Aliases: F23E13.30, F23E13_30	3.5	3.6	-0.1	-0.2	100.0%	-4.9
17216	AT1G33080.2   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:11985699-11990391 FORWARD   Aliases: T9L6.14, T9L6_14	2.9	3.0	-0.1	-0.2	100.0%	-4.8
17217	AT5G35540.1   hypothetical protein   chr5:13739367-13740223 FORWARD   Aliases: MOK9.17, MOK9_17	2.8	2.9	-0.0	-0.2	100.0%	-5.5
17218	AT3G53520.2   Symbol: UXS1   NAD-dependent epimerase/dehydratase family protein, similar to UDP-glucuronic acid decarboxylase Uxs1p from Filobasidiella neoformans GI:14318327; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family   chr3:19852613-19855285 FORWARD   Aliases: ATUXS1, F4P12.220, UDP GLUCURONIC ACID DECARBOXYLASE 1	6.9	7.0	-0.1	-0.2	100.0%	-4.9
17219	AT3G57850.1   hypothetical protein   chr3:21435354-21435768 FORWARD   Aliases: T10K17.60	3.1	3.2	-0.0	-0.2	100.0%	-5.4
17220	AT3G06560.1   poly (A) polymerase family protein, similar to SP:Q9BWT3 Poly(A) polymerase gamma (EC 2.7.7.19) (PAP gamma) (Polynucleotide adenylyltransferase gamma) (SRP RNA 3' adenylylating enzyme) {Homo sapiens}; contains Pfam profiles PF04926: Poly(A) polymerase predicted RNA binding domain, PF04928: Poly(A) polymerase central domain   chr3:2044782-2047040 FORWARD   Aliases: F5E6.11, F5E6_11	3.3	3.4	-0.0	-0.2	100.0%	-5.4
17221	AT2G35100.1   exostosin family protein, contains Pfam profile: PF03016	5.9	5.8	0.1	0.2	100.0%	-4.9
17222	AT2G37160.2   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g53390.1); similar to CreC [Emericella nidulans] (GB:AAF63188.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr2:15615907-15620013 FORWARD   Aliases: T2N18.8, T2N18_8	4.5	4.5	0.0	0.2	100.0%	-5.0
17223	AT3G09280.1   expressed protein, ; expression supported by MPSS   chr3:2850926-2851264 REVERSE   Aliases: F3L24.15	3.2	3.2	0.0	0.2	100.0%	-5.2
17224	AT4G26410.1   expressed protein   chr4:13346757-13349025 FORWARD   Aliases: M3E9.160, M3E9_160	9.3	9.3	0.1	0.2	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17225	AT5G62320.1   Symbol: MYB99   myb family transcription factor (MYB99), contains PFAM profile: myb DNA binding domain PF00249   chr5:25045959-25047012 REVERSE   Aliases: MMI9.18, MMI9_18	3.1	3.2	-0.0	-0.2	100.0%	-5.2
17226	AT5G51230.2   Symbol: EMF2   embryonic flower 2 (EMF2), identical to embryonic flower 2 (Arabidopsis thaliana) GI:14276050; supporting cDNA gi:14276049:dbj:AB053171.1:   chr5:20841013-20846790 FORWARD   Aliases: AT5G51240, CYR1, CYTOKININ RESISTANT 1, EMBRYONIC FLOWER 2, MWD22.18, MWD22_18, VEF2	5.1	5.2	-0.1	-0.2	100.0%	-5.1
17227	AT5G38610.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pistil-specific gene sts15 (Solanum tuberosum) GI:1616628; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:15478075-15478674 REVERSE   Aliases: MBB18.16, MBB18_16	4.0	3.9	0.1	0.2	100.0%	-4.5
17228	AT5G24313.1   expressed protein   chr5:8276788-8277405 REVERSE   Aliases: None	2.6	2.7	-0.1	-0.2	100.0%	-4.9
17229	AT1G09100.1   26S protease regulatory subunit 6A, putative, identical to SP:O04019 from (Arabidopsis thaliana)	7.3	7.2	0.1	0.2	100.0%	-4.8
17230	AT2G38220.1   expressed protein   chr2:16015190-16017136 FORWARD   Aliases: F16M14.15, F16M14_15	2.8	2.9	-0.0	-0.2	100.0%	-4.9
17231	AT1G06260.1   cysteine proteinase, putative, contains similarity to thiol-protease, pre-pro-TPE4A protein GI:3688528 (Pisum sativum)   chr1:1916448-1917584 FORWARD   Aliases: F9P14.12, F9P14_12	3.0	3.0	-0.1	-0.2	100.0%	-5.0
17232	AT3G15740.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:5333886-5334560 REVERSE   Aliases: MSJ11.14	3.6	3.5	0.1	0.2	100.0%	-4.8
17233	AT2G27775.2   expressed protein   chr2:11849812-11850370 REVERSE   Aliases: None	4.7	4.6	0.1	0.2	100.0%	-5.1
17234	AT5G03060.1   expressed protein, ; expression supported by MPSS   chr5:716721-717677 REVERSE   Aliases: F15A17.90, F15A17_90	2.7	2.7	0.0	0.2	100.0%	-5.7
17235	AT2G24840.1   MADS-box family protein   chr2:10588161-10588955 FORWARD   Aliases: F27C12.24, F27C12_24	3.5	3.5	0.1	0.2	100.0%	-5.0
17236	AT4G31300.2   Symbol: PBA1   similar to 20S proteasome beta subunit E1 (PBE1) (PRCE) [Arabidopsis thaliana] (TAIR:At1g13060.1); similar to PREDICTED OJ1079_F11.26 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_507536.1); contains InterPro domain Proteasome B-type subunit (InterPro:IPR000243); contains InterPro domain Multispecific proteasome protease (InterPro:IPR001353)   chr4:15188769-15191159 FORWARD   Aliases: 20S PROTEASOME SUBUNIT PBA1, F8F16.120, F8F16_120	11.1	11.0	0.1	0.2	100.0%	-4.9
17237	AT2G15750.1   expressed protein   chr2:6870004-6871198 FORWARD   Aliases: F9O13.30	3.2	3.2	-0.0	-0.2	100.0%	-5.6
17238	AT3G61880.1   Symbol: CYP78A9   cytochrome P450, putative, similar to cytochrome p450 SP:O48927 from (Arabidopsis thaliana)   chr3:22916843-22918933 REVERSE   Aliases: CYTOCHROME P450 78A9, F21F14.50	3.8	3.7	0.1	0.2	100.0%	-4.5
17239	AT2G33690.1   late embryogenesis abundant protein, putative / LEA protein, putative, similar to responsive to water deficit, novel late embryogenesis abundant-like protein PvLEA-18 (GI:2347086) (Phaseolus vulgaris)	2.4	2.4	0.0	0.2	100.0%	-6.0
17240	AT3G49640.1   nitrogen regulation family protein, similar to NITROGEN REGULATION PROTEIN NIFR3 (SP:Q08111) (Rhodobacter capsulatus); contains Pfam domain PF01207: Dihydrouridine synthase (Dus)   chr3:18411764-18415791 REVERSE   Aliases: T9C5.230	5.9	5.9	-0.1	-0.2	100.0%	-4.7
17241	AT2G41110.1   Symbol: ATCAL4	9.1	8.9	0.1	0.2	100.0%	-4.7
17242	AT3G50230.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase (RKL1), Arabidopsis thaliana, EMBL:AF084034   chr3:18631581-18634182 FORWARD   Aliases: F11C1.70	2.9	2.9	-0.0	-0.2	100.0%	-5.3
17243	AT3G24710.1   expressed protein   chr3:9023967-9024374 REVERSE   Aliases: MSD24.9	3.3	3.3	-0.0	-0.2	100.0%	-5.1
17244	AT1G50900.1   expressed protein   chr1:18869874-18870872 FORWARD   Aliases: F8A12.12, F8A12_12	4.3	4.2	0.1	0.2	100.0%	-4.7
17245	AT2G43010.2   Symbol: PIF4   phytochrome-interacting factor 4 (PIF4) / basic helix-loop-helix protein 9 (bHLH9) / short under red-light 2 (SRL2), identical to SP:Q8W2F3 Phytochrome-interacting factor 4 (Basic helix-loop-helix protein 9) (bHLH9) (Short under red-light 2) {Arabidopsis thaliana}; supporting cDNA gi:18026965:gb:AF251694.1:AF251694   chr2:17893504-17896127 FORWARD   Aliases: MFL8.13, MFL8_13, PHYTOCHROME INTERACTING FACTOR 4, SRL2	2.8	2.8	0.0	0.2	100.0%	-5.2
17246	AT2G04050.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile: PF01554 uncharacterized membrane protein family   chr2:1337383-1339267 REVERSE   Aliases: F3L12.12, F3L12_12	3.5	3.5	0.0	0.2	100.0%	-5.3
17247	AT4G00050.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	3.0	0.0	0.2	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17248	AT5G51710.1   Symbol: KEA5   K+ efflux antiporter, putative (KEA5), Monovalent cation:proton antiporter family 2 (CPA2 family) member, PMID:11500563; related to glutathione-regulated potassium-efflux system protein (Escherichia coli) GP:606284:gb:AAA58147   chr5:21021504-21025944 REVERSE   Aliases: ATKEA5, MIO24.16, MIO24_16	4.2	4.3	-0.1	-0.2	100.0%	-5.0
17249	AT2G11830.1   expressed protein   chr2:4778947-4780327 REVERSE   Aliases: F7E22.2, F7E22_2	3.4	3.5	-0.0	-0.2	100.0%	-5.4
17250	AT1G69960.1   Symbol: PP2A   serine/threonine protein phosphatase PP2A-5 catalytic subunit (PP2A5), identical to SP:O04951:P2A5_ARATH Serine/threonine protein phosphatase PP2A-5 catalytic subunit (EC 3.1.3.16) {Arabidopsis thaliana}; contains Pfam profile PF00149: Ser/Thr protein phosphatase   chr1:26352384-26354329 REVERSE   Aliases: F20P5.30, F20P5_30, SERINE/THREONINE PROTEIN PHOSPHATASE 2A, TYPE 2A SERINE/THREONINE PROTEIN PHOSPHATASE	7.4	7.2	0.1	0.2	100.0%	-4.9
17251	AT5G14560.1   expressed protein   chr5:4693967-4694089 FORWARD   Aliases: T15N1.50, T15N1_50	3.1	3.1	0.0	0.2	100.0%	-5.7
17252	AT3G13490.1   tRNA synthetase class II (D, K and N) family protein, similar to SP:Q9RHHV9 Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) {Bacillus stearothermophilus}; contains Pfam profile: PF00152 tRNA synthetases class II (D, K and N)	5.3	5.2	0.1	0.2	100.0%	-5.1
17253	AT3G30210.1   Symbol: MYB121	5.8	5.8	0.1	0.2	100.0%	-5.0
17254	AT4G22140.2   similar to bromo-adjacent homology (BAH) domain-containing protein [Arabidopsis thaliana] (TAIR:At4g04260.1); similar to receptor like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_482453.1); contains InterPro domain Zn-finger-like, PHD finger (InterPro:IPR001965); contains InterPro domain Bromo adjacent region (InterPro:IPR001025)   chr4:11727755-11730501 REVERSE   Aliases: F1N20.240, F1N20_240	4.0	3.9	0.1	0.2	100.0%	-4.9
17255	AT1G09830.1   phosphoribosylamine--glycine ligase (PUR2), Identical to phosphoribosylamine--glycine ligase, chloroplast (precursor) SP:P52420 from (Arabidopsis thaliana)   chr1:3192683-3195008 REVERSE   Aliases: F21M12.22, F21M12_22	9.2	9.3	-0.1	-0.2	100.0%	-4.6
17256	AT4G31540.1   exocyst subunit EXO70 family protein (EXO70-G1), tomato leucine zipper-containing protein - Lycopersicon esculentum, PIR2:S21495; contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr4:15284395-15287312 REVERSE   Aliases: F3L17.110, F3L17_110	4.1	4.0	0.1	0.2	100.0%	-5.1
17257	AT1G52600.1   signal peptidase, putative, similar to SP:P13679 Microsomal signal peptidase 21 kDa subunit (EC 3.4.-.-) {Canis familiaris}; contains Pfam profile PF00461: Signal peptidase I   chr1:19594194-19596343 FORWARD   Aliases: F6D8.18, F6D8_18	8.7	8.6	0.1	0.2	100.0%	-4.8
17258	AT1G24938.1   expressed protein   chr1:8789363-8792067 REVERSE   Aliases: None	2.7	2.7	-0.1	-0.2	100.0%	-5.0
17259	AT2G03520.1   Symbol: ATUPS4	2.2	2.2	-0.0	-0.2	100.0%	-5.6
17260	AT3G59180.1   expressed protein, contains a novel domain with similarity to F-box domain;   chr3:21891696-21893436 FORWARD   Aliases: F25L23.40	2.8	2.8	-0.0	-0.2	100.0%	-5.8
17261	AT5G49440.1   expressed protein   chr5:20065465-20066823 FORWARD   Aliases: K7J8.12, K7J8_12	3.1	3.0	0.1	0.2	100.0%	-5.0
17262	AT5G25910.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596;   chr5:9038863-9041380 FORWARD   Aliases: T1N24.21, T1N24_21	2.3	2.3	0.0	0.2	100.0%	-5.7
17263	AT3G57000.1   nucleolar essential protein-related, contains weak similarity to Nucleolar essential protein 1 (Essential for mitotic growth 1) (Swiss-Prot:Q06287) (Saccharomyces cerevisiae)   chr3:21103247-21105271 FORWARD   Aliases: F24I3.80	7.8	7.8	-0.1	-0.2	100.0%	-4.8
17264	AT3G30530.1   bZIP transcription factor family protein, similar to bZIP protein(G/HBF-1) GI:1905785 from (Glycine max ); contains PFAM profile: bZIP transcription factor PF00170   chr3:12141991-12142512 FORWARD   Aliases: MQP15.3	2.4	2.4	0.0	0.2	100.0%	-5.6
17265	AT2G02490.1   similar to proline-rich family protein [Arabidopsis thaliana] (TAIR:At5g59170.1); similar to LENOD2 [Lupinus luteus] (GB:CAA39050.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr2:667040-668268 FORWARD   Aliases: T8K22.21, T8K22_21	1.9	1.8	0.1	0.2	100.0%	-5.2
17266	AT4G29990.1   light repressible receptor protein kinase, identical to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376	4.0	3.9	0.1	0.2	100.0%	-5.0
17267	AT1G75920.1   family II extracellular lipase 5 (EXL5), EXL5 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 (Arabidopsis thaliana (Mouse-ear cress))   chr1:28509252-28510684 FORWARD   Aliases: T4O12.14, T4O12_14	3.8	3.9	-0.1	-0.2	100.0%	-4.9
17268	AT3G56100.1   Symbol: MRLK   leucine-rich repeat transmembrane protein kinase, putative, hypothetical proteins - Arabidopsis thaliana	3.2	3.3	-0.1	-0.2	100.0%	-5.0
17269	AT1G24000.1   Bet v I allergen family protein, contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:8496046-8496515 REVERSE   Aliases: T23E23.17, T23E23_17	3.8	3.8	0.1	0.2	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17270	AT3G30390.2   similar to amino acid transporter family protein [Arabidopsis thaliana] (TAIR:At5g38820.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910699.1); similar to putative system A transporter isoform 2 [Oryza sativa (japonica cultivar-group)] (GB:BAD37809.1); contains InterPro domain Amino acid/polyamine transporter, family II (InterPro:IPR002422); contains InterPro domain Aromatic amino acid permease (InterPro:IPR002091)   chr3:11979316-11982100 REVERSE   Aliases: T6J22.19	6.0	5.8	0.2	0.2	100.0%	-4.6
17271	AT1G17160.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr1:5867639-5869323 FORWARD   Aliases: F20D23.14, F20D23_14	9.0	9.1	-0.1	-0.2	100.0%	-5.0
17272	AT5G51310.1   gibberellin 20-oxidase-related, low similarity to GI:9791186, GI:1109695	2.8	2.9	-0.1	-0.2	100.0%	-4.8
17273	AT4G01460.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	3.0	0.0	0.2	100.0%	-5.5
17274	AT1G20575.1   dolichyl-phosphate beta-D-mannosyltransferase, putative / dolichol-phosphate mannosyltransferase, putative / mannose-P-dolichol synthase, putative, similar to DPM1 from Homo sapiens (SP:O60762); member of glycosyltransferase family 2   chr1:7126785-7128735 REVERSE   Aliases: None	8.1	8.1	0.1	0.2	100.0%	-5.0
17275	AT5G57320.1   villin, putative, similar to villin 2 (VLN2) (Arabidopsis thaliana) GI:3415115, villin 3 (VLN3) (Arabidopsis thaliana) GI:3415117; contains Pfam profiles PF00626: Gelsolin repeat, PF02209: Villin headpiece domain   chr5:23229916-23234775 FORWARD   Aliases: MJB24.13, MJB24_13	2.6	2.7	-0.0	-0.2	100.0%	-5.3
17276	AT4G26670.1   mitochondrial import inner membrane translocase subunit Tim17/Tim22/Tim23 family protein, weak similarity to SP:Q9Z0V8 Mitochondrial import inner membrane translocase subunit TIM17 A {Mus musculus}; contains Pfam profile PF02466: Mitochondrial import inner membrane translocase subunit Tim17   chr4:13452178-13453990 FORWARD   Aliases: F10M23.10, F10M23_10	6.7	6.8	-0.1	-0.2	100.0%	-4.7
17277	AT5G60980.2   nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing protein, G3BP ras-GTPase-activating protein SH3-domain binding protein, Mus musculus, EMBL:MMU65313   chr5:24560586-24563495 FORWARD   Aliases: MSL3.12, MSL3_12	5.1	5.0	0.0	0.2	100.0%	-5.2
17278	AT1G09930.1   Symbol: ATOPT2	3.0	3.0	0.0	0.2	100.0%	-5.4
17279	AT1G34340.1   esterase/lipase/thioesterase family protein, similar to late embryogenesis abundant protein (EMB8) GI:1350544 SP:Q40863 from (Picea glauca); contains Interpro entry IPR000379 esterase/lipase/thioesterase family   chr1:12530805-12534140 FORWARD   Aliases: F7P12.5	5.5	5.6	-0.1	-0.2	100.0%	-4.7
17280	AT3G51760.1   expressed protein   chr3:19209125-19210477 REVERSE   Aliases: ATEM1.1	3.1	3.2	-0.1	-0.2	100.0%	-5.1
17281	AT4G32390.1   phosphate translocator-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}   chr4:15636556-15637608 FORWARD   Aliases: F8B4.90, F8B4_90	4.9	5.0	-0.1	-0.2	100.0%	-4.8
17282	AT3G02850.1   Symbol: SKOR   stelar K+ outward rectifier (SKOR) / potassium channel protein, identical to SKOR (Arabidopsis thaliana) gi:3810676:emb:CAA11280; member of the 1 pore, 6 transmembrane (1P/6TM) Shaker K+ channel family, PMID:11500563	2.8	2.7	0.1	0.2	100.0%	-4.1
17283	AT3G04520.1   threonine aldolase family protein, similar to L-allo-threonine aldolase SP:O07051 from (Aeromonas jandaei)   chr3:1217248-1219765 REVERSE   Aliases: None	6.6	6.6	0.1	0.2	100.0%	-4.9
17284	AT5G53810.1   O-methyltransferase, putative, similar to GI:2781394   chr5:21867405-21870237 REVERSE   Aliases: MGN6.20, MGN6_20	3.2	3.1	0.1	0.2	100.0%	-5.3
17285	AT5G05280.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:1565448-1566392 REVERSE   Aliases: K18I23.8, K18I23_8	2.5	2.5	-0.0	-0.2	100.0%	-5.6
17286	AT4G28080.1   expressed protein   chr4:13948609-13957424 REVERSE   Aliases: T13J8.190, T13J8_190	3.9	3.9	0.0	0.2	100.0%	-5.3
17287	AT4G37010.2   similar to caltractin / centrin [Arabidopsis thaliana] (TAIR:At3g50360.1); similar to centrin [Nicotiana tabacum] (GB:AAF07221.1); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048); contains InterPro domain Flagellar calcium-binding protein (calflagin) (InterPro:IPR003299)   chr4:17444303-17445609 FORWARD   Aliases: AP22.11, AP22_11	3.2	3.1	0.1	0.2	100.0%	-4.3
17288	AT1G75950.1   Symbol: SKP1   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At1), E3 ubiquitin ligase; skp1a; identical to Skp1a GI:3068807, Skp1p GI:1432083 and UIP1 GI:3719209 from (Arabidopsis thaliana); contains Pfam profiles PF01466: Skp1 family, dimerisation domain and PF03931: Skp1 family, tetramerisation domain;   chr1:28520258-28521360 FORWARD   Aliases: ARABIDOPSIS SKP1 HOMOLOGUE, ASK1, ATSKP1, SKP1A, T4O12.17, T4O12_17, UFO INTERACTING PROTEIN 1, UIP1	10.6	10.7	-0.1	-0.2	100.0%	-5.2
17289	AT2G04360.1   expressed protein   chr2:1519394-1521053 REVERSE   Aliases: T23O15.18	5.4	5.3	0.1	0.2	100.0%	-4.8
17290	AT5G47260.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.8	2.9	-0.0	-0.2	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17291	AT1G63950.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr1:23738660-23739219 FORWARD   Aliases: T12P18.3, T12P18_3	3.3	3.2	0.0	0.2	100.0%	-5.4
17292	AT1G36670.1   expressed protein   chr1:13865447-13866548 REVERSE   Aliases: T15P17.10, T15P17_10	3.2	3.2	0.0	0.2	100.0%	-5.6
17293	AT5G11640.1   expressed protein, predicted proteins, Drosophila melanogaster and Homo sapiens   chr5:3742009-3743980 FORWARD   Aliases: T22P22.30, T22P22_30	6.4	6.4	0.0	0.2	100.0%	-5.1
17294	AT5G26070.1   Encodes a protein with 23.5% proline residues and proline-rich extensin domains, INTERPRO:IPR002965; similar to root nodule extensin (Pisum sativum) gi:15021750/gb:AAK77902; Common family members: At5g19800, At5g57070, At1g72790 (Arabidopsis thaliana)   chr5:9106344-9106652 FORWARD   Aliases: T1N24.104, T1N24_104	2.3	2.3	0.0	0.2	100.0%	-5.8
17295	AT1G69990.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor-like protein kinase GI:8777368 from (Arabidopsis thaliana)   chr1:26363898-26365673 REVERSE   Aliases: F20P5.27, F20P5_27	3.1	3.1	-0.1	-0.2	100.0%	-5.1
17296	AT2G37630.1   Symbol: AS1   myb family transcription factor (MYB91), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:15788693-15790476 REVERSE   Aliases: ASYMMETRIC LEAVES 1, ATPHAN, F13M22.13, F13M22_13, MYB91	5.7	5.8	-0.1	-0.2	100.0%	-4.4
17297	AT5G60590.2   yrdC protein-related   chr5:24374251-24375976 FORWARD   Aliases: MUP24.1	2.6	2.6	0.0	0.2	100.0%	-5.4
17298	AT2G36370.1   F-box family protein (FBL11), contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from (Homo sapiens)   chr2:15254847-15260043 FORWARD   Aliases: F2H17.2, F2H17_2	3.7	3.6	0.0	0.2	100.0%	-5.2
17299	AT1G68170.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr1:25555585-25557921 FORWARD   Aliases: T22E19.23, T22E19_23	3.3	3.4	-0.1	-0.2	100.0%	-5.0
17300	AT3G04350.1   expressed protein   chr3:1153734-1156783 REVERSE   Aliases: T6K12.3, T6K12_3	5.0	5.0	-0.1	-0.2	100.0%	-5.0
17301	AT1G77655.1   expressed protein   chr1:29187502-29188066 REVERSE   Aliases: None	3.9	3.8	0.0	0.2	100.0%	-5.4
17302	AT5G25760.2   similar to ubiquitin-conjugating enzyme 10 (UBC10) [Arabidopsis thaliana] (TAIR:At5g53300.2); similar to ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] (TAIR:At2g16740.1); similar to ubiquitin-conjugating enzyme 10 (UBC10) [Arabidopsis thaliana] (TAIR:At5g53300.1); similar to ubiquitin-conjugating enzyme E2-17 kDa 9 (UBC9) [Arabidopsis thaliana] (TAIR:At4g27960.2); similar to ubiquitin-conjugating enzyme E2 [Pavlova lutheri] (GB:AAN16047.1); contains InterPro domain Ubiquitin-conjugating enzymes (InterPro:IPR000608)	6.6	6.7	-0.1	-0.2	100.0%	-4.8
17303	AT5G06260.1   nucleolar protein-related, contains weak similarity to nucleolar protein C7C (GI:13540302) (Rattus norvegicus)   chr5:1902600-1905102 REVERSE   Aliases: MHF15.22, MHF15_22	6.8	6.6	0.1	0.2	100.0%	-4.6
17304	AT1G61750.1   expressed protein, contains Pfam profile: PF01657 domain of unknown function   chr1:22808660-22809983 REVERSE   Aliases: T13M11.11, T13M11_11	2.4	2.4	0.0	0.2	100.0%	-5.6
17305	AT1G67760.1   similar to T-complex protein 1 epsilon subunit, putative / TCP-1-epsilon, putative / chaperonin, putative [Arabidopsis thaliana] (TAIR:At1g24510.1); similar to T complex protein (GB:2206327A)   chr1:25409243-25410035 REVERSE   Aliases: F12A21.11, F12A21_11	3.6	3.7	-0.1	-0.2	100.0%	-4.9
17306	AT4G31100.1   wall-associated kinase, putative	3.6	3.6	-0.0	-0.2	100.0%	-5.4
17307	AT1G43780.1   Symbol: SCPL44	2.5	2.5	0.0	0.2	100.0%	-4.9
17308	AT5G48050.1   expressed protein, low similarity to copia-like polyprotein (Arabidopsis thaliana) GI:13872712   chr5:19489887-19490996 REVERSE   Aliases: MDN11.13, MDN11_13	2.8	2.8	-0.0	-0.2	100.0%	-5.5
17309	AT3G27590.1   expressed protein   chr3:10222384-10222952 FORWARD   Aliases: MMJ24.15	2.6	2.6	-0.0	-0.2	100.0%	-5.1
17310	AT3G58280.1   expressed protein   chr3:21589594-21590261 REVERSE   Aliases: F9D24.190	2.7	2.7	0.0	0.2	100.0%	-5.5
17311	AT5G16460.1   expressed protein, similar to unknown protein (pir::T02326)   chr5:5377088-5378536 REVERSE   Aliases: MQK4.19, MQK4_19	2.2	2.2	-0.0	-0.2	100.0%	-5.8
17312	AT5G51900.1   cytochrome P450 family, similar to cytochrome P450 86A1 (SP:P48422) (Arabidopsis thaliana)   chr5:21110907-21111680 REVERSE   Aliases: MJM18.5, MJM18_5	2.5	2.4	0.0	0.2	100.0%	-5.9
17313	AT2G41440.1   expressed protein   chr2:17278281-17284775 FORWARD   Aliases: T26J13.3, T26J13_3	2.7	2.8	-0.0	-0.2	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17314	AT5G55340.1   long-chain-alcohol O-fatty-acyltransferase family protein / wax synthase family protein, contains similarity to wax synthase similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis	4.5	4.4	0.1	0.2	100.0%	-4.8
17315	AT5G09300.2   2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 alpha subunit, putative, similar to branched-chain alpha-keto acid dehydrogenase E1-alpha subunit (Gallus gallus) GI:12964598; contains Pfam profile PF00676: Dehydrogenase E1 component   chr5:2884181-2886474 REVERSE   Aliases: T5E8.100, T5E8_100	8.3	8.4	-0.1	-0.2	100.0%	-4.7
17316	AT1G53710.1   similar to putative cell division control protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470871.1); contains InterPro domain Metallophosphoesterase (InterPro:IPR004843)   chr1:20056829-20060064 REVERSE   Aliases: F22G10.25, F22G10_25	4.9	4.9	-0.0	-0.2	100.0%	-5.6
17317	AT5G58782.1   dehydrodolichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076   chr5:23755373-23756690 REVERSE   Aliases: None	2.6	2.6	0.0	0.2	100.0%	-5.5
17318	AT5G13850.1   nascent polypeptide-associated complex (NAC) domain-containing protein, similar to alpha-NAC, non-muscle form (Mus musculus) GI:1666690; contains Pfam profile PF01849: NAC domain   chr5:4471315-4472857 FORWARD   Aliases: MAC12.19, MAC12_19	8.4	8.5	-0.1	-0.2	100.0%	-4.6
17319	AT5G51680.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; similar to hydroxyproline-rich Glycoprotein (HRGP) (Zea mays) gi:4007865:emb:CAA10387   chr5:21014546-21016067 FORWARD   Aliases: MIO24.19, MIO24_19	2.8	2.8	-0.1	-0.2	100.0%	-4.8
17320	AT2G47220.1   3' exoribonuclease family domain 1 protein-related, similar to polynucleotide phosphorylase (Pisum sativum) GI:2286200, polyribonucleotide phosphorylase (Spinacia oleracea) GI:1924972; contains Pfam profiles PF05266: Protein of unknown function (DUF724), weak hit to PF01138: 3' exoribonuclease family, domain 1   chr2:19390813-19394024 FORWARD   Aliases: T8I13.6	2.3	2.3	-0.0	-0.2	100.0%	-5.3
17321	AT2G37670.1   WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); similar to rab11 binding protein (GI:4512103) (Bos taurus)   chr2:15804462-15807614 REVERSE   Aliases: F13M22.17, F13M22_17	4.4	4.4	-0.1	-0.2	100.0%	-5.0
17322	AT5G05050.1   peptidase C1A papain family protein, weak similarity to berghepain-2 (Plasmodium berghei) GI:17978639; contains Pfam profile PF00112: Papain family cysteine protease   chr5:1491640-1493458 FORWARD   Aliases: MUG13.9, MUG13_9	2.5	2.5	-0.0	-0.2	100.0%	-5.6
17323	AT2G38680.1   pyrimidine 5'-nucleotidase family protein / uridine monophosphate hydrolase-1 (UMPH-1) family protein, similar to pyrimidine 5'-nucleotidase (Homo sapiens) GI:11245474; contains Pfam profile PF05822: Pyrimidine 5'-nucleotidase (UMPH-1)   chr2:16181536-16182951 REVERSE   Aliases: T6A23.12, T6A23_12	4.8	4.8	0.1	0.2	100.0%	-4.7
17324	AT5G37140.1   tRNA-splicing endonuclease positive effector-related, contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease (Saccharomyces cerevisiae) gi:172574:gb:AAB63976   chr5:14707666-14710081 FORWARD   Aliases: MJG14.20, MJG14_20	3.3	3.2	0.0	0.2	100.0%	-5.2
17325	AT5G64010.1   expressed protein   chr5:25635445-25637405 REVERSE   Aliases: MBM17.11, MBM17_11	7.1	7.2	-0.1	-0.2	100.0%	-4.8
17326	AT1G11820.1   similar to glycosyl hydrolase family 17 protein / beta-1,3-glucanase, putative [Arabidopsis thaliana] (TAIR:At2g01630.1); similar to E131_ARATH Putative glucan endo-1,3-beta-glucosidase 1 precursor ((1->3)-beta-glucan endohydrolase) ((1->3)-beta-glucanase) (Beta-1,3-endoglucanase) (Beta-1,3-glucanase) (GB:O65399); contains InterPro domain Glycoside hydrolase, family 17 (InterPro:IPR000490)	5.6	5.7	-0.1	-0.2	100.0%	-4.4
17327	AT1G27210.1   expressed protein   chr1:9455455-9458013 REVERSE   Aliases: T7N9.27, T7N9_27	4.6	4.5	0.1	0.2	100.0%	-4.7
17328	AT3G14160.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to alkB protein (Caulobacter crescentus)(GI:2055386); contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily   chr3:4694070-4695611 FORWARD   Aliases: MAG2.12	3.7	3.7	-0.0	-0.2	100.0%	-5.4
17329	AT1G73570.1   suppressor of lin-12-like protein-related / sel-1 protein-related, similar to Sel-1 homolog precursor (Suppressor of lin-12-like protein) (Sel-1L)(SP:Q9UBV2) {Homo sapiens}   chr1:27654653-27657603 FORWARD   Aliases: F6D5.4, F6D5_4	3.4	3.4	-0.0	-0.2	100.0%	-5.4
17330	AT1G03630.2   Symbol: POR   similar to protochlorophyllide reductase A, chloroplast / PCR A / NADPH-protochlorophyllide oxidoreductase A (PORA) [Arabidopsis thaliana] (TAIR:At5g54190.1); similar to protochlorophyllide reductase B, chloroplast / PCR B / NADPH-protochlorophyllide oxidoreductase B (PORB) [Arabidopsis thaliana] (TAIR:At4g27440.1); similar to NADPH-protochlorophyllide oxidoreductase [Cucumis sativus] (GB:BAA21089.1); contains InterPro domain Glucose/ribitol dehydrogenase (InterPro:IPR002347); contains InterPro domain Light-dependent protochlorophyllide reductase (InterPro:IPR005979); contains InterPro domain Short-chain dehydrogenase/reductase SDR (InterPro:IPR002198)   chr1:907650-909375 FORWARD   Aliases: F21B7.24, NADPH:PROTOCHLOROPHYLLIDE OXIDOREDUCTASE, PROTOCHLOROPHYLLIDE OXIDOREDUCTASE	7.6	7.7	-0.1	-0.2	100.0%	-4.3
17331	AT1G64520.1   26S proteasome regulatory subunit, putative (RPN12), similar to 26S proteasome regulatory complex subunit p30 GB:AAF08395 GI:6434966 from (Drosophila melanogaster)   chr1:23960061-23961981 FORWARD   Aliases: F1N19.9, F1N19_9	9.8	9.7	0.1	0.2	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17332	AT5G51800.1   expressed protein   chr5:21065417-21069238 FORWARD   Aliases: MIO24.6, MIO24_6	2.7	2.7	-0.0	-0.2	100.0%	-5.8
17333	AT4G37460.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile PF00515: TPR Domain   chr4:17608371-17615770 REVERSE   Aliases: F6G17.110, F6G17_110	7.0	7.1	-0.1	-0.2	100.0%	-4.8
17334	AT3G21700.3   expressed protein   chr3:7644482-7646362 FORWARD   Aliases: MSD21.1	3.0	3.1	-0.1	-0.2	100.0%	-5.0
17335	AT2G17060.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr2:7429493-7433959 FORWARD   Aliases: F6P23.21, F6P23_21	2.3	2.2	0.0	0.2	100.0%	-5.1
17336	AT3G49440.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr3:18346700-18347302 REVERSE   Aliases: T9C5.40	2.3	2.3	-0.0	-0.2	100.0%	-5.9
17337	AT1G53730.1   leucine-rich repeat transmembrane protein kinase, putative, similar to GI:3360289 from (Zea mays) (Plant Mol. Biol. 37 (5), 749-761 (1998))   chr1:20065398-20069369 FORWARD   Aliases: F22G10.31, F22G10_31	6.5	6.5	0.1	0.2	100.0%	-5.0
17338	AT1G70280.2   NHL repeat-containing protein, contains Pfam profile PF01436: NHL repeat	4.9	5.0	-0.1	-0.2	100.0%	-4.7
17339	AT1G26900.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:9319743-9321461 REVERSE   Aliases: T2P11.9, T2P11_9	4.3	4.4	-0.1	-0.2	100.0%	-4.7
17340	AT1G22610.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr1:7994280-7997574 FORWARD   Aliases: F12K8.4, F12K8_4	7.9	7.9	0.0	0.2	100.0%	-5.2
17341	AT4G21080.1   Dof-type zinc finger domain-containing protein, prolamin box binding factor, Zea mays, PATCHX:G2393775   chr4:11254613-11255362 REVERSE   Aliases: F7J7.20, F7J7_20	2.5	2.5	-0.0	-0.2	100.0%	-5.7
17342	AT1G78160.1   pumilio/Puf RNA-binding domain-containing protein, contains Pfam profile: PF00806 Pumilio-family RNA binding domains (aka PUM-HD, Pumilio homology domain) (8 copies at C-terminal half of protein)   chr1:29412793-29415077 FORWARD   Aliases: T11I11.10, T11I11_10	2.7	2.8	-0.0	-0.2	100.0%	-5.5
17343	AT4G16780.1   Symbol: ATHB 2	3.8	3.7	0.1	0.2	100.0%	-5.0
17344	AT5G56770.1   expressed protein   chr5:22980220-22981215 REVERSE   Aliases: MIK19.24, MIK19_24	2.7	2.6	0.0	0.2	100.0%	-5.4
17345	AT4G35970.1   L-ascorbate peroxidase, putative, similar to ascorbate peroxidase (Gossypium hirsutum) gi:1019946:gb:AAB52954; identical to putative ascorbate peroxidase APX5 (AT4g35970) mRNA, partial cds GI:31980501; contains Pfam domain PF00141: Peroxidase   chr4:17028609-17030296 FORWARD   Aliases: T19K4.100	3.1	3.1	-0.1	-0.2	100.0%	-4.8
17346	AT4G31160.1   transducin family protein / WD-40 repeat family protein, contains 2 WD-40 repeats (PF00400); KIAA0800 protein, Homo sapiens GI:3882321 EMBL:AB018343   chr4:15145942-15152945 FORWARD   Aliases: F6E21.80, F6E21_80	5.2	5.2	0.1	0.2	100.0%	-4.8
17347	AT1G76430.1   phosphate transporter family protein, similar to phosphate transporters from (Catharanthus roseus) GI:2208908 and (Nicotiana tabacum) GI:12641853, transmembrane protein (Solanum tuberosum) GI:17065936; contains Pfam profile: PF00083 major facilitator superfamily protein   chr1:28683829-28686768 REVERSE   Aliases: F15M4.7	3.3	3.3	-0.1	-0.2	100.0%	-5.1
17348	AT4G30170.1   peroxidase, putative, identical to peroxidase ATP8a (Arabidopsis thaliana) gi:1546706:emb:CAA67361   chr4:14762847-14764633 FORWARD   Aliases: F9N11.20, F9N11_20	2.4	2.5	-0.1	-0.2	100.0%	-4.6
17349	AT5G64530.1   Symbol: ANAC104/XND1   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to NAM (no apical meristem)   chr5:25812459-25814164 FORWARD   Aliases: ANAC104, MUB3.5, MUB3_5, XND1	2.4	2.4	0.0	0.2	100.0%	-5.3
17350	AT2G20720.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam TIGR00756: pentatricopeptide repeat domain   chr2:8934903-8937193 REVERSE   Aliases: F5H14.31, F5H14_31	4.6	4.7	-0.1	-0.2	100.0%	-4.7
17351	AT1G15600.1   expressed protein   chr1:5368918-5369756 FORWARD   Aliases: T16N11.10, T16N11_10	4.3	4.4	-0.1	-0.2	100.0%	-5.1
17352	AT2G28360.1   SIT4 phosphatase-associated family protein, contains Pfam profile: PF04499 SIT4 phosphatase-associated protein   chr2:12131681-12136956 REVERSE   Aliases: T1B3.12, T1B3_12	2.9	2.9	-0.0	-0.2	100.0%	-5.1
17353	AT5G01030.2   expressed protein   chr5:9933-13234 FORWARD   Aliases: F7J8.10, F7J8_10	7.1	7.1	-0.1	-0.2	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17354	AT3G54820.1   Symbol: PIP2;5/PIP2D   aquaporin, putative, similar to plasma membrane aquaporin GI:3551133 from (Raphanus sativus)   chr3:20312999-20314988 FORWARD   Aliases: F28P10.200, PIP2;5, PIP2D	4.0	4.1	-0.1	-0.2	100.0%	-4.5
17355	AT5G41940.1   RabGAP/TBC domain-containing protein, similar to GTPase activating protein (Yarrowia lipolytica) GI:2370595; contains Pfam profile PF00566: TBC domain   chr5:16799224-16802804 FORWARD   Aliases: MJC20.4, MJC20_4	7.1	7.1	-0.0	-0.2	100.0%	-5.1
17356	AT3G24270.1   expressed protein   chr3:8796548-8797038 REVERSE   Aliases: K7M2.3	3.2	3.1	0.1	0.2	100.0%	-4.9
17357	AT1G74200.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591 disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591   chr1:27910570-27913019 REVERSE   Aliases: F1O17.13, F1O17_13	3.3	3.3	-0.1	-0.2	100.0%	-4.9
17358	AT1G79400.1   Symbol: ATCHX2	3.6	3.5	0.0	0.2	100.0%	-5.0
17359	AT4G35780.1   protein kinase family protein, similar to protein kinase (gi:170047) from Glycine max, (gi:13124865) from Arachis hypogaea; contains Pfam protein kinase domain PF00069   chr4:16946526-16950462 REVERSE   Aliases: F4B14.1	6.7	6.8	-0.1	-0.2	100.0%	-4.8
17360	AT5G61370.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:24689022-24690883 REVERSE   Aliases: MFB13.15, MFB13_15	6.2	6.1	0.1	0.2	100.0%	-4.6
17361	AT5G61110.1   expressed protein   chr5:24598304-24599217 REVERSE   Aliases: MAF19.11, MAF19_11	2.2	2.2	0.0	0.2	100.0%	-5.9
17362	AT3G60180.2   uridylate kinase, putative / uridine monophosphate kinase, putative / UMP kinase, putative, similar to uridylate kinase (EC 2.7.4.-) (UK) (Uridine monophosphate kinase) (UMP kinase) (UMP/CMP kinase) (Swiss-Prot:O04905) (Arabidopsis thaliana)   chr3:22253715-22255030 REVERSE   Aliases: F27H5.2	4.6	4.5	0.1	0.2	100.0%	-4.6
17363	AT1G65630.1   DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana)   chr1:24410205-24412731 REVERSE   Aliases: F1E22.1	2.4	2.4	-0.0	-0.2	100.0%	-6.0
17364	AT1G69620.1   Symbol: RPL34   60S ribosomal protein L34 (RPL34B), similar to SP:Q42351 from (Arabidopsis thaliana)   chr1:26193501-26194986 FORWARD   Aliases: F24J1.23, RIBOSOMAL PROTEIN L34, RPL34	12.3	12.2	0.0	0.2	100.0%	-5.4
17365	AT1G55120.1   Symbol: ATFRUCT5   beta-fructosidase, putative / beta-fructofuranosidase, putative, similar to beta-fructofuranosidase GI:402740   chr1:20570265-20572943 FORWARD   Aliases: BETA FRUCTOFURANOSIDASE, BETA FRUCTOFURANOSIDASE 5, T7N22.6, T7N22_6	6.2	6.1	0.1	0.2	100.0%	-4.4
17366	AT2G36630.1   expressed protein, contains Pfam profile: PF01925 domain of unknown function DUF81   chr2:15359570-15362213 REVERSE   Aliases: F13K3.3, F13K3_3	4.7	4.6	0.0	0.2	100.0%	-5.1
17367	AT1G08980.1   Symbol: ATAMI1	6.8	6.8	0.1	0.2	100.0%	-4.6
17368	AT4G38630.1   Symbol: AT MCB1   26S proteasome regulatory subunit S5A (RPN10), identical to multiubiquitin chain binding protein (MBP1) SP:P55034, GI:1165206	8.0	7.9	0.1	0.2	100.0%	-5.3
17369	AT1G06900.1   peptidase M16 family protein / insulinase family protein, contains Pfam domain, PF05193: Peptidase M16 inactive domain; similar to insulin-degrading enzyme (Insulysin, Insulinase, Insulin protease) (Mouse) SWISS-PROT:Q9JHR7   chr1:2114927-2120744 REVERSE   Aliases: F4H5.4, F4H5_4	6.2	6.2	0.0	0.2	100.0%	-5.0
17370	AT1G23790.1   expressed protein   chr1:8409952-8412030 FORWARD   Aliases: F5O8.34, F5O8_34	3.6	3.6	-0.1	-0.2	100.0%	-5.0
17371	AT1G10300.1   GTP-binding protein-related, contains similarity to nucleolar GTP-binding protein 1 SP: Q9BZE4 from (Homo sapiens);   chr1:3378144-3380228 FORWARD   Aliases: F14N23.18, F14N23_18	3.2	3.1	0.0	0.2	100.0%	-5.5
17372	AT3G06520.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr3:2020290-2021961 FORWARD   Aliases: F5E6.15, F5E6_15	4.1	4.0	0.1	0.2	100.0%	-5.0
17373	AT3G16950.1   Symbol: LPD1   dihydrolipoamide dehydrogenase 1, plastidic / lipoamide dehydrogenase 1 (PTLPD1), identical to plastidic lipoamide dehydrogenase from Arabidopsis thaliana (gi:7159282)   chr3:5786391-5790531 REVERSE   Aliases: K14A17.6, LIPOAMIDE DEHYDROGENASE, LIPOAMIDE DEHYDROGENASE 1	6.1	6.3	-0.1	-0.2	100.0%	-4.5
17374	AT2G23130.2   Symbol: AGP17   arabinogalactan-protein (AGP17), identical to gi_11935086_gb_AAG41963   chr2:9851379-9852169 FORWARD   Aliases: ARABINOGALACTAN PROTEIN 17, ATAGP17, T20D16.24	2.5	2.5	0.0	0.2	100.0%	-5.2
17375	AT5G65320.1   basic helix-loop-helix (bHLH) family protein, contains similarity to bHLH DNA-binding protein   chr5:26124395-26125952 REVERSE   Aliases: MNA5.5, MNA5_5	3.6	3.7	-0.0	-0.2	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17376	AT3G15352.1   Symbol: ATCOX17   cytochrome c oxidase copper chaperone-related, contains similarity to cytochrome c oxidase copper chaperone (Mus musculus) SWISS-PROT:P56394   chr3:5179507-5180672 FORWARD   Aliases: COX17	7.4	7.3	0.1	0.2	100.0%	-5.2
17377	AT5G57660.1   zinc finger (B-box type) family protein, contains Pfam domain, PF00643: B-box zinc finger   chr5:23372690-23374215 FORWARD   Aliases: MRI1.1, MRI1_1	5.6	5.7	-0.1	-0.2	100.0%	-4.9
17378	AT5G57510.1   expressed protein   chr5:23306390-23306782 REVERSE   Aliases: MUA2.8, MUA2_8	3.1	3.0	0.0	0.2	100.0%	-5.3
17379	AT3G60300.1   RWD domain-containing protein, contains weak similarity to RING finger protein 25 (RING finger protein AO7) (Swiss-Prot:Q9QZR0) (Mus musculus)   chr3:22296306-22298454 FORWARD   Aliases: F27H5.90	11.1	11.1	0.0	0.2	100.0%	-5.3
17380	AT1G09610.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr1:3111791-3112639 FORWARD   Aliases: F14J9.29, F14J9_29	2.4	2.5	-0.0	-0.2	100.0%	-5.5
17381	AT1G27740.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.7	2.8	-0.1	-0.2	100.0%	-4.1
17382	AT5G60720.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547   chr5:24435455-24439460 REVERSE   Aliases: MUP24.14, MUP24_14	3.3	3.2	0.1	0.2	100.0%	-4.6
17383	AT5G16530.1   auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547   chr5:5400738-5402479 FORWARD   Aliases: MQK4.28, MQK4_28	2.6	2.6	0.0	0.2	100.0%	-5.6
17384	AT4G09290.1   expressed protein   chr4:5893341-5894966 REVERSE   Aliases: T30A10.50, T30A10_50	2.7	2.8	-0.0	-0.2	100.0%	-5.8
17385	AT4G00160.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	0.0	0.2	100.0%	-5.9
17386	AT5G53290.1   encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	3.4	3.4	0.0	0.2	100.0%	-5.2
17387	AT4G16730.1   terpene synthase/cyclase family protein, similar to myrcene/ocimene synthase (GI:9957293); contains Pfam profile: PF01397 terpene synthase family   chr4:9402989-9406025 FORWARD   Aliases: DL4390W, FCAALL.15	2.2	2.2	0.0	0.2	100.0%	-6.0
17388	AT1G12810.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr1:4367306-4368800 FORWARD   Aliases: F13K23.6, F13K23_6	5.2	5.2	-0.1	-0.2	100.0%	-4.9
17389	AT4G18090.1   expressed protein   chr4:10034023-10034859 REVERSE   Aliases: F15J5.60, F15J5_60	2.9	2.9	-0.0	-0.2	100.0%	-5.7
17390	AT5G09920.1   Symbol: RPB15.9   RNA polymerase II 15.9 kDa subunit (RPB15.9), identical to 15.9 kDa subunit of RNA polymerase II GI:2760362 from (Arabidopsis thaliana)   chr5:3096184-3097576 FORWARD   Aliases: ATRPB15.9, MYH9.13, MYH9_13, RNA POLYMERASE II 15.9 KDA SUBUNIT, RPB15.9.9	8.0	8.1	-0.1	-0.2	100.0%	-4.6
17391	AT2G17520.1   Symbol: IRE1A   protein kinase family protein / Ire1 homolog-2 (IRE1-2), contains protein kinase domain, Pfam:PF00069; identical to Ire1 homolog-2 (Arabidopsis thaliana) GI:15277139, cDNA Ire1 homolog-2 GI:15277138   chr2:7624292-7628175 FORWARD   Aliases: MJB20.8, MJB20_8, TRANSMEMBRANE PROTEIN KINASE/RIBONUCLEASE	6.9	6.8	0.1	0.2	100.0%	-4.6
17392	AT4G38640.1   choline transporter-related, contains weak similarity to CD92 protein (Homo sapiens) gi:16945323:emb:CAC82175   chr4:18059647-18062283 REVERSE   Aliases: T9A14.3	5.3	5.4	-0.1	-0.2	100.0%	-4.8
17393	AT5G41250.1   exostosin family protein, contains Pfam profile: PF03016	2.2	2.2	-0.0	-0.2	100.0%	-5.9
17394	AT2G40370.1   laccase, putative / diphenol oxidase, putative, similar to laccase (Populus balsamifera subsp. trichocarpa)(GI:3805960)   chr2:16865248-16867684 REVERSE   Aliases: T3G21.14, T3G21_14	3.0	3.0	-0.0	-0.2	100.0%	-5.0
17395	AT5G47480.1   expressed protein   chr5:19274647-19280651 FORWARD   Aliases: MNJ7.7, MNJ7_7	8.2	8.3	-0.1	-0.2	100.0%	-5.1
17396	AT3G28870.1   expressed protein   chr3:10891592-10893076 FORWARD   Aliases: MLD15.4	2.4	2.4	0.0	0.2	100.0%	-6.0
17397	AT5G07760.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr5:2468240-2473658 FORWARD   Aliases: MBK20.22, MBK20_22	2.5	2.4	0.0	0.2	100.0%	-5.9
17398	AT2G04380.1   expressed protein   chr2:1525639-1526764 FORWARD   Aliases: T1O3.21, T1O3_21	2.9	2.9	-0.0	-0.2	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17399	AT1G49230.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:18212952-18213765 FORWARD   Aliases: F27J15.2, F27J15_2	3.8	3.7	0.1	0.2	100.0%	-4.7
17400	AT1G68150.1   Symbol: WRKY9   WRKY family transcription factor, similar to DNA-binding protein ABF2 GI:1159879 from (Avena fatua)   chr1:25547633-25549380 FORWARD   Aliases: ATWRKY9, T22E19.22, T22E19_22, WRKY9	3.0	3.2	-0.1	-0.2	100.0%	-4.7
17401	AT3G15470.1   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP:Q9UGP9) (Homo sapiens)   chr3:5216269-5220225 REVERSE   Aliases: MJK13.13	4.7	4.6	0.0	0.2	100.0%	-5.5
17402	AT2G19050.1   GDSL-motif lipase/hydrolase family protein, low similarity to SP:P40603 Anter-specific proline-rich protein APG (Protein CEX) (Fragment) {Brassica napus}; contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	2.8	2.8	-0.0	-0.2	100.0%	-5.5
17403	AT1G36990.1   expressed protein, contains PS00070: Aldehyde dehydrogenases cysteine active site; similar to high molecular mass nuclear antigen (GI:2754696) (Gallus gallus);similar to streptococcal hemagglutinin (GI:8885520) (Streptococcus gordonii) similar to proteophosphoglycan (GI:5420389) (Leishmania major)   chr1:14029733-14032941 REVERSE   Aliases: T32E20.28, T32E20_28	3.3	3.3	-0.1	-0.2	100.0%	-4.9
17404	AT2G22750.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.2	2.2	0.0	0.2	100.0%	-5.7
17405	AT1G51610.1   cation efflux family protein / metal tolerance protein, putative (MTPc4), member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr1:19140069-19143586 FORWARD   Aliases: F19C24.16	4.8	4.9	-0.1	-0.2	100.0%	-5.0
17406	AT5G58720.1   PRLI-interacting factor, putative, similar to PRLI-interacting factor N (Arabidopsis thaliana) GI:11139276; contains Pfam profile PF01713: Smr domain   chr5:23736607-23740363 REVERSE   Aliases: MZN1.26, MZN1_26	5.0	4.9	0.1	0.2	100.0%	-4.7
17407	AT1G67750.1   pectate lyase family protein, similar to pectate lyase GI:14289169 from (Salix gilgiana)	6.1	6.0	0.1	0.2	100.0%	-4.1
17408	AT4G21130.1   Symbol: EMB2271   transducin family protein / WD-40 repeat family protein, contains 6 WD-40 repeats (PF00400); some similarity to a group of proteins with homology to mammalian apoptosis regulators identified in zebrafish (PUBMED:10917738)Apaf-1(gi:7677507)   chr4:11274319-11276410 FORWARD   Aliases: EMB2271, EMBRYO DEFECTIVE 2271, F7J7.70, F7J7_70	3.4	3.4	-0.1	-0.2	100.0%	-5.0
17409	AT1G70150.1   zinc finger (MYND type) family protein, contains Pfam profile PF01753: MYND finger   chr1:26420561-26422880 FORWARD   Aliases: F20P5.13, F20P5_13	4.1	4.0	0.1	0.2	100.0%	-4.9
17410	AT3G03130.1   expressed protein, ; expression supported by MPSS   chr3:721446-723571 REVERSE   Aliases: T17B22.18, T17B22_18	4.4	4.5	-0.1	-0.2	100.0%	-5.0
17411	AT1G42550.1   expressed protein   chr1:15979855-15982392 FORWARD   Aliases: T8D8.2, T8D8_2	4.9	4.7	0.2	0.2	100.0%	-4.7
17412	AT3G20180.1   hypothetical protein   chr3:7043391-7043847 REVERSE   Aliases: MAL21.22	2.8	2.7	0.0	0.2	100.0%	-5.4
17413	AT2G20870.1   cell wall protein precursor, putative, identical to Putative cell wall protein precursor (Swiss-Prot:P47925) (Arabidopsis thaliana); weak similarity to mu-protocadherin (GI:7861967) (Rattus norvegicus)   chr2:8989071-8989793 REVERSE   Aliases: F5H14.16, F5H14_16	2.9	2.9	-0.0	-0.2	100.0%	-5.2
17414	AT2G29740.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:12713787-12715444 FORWARD   Aliases: T27A16.16, T27A16_16	4.3	4.2	0.1	0.2	100.0%	-4.7
17415	AT5G40340.1   PWWP domain-containing protein, KED, Nicotiana tabacum, EMBL:AB009883   chr5:16148882-16151908 REVERSE   Aliases: MPO12.6, MPO12_6	3.9	4.0	-0.1	-0.2	100.0%	-4.5
17416	AT2G33320.1   C2 domain-containing protein, low similarity to splicing coactivator subunit SRm300 (Homo sapiens) GI:6649242; contains Pfam profile PF00168: C2 domain   chr2:14126603-14129171 REVERSE   Aliases: F4P9.9, F4P9_9	4.0	4.0	-0.1	-0.2	100.0%	-4.9
17417	AT5G51080.3   similar to RNase H domain-containing protein [Arabidopsis thaliana] (TAIR:At1g24090.1); similar to putative RNase [Oryza sativa (japonica cultivar-group)] (GB:AAP54111.1); contains InterPro domain RNase H (InterPro:IPR002156)   chr5:20786050-20788219 REVERSE   Aliases: MWD22.2, MWD22_2	2.6	2.5	0.0	0.2	100.0%	-5.5
17418	AT4G03890.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr4:1836408-1837816 FORWARD   Aliases: T25H8.3, T25H8_3	2.6	2.5	0.0	0.2	100.0%	-5.8
17419	AT3G05730.1   Encodes a defensin-like (DEFL) family protein.   chr3:1695982-1696714 FORWARD   Aliases: F18C1.19	3.4	3.4	-0.0	-0.2	100.0%	-5.1
17420	AT1G34150.1   tRNA pseudouridine synthase family protein, similar to pseudouridine synthase 3 (Mus musculus) GI:9652099; contains Pfam profile PF01416: tRNA pseudouridine synthase   chr1:12435932-12439477 FORWARD   Aliases: F12G12.3, F12G12_3	6.9	7.0	-0.1	-0.2	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17421	AT5G38820.1   amino acid transporter family protein, low similarity to N system amino acids transporter NAT-1 (Mus musculus) GI:7406950; contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr5:15560711-15562412 FORWARD   Aliases: K15E6.7	4.9	5.0	-0.1	-0.2	100.0%	-4.3
17422	AT5G43200.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 finger protein RHY1a (Arabidopsis thaliana) GI:3790593; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:17363369-17363992 REVERSE   Aliases: MNL12.2, MNL12_2	2.5	2.5	-0.0	-0.2	100.0%	-5.9
17423	AT3G01010.1   UDP-glucose/GDP-mannose dehydrogenase family protein, similar to SP:Q96558 UDP-glucose 6-dehydrogenase (EC 1.1.1.22) (UDP-Glc dehydrogenase) (UDP-GlcDH) (UDPGDH) {Glycine max}; contains Pfam profile PF03720: UDP-glucose/GDP-mannose dehydrogenase family UDP binding domain   chr3:4349-4825 FORWARD   Aliases: T4P13.31	2.6	2.6	-0.0	-0.2	100.0%	-5.7
17424	AT1G52790.1   encodes a putative oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to GS-AOP loci (GI:16118889, GI:16118887, GI:16118891, GI:16118893); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:19665862-19666969 REVERSE   Aliases: F14G24.6, F14G24_6	2.7	2.7	0.0	0.2	100.0%	-6.1
17425	AT3G24090.1   glucosamine--fructose-6-phosphate aminotransferase (isomerizing), putative / hexosephosphate aminotransferase, putative / glucosamine-6-phosphate synthase, putative / D-fructose-6-phosphate amidotransferase, putative / GLCN6P synthase, putative, similar to SP:O94808 Glucosamine--fructose-6-phosphate aminotransferase (isomerizing) 2 (EC 2.6.1.16) (Hexosephosphate aminotransferase 2) (D-fructose-6-phosphate amidotransferase 2) {Homo sapiens}; contains Pfam profiles PF00310: Glutamine amidotransferases class-II, PF01380:SIS domain   chr3:8697845-8700978 REVERSE   Aliases: F14O13.29	4.2	4.2	-0.1	-0.2	100.0%	-4.8
17426	AT2G35860.1   beta-Ig-H3 domain-containing protein / fasciclin domain-containing protein, contains Pfam profile PF02469: Fasciclin domain   chr2:15066842-15069199 FORWARD   Aliases: F11F19.23, F11F19_23	6.0	6.0	-0.1	-0.2	100.0%	-5.0
17427	AT5G08030.1   glycerophosphoryl diester phosphodiesterase family protein, similar to glycerophosphodiester phosphodiesterase (Borrelia hermsii) GI:1399038; contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family   chr5:2575034-2576771 REVERSE   Aliases: T22D6.1	2.8	2.7	0.0	0.2	100.0%	-5.4
17428	AT3G27520.1   expressed protein   chr3:10193659-10194736 FORWARD   Aliases: MMJ24.7	3.1	3.1	0.0	0.2	100.0%	-5.3
17429	AT3G09840.1   Symbol: CDC48   cell division cycle protein 48 (CDC48A) (CDC48), identical to SP:P54609 Cell division cycle protein 48 homolog {Arabidopsis thaliana}   chr3:3019345-3023050 FORWARD   Aliases: ATCDC48, CDC48A, CELL DIVISION CYCLE 48, F8A24.11	9.3	9.2	0.1	0.2	100.0%	-4.8
17430	AT1G28040.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:9773567-9775468 REVERSE   Aliases: F13K9.14, F13K9_14	3.4	3.4	0.0	0.2	100.0%	-5.5
17431	AT5G49390.1   expressed protein   chr5:20045228-20047286 FORWARD   Aliases: K7J8.6, K7J8_6	3.5	3.6	-0.0	-0.2	100.0%	-5.1
17432	AT5G58180.1   Symbol: ATYKT62   SNARE protein-related, similar to SNARE protein Ykt6 (Homo sapiens) GI:2507637   chr5:23561237-23562383 FORWARD   Aliases: MCK7.5, MCK7_5, YKT62	2.3	2.3	0.0	0.2	100.0%	-5.8
17433	AT3G49130.1   expressed protein   chr3:18221438-18222693 FORWARD   Aliases: F2K15.1	3.5	3.4	0.1	0.2	100.0%	-4.9
17434	AT3G19540.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr3:6780625-6783172 FORWARD   Aliases: T31J18.4	3.2	3.2	-0.0	-0.2	100.0%	-5.2
17435	AT1G69980.1   expressed protein   chr1:26360043-26361330 REVERSE   Aliases: F20P5.28, F20P5_28	5.2	5.3	-0.1	-0.2	100.0%	-4.6
17436	AT1G20850.1   Symbol: XCP2   cysteine endopeptidase, papain-type (XCP2), identical to papain-type cysteine endopeptidase XCP2 GI:6708183 from (Arabidopsis thaliana)   chr1:7252173-7253716 FORWARD   Aliases: F9H16.17, F9H16_17, PAPAINE TYPE CYSTEINE ENDOPEPTIDASE XCP2, XYLEM CYSTEINE PEPTIDASE 2	5.0	5.2	-0.2	-0.2	100.0%	-4.4
17437	AT2G34630.2   similar to geranyl diphosphate synthase, putative / GPPS, putative / dimethylallyltransferase, putative / prenyl transferase, putative [Arabidopsis thaliana] (TAIR:At1g17050.1); similar to geranyl diphosphat synthase [Quercus robur] (GB:CAC20852.1); contains InterPro domain Polyprenyl synthetase (InterPro:IPR000092)   chr2:14585632-14588806 FORWARD   Aliases: T31E10.3, T31E10_3	7.4	7.5	-0.1	-0.2	100.0%	-4.6
17438	AT1G30750.1   expressed protein   chr1:10904889-10905691 REVERSE   Aliases: T5I8.20	2.6	2.6	-0.1	-0.2	100.0%	-4.5
17439	AT1G02170.1   Symbol: LOL3   Metacaspase AtMCP1b. Arginine/lysine-specific cysteine protease activity. Induces apoptosis in yeast. Contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain   chr1:411883-413932 FORWARD   Aliases: AMC1, ATMCPB1, LSD ONE LIKE 3, MCP1B, T6A9.24	7.3	7.3	0.1	0.2	100.0%	-4.8
17440	AT5G07190.2   Symbol: ATS3   similar to embryo-specific protein-related [Arabidopsis thaliana] (TAIR:At5g62210.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:NP_916465.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr5:2237508-2238672 FORWARD   Aliases: ARABIDOPSIS THALIANA SEED GENE 3, T28J14.130, T28J14_130	2.4	2.4	0.0	0.2	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17441	AT4G01630.1   Symbol: ATEXPA17   expansin, putative (EXP17), similar to alpha-expansin precursor GI:4027891 from (Nicotiana tabacum); alpha-expansin gene family, PMID:11641069   chr4:700653-701527 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A17, ATEXP17, ATHEXP ALPHA 1.13, T15B16.16, T15B16_16	3.2	3.2	0.0	0.2	100.0%	-5.1
17442	AT1G57620.1   emp24/gp25L/p24 family protein, similar to SP:P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family   chr1:21346386-21348423 FORWARD   Aliases: T8L23.9, T8L23_9	5.7	5.8	-0.1	-0.2	100.0%	-4.6
17443	AT2G23430.1   Symbol: ICK1   kip-related protein 1 (KRP1) / cyclin-dependent kinase inhibitor 1 (ICK1), identical to cyclin-dependent kinase inhibitor (ICK1) (Arabidopsis thaliana) GI:3550262, GI:2052502   chr2:9983826-9985040 REVERSE   Aliases: CYCLIN DEPENDENT KINASE INHIBITOR PROTEIN, F26B6.8, F26B6_8, KIP RELATED PROTEIN 1, KRP1, Kip related protein 1	4.8	4.7	0.1	0.2	100.0%	-4.5
17444	AT3G21570.1   expressed protein   chr3:7600303-7600713 REVERSE   Aliases: MIL23.14	2.7	2.8	-0.0	-0.2	100.0%	-5.5
17445	AT3G57870.1   Symbol: AHUS5   ubiquitin-conjugating enzyme, putative, strong similarity to SP:P50550 Ubiquitin-like protein SUMO-1 conjugating enzyme (EC 6.3.2.19) (SUMO-1-protein ligase) (Ubiquitin carrier protein) (Ubiquitin-conjugating enzyme UbcE2A) {Xenopus laevis}; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr3:21439624-21441155 REVERSE   Aliases: EMB1637, EMBRYO DEFECTIVE 1637, T10K17.80	12.4	12.5	-0.1	-0.2	100.0%	-5.6
17446	AT3G27730.1   Symbol: MER3   ATP-dependent DNA helicase, putative, similar to SP:P51979 ATP-dependent DNA helicase MER3 (EC 3.6.1.-) {Saccharomyces cerevisiae}; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF02889: Sec63 domain   chr3:10275084-10281450 REVERSE   Aliases: MGF10.13	2.4	2.4	0.0	0.2	100.0%	-5.9
17447	AT3G15910.1   expressed protein   chr3:5382067-5383075 FORWARD   Aliases: MVC8.3	3.3	3.4	-0.0	-0.2	100.0%	-5.1
17448	AT2G37800.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.5	0.0	0.2	100.0%	-5.5
17449	AT2G14690.1   similar to glycosyl hydrolase family 10 protein [Arabidopsis thaliana] (TAIR:At4g33820.1); similar to glycosyl hydrolase family 10 protein [Arabidopsis thaliana] (TAIR:At4g33810.1); similar to putative 1,4-beta-xylanase [Oryza sativa (japonica cultivar-group)] (GB:AA53220.1); contains InterPro domain Glycoside hydrolase, family 10 (InterPro:IPR001000)   chr2:6290586-6293137 REVERSE   Aliases: T6B13.7, T6B13_7	2.8	2.9	-0.0	-0.2	100.0%	-5.3
17450	AT2G43480.1   peroxidase, putative, similar to peroxidase; peroxidase ATP14a (Arabidopsis thaliana) gi:1546690:emb:CAA67335   chr2:18060079-18061464 FORWARD   Aliases: T1O24.22	2.3	2.3	0.0	0.2	100.0%	-6.0
17451	AT5G21090.1   leucine-rich repeat protein, putative, similar to leucine rich repeat protein (LRP) GI:1619300 from (Lycopersicon esculentum); contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611   chr5:7164614-7167257 FORWARD   Aliases: T10F18.120, T10F18_120	9.4	9.3	0.2	0.2	100.0%	-4.5
17452	AT1G73990.1   Symbol: SPPA   peptidase U7 family protein, similar to protease IV GB:AAA57008 from (Escherichia coli); contains Pfam profile PF01343: Peptidase family U7   chr1:27828094-27832587 FORWARD   Aliases: F2P9.14, F2P9_14, SPPA	8.9	9.0	-0.0	-0.2	100.0%	-5.1
17453	AT1G68610.1   expressed protein, similar to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr1:25767286-25767768 FORWARD   Aliases: F24J5.15, F24J5_15	2.7	2.7	-0.0	-0.2	100.0%	-5.3
17454	AT3G26780.1   phosphoglycerate/bisphosphoglycerate mutase family protein, similar to X4 protein GI:21386798, Y4 protein GI:21386800 from (Silene dioica); contains Pfam profiles PF00300: phosphoglycerate mutase family, PF01535: PPR repeat	3.7	3.7	0.0	0.2	100.0%	-5.2
17455	AT5G44660.1   expressed protein, similar to unknown protein (pir::T05327)   chr5:18033037-18034404 FORWARD   Aliases: K15C23.11, K15C23_11	2.6	2.7	-0.0	-0.2	100.0%	-5.2
17456	AT2G21490.1   dehydrin family protein, contains Pfam domain, PF00257: Dehydrin	2.8	2.7	0.0	0.2	100.0%	-5.3
17457	AT5G17300.1   myb family transcription factor, similar to CCA1 (Arabidopsis thaliana) GI:4090569; contains Pfam profile PF00249: Myb-like DNA-binding domain   chr5:5690229-5692904 REVERSE   Aliases: MKP11.15, MKP11_15	3.9	4.0	-0.0	-0.2	100.0%	-5.1
17458	AT2G25110.1   MIR domain-containing protein, similar to SP:Q99470 Stromal cell-derived factor 2 precursor (SDF-2) {Homo sapiens}; contains Pfam profile PF02815: MIR domain   chr2:10691214-10693164 FORWARD   Aliases: F13D4.70, F13D4_70	7.5	7.6	-0.1	-0.2	100.0%	-4.7
17459	AT2G34315.1   disease resistance protein-related, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}   chr2:14487333-14490135 REVERSE   Aliases: None	2.5	2.5	-0.0	-0.2	100.0%	-5.7
17460	AT5G01720.1   F-box family protein (FBL3), contains similarity to leucine-rich repeats containing F-box protein FBL3 GI:5919219 from (Homo sapiens)   chr5:266720-270480 REVERSE   Aliases: F7A7.240, F7A7_240	4.7	4.7	-0.1	-0.2	100.0%	-5.0
17461	AT1G63730.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr1:23645433-23648795 FORWARD   Aliases: F24D7.8, F24D7_8	2.2	2.2	-0.0	-0.2	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17462	AT5G62340.1   invertase/pectin methylesterase inhibitor family protein, similar to SP:Q42534 Pectinesterase 2 precursor (EC 3.1.1.11) (Pectin methylesterase 2) (PE 2) {Arabidopsis thaliana}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:25050828-25051535 FORWARD   Aliases: MMI9.17, MMI9_17	2.7	2.8	-0.0	-0.2	100.0%	-5.3
17463	AT2G26510.1   Symbol: PDE135	7.2	7.2	0.0	0.2	100.0%	-4.9
17464	AT3G20580.1   phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region; supporting cDNA gi:26452232:dbj:AK118605.1   chr3:7187862-7190568 REVERSE   Aliases: K10D20.12	2.8	2.7	0.0	0.2	100.0%	-5.3
17465	AT5G01680.1   Symbol: ATCHX26   cation/hydrogen exchanger, putative (CHX26), monovalent cation:proton antiporter family 2 (CPA2) member, PMID:11500563   chr5:253993-256637 REVERSE   Aliases: CHX26, F7A7.200, F7A7_200	2.6	2.6	0.0	0.2	100.0%	-5.4
17466	AT4G32375.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Lycopersicon esculentum) GI:4325090; contains Pfam profile PF00295: Polygalacturonase (pectinase)   chr4:15628879-15631602 FORWARD   Aliases: None	2.9	2.9	-0.0	-0.2	100.0%	-5.4
17467	AT3G01070.1   plastocyanin-like domain-containing protein   chr3:19599-20726 FORWARD   Aliases: T4P13.25, T4P13_25	3.3	3.4	-0.0	-0.2	100.0%	-5.0
17468	AT1G71780.1   expressed protein   chr1:26998748-27000312 REVERSE   Aliases: F14O23.16, F14O23_16	7.1	7.0	0.1	0.2	100.0%	-4.7
17469	AT3G06080.2   expressed protein, identical to unknown protein GB:AAF30301 from (Arabidopsis thaliana)   chr3:1834713-1837990 REVERSE   Aliases: F24F17.6, F24F17_6	3.0	3.0	-0.0	-0.2	100.0%	-5.8
17470	AT5G64160.1   expressed protein   chr5:25688156-25689689 FORWARD   Aliases: MHJ24.14, MHJ24_14	7.3	7.4	-0.1	-0.2	100.0%	-4.7
17471	AT4G15240.1   fringe-related protein, + weak similarity to Fringe (Schistocerca gregaria)(GI:6573138);Fringe encodes an extracellular protein that regulates Notch signalling.	4.2	4.2	0.1	0.2	100.0%	-4.7
17472	AT2G46375.1   expressed protein   chr2:19044937-19045452 FORWARD   Aliases: None	3.4	3.3	0.0	0.2	100.0%	-5.4
17473	AT1G61780.1   postsynaptic protein-related, similar to postsynaptic protein CRIPT GI:3098551 from (Rattus norvegicus)   chr1:22816280-22817806 REVERSE   Aliases: T13M11.14, T13M11_14	10.7	10.8	-0.0	-0.2	100.0%	-5.5
17474	AT4G28660.1   photosystem II reaction centre W (PsbW) family protein, contains Pfam profile: PF03912 photosystem II reaction centre W protein, PsbW   chr4:14149922-14151103 FORWARD   Aliases: T5F17.110, T5F17_110	6.1	6.0	0.1	0.2	100.0%	-4.8
17475	AT3G08610.1   expressed protein   chr3:2615432-2616809 REVERSE   Aliases: F17O14.8	12.5	12.4	0.0	0.2	100.0%	-6.0
17476	AT4G35030.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:16676134-16677541 FORWARD   Aliases: M4E13.90, M4E13_90	3.2	3.0	0.2	0.2	100.0%	-3.8
17477	AT5G47760.1   Symbol: ATPK5   phosphoglycolate phosphatase, putative, similar to phosphoglycolate phosphatase precursor (Chlamydomonas reinhardtii) GI:15982558; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:19360113-19362220 REVERSE   Aliases: MCA23.8, MCA23_8	7.6	7.5	0.1	0.2	100.0%	-4.8
17478	AT3G14210.1   myrosinase-associated protein, putative, similar to GB:CAA71238 from (Brassica napus); contains Pfam profile:PF00657 Lipase/Acylhydrolase with GDSL-like motif   chr3:4729830-4731810 FORWARD   Aliases: MAG2.6	2.3	2.3	-0.0	-0.2	100.0%	-5.8
17479	AT4G17020.2   transcription factor-related, contains weak similarity to Swiss-Prot:Q92759 TFIIH basal transcription factor complex p52 subunit (Basic transcription factor 52 kDa subunit, BTF2-p52, General transcription factor IIH polypeptide 4) (Homo sapiens)   chr4:9577443-9581390 REVERSE   Aliases: DL4540C, FCAALL.340	3.0	3.0	0.0	0.2	100.0%	-5.7
17480	AT4G35710.1   hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr4:16925306-16926157 FORWARD   Aliases: F8D20.220, F8D20_220	4.3	4.3	0.1	0.2	100.0%	-5.0
17481	AT4G01550.1   Symbol: ANAC069   no apical meristem (NAM) family protein, similar to NAC1 (GI:7716952) {Medicago truncatula}; contains Pfam PF02365 : No apical meristem (NAM) protein   chr4:673868-676392 REVERSE   Aliases: ANAC069, F11O4.5, F11O4_5	2.3	2.2	0.0	0.2	100.0%	-4.8
17482	AT5G49270.1   phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region   chr5:19989138-19991670 REVERSE   Aliases: K21P3.15, K21P3_15	3.6	3.7	-0.1	-0.2	100.0%	-4.3
17483	AT5G54140.1   Symbol: ILL3   IAA-amino acid hydrolase, putative (ILL3), identical to IAA-amino acid hydrolase homolog ILL3 (Arabidopsis thaliana) gi:3420801:gb:AAC31939   chr5:21983059-21985287 FORWARD   Aliases: MJP23.12, MJP23_12	6.0	6.0	0.1	0.2	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17484	AT1G75470.1   Symbol: ATPUP15   purine permease-related, contains Pfam profile PF03151: Domain of unknown function, DUF250; low similarity to purine permease (Arabidopsis thaliana) GI:7620007   chr1:28333733-28334961 FORWARD   Aliases: F1B16.15	3.5	3.4	0.0	0.2	100.0%	-5.3
17485	AT1G23650.1   expressed protein, ; expression supported by MPSS   chr1:8371009-8371095 REVERSE   Aliases: F5O8.41, F5O8_41	2.9	3.0	-0.1	-0.2	100.0%	-5.5
17486	AT1G76390.1   armadillo/beta-catenin repeat family protein / U-box domain-containing protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr1:28660298-28663425 FORWARD   Aliases: F15M4.11, F15M4_11	5.0	4.9	0.0	0.2	100.0%	-4.9
17487	AT1G17680.2   transcription factor-related, low similarity to SP:P33339 Transcription factor tau 131 kDa subunit (TFIIIC 131 kDa subunit) Saccharomyces cerevisiae, transcription factor IIIC102 short isoform (Homo sapiens) GI:18481637   chr1:6076123-6082330 FORWARD   Aliases: F11A6.2, F11A6_2	4.9	4.8	0.1	0.2	100.0%	-4.9
17488	AT5G45970.1   Symbol: ARAC2   Rac-like GTP-binding protein (ARAC2), identical to RAC-like GTP binding protein ARAC2 SP:Q38903	2.8	2.8	-0.0	-0.2	100.0%	-5.0
17489	AT1G52830.1   Symbol: IAA6   auxin-responsive protein / indoleacetic acid-induced protein 6 (IAA6), nearly identical to SP:Q38824 Auxin-responsive protein IAA6 (Indoleacetic acid-induced protein 6) {Arabidopsis thaliana}   chr1:19676164-19677312 REVERSE   Aliases: F14G24.10, F14G24_10, IAA6, SHY1	3.8	3.8	-0.0	-0.2	100.0%	-5.2
17490	AT4G31000.1   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum); contains non-consensus donor splice site AT at exon 4; supported by cDNA gi:17065559   chr4:15103165-15105985 FORWARD   Aliases: F6I18.90, F6I18_90	3.4	3.4	0.1	0.2	100.0%	-5.1
17491	AT2G28550.2   Symbol: TOE1   AP2 domain-containing transcription factor RAP2.7 (RAP2.7), nearly identical to AP2 domain transcription factor RAP2.7 (GI:2281639) (Arabidopsis thaliana)   chr2:12233168-12235620 REVERSE   Aliases: RAP2.7, T17D12.11, T17D12_11	4.5	4.4	0.1	0.2	100.0%	-4.6
17492	AT1G79430.2   Symbol: APL   myb family transcription factor-related   chr1:29882121-29884097 REVERSE   Aliases: ALTERED PHLOEM DEVELOPMENT, T8K14.15, T8K14_15, WDY, WOODY	3.0	3.0	0.1	0.2	100.0%	-4.6
17493	AT1G05750.1   Symbol: PDE247	2.7	2.7	0.0	0.2	100.0%	-5.6
17494	AT1G62330.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g11990.1); similar to putative growth regulator [Gossypium hirsutum] (GB:AAT64033.1); contains InterPro domain Hypothetical plant protein (InterPro:IPR004348)   chr1:23050558-23053858 FORWARD   Aliases: F24O1.5, F24O1_5	3.9	4.0	-0.0	-0.2	100.0%	-5.0
17495	AT2G43520.1   Symbol: ATTI2   Encodes a defensin-like (DEFL) family protein.   chr2:18075638-18076219 FORWARD   Aliases: T1O24.26	3.0	3.0	0.0	0.2	100.0%	-5.4
17496	AT1G18720.1   expressed protein, similar to YGL010w-like protein GI:2982301 from (Picea mariana)   chr1:6457813-6459707 REVERSE   Aliases: F6A14.17, F6A14_17	8.0	8.0	0.1	0.2	100.0%	-5.0
17497	AT3G08580.2   Symbol: AAC1   ADP, ATP carrier protein 1, mitochondrial / ADP/ATP translocase 1 / adenine nucleotide translocator 1 (ANT1), identical to SWISS-PROT:P31167 ADP,ATP carrier protein 1 (Adenine nucleotide translocator 1) (Arabidopsis thaliana)   chr3:2605448-2607793 REVERSE   Aliases: ADP/ATP CARRIER 1, F17O14.5	12.3	12.4	-0.1	-0.2	100.0%	-5.6
17498	AT1G54640.1   F-box family protein-related, contains TIGRFAM TIGR01640 : F-box protein interaction domain   chr1:20407559-20408474 REVERSE   Aliases: T22H22.8, T22H22_8	3.2	3.2	-0.0	-0.2	100.0%	-5.5
17499	AT5G13030.1   expressed protein, contains Pfam profile PF02696: Uncharacterized ACR, YdiU/UPF0061 family   chr5:4133219-4136921 FORWARD   Aliases: AT5G13040, T19L5.1	6.3	6.4	-0.0	-0.2	100.0%	-5.4
17500	AT4G07435.1   cytochrome P-450 aromatase-related, similar to minor outer capsid protein VP4 (GI:13446784) (Human rotavirus C); similar to cytochrome P-450 aromatase (GI:21170) (Gallus gallus);   chr4:4224486-4225573 REVERSE   Aliases: None	2.2	2.2	0.0	0.2	100.0%	-4.8
17501	AT5G37010.1   expressed protein   chr5:14637962-14640171 REVERSE   Aliases: K15O15.3, K15O15_3	7.4	7.4	0.0	0.2	100.0%	-4.9
17502	AT2G43560.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, identical to Probable FKBP-type peptidyl-prolyl cis-trans isomerase 2, chloroplast precursor (Ppiase) (Rotamase) (SP:O22870)(Arabidopsis thaliana); contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr2:18080566-18082514 REVERSE   Aliases: T1O24.30	6.5	6.6	-0.1	-0.2	100.0%	-4.3
17503	AT3G56850.1   Symbol: AREB3   ABA-responsive element-binding protein 3 (AREB3), identical to ABA-responsive element binding protein 3 (AREB3) (Arabidopsis thaliana) GI:9967421   chr3:21057320-21059495 REVERSE   Aliases: ABA RESPONSIVE ELEMENT BINDING PROTEIN 3, DPBF3, T8M16.180	6.0	5.9	0.0	0.2	100.0%	-5.0
17504	AT2G44660.1   ALG6, ALG8 glycosyltransferase family protein, similar to SP:P40351 Dolichyl pyrophosphate Glc1Man9GlcNAc2 alpha-1,3-glycosyltransferase (EC 2.4.1.-) (Dolichyl-P-Glc:Glc1Man9GlcNAc2-PP-dolichyl glycosyltransferase) {Saccharomyces cerevisiae}; contains Pfam profile PF03155: ALG6, ALG8 glycosyltransferase family   chr2:18428171-18429902 REVERSE   Aliases: F16B22.15	3.8	3.8	-0.0	-0.2	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17505	AT2G46490.1   expressed protein (APS2), identical to cDNA Aps2, partial cds GI:4519894	8.6	8.8	-0.1	-0.2	100.0%	-4.6
17506	AT4G14450.1   Symbol: ATBET12   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g23170.1)   chr4:8309487-8310054 FORWARD   Aliases: ATBET12, BET12, DL3265W, FCAALL.213	2.8	2.8	-0.0	-0.2	100.0%	-5.4
17507	AT5G57540.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endotransglycosylase (XTR9) GI:4218963 from (Arabidopsis thaliana)   chr5:23320222-23321275 REVERSE   Aliases: MUA2.11, MUA2_11	3.0	3.1	-0.1	-0.2	100.0%	-4.2
17508	AT5G49770.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:20240086-20244493 FORWARD   Aliases: K2I5.14, K2I5_14	2.4	2.5	-0.1	-0.2	100.0%	-4.5
17509	AT4G24250.1   Symbol: MLO13   seven transmembrane MLO family protein / MLO-like protein 13 (MLO13), identical to membrane protein Mlo13 (Arabidopsis thaliana) gi:14091596:gb:AAK53806; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr4:12574822-12577593 REVERSE   Aliases: T22A6.80, T22A6_80	2.6	2.6	0.1	0.2	100.0%	-5.1
17510	AT3G01020.1   Symbol: ATISU2/ISU2   Encodes a mitochondrial protein similar to E.coli IscU. In bacteria, IscU is a scaffold protein accepting sulfur and iron to build a transient Fe-S cluster, which is subsequently transferred to a target apoprotein.   chr3:5146-5900 FORWARD   Aliases: ATISU2, ISU2, T4P13.30, T4P13_30	3.6	3.7	-0.0	-0.2	100.0%	-5.4
17511	AT5G17130.1   hypothetical protein   chr5:5636975-5637537 FORWARD   Aliases: F2K13.280, F2K13_280	3.7	3.7	0.1	0.2	100.0%	-5.2
17512	AT5G11860.3   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr5:3821804-3824254 REVERSE   Aliases: F14F18.30, F14F18_30	5.9	5.9	-0.1	-0.2	100.0%	-5.0
17513	AT3G16740.1   F-box family protein, contains F-box domain Pfam:PF00646	4.8	4.7	0.0	0.2	100.0%	-5.2
17514	AT5G55860.1   expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827); expression supported by MPSS   chr5:22627372-22629392 FORWARD   Aliases: MWJ3.4, MWJ3_4	5.8	5.7	0.1	0.2	100.0%	-4.6
17515	AT5G23190.1   Symbol: CYP86B1   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr5:7803144-7805818 REVERSE   Aliases: MKD15.5, MKD15_5	2.1	2.2	-0.1	-0.2	100.0%	-4.7
17516	AT4G18840.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:10338730-10340367 REVERSE   Aliases: F13C5.10, F13C5_10	4.4	4.3	0.0	0.2	100.0%	-5.1
17517	AT1G08030.1   expressed protein   chr1:2490951-2491919 REVERSE   Aliases: T6D22.29, T6D22_29	3.5	3.5	-0.0	-0.2	100.0%	-5.2
17518	AT1G58420.1   expressed protein   chr1:21711044-21711783 FORWARD   Aliases: F9K23.5, F9K23_5	3.0	3.1	-0.1	-0.2	100.0%	-4.7
17519	AT3G19090.1   RNA-binding protein, putative, similar to RNA-binding protein homolog GB:AAF00075 GI:6449448 from (Brassica napus); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:6601472-6603715 FORWARD   Aliases: MHP21.1	4.8	4.9	-0.1	-0.2	100.0%	-5.1
17520	AT2G45690.1   Symbol: SSE1   shrunken seed protein (SSE1), identical to shrunken seed protein (Arabidopsis thaliana) GI:4837733; annotation based on supporting cDNA gi:4837732:gb:AF085354.1:AF085354   chr2:18830298-18832796 REVERSE   Aliases: F17K2.22, PEX16, SHRUNKEN SEED 1, SSE	5.0	4.9	0.1	0.2	100.0%	-4.9
17521	AT5G22530.1   expressed protein   chr5:7480530-7481197 FORWARD   Aliases: MQJ16.7, MQJ16_7	3.0	3.0	0.0	0.2	100.0%	-5.3
17522	AT4G27060.1   Symbol: TOR1   expressed protein   chr4:13581414-13585161 REVERSE   Aliases: CN, CONVOLUTA, SPIRAL 2, SPR2, T24A18.10, T24A18_10, TORTIFOLIA 1	7.1	7.0	0.1	0.2	100.0%	-4.9
17523	AT5G04220.2   C2 domain-containing protein (sytC), GC donor splice site at exon 3; similar to Ca2+-dependent lipid-binding protein (CLB1) GI:2789434 from (Lycopersicon esculentum)   chr5:1155866-1158877 REVERSE   Aliases: F21E1.140, F21E1_140	3.7	3.8	-0.1	-0.2	100.0%	-5.2
17524	AT1G01280.1   Symbol: CYP703A2   cytochrome P450 family protein, similar to cytochrome P450 GB:BAA92894 GI:7339658 from (Petunia hybrida)   chr1:112263-113947 FORWARD   Aliases: F6F3.8, F6F3_8	2.7	2.7	0.0	0.2	100.0%	-5.6
17525	AT4G28780.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr4:14215551-14217585 FORWARD   Aliases: F16A16.110, F16A16_110	2.3	2.3	-0.0	-0.2	100.0%	-5.7
17526	AT4G32070.1   octicosapeptide/Phox/Bem1p (PB1) domain-containing protein / tetratricopeptide repeat (TPR)-containing protein, similar to SP:Q99614 Tetratricopeptide repeat protein 1 {Homo sapiens}; contains Pfam profiles PF00564: PB1 domain, PF00515: TPR Domain   chr4:15504668-15507103 REVERSE   Aliases: F10N7.120, F10N7_120	3.6	3.7	-0.1	-0.2	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17527	AT3G18540.1   expressed protein   chr3:6375815-6377473 FORWARD   Aliases: K24M9.3	3.4	3.3	0.1	0.2	100.0%	-4.6
17528	AT3G50730.1   protein kinase, putative, similar to protein kinase ATN1 (Arabidopsis thaliana) gi:1054633:emb:CAA63387   chr3:18862514-18864118 REVERSE   Aliases: F18B3.10	2.6	2.5	0.0	0.2	100.0%	-5.4
17529	AT1G22500.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:7949465-7950845 FORWARD   Aliases: F12K8.15, F12K8_15	3.0	2.9	0.1	0.2	100.0%	-4.5
17530	AT5G14870.1   Symbol: ATCNGC18   cyclic nucleotide-regulated ion channel, putative (CNGC18), similar to cyclic nucleotide and calmodulin-regulated ion channel (cngc6) GI:4581207 from (Arabidopsis thaliana)	2.6	2.6	-0.0	-0.2	100.0%	-5.6
17531	AT4G36640.1   SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein, similar to polyphosphoinositide binding protein Ssh1p (GI:2739044) {Glycine max, SEC14 cytosolic factor (Phosphatidylinositol/phosphatidylcholine transfer protein) (PI/PCTP) (SP:P24859) (Kluyveromyces lactis) and to SEC14 cytosolic factor (SP:P53989) (Candida glabrata)   chr4:17276941-17279173 REVERSE   Aliases: AP22.47, AP22_47	6.1	6.1	-0.1	-0.2	100.0%	-5.0
17532	AT3G52810.1   purple acid phosphatase (PAP21), identical to purple acid phosphatase GI:20257492 from (Arabidopsis thaliana); contains Pfam profile PF00149: Ser/Thr protein phosphatase   chr3:19581980-19584711 REVERSE   Aliases: F3C22.210	3.2	3.2	0.0	0.2	100.0%	-5.4
17533	AT3G50220.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr3:18628406-18629711 REVERSE   Aliases: F11C1.60	3.1	3.1	-0.0	-0.2	100.0%	-5.0
17534	AT3G50580.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:18779612-18780500 REVERSE   Aliases: T20E23.180	3.7	3.7	0.1	0.2	100.0%	-5.1
17535	AT4G37900.1   glycine-rich protein   chr4:17821731-17824439 REVERSE   Aliases: F20D10.20, F20D10_20	5.0	5.0	0.1	0.2	100.0%	-4.8
17536	AT1G15250.1   60S ribosomal protein L37 (RPL37A), almost identical to GB:Q43292   chr1:5248660-5249457 REVERSE   Aliases: F9L1.46, F9L1_46	9.1	9.0	0.1	0.2	100.0%	-4.5
17537	AT1G55805.1   BolA-like family protein, contains Pfam profile: PF01722 BolA-like protein   chr1:20862397-20863105 REVERSE   Aliases: None	8.8	8.7	0.1	0.2	100.0%	-4.5
17538	AT3G24260.1   hypothetical protein   chr3:8793844-8794968 REVERSE   Aliases: K7M2.2	2.9	2.9	-0.0	-0.2	100.0%	-5.4
17539	AT3G48090.2   Symbol: EDS1   similar to lipase class 3 family protein / disease resistance protein-related [Arabidopsis thaliana] (TAIR:At3g48080.1); similar to EDS1-like protein [Nicotiana benthamiana] (GB:AAL85347.1)   chr3:17766359-17768742 REVERSE   Aliases: EDS1 PROTEIN, ENHANCED DISEASE SUSCEPTIBILITY 1, T17F15.40	3.7	3.8	-0.0	-0.2	100.0%	-4.9
17540	AT1G14670.1   endomembrane protein 70, putative, similar to endomembrane protein emp70 precursor isolog GB:AAF67014 GI:7677068 (Homo sapiens)   chr1:5037607-5040523 FORWARD   Aliases: F10B6.3, F10B6_3	7.9	8.0	-0.1	-0.2	100.0%	-5.0
17541	AT1G79050.1   DNA repair protein recA, identical to DNA repair protein recA, chloroplast (Precursor) SP:Q39199 from (Arabidopsis thaliana) ;contains Pfam profile: PF00154 recA bacterial DNA recombination protein   chr1:29741854-29745049 REVERSE   Aliases: YUP8H12R.33, YUP8H12R_33	8.8	8.7	0.1	0.2	100.0%	-4.6
17542	AT2G44940.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr2:18544332-18545488 FORWARD   Aliases: T13E15.25	4.6	4.6	-0.1	-0.2	100.0%	-4.6
17543	AT1G34350.1   expressed protein   chr1:12534432-12536073 FORWARD   Aliases: F7P12.4, F7P12_4	7.0	6.9	0.1	0.2	100.0%	-4.5
17544	AT1G13080.2   Symbol: CYP71B2   cytochrome P450 family protein, identical to gb:D78605 cytochrome P450 monooxygenase from Arabidopsis thaliana and is a member of the PF:00067 Cytochrome P450 family. ESTs gb:Z18072, gb:Z35218 and gb:T43466 come from this gene   chr1:4459164-4460938 FORWARD   Aliases: CYTOCHROME P450 71B2, CYTOCHROME P450 MONOOXYGENASE 71B2, F3F19.10, F3F19_10	3.0	2.9	0.1	0.2	100.0%	-4.5
17545	AT5G48210.1   expressed protein   chr5:19565640-19566367 FORWARD   Aliases: MIF21.10, MIF21_10	2.7	2.7	-0.0	-0.2	100.0%	-5.8
17546	AT2G02860.2   Symbol: SUT2   sucrose transporter / sucrose-proton symporter (SUC3), identical to sucrose transporter (Arabidopsis thaliana) GI:8052190; similar to sucrose transporters from (Oryza sativa (japonica cultivar-group)) GI:2723471, (Zea mays) GI:5771354, (Triticum aestivum) GI:19548165; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:828351-832454 REVERSE   Aliases: ATSUC3, SUC3, T17M13.3, T17M13_3	5.5	5.4	0.1	0.2	100.0%	-4.8
17547	AT2G38900.1   serine protease inhibitor, potato inhibitor I-type family protein, similar to SP:P24076 Glu S.griseus protease inhibitor (BGIA) {Momordica charantia}, SP:P20076 Ethylene-responsive proteinase inhibitor I precursor {Lycopersicon esculentum}; contains Pfam profile PF00280: Potato inhibitor I family   chr2:16250312-16251132 FORWARD   Aliases: T7F6.7, T7F6_7	2.9	3.0	-0.0	-0.2	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17548	AT4G26770.1   phosphatidate cytidyltransferase, putative / CDP-diglyceride synthetase, putative, similar to CDP-diacylglycerol synthetase GI:2182104 from ( <i>Solanum tuberosum</i> )   chr4:13482082-13484846 FORWARD   Aliases: F10M23.110, F10M23_110	2.6	2.6	-0.0	-0.2	100.0%	-5.4
17549	AT5G04730.1   expressed protein, ; expression supported by MPSS   chr5:1364102-1365067 REVERSE   Aliases: MUK11.5	2.4	2.4	-0.1	-0.2	100.0%	-4.6
17550	AT1G71210.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:26841951-26845152 REVERSE   Aliases: F23N20.20, F23N20_20	3.0	3.0	0.0	0.2	100.0%	-5.5
17551	AT4G21020.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to SP:P23283 Desiccation-related protein { <i>Craterostigma plantagineum</i> }; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr4:11228198-11229588 FORWARD   Aliases: T13K14.180, T13K14_180	2.9	2.9	-0.0	-0.2	100.0%	-5.6
17552	AT4G17250.1   expressed protein   chr4:9671101-9673430 FORWARD   Aliases: DL4660W, FCAALL.204	2.2	2.2	0.0	0.2	100.0%	-6.0
17553	AT1G42460.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr1:15915960-15919925 REVERSE   Aliases: F7F22.2, F7F22_2	2.7	2.6	0.1	0.2	100.0%	-4.9
17554	AT5G12990.1   Symbol: CLE40   CLE40, putative, CLAVATA3/ESR-Related 40 (CLE40); similarity to CLAVATA3 signature   chr5:4109237-4109771 REVERSE   Aliases: CLAVATA3/ESR RELATED 40, T24H18.160, T24H18_160	2.8	2.8	0.0	0.2	100.0%	-5.6
17555	AT3G52920.2   expressed protein, weak similarity to enterophilin-2L ( <i>Cavia porcellus</i> ) GI:12718845; contains Pfam profile PF04949: Family of unknown function (DUF662)   chr3:19635358-19637236 FORWARD   Aliases: F8J2.90	7.8	7.7	0.2	0.2	100.0%	-4.7
17556	AT4G08740.1   expressed protein   chr4:5579031-5579742 FORWARD   Aliases: T32A17.50, T32A17_50	2.3	2.3	0.0	0.2	100.0%	-5.7
17557	AT2G35000.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:14758653-14760398 REVERSE   Aliases: F19I3.23, F19I3_23	2.3	2.4	-0.1	-0.2	100.0%	-4.4
17558	AT4G30130.1   expressed protein, contains Pfam domains, PF04782: Protein of unknown function (DUF632) and PF04783: Protein of unknown function (DUF630)   chr4:14734825-14737984 FORWARD   Aliases: F6G3.160, F6G3_160	2.9	2.9	0.0	0.2	100.0%	-5.3
17559	AT3G30240.1   hypothetical protein   chr3:11886304-11886966 FORWARD   Aliases: MIL15.14	3.0	3.0	0.0	0.2	100.0%	-5.5
17560	AT3G20070.2   Symbol: TTN9   expressed protein   chr3:7004678-7006888 REVERSE   Aliases: MAL21.7, TITAN9	3.9	3.9	-0.0	-0.2	100.0%	-5.0
17561	AT3G14395.1   expressed protein   chr3:4810930-4811486 FORWARD   Aliases: None	3.3	3.3	0.0	0.2	100.0%	-5.6
17562	AT1G76250.1   expressed protein   chr1:28611344-28614022 REVERSE   Aliases: T23E18.18, T23E18_18	2.6	2.6	-0.1	-0.2	100.0%	-4.9
17563	AT4G25970.1   Symbol: PSD2   similar to phosphatidylserine decarboxylase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g57190.1); similar to putative phosphatidylserine decarboxylase [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:NP_914239.1); contains InterPro domain Phosphatidylserine decarboxylase (InterPro:IPR005221); contains InterPro domain Phosphatidylserine decarboxylase-related (InterPro:IPR003817); contains InterPro domain Calcium-binding EF-hand (InterPro:IPR002048)   chr4:13185739-13189444 FORWARD   Aliases: F20B18.80, F20B18_80, PHOSPHATIDYLSERINE DECARBOXYLASE 2	7.0	6.9	0.1	0.2	100.0%	-4.8
17564	AT5G22870.1   harpin-induced protein-related / HIN1-related / harpin-responsive protein-related, weak similarity to hin1 ( <i>Nicotiana tabacum</i> ) GI:1619321   chr5:7647059-7647682 REVERSE   Aliases: MRN17.10, MRN17_10	2.3	2.3	-0.0	-0.2	100.0%	-5.2
17565	AT1G13760.1   expressed protein   chr1:4720178-4720507 REVERSE   Aliases: F21F23.20, F21F23_20	2.3	2.3	-0.0	-0.2	100.0%	-5.6
17566	AT3G51570.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr3:19137337-19141435 FORWARD   Aliases: T18N14.4	2.3	2.3	-0.0	-0.2	100.0%	-5.1
17567	AT1G01180.1   expressed protein   chr1:75633-77446 FORWARD   Aliases: F6F3.5	3.0	3.1	-0.0	-0.2	100.0%	-5.0
17568	AT1G52100.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog ( <i>Arabidopsis thaliana</i> ) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain; contains non-consensus AG donor splice site at exon3   chr1:19386791-19389202 REVERSE   Aliases: F5F19.16, F5F19_16	3.9	3.9	0.1	0.2	100.0%	-5.1
17569	AT2G19510.1   LOB domain family protein / lateral organ boundaries domain family protein (LBD8), identical to SP:Q9ZUP0: Putative LOB domain protein 8 { <i>Arabidopsis thaliana</i> }; similar to lateral organ boundaries (LOB) domain-containing proteins from <i>Arabidopsis thaliana</i> ; identical to ASYMMETRIC LEAVES2-like protein 34 ( <i>Arabidopsis thaliana</i> ) GI:19919039   chr2:8460312-8460758 FORWARD   Aliases: F3P11.11, F3P11_11	2.7	2.7	0.0	0.2	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17570	AT3G26930.1   hypothetical protein   chr3:9927168-9928588 FORWARD   Aliases: MQP17.1	3.1	3.2	-0.0	-0.2	100.0%	-5.3
17571	AT3G13090.1   Symbol: ATMRP8	3.8	3.8	0.0	0.2	100.0%	-5.1
17572	AT4G24610.1   expressed protein   chr4:12700607-12707909 REVERSE   Aliases: F22K18.190, F22K18_190	5.9	5.8	0.1	0.2	100.0%	-4.7
17573	AT2G44740.1   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr2:18449064-18450471 REVERSE   Aliases: F16B22.23	3.0	3.0	-0.0	-0.2	100.0%	-5.1
17574	AT5G04740.1   ACT domain-containing protein, contains Pfam profile PF01842: ACT domain	9.5	9.6	-0.1	-0.2	100.0%	-4.8
17575	AT1G21090.1   hydroxyproline-rich glycoprotein family protein   chr1:7384618-7386547 FORWARD   Aliases: T22I11.8, T22I11_8	2.8	2.8	-0.0	-0.2	100.0%	-5.4
17576	AT3G50660.1   Symbol: DWF4   steroid 22-alpha-hydroxylase (CYP90B1) (DWF4), identical to gi:2935342   chr3:18825122-18828214 REVERSE   Aliases: CLAM, CLM, CYP90B1, DWARF 4, DWF4, STEROID 22 ALPHA HYDROXYLASE, T3A5.40	7.3	7.3	-0.1	-0.2	100.0%	-5.0
17577	AT5G48270.1   expressed protein   chr5:19581970-19582938 REVERSE   Aliases: MIF21.16, MIF21_16	2.7	2.7	0.0	0.2	100.0%	-5.4
17578	AT1G56190.1   phosphoglycerate kinase, putative, similar to SP:P41758 Phosphoglycerate kinase, chloroplast precursor (EC 2.7.2.3) {Chlamydomonas reinhardtii}; contains Pfam profile PF00162: phosphoglycerate kinase   chr1:21032030-21034314 FORWARD   Aliases: F14G9.19, F14G9_19	10.3	10.4	-0.1	-0.2	100.0%	-5.0
17579	AT5G42660.1   expressed protein, contains Pfam profile PF04765: Protein of unknown function (DUF616)   chr5:17120152-17123192 REVERSE   Aliases: MJB21.3, MJB21_3	3.9	4.0	-0.1	-0.2	100.0%	-4.8
17580	AT1G62800.2   Symbol: ASP4   aspartate aminotransferase, cytoplasmic isozyme 2 / transaminase A (ASP4), identical to aspartate aminotransferase, cytoplasmic isozyme 2 SP:P46646 (Arabidopsis thaliana)   chr1:23257368-23261128 REVERSE   Aliases: ASPARTATE AMINOTRANSFERASE 4, F23N19.17, F23N19_17	7.1	7.2	-0.1	-0.2	100.0%	-4.9
17581	AT5G03000.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr5:703266-704435 FORWARD   Aliases: F15A17.30, F15A17_30	2.9	2.9	0.0	0.2	100.0%	-5.5
17582	AT1G22370.2   UDP-glucuronosyl/UDP-glucosyl transferase family protein, glycosyltransferase family   chr1:7898105-7899868 REVERSE   Aliases: T16E15.2, T16E15_2	3.4	3.5	-0.1	-0.2	100.0%	-4.9
17583	AT4G19470.1   disease resistance protein-related, similar to disease resistance protein RPS4-Ler (GI:5823587)(Arabidopsis thaliana); similar to TMV resistance protein N, Nicotiana glutinosa, PIR2:A54810; contains Pfam PF00560: Leucine Rich Repeat domains	2.4	2.5	-0.0	-0.2	100.0%	-5.8
17584	AT5G47430.1   expressed protein   chr5:19252858-19258448 REVERSE   Aliases: MQL5.29, MQL5_29	3.2	3.1	0.0	0.2	100.0%	-5.3
17585	AT1G14110.1   xyloglucan fucosyltransferase family protein, contains Pfam profile: PF03254 xyloglucan fucosyltransferase   chr1:4827958-4831912 FORWARD   Aliases: F7A19.19, F7A19_19	2.5	2.4	0.0	0.2	100.0%	-6.0
17586	AT5G09950.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:3102878-3105865 REVERSE   Aliases: MYH9.16, MYH9_16	2.5	2.5	0.0	0.2	100.0%	-5.7
17587	AT1G25490.1   Symbol: RCN1   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit A (RCN1), identical to phosphoprotein phosphatase 2A, regulatory subunit A GI:1262171 from (Arabidopsis thaliana)   chr1:8951207-8955088 FORWARD   Aliases: ATB BETA BETA, EER1, ENHANCED ETHYLENE RESPONSE 1, F2J7.19, F2J7_19, PHOSPHOPROTEIN PHOSPHATASE 2A REGULATORY SUBUNIT A, PR65, REGA, ROOTS CURL IN NPA, SERINE/THREONINE PROTEIN PHOSPHATASE TYPE 2A REGULATORY SUBUNIT A	6.6	6.7	-0.1	-0.2	100.0%	-5.1
17588	AT1G48510.1   cytochrome c oxidase assembly protein surfeit-related, contains similarity to Swiss-Prot:Q9QXU2 surfeit locus protein 1 (Rattus norvegicus)   chr1:17938557-17940583 FORWARD   Aliases: T1N15.12, T1N15_12	3.3	3.4	-0.0	-0.2	100.0%	-5.4
17589	AT3G20120.2   Symbol: CYP705A21   similar to cytochrome P450 family protein [Arabidopsis thaliana] (TAIR:At3g20110.1); similar to C93A2_SOYBN Cytochrome P450 93A2 (GB:Q42799); contains InterPro domain E-class P450, group I (InterPro:IPR002401); contains InterPro domain Cytochrome P450 (InterPro:IPR001128)   chr3:7023317-7025929 FORWARD   Aliases: MAL21.16	8.6	8.6	-0.0	-0.2	100.0%	-5.3
17590	AT1G73760.1   zinc finger (C3HC4-type RING finger) family protein, similar to Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:27742869-27744868 REVERSE   Aliases: F25P22.18, F25P22_18	4.3	4.3	0.0	0.2	100.0%	-5.3
17591	AT1G09770.1   Symbol: ATCDC5	8.9	9.0	-0.1	-0.2	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17592	AT4G11980.1   MutT/nudix family protein, low similarity to SP:P54570 ADP-ribose pyrophosphatase (EC 3.6.1.13) {Bacillus subtilis}; contains Pfam profile PF00293: NUDIX domain	6.6	6.5	0.1	0.2	100.0%	-4.6
17593	AT5G57340.2   expressed protein   chr5:23244526-23246429 FORWARD   Aliases: MJB24.15, MJB24_15	5.3	5.4	-0.1	-0.2	100.0%	-4.9
17594	AT1G50310.1   monosaccharide transporter (STP9), identical to monosaccharide transporter STP9 protein (Arabidopsis thaliana) GI:15487254; contains Pfam profile PF00083: major facilitator superfamily protein	3.0	3.0	-0.0	-0.2	100.0%	-5.2
17595	AT5G04200.1   latex-abundant protein, putative (AMC9) / caspase family protein, similar to latex-abundant protein (Hevea brasiliensis) gb:AAD13216; contains Pfam profile PF00656: ICE-like protease (caspase) p20 domain   chr5:1153791-1155041 FORWARD   Aliases: F21E1.120, F21E1_120	2.5	2.6	-0.0	-0.2	100.0%	-5.0
17596	AT3G32040.1   geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltransferase, putative, identical to gi:413730; similar to GB:P34802 from (Arabidopsis thaliana) (Plant Physiol. 104 (4), 1469-1470 (1994))   chr3:13051535-13052722 REVERSE   Aliases: F1M23.7	4.5	4.6	-0.1	-0.2	100.0%	-4.6
17597	AT3G04540.1   Encodes a defensin-like (DEFL) family protein.   chr3:1223356-1223720 FORWARD   Aliases: F7O18.19	2.9	2.8	0.1	0.2	100.0%	-4.9
17598	AT5G27230.1   expressed protein, ; expression supported by MPSS   chr5:9584258-9587841 FORWARD   Aliases: T21B4.140, T21B4_140	2.4	2.4	0.0	0.2	100.0%	-5.7
17599	AT2G25630.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) (Prunus serotina)	2.5	2.5	0.0	0.2	100.0%	-5.4
17600	AT1G31350.1   F-box family protein, similar to hypothetical protein GB:AAF24593 GI:6692128 from (Arabidopsis thaliana) ; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:11221321-11222764 REVERSE   Aliases: T19E23.14, T19E23_14	4.9	4.8	0.1	0.2	100.0%	-4.8
17601	AT2G31480.1   expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313)   chr2:13416055-13418076 REVERSE   Aliases: T28P16.3, T28P16_3	3.3	3.4	-0.0	-0.2	100.0%	-4.9
17602	AT2G22510.1   hydroxyproline-rich glycoprotein family protein, similar to proline-rich cell wall protein (Gossypium barbadense) gi:451544:gb:AAA79364; contains proline-rich extensin domains, INTERPRO:IPR002965   chr2:9576106-9576838 REVERSE   Aliases: F14M13.9, F14M13_9	2.4	2.5	-0.1	-0.2	100.0%	-5.3
17603	AT1G24070.1   Symbol: ATCSLA10   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	2.5	2.5	-0.0	-0.2	100.0%	-5.3
17604	AT3G10060.1   immunophilin, putative / FKBP-type peptidyl-prolyl cis-trans isomerase, putative, Pfam:PF-254: FKBP-type peptidyl-prolyl cis-trans isomerases   chr3:3102229-3104001 FORWARD   Aliases: T22K18.11	3.8	3.7	0.1	0.2	100.0%	-4.8
17605	AT3G42700.1   hypothetical protein   chr3:14783620-14784282 FORWARD   Aliases: T12K4.150	3.1	3.1	0.0	0.2	100.0%	-5.4
17606	AT3G19810.1   expressed protein, contains Pfam PF02620: Uncharacterized ACR, COG1399   chr3:6877581-6879405 REVERSE   Aliases: MPN9.5	5.5	5.4	0.1	0.2	100.0%	-4.8
17607	AT2G25355.1   exonuclease-related, similar to Exosome complex exonuclease RRP40 (EC 3.1.13.-) (Ribosomal RNA processing protein 40) (p10) (CGI-102) (Swiss-Prot:Q9NQT5) (Homo sapiens)	6.4	6.5	-0.1	-0.2	100.0%	-4.7
17608	AT5G39680.1   Symbol: EMB2744   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:15900407-15903616 REVERSE   Aliases: EMB2744, EMBRYO DEFECTIVE 2744, MIJ24.150, MIJ24_150	3.1	3.2	-0.0	-0.2	100.0%	-5.5
17609	AT1G74300.1   esterase/lipase/thioesterase family protein, low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase (Rhodococcus sp. RHA1) GI:8978311; contains Interpro entry IPR000379   chr1:27938959-27940650 FORWARD   Aliases: F1O17.3, F1O17_3	4.4	4.3	0.0	0.2	100.0%	-4.9
17610	AT4G09610.1   Symbol: GASA2   gibberellin-regulated protein 2 (GASA2) / gibberellin-responsive protein 2, identical to SP:P46688 Gibberellin-regulated protein 2 precursor {Arabidopsis thaliana}   chr4:6074767-6075642 REVERSE   Aliases: GAST1 PROTEIN HOMOLOG, T25P22.50, T25P22_50	2.8	2.7	0.0	0.2	100.0%	-5.4
17611	AT3G51780.1   BAG domain-containing protein, low similarity to SP:Q99933 BAG-family molecular chaperone regulator-1 {Homo sapiens}; contains Pfam profile PF02179: BAG (Apoptosis regulator Bcl-2 protein) domain   chr3:19217745-19219260 REVERSE   Aliases: ATEM1.3	7.6	7.5	0.1	0.2	100.0%	-5.0
17612	AT1G51850.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376   chr1:19256516-19260452 REVERSE   Aliases: T14L22.6, T14L22_6	2.4	2.5	-0.1	-0.2	100.0%	-4.4
17613	AT1G21340.1   Dof-type zinc finger domain-containing protein, contains similaity to DNA-binding protein GB:X66076 GI:517257 from (Zea mays)   chr1:7476075-7476857 FORWARD   Aliases: F24J8.23, F24J8_23	3.2	3.2	-0.0	-0.2	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17614	AT4G24500.2   hydroxyproline-rich glycoprotein family protein   chr4:12658742-12660615 FORWARD   Aliases: F22K18.300, F22K18_300	3.7	3.7	-0.0	-0.2	100.0%	-5.3
17615	AT5G05310.3   expressed protein   chr5:1571272-1574580 FORWARD   Aliases: K18I23.11, K18I23_11	4.8	4.8	0.0	0.2	100.0%	-4.9
17616	AT1G65720.1   expressed protein   chr1:24443922-24444736 REVERSE   Aliases: F1E22.9, F1E22_9	8.9	8.8	0.1	0.2	100.0%	-4.6
17617	AT2G40410.2   Ca(2+)-dependent nuclease, putative, similar to Ca(2+)-dependent nuclease (Arabidopsis thaliana) GI:7684292   chr2:16880519-16882474 FORWARD   Aliases: T3G21.18, T3G21_18	6.9	6.8	0.0	0.2	100.0%	-5.0
17618	AT5G57740.1   Symbol: XBAT32	3.3	3.2	0.0	0.2	100.0%	-4.8
17619	AT3G54980.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:20381211-20384046 FORWARD   Aliases: T15C9.5	4.9	4.9	-0.1	-0.2	100.0%	-4.7
17620	AT1G34640.1   expressed protein   chr1:12687208-12688488 REVERSE   Aliases: F12K21.2	4.0	4.0	-0.0	-0.2	100.0%	-5.2
17621	AT2G14620.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endo-transglycosylase-like protein XET-1 GI:5070246 from (Medicago truncatula)   chr2:6251863-6253315 FORWARD   Aliases: T6B13.14, T6B13_14	2.9	2.9	-0.0	-0.2	100.0%	-5.3
17622	AT4G24640.1   Symbol: APPB1   invertase/pectin methylesterase inhibitor family protein, annotation temporarily based on supporting cDNA gi:4097527:gb:U63898.1:U63898	2.3	2.3	0.0	0.2	100.0%	-5.5
17623	AT1G17120.1   Symbol: CAT8   amino acid permease family protein, low similarity to SP:O43246 Cationic amino acid transporter-4 (CAT-4) {Homo sapiens}; contains Pfam profile PF00324: Amino acid permease   chr1:5851946-5853948 FORWARD   Aliases: CATIONIC AMINO ACID TRANSPORTER 8, F20D23.19, F20D23_19	5.6	5.5	0.0	0.2	100.0%	-5.0
17624	AT5G57310.1   expressed protein   chr5:23228256-23228846 FORWARD   Aliases: MJB24.12, MJB24_12	3.2	3.2	0.0	0.2	100.0%	-5.3
17625	AT3G04660.1   F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.5	0.0	0.2	100.0%	-5.2
17626	AT1G75590.1   auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana)   chr1:28386557-28387429 REVERSE   Aliases: F10A5.20, F10A5_20	2.8	2.8	0.0	0.2	100.0%	-5.2
17627	AT1G50890.1   expressed protein   chr1:18865839-18869707 REVERSE   Aliases: F8A12.11, F8A12_11	4.2	4.3	-0.0	-0.2	100.0%	-4.9
17628	AT5G15630.1   Symbol: COBL4/IRX6   Encodes a member of the COBRA family, similar to phytochelatin synthetase. Involved in secondary cell wall biosynthesis. Mutants make smaller plants with reduced levels of cellulose and cell wall sugars.   chr5:5084708-5086795 FORWARD   Aliases: COBL4, COBRA LIKE4, F14F8.10, F14F8_10, IRX6	3.3	3.4	-0.1	-0.2	100.0%	-4.7
17629	AT5G03415.1   Symbol: DPB   DPB-1 transcription factor, putative (DPB), similar to Swiss-Prot:Q14186 transcription factor DP-1 (Homo sapiens); contains Pfam profile PF02319: Transcription factor E2F/dimerisation partner (TDP)   chr5:842499-845411 FORWARD   Aliases: ATDPB, DPB TRANSCRIPTION FACTOR	3.8	3.9	-0.1	-0.2	100.0%	-5.2
17630	AT2G31890.1   expressed protein   chr2:13563222-13566844 REVERSE   Aliases: F20M17.7, F20M17_7	6.7	6.7	-0.1	-0.2	100.0%	-4.8
17631	AT2G26480.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:11271041-11272762 FORWARD   Aliases: T9J22.15, T9J22_15	2.9	2.8	0.1	0.2	100.0%	-4.6
17632	AT3G20340.1   expressed protein   chr3:7092906-7093428 REVERSE   Aliases: MQC12.8	2.5	2.4	0.1	0.2	100.0%	-4.7
17633	AT1G67050.1   expressed protein   chr1:25032290-25033451 REVERSE   Aliases: F1O19.11, F1O19_11	4.2	4.1	0.1	0.2	100.0%	-4.5
17634	AT1G29720.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr1:10393783-10395589 REVERSE   Aliases: T3M22.6, T3M22_6	2.8	2.7	0.0	0.2	100.0%	-5.6
17635	AT5G41720.1   similar to F-box protein-related [Arabidopsis thaliana] (TAIR:At1g64290.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810)   chr5:16700393-16701170 REVERSE   Aliases: MBK23.26, MBK23_26	3.1	3.2	-0.0	-0.2	100.0%	-5.4
17636	AT1G71430.1   expressed protein   chr1:26924102-26924801 FORWARD   Aliases: F3I17.24, F3I17_24	6.8	6.7	0.1	0.2	100.0%	-4.3
17637	AT5G14070.1   glutaredoxin family protein, contains INTERPRO Domain IPR002109, Glutaredoxin (thioltransferase)	3.6	3.5	0.1	0.2	100.0%	-4.7
17638	AT1G47300.1   F-box family protein, similar to hypothetical protein GB:AAD22295 GI:4544385 from (Arabidopsis thaliana)	2.3	2.3	-0.0	-0.2	100.0%	-6.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17639	AT1G03930.1   Symbol: ADK1   protein kinase (ADK1), identical to dual specificity kinase 1 (ADK1) (Arabidopsis thaliana) gi:1216484:gb:AAB47968; supported by cDNA gi:18700076 and gi:1216483. Note: differences between cDNAs in the 11th exon, possibly due to errors or alternative splicing.   chr1:1004768-1008369 FORWARD   Aliases: DUAL SPECIFICITY KINASE 1, F21M11.14, F21M11_14	2.3	2.2	0.0	0.2	100.0%	-5.8
17640	AT5G44100.1   casein kinase, putative, similar to dual specificity kinase 1 gi:1216484:gb:AAB47968   chr5:17766345-17769920 REVERSE   Aliases: MLN1.2, MLN1_2	2.3	2.2	0.0	0.2	100.0%	-5.8
17641	AT4G34830.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:16602433-16606014 REVERSE   Aliases: F11I11.70, F11I11_70	2.7	2.7	-0.0	-0.2	100.0%	-5.7
17642	AT5G48860.1   hypothetical protein   chr5:19828877-19830091 REVERSE   Aliases: K24G6.20, K24G6_20	2.2	2.2	-0.0	-0.2	100.0%	-5.7
17643	AT2G39630.2   glycosyl transferase family 2 protein, similar to dolichyl-phosphate beta-glucosyltransferase from Saccharomyces cerevisiae (SP:P40350); contains Pfam glycosyltransferase group 2 domain PF00535   chr2:16528822-16531726 REVERSE   Aliases: F12L6.29, F12L6_29	7.0	7.0	-0.1	-0.2	100.0%	-4.8
17644	AT1G28135.1   expressed protein   chr1:9829319-9829474 FORWARD   Aliases: F3H9.27, F3H9_27	2.5	2.5	0.0	0.2	100.0%	-5.8
17645	AT5G39560.1   similar to kelch repeat-containing F-box family protein [Arabidopsis thaliana] (TAIR:At4g19870.2); similar to kelch repeat-containing F-box family protein [Arabidopsis thaliana] (TAIR:At4g19870.1); similar to kelch repeat-containing F-box protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_465877.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Kelch repeat (InterPro:IPR006652)   chr5:15858920-15860397 REVERSE   Aliases: MIJ24.5, MIJ24_5	3.1	3.0	0.0	0.2	100.0%	-5.3
17646	AT2G47600.1   Symbol: ATMHX   magnesium/proton exchanger (MHX1), identical to magnesium/proton exchanger AtMHX (Arabidopsis thaliana) gi:6492237:gb:AAF14229; Ca2+:Cation Antiporter (CaCA) Family member PMID:11500563   chr2:19531230-19534483 REVERSE   Aliases: ATMHX1, MAGNESIUM/PROTON EXCHANGER, MHX1, T30B22.10	6.8	6.7	0.1	0.2	100.0%	-5.1
17647	AT5G27510.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	3.1	3.1	0.1	0.2	100.0%	-5.1
17648	AT2G23780.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type   chr2:10130386-10131716 REVERSE   Aliases: F27L4.4, F27L4_4	4.2	4.1	0.1	0.2	100.0%	-5.1
17649	AT1G34170.2   Symbol: ARF13   similar to transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related [Arabidopsis thaliana] (TAIR:At1g35540.1); similar to ARFT_ARATH Putative auxin response factor 20 (GB:Q9C7I9); contains InterPro domain Transcriptional factor B3 (InterPro:IPR003340)   chr1:12443525-12446742 REVERSE   Aliases: ARF13, AUXIN RESPONSE FACTOR 13, F12G12.1, F12G12_1	3.0	3.0	-0.0	-0.2	100.0%	-5.3
17650	AT3G46360.1   expressed protein   chr3:17053200-17054485 REVERSE   Aliases: F18L15.80	3.7	3.8	-0.1	-0.2	100.0%	-5.0
17651	AT1G03280.1   transcription initiation factor IIE (TFIIE) alpha subunit family protein / general transcription factor TFIIE family protein, contains Pfam profile: PF02002 TFIIE alpha subunit	8.1	8.0	0.1	0.2	100.0%	-5.0
17652	AT1G25410.1   Symbol: ATIPT6	3.5	3.4	0.0	0.2	100.0%	-5.1
17653	AT2G29310.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12597145-12598427 FORWARD   Aliases: F16P2.31, F16P2_31	2.8	2.7	0.0	0.2	100.0%	-5.3
17654	AT1G06680.1   Symbol: PSBP   photosystem II oxygen-evolving complex 23 (OEC23), JBC 14:211-238 (2002); identical to 23 kDa polypeptide of oxygen-evolving complex (OEC) GB:CAA66785 GI:1769905 (Arabidopsis thaliana)   chr1:2047878-2049417 FORWARD   Aliases: F12K11.3, F12K11_3, OE23, OEE2, OXYGEN EVOLVING ENHANCER PROTEIN 2	10.6	10.5	0.1	0.2	100.0%	-4.6
17655	AT3G55330.1   photosystem II reaction center PsbP family protein, contains Pfam profile PF01789: PsbP   chr3:20524870-20526328 REVERSE   Aliases: T26I12.210	5.0	5.0	-0.1	-0.2	100.0%	-4.5
17656	AT1G03900.1   Symbol: ATNAP4	7.5	7.4	0.1	0.2	100.0%	-4.9
17657	AT2G37140.1   terpene synthase/cyclase-related, contains Pfam profile PF03936: Terpene synthase family, metal binding domain   chr2:15609942-15610408 FORWARD   Aliases: T2N18.10, T2N18_10	2.6	2.6	-0.0	-0.2	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17658	AT2G22780.1   Symbol: PMDH1   malate dehydrogenase, glyoxysomal, putative, strong similarity to glyoxysomal malate dehydrogenase (EC 1.1.1.37) SP:P19446 {Citrus lanatus}, SP:P46488 {Cucumis sativus}, (Medicago sativa) GI:2827078, SP:Q42972 {Oryza sativa}, SP:Q9ZP05 {Arabidopsis thaliana}, SP:P37228 {Glycine max}; contains InterPro entry IPR001236: Lactate/malate dehydrogenase	8.4	8.6	-0.2	-0.2	100.0%	-4.6
17659	AT4G36260.1   Symbol: STY2   zinc finger protein-related, similar to lateral root primordium 1 (LRP1) (Arabidopsis thaliana) GI:882341; contains Pfam profile PF05142: Domain of unknown function (DUF702), TIGR01624: LRP1 C-terminal domain, TIGR01623: putative zinc finger domain, LRP1 type   chr4:17155559-17157248 REVERSE   Aliases: F23E13.150, F23E13_150, SHI RELATED SEQUENCE 2, SRS2, STYLISH 2	2.8	2.8	-0.0	-0.2	100.0%	-5.2
17660	AT1G57670.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr1:21360834-21363537 REVERSE   Aliases: T8L23.14, T8L23_14	3.3	3.3	0.0	0.2	100.0%	-5.1
17661	AT1G78170.1   expressed protein   chr1:29418952-29419987 FORWARD   Aliases: T11I11.11, T11I11_11	1.9	1.9	0.0	0.2	100.0%	-6.1
17662	AT3G19760.1   eukaryotic translation initiation factor 4A, putative / eIF-4A, putative / DEAD box RNA helicase, putative, contains DEAD/DEAH helicase domain; similar to RNA helicase GB:CAA09195 from (Arabidopsis thaliana); identical to cDNA DEAD box RNA helicase, RH2 GI:3775984	8.3	8.2	0.1	0.2	100.0%	-5.0
17663	AT4G28560.1   Symbol: RIC7   leucine-rich repeat family protein (fragment), contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611;   chr4:14116021-14117373 REVERSE   Aliases: ROP INTERACTIVE CRIB MOTIF CONTAINING PROTEIN 7, T5F17.10	3.7	3.6	0.1	0.2	100.0%	-4.7
17664	AT3G59080.2   similar to aspartyl protease family protein [Arabidopsis thaliana] (TAIR:At2g42980.1); similar to Avr9/Cf-9 rapidly elicited protein 36 [Nicotiana tabacum] (GB:AAV92892.1); contains InterPro domain Aspartic protease A1, pepsin (InterPro:IPR001461)   chr3:21847556-21849597 FORWARD   Aliases: F17J16.130	3.7	3.7	-0.0	-0.2	100.0%	-5.4
17665	AT4G30620.1   expressed protein, contains Pfam domain PF02575: Uncharacterized BCR, YbaB family COG0718; contains similarity to complex interacting protein 9 (CIP9) GI: 32892212   chr4:14948592-14950078 REVERSE   Aliases: F17I23.40, F17I23_40	6.6	6.5	0.1	0.2	100.0%	-4.2
17666	AT3G44180.1   syntaxin-related family protein, contains a novel domain similar to F-box that is shared among other proteins in Arabidopsis; similar to proteins At3g54160, At1g47920 (syntaxin SYP81), At5g41830, At3g58890, At1g56610, At1g48390, At3g59270 (Arabidopsis thaliana)   chr3:15911782-15912703 FORWARD   Aliases: F26G5.130	3.0	3.0	0.0	0.2	100.0%	-5.2
17667	AT4G18650.1   transcription factor-related, contains weak similarity to TGACG-sequence specific DNA-binding protein TGA-2.1 (TGA2.1) (Swiss-Prot:O24160) (Nicotiana tabacum)   chr4:10263980-10265450 REVERSE   Aliases: F28A21.60, F28A21_60	4.0	4.1	-0.1	-0.2	100.0%	-4.1
17668	AT3G45670.1   protein kinase-related, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:16776305-16777444 FORWARD   Aliases: T6D9.3	3.2	3.1	0.0	0.2	100.0%	-5.4
17669	AT2G25160.1   Symbol: CYP82F1   cytochrome P450, putative, similar to cytochrome p450(CYP82C1p) GI:2739004 from (Glycine max)	2.6	2.7	-0.1	-0.2	100.0%	-4.3
17670	AT3G02270.1   eIF4-gamma/eIF5/eIF2-epsilon domain-containing protein, similar to SP:Q13144 Translation initiation factor eIF-2B epsilon subunit (eIF-2B GDP-GTP exchange factor) {Homo sapiens}; contains Pfam profile PF02020: eIF4-gamma/eIF5/eIF2-epsilon   chr3:448984-451014 REVERSE   Aliases: F14P3.8, F14P3_8	3.0	2.9	0.0	0.2	100.0%	-5.2
17671	AT1G21730.1   kinesin-related protein (MKRP1), Similar to gb:U06698 neuronal kinesin heavy chain from Homo sapiens and contains a PF:00225 Kinesin motor domain. EST gb:AA042507 comes from this gene; identical to cDNA MKRP1 mRNA for kinesin-related protein, GI:16902291, kinesin-related protein (Arabidopsis thaliana) GI:16902292   chr1:7630096-7636583 FORWARD   Aliases: F8K7.17, F8K7_17	3.3	3.4	-0.0	-0.2	100.0%	-5.5
17672	AT5G11550.1   expressed protein   chr5:3708010-3709247 REVERSE   Aliases: F15N18.140, F15N18_140	3.6	3.7	-0.1	-0.2	100.0%	-4.9
17673	AT4G03740.1   expressed protein   chr4:1661990-1663513 REVERSE   Aliases: T5L23.25, T5L23_25	2.3	2.3	-0.0	-0.2	100.0%	-5.8
17674	AT4G07460.1   hypothetical protein   chr4:4257794-4259250 FORWARD   Aliases: F28D6.2, F28D6_2	2.3	2.3	-0.0	-0.2	100.0%	-5.8
17675	AT5G18350.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:6074525-6078571 REVERSE   Aliases: F20L16.70, F20L16_70	2.4	2.4	-0.0	-0.2	100.0%	-5.1
17676	AT2G20110.2   tesmin/TSO1-like CXC domain-containing protein, similar to SP:Q9WTJ6 Tesmin (Metallothionein-like 5, testis-specific) {Mus musculus}; contains Pfam profile PF03638: Tesmin/TSO1-like CXC domain	2.4	2.4	0.0	0.2	100.0%	-5.3
17677	AT5G37520.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr5:14919900-14921441 FORWARD   Aliases: MPA22.6, MPA22_6	3.3	3.4	-0.0	-0.2	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17678	AT4G01890.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase ( <i>Lycopersicon esculentum</i> ) GI:7381227; contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr4:816210-818428 FORWARD   Aliases: T7B11.15, T7B11_15	3.9	3.8	0.1	0.2	100.0%	-4.8
17679	AT3G51790.1   Symbol: ATG1   cytochrome c biogenesis protein CcmE family, contains Pfam profile: PF03100 cytochrome c-type biogenesis protein CcmE   chr3:19220562-19221721 REVERSE   Aliases: ATEM1.4	4.8	4.7	0.0	0.2	100.0%	-4.9
17680	AT5G41810.2   expressed protein   chr5:16755290-16756891 FORWARD   Aliases: K16L22.9, K16L22_9	3.5	3.4	0.1	0.2	100.0%	-4.5
17681	AT1G79610.1   sodium proton exchanger, putative (NHX6), identical to Na <sup>+</sup> /H <sup>+</sup> exchanger 6 ( <i>Arabidopsis thaliana</i> ) gi:19919848:gb:AAM08407 (Plant J. (2002) In press); contains similarity to Na <sup>+</sup> /H <sup>+</sup> antiporter GI:1655701 from ( <i>Xenopus laevis</i> ); contains non-consensus AT/AC splice sites; Member of The Monovalent Cation:Proton Antiporter (CPA1) Family, PMID:11500563   chr1:29957836-29962082 REVERSE   Aliases: F20B17.4, F20B17_4	6.4	6.4	-0.1	-0.2	100.0%	-4.7
17682	AT1G60280.1   Symbol: ANAC023   no apical meristem (NAM) protein-related, contains Pfam PF02365: No apical meristem (NAM) protein; contains similarity to NAM-like protein GI:4337200 from ( <i>Arabidopsis thaliana</i> )   chr1:22230550-22231593 REVERSE   Aliases: ANAC023, T13D8.17, T13D8_17	3.2	3.1	0.0	0.2	100.0%	-5.3
17683	AT4G17895.1   ubiquitin-specific protease 20, putative (UBP20), identical to ubiquitin-specific protease 20 GI:11993480 ( <i>Arabidopsis thaliana</i> )	4.3	4.4	-0.1	-0.2	100.0%	-4.9
17684	AT4G35860.1   Symbol: ATGB2   Ras-related GTP-binding protein, putative, similar to Rab2-like GTP-binding protein GI:1765896 from ( <i>Arabidopsis thaliana</i> )   chr4:16986843-16989041 REVERSE   Aliases: F4B14.130, F4B14_130, GTP BINDING 2, GTP BINDING PROTEIN ATGB2	7.4	7.3	0.1	0.2	100.0%	-4.9
17685	AT1G56450.1   Symbol: PBG1   20S proteasome beta subunit G1 (PBG1) (PRCH), identical to 20S proteasome beta subunit (PBG1) GI:3421123 ( <i>Arabidopsis thaliana</i> ); identical to cDNA proteasome subunit prch GI:2511597   chr1:21145558-21148065 FORWARD   Aliases: F13N6.3, F13N6_3, PROTEASOME BETA SUBUNIT PBG1	10.8	10.9	-0.1	-0.2	100.0%	-4.7
17686	AT1G71460.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:26931646-26933978 REVERSE   Aliases: F26A9.16	3.7	3.8	-0.0	-0.2	100.0%	-5.3
17687	AT1G74380.1   galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, <i>Schizosaccharomyces pombe</i> (SP:Q09174)	6.1	6.0	0.1	0.2	100.0%	-5.0
17688	AT5G28440.1   expressed protein   chr5:10367675-10369018 REVERSE   Aliases: F21B23.100, F21B23_100	2.9	2.9	-0.0	-0.2	100.0%	-5.2
17689	AT4G16310.1   amine oxidase family protein / SWIRM domain-containing protein, low similarity to polyamine oxidase isoform-1 ( <i>Homo sapiens</i> ) GI:14860862; contains Pfam profiles PF01593: amine oxidase flavin-containing, PF04433: SWIRM domain	2.7	2.7	0.0	0.2	100.0%	-5.6
17690	AT1G60930.1   DNA helicase, putative, strong similarity to DNA Helicase recQ14B ( <i>Arabidopsis thaliana</i> ) GI:11121451; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain, PF00570: HRDC domain   chr1:22435025-22441637 REVERSE   Aliases: T7P1.7, T7P1_7	3.0	2.9	0.0	0.2	100.0%	-5.4
17691	AT4G39560.2   kelch repeat-containing F-box family protein, contains Pfam PF00646: F-box domain; contains Pfam PF01344 : Kelch motif; contains Prosite PS00018: EF-hand calcium-binding domain	4.6	4.6	-0.0	-0.2	100.0%	-4.9
17692	AT4G19480.1   expressed protein   chr4:10614791-10615327 REVERSE   Aliases: F24J7.40, F24J7_40	2.8	2.9	-0.0	-0.2	100.0%	-5.3
17693	AT5G26130.1   pathogenesis-related protein, putative, similar to PR-1a protein ( <i>Nicotiana tabacum</i> ) GI:19944; contains Pfam profile PF00188: SCP-like extracellular protein   chr5:9128113-9128607 REVERSE   Aliases: T1N24.14, T1N24_14	3.5	3.5	0.0	0.2	100.0%	-5.5
17694	AT1G78710.1   expressed protein, similar to hypothetical protein GI:3201617 from ( <i>Arabidopsis thaliana</i> ); expression supported by MPSS   chr1:29607601-29609450 FORWARD   Aliases: F9K20.25, F9K20_25	3.5	3.6	-0.0	-0.2	100.0%	-4.9
17695	AT2G25440.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to NLOE ( <i>Lycopersicon esculentum</i> ) gi:4235643:gb:AAD13303   chr2:10833814-10836481 FORWARD   Aliases: F13B15.10, F13B15_10	2.9	2.9	-0.0	-0.2	100.0%	-5.8
17696	AT2G30050.1   transducin family protein / WD-40 repeat family protein, similar to SEC13-related protein (SP:P55735) ( <i>Homo sapiens</i> )   chr2:12831528-12833761 FORWARD   Aliases: T27E13.21, T27E13_21	6.3	6.2	0.1	0.2	100.0%	-4.6
17697	AT3G19380.1   U-box domain-containing protein, contains similarity to immediate-early fungal elicitor protein CMPG1 GI:14582200 ( <i>Petroselinum crispum</i> ); contains Pfam profile PF04564: U-box domain   chr3:6714398-6716105 REVERSE   Aliases: MLD14.11	3.2	3.1	0.0	0.2	100.0%	-5.2
17698	AT2G31700.1   hypothetical protein   chr2:13487587-13488645 FORWARD   Aliases: T9H9.22, T9H9_22	2.7	2.6	0.0	0.2	100.0%	-5.4
17699	AT5G57480.1   AAA-type ATPase family protein, contains Pfam profile: PF00004 ATPase family   chr5:23296632-23298194 REVERSE   Aliases: MUA2.5, MUA2_5	6.3	6.5	-0.1	-0.2	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17700	AT5G27810.1   expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr5:9855831-9856190 FORWARD   Aliases: T1G16.140, T1G16_140	2.6	2.6	-0.0	-0.2	100.0%	-5.8
17701	AT5G23010.1   Symbol: MAM1   2-isopropylmalate synthase 3 (IMS3), identical to 2-isopropylmalate synthase (IMS3) (Arabidopsis thaliana) GI:15983745; identical to cDNA 2-isopropylmalate synthase (IMS3) GI:15983744	3.5	3.6	-0.1	-0.2	100.0%	-4.3
17702	AT2G39725.2   complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)   chr2:16576508-16577595 FORWARD   Aliases: None	7.0	7.1	-0.1	-0.2	100.0%	-4.6
17703	AT1G25370.1   expressed protein   chr1:8897744-8899089 REVERSE   Aliases: F4F7.1	5.4	5.4	0.0	0.2	100.0%	-5.2
17704	AT5G40230.1   nodulin-related, low similarity to MtN21 (Medicago truncatula) GI:2598575; contains Pfam profile PF00892: Integral membrane protein   chr5:16096876-16098963 REVERSE   Aliases: MSN9.130, MSN9_130	3.7	3.7	0.0	0.2	100.0%	-5.0
17705	AT5G03550.1   hypothetical protein   chr5:895812-896144 REVERSE   Aliases: F12E4.340, F12E4_340	2.4	2.4	0.0	0.2	100.0%	-5.4
17706	AT3G14480.1   glycine/proline-rich protein, contains 1 predicted transmembrane domain;	2.4	2.4	0.0	0.2	100.0%	-5.5
17707	AT4G11510.1   Symbol: RALFL28   expressed protein, ; expression supported by MPSS   chr4:6984046-6984303 REVERSE   Aliases: F25E4.130, F25E4_130, RALF LIKE 28	2.9	3.0	-0.1	-0.2	100.0%	-5.1
17708	AT4G04990.1   expressed protein, contains Pfam domain PF05553: Cotton fiber expressed protein   chr4:2555088-2557044 FORWARD   Aliases: C17L7.3	3.1	3.0	0.1	0.2	100.0%	-4.8
17709	AT4G33670.1   L-galactose dehydrogenase (L-GalDH), identical to L-galactose dehydrogenase (Arabidopsis thaliana) GI:16555790; similar to L-fucose dehydrogenase (Pseudomonas sp.) GI:829054; contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family	8.5	8.5	0.1	0.2	100.0%	-4.7
17710	AT1G33070.1   hypothetical protein   chr1:11982869-11985279 FORWARD   Aliases: T9L6.11, T9L6_11	2.3	2.3	0.0	0.2	100.0%	-5.8
17711	AT3G52850.1   Symbol: ATELP1	9.6	9.5	0.1	0.2	100.0%	-5.0
17712	AT2G47320.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr2:19434442-19435987 FORWARD   Aliases: T8I13.16	10.1	10.0	0.1	0.2	100.0%	-4.8
17713	AT1G77110.1   Symbol: PIN6   auxin transport protein, putative, similar to auxin transport protein EIR1 GI:3377507 from (Arabidopsis thaliana)   chr1:28975698-28979497 FORWARD   Aliases: F22K20.18, F22K20_18, PIN FORMED 6, PIN6	4.0	4.0	0.1	0.2	100.0%	-4.9
17714	AT5G62790.1   Symbol: DXR   1-deoxy-D-xylulose 5-phosphate reductoisomerase (DXR), nearly identical to 1-deoxy-d-xylulose-5-phosphate reductoisomerase (Arabidopsis thaliana) GI:4886307; contains Pfam profile PF02670: 1-deoxy-D-xylulose 5-phosphate reductoisomerase   chr5:25231351-25234665 REVERSE   Aliases: 1 DEOXY D XYLULOSE 5 PHOSPHATE REDUCTOISOMERASE, MQB2.90, MQB2_90, PDE129, PIGMENT DEFECTIVE EMBRYO	7.3	7.4	-0.1	-0.2	100.0%	-4.9
17715	AT1G80060.1   expressed protein   chr1:30121195-30122417 REVERSE   Aliases: F18B13.35, F18B13_35	4.1	4.1	0.1	0.2	100.0%	-4.8
17716	AT1G18080.1   Symbol: ATARCA	9.2	9.0	0.2	0.2	100.0%	-4.4
17717	AT4G32570.1   expressed protein   chr4:15716039-15718864 REVERSE   Aliases: F4D11.230, F4D11_230	3.7	3.7	-0.1	-0.2	100.0%	-5.4
17718	AT1G46336.1   hypothetical protein   chr1:17232851-17233093 REVERSE   Aliases: F2G19.35, F2G19_35	2.5	2.5	0.0	0.2	100.0%	-6.0
17719	AT3G17950.2   expressed protein   chr3:6146247-6147324 FORWARD   Aliases: MEB5.1	2.9	3.0	-0.0	-0.2	100.0%	-5.0
17720	AT5G06020.1   self-incompatibility protein-related, similar to self-incompatibility (Papaver rhoeas) GI:3097260   chr5:1811939-1812394 FORWARD   Aliases: K18J17.22, K18J17_22	2.5	2.4	0.0	0.2	100.0%	-5.7
17721	AT1G80530.1   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr1:30282844-30285216 REVERSE   Aliases: T21F11.14, T21F11_14	5.4	5.4	0.1	0.2	100.0%	-5.1
17722	NA	2.2	2.2	0.0	0.2	100.0%	-6.4
17723	AT5G63610.1   Symbol: HEN3   protein kinase, putative, similar to cyclin-dependent kinase cdc2MsE (Medicago sativa) gi:1806144:emb:CAA65981; contains protein kinase domain, Pfam:PF00069   chr5:25480665-25483112 REVERSE   Aliases: CDKE;1, Cyclin dependent kinase E;1, HUA ENHANCER 3, MBK5.8, MBK5_8	5.7	5.6	0.1	0.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17724	AT3G49390.2   Symbol: CID10   similar to RNA-binding protein, putative [Arabidopsis thaliana] (TAIR:At1g32790.1); similar to putative RNA-binding protein RBP37 [Oryza sativa (japonica cultivar-group)] (GB:XP_479783.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr3:18325512-18328983 REVERSE   Aliases: CID10, F2K15.250	6.3	6.2	0.1	0.2	100.0%	-4.9
17725	AT2G32600.1   hydroxyproline-rich glycoprotein family protein, similar to SWISS-PROT:Q15428   chr2:13840622-13842736 REVERSE   Aliases: T26B15.16, T26B15_16	4.0	4.1	-0.1	-0.2	100.0%	-5.1
17726	AT3G60570.1   Symbol: ATEXPB5   beta-expansin, putative (EXPB5), contains similarity to beta-expansin GI:8118428 from (Oryza sativa); beta-expansin gene family, PMID:11641069   chr3:22402222-22403438 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN B5, ATHEXP BETA 1.3, EXPB5, T8B10.230	3.2	3.2	-0.0	-0.2	100.0%	-5.0
17727	AT2G20580.1   26S proteasome regulatory subunit S2 (RPN1), contains an APC-complex (cyclosome) and proteasome component repeat ( P550248)   chr2:8866091-8871946 FORWARD   Aliases: F23N11.10, F23N11_10	8.0	8.1	-0.1	-0.2	100.0%	-4.7
17728	AT4G04110.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr4:1972589-1974012 FORWARD   Aliases: T24H24.18, T24H24_18	3.7	3.7	-0.0	-0.2	100.0%	-5.3
17729	AT5G48690.1   similar to ubiquitin-associated (UBA)/TS-N domain-containing protein [Arabidopsis thaliana] (TAIR:At1g04850.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_483435.1); contains InterPro domain Ubiquitin-associated domain (InterPro:IPR000449); contains InterPro domain PUG (InterPro:IPR006567)   chr5:19764330-19766284 REVERSE   Aliases: K24G6.2, K24G6_2	2.6	2.7	-0.0	-0.2	100.0%	-5.0
17730	AT5G62890.3   similar to xanthine/uracil permease family protein [Arabidopsis thaliana] (TAIR:At1g10540.1); similar to xanthine/uracil permease family protein [Arabidopsis thaliana] (TAIR:At1g60030.1); similar to xanthine/uracil permease family protein [Arabidopsis thaliana] (TAIR:At5g49990.1); similar to putative permease 1 [Lycopersicon esculentum] (GB:AAX95758.1); similar to putative permease [Oryza sativa (japonica cultivar-group)] (GB:XP_482444.1); similar to putative permease 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_450798.1); similar to putative permease 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_467723.1); similar to putative permease [Oryza sativa (japonica cultivar-group)] (GB:NP_910042.1); contains InterPro domain Xanthine/uracil/vitamin C permease family (InterPro:IPR006043)   chr5:25260477-25264068 FORWARD   Aliases: MQB2.190, MQB2_190	5.2	5.3	-0.1	-0.2	100.0%	-4.7
17731	AT5G65770.1   nuclear matrix constituent protein-related, low similarity to nuclear matrix constituent protein 1 (NMCP1) (Daucus carota) GI:2190187   chr5:26328813-26332770 FORWARD   Aliases: MPA24.12, MPA24_12	4.4	4.3	0.1	0.2	100.0%	-4.8
17732	AT4G02600.2   similar to seven transmembrane MLO family protein / MLO-like protein 15 (MLO15) [Arabidopsis thaliana] (TAIR:At2g44110.1); similar to seven transmembrane MLO family protein / MLO-like protein 15 (MLO15) [Arabidopsis thaliana] (TAIR:At2g44110.2); similar to putative seven transmembrane protein [Oryza sativa (japonica cultivar-group)] (GB:NP_915093.1); contains InterPro domain Mlo-related protein (InterPro:IPR004326)   chr4:1143962-1147422 FORWARD   Aliases: T10P11.12, T10P11_12	5.6	5.7	-0.0	-0.2	100.0%	-5.1
17733	AT4G18550.1   lipase class 3 family protein, similar to lipase (Dianthus caryophyllus) GI:4103627; contains Pfam profile PF01764: Lipase   chr4:10225017-10226873 REVERSE   Aliases: F28J12.210, F28J12_210	2.7	2.6	0.1	0.2	100.0%	-4.6
17734	AT4G01040.1   glycosyl hydrolase family 18 protein, contains Pfam profile PF00704: Glycosyl hydrolases family 18   chr4:453370-455548 FORWARD   Aliases: F2N1.39_01, F2N1_39_01	8.2	8.2	0.1	0.2	100.0%	-5.0
17735	AT1G17150.1   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, similar to polygalacturonase (Salix gilgiana) GI:6714524; contains Pfam profile PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr1:5865700-5867488 FORWARD   Aliases: F20D23.15, F20D23_15	2.9	2.8	0.0	0.2	100.0%	-5.4
17736	AT4G28320.1   glycosyl hydrolase family 5 protein / cellulase family protein, mannan endo-1,4-beta-mannosidase (EC 3.2.1.78) - tomato, PIR2:T04323   chr4:14018189-14020223 REVERSE   Aliases: F26K10.200, F26K10_200	3.4	3.4	-0.0	-0.2	100.0%	-5.4
17737	AT5G51750.1   subtilase family protein, similar to subtilisin-like protease GI:3687307 from (Lycopersicon esculentum)   chr5:21037433-21040007 FORWARD   Aliases: MIO24.12, MIO24_12	3.1	3.1	-0.0	-0.2	100.0%	-5.4
17738	AT4G02180.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.5	3.4	0.1	0.2	100.0%	-4.6
17739	AT5G36150.1   Symbol: ATPEN3	2.5	2.5	0.0	0.2	100.0%	-5.7
17740	AT4G21600.1   bifunctional nuclease, putative, similar to bifunctional nuclease (Zinnia elegans) gi:4099833:gb:AAD00694   chr4:11485131-11487428 FORWARD   Aliases: F17L22.60	7.8	7.9	-0.1	-0.2	100.0%	-4.9
17741	AT5G04630.1   Symbol: CYP77A9   cytochrome P450, putative, cytochrome P450 77A3p, Glycine max, PIR:T05948   chr5:1330579-1332108 FORWARD   Aliases: T1E3.4	4.0	4.0	-0.0	-0.2	100.0%	-5.4
17742	AT3G55170.2   60S ribosomal protein L35 (RPL35C), various ribosomal L35 proteins   chr3:20463946-20465316 REVERSE   Aliases: T26I12.50	9.3	9.4	-0.1	-0.2	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17743	AT5G02000.1   hypothetical protein   chr5:380152-380592 REVERSE   Aliases: T7H20.50, T7H20_50	3.2	3.1	0.0	0.2	100.0%	-5.0
17744	AT1G12430.1   Symbol: PAK   armadillo/beta-catenin repeat family protein / kinesin motor family protein   chr1:4233871-4238757 REVERSE   Aliases: None	4.1	4.1	-0.1	-0.2	100.0%	-4.6
17745	AT2G19060.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL6 GI:15054390, EXL1 GI:15054382, EXL2 GI:15054384 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	3.6	3.5	0.1	0.2	100.0%	-4.4
17746	AT2G41770.1   expressed protein, contains Pfam domain PF03385: Protein of unknown function, DUF288   chr2:17431436-17434360 REVERSE   Aliases: T11A7.13, T11A7_13	5.2	5.3	-0.1	-0.2	100.0%	-4.8
17747	AT5G51610.1   ribosomal protein L11 family protein   chr5:20982803-20984031 FORWARD   Aliases: K17N15.16, K17N15_16	2.5	2.5	-0.0	-0.2	100.0%	-5.5
17748	AT2G05600.1   hypothetical protein   chr2:2072643-2073544 FORWARD   Aliases: T20G20.5, T20G20_5	2.9	2.8	0.0	0.2	100.0%	-5.3
17749	AT1G02310.1   glycosyl hydrolase family protein 5 / cellulase family protein / (1-4)-beta-mannan endohydrolase, putative, similar to (1-4)-beta-mannan endohydrolase precursor GI:9836826 from ( <i>Lycopersicon esculentum</i> )   chr1:458133-460696 REVERSE   Aliases: T6A9.1, T6A9_1	3.9	3.9	0.0	0.2	100.0%	-4.8
17750	AT2G10930.1   expressed protein   chr2:4310363-4311049 REVERSE   Aliases: F16G22.1, F16G22_1	5.0	5.0	-0.1	-0.2	100.0%	-5.2
17751	AT5G47950.1   transferase family protein, similar to deacetylindoline 4-O-acetyltransferase ( <i>Catharanthus roseus</i> )(GI:4091808)(PMID:9681034), acetyl-CoA:benzylalcohol acetyltransferase ( <i>Clarkia concinna</i> )(GI:6166328)(PMID:10588064)	3.8	3.7	0.1	0.2	100.0%	-4.5
17752	AT3G10700.1   GHMP kinase family protein, contains Pfam profile: PF00288 GHMP kinases putative ATP-binding proteins   chr3:3346583-3351028 REVERSE   Aliases: T7M13.22	3.4	3.4	0.0	0.2	100.0%	-5.3
17753	AT2G40300.1   Symbol: ATFER4	5.8	5.9	-0.1	-0.2	100.0%	-4.3
17754	AT5G01060.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:22739-24846 FORWARD   Aliases: F7J8.40, F7J8_40	3.9	3.8	0.1	0.2	100.0%	-4.4
17755	AT2G30340.1   LOB domain protein 13 / lateral organ boundaries domain protein 13 (LBD13), identical to LOB DOMAIN 13 ( <i>Arabidopsis thaliana</i> ) GI:17227158 SP:Q9AT61   chr2:12938321-12939659 REVERSE   Aliases: T9D9.15, T9D9_15	2.1	2.2	-0.1	-0.2	100.0%	-4.9
17756	AT5G50770.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to sterol-binding dehydrogenase steroleosin GI:15824408 from ( <i>Sesamum indicum</i> )	3.1	3.0	0.0	0.2	100.0%	-5.3
17757	AT5G17240.1   SET domain-containing protein, contains Pfam profile PF00856: SET domain	2.7	2.7	0.0	0.2	100.0%	-5.5
17758	AT5G13110.1   Symbol: G6PD2   Encodes a plastidic glucose-6-phosphate dehydrogenase that is sensitive to reduction by DTT and whose mRNA is most highly expressed in root.   chr5:4158814-4161823 FORWARD   Aliases: G6PD2, GLUCOSE 6 PHOSPHATE DEHYDROGENASE 2, T19L5.70, T19L5_70	9.0	9.1	-0.1	-0.2	100.0%	-4.9
17759	AT5G60970.1   TCP family transcription factor, putative, putative basic helix-loop-helix DNA binding protein TCP2, <i>Arabidopsis thaliana</i> , EMBL:AF072691	2.1	2.1	0.0	0.2	100.0%	-6.1
17760	AT1G64900.1   Symbol: CYP89A2   cytochrome P450, putative, similar to cytochrome p450 GI:438240 from ( <i>Solanum melongena</i> )   chr1:24116878-24118647 FORWARD   Aliases: CYP89, CYP89A2, CYTOCHROME P450 89A2, F13O11.20, F13O11_20	3.0	3.0	0.0	0.2	100.0%	-5.5
17761	AT1G73340.1   cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) ( <i>Arabidopsis thaliana</i> ); contains Pfam profile: PF00067 cytochrome P450   chr1:27576797-27578934 FORWARD   Aliases: T9L24.44, T9L24_44	2.6	2.6	-0.0	-0.2	100.0%	-5.3
17762	AT4G39150.1   DNAJ heat shock N-terminal domain-containing protein, similar to SP:P39101 CAJ1 protein, <i>Saccharomyces cerevisiae</i> , PIR2:S48085; contains Pfam profile PF00226 DnaJ domain   chr4:18233499-18236058 REVERSE   Aliases: T22F8.50, T22F8_50	8.1	8.1	0.0	0.2	100.0%	-5.1
17763	AT2G47540.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr2:19512948-19513578 FORWARD   Aliases: T30B22.16	2.4	2.4	-0.0	-0.2	100.0%	-5.0
17764	AT5G66100.1   La domain-containing protein, similar to SP:P40796 La protein homolog (La ribonucleoprotein) (La autoantigen homolog) { <i>Drosophila melanogaster</i> }; contains Pfam profile PF05383: La domain   chr5:26444715-26447232 FORWARD   Aliases: K2A18.18, K2A18_18	4.0	3.9	0.0	0.2	100.0%	-5.1
17765	AT5G16900.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase ( <i>Arabidopsis thaliana</i> ) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:5555257-5559718 FORWARD   Aliases: F2K13.50, F2K13_50	3.3	3.3	0.0	0.2	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17766	AT1G74210.1   glycerophosphoryl diester phosphodiesterase family protein, low similarity to glycerophosphodiester phosphodiesterase ( <i>Borrelia hermsii</i> ) GI:1399038; contains Pfam profile PF03009: Glycerophosphoryl diester phosphodiesterase family   chr1:27913979-27916602 FORWARD   Aliases: F1O17.12, F1O17_12	10.0	10.1	-0.1	-0.2	100.0%	-4.8
17767	AT3G56010.1   expressed protein   chr3:20799670-20800903 FORWARD   Aliases: F27K19.190	5.1	5.1	-0.0	-0.2	100.0%	-4.9
17768	AT1G16880.2   uridylyltransferase-related, similar to (Protein-PII) uridylyltransferase (PII uridylyl-transferase) (Uridylyl removing enzyme) (UTase)(SP:Q9AC53) ( <i>Caulobacter crescentus</i> )   chr1:5773671-5775497 FORWARD   Aliases: F17F16.13	8.0	7.9	0.1	0.2	100.0%	-4.7
17769	AT2G24810.1   pathogenesis-related thaumatin family protein, similar to thaumatin-like protein ( <i>Arabidopsis thaliana</i> ) GI:2435406; contains Pfam profile PF00314: Thaumatin family   chr2:10580941-10581778 FORWARD   Aliases: F27C12.27, F27C12_27	2.5	2.5	0.0	0.2	100.0%	-5.5
17770	AT2G14590.1   hypothetical protein   chr2:6235919-6236890 FORWARD   Aliases: T13P21.3	2.6	2.6	-0.0	-0.2	100.0%	-5.7
17771	AT4G30410.2   expressed protein, similar to cDNA bHLH transcription factor (bHLH eta gene) gi:32563007	5.5	5.5	0.1	0.2	100.0%	-4.5
17772	AT3G09350.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr3:2871051-2873318 FORWARD   Aliases: F3L24.22	5.1	5.2	-0.1	-0.2	100.0%	-4.4
17773	AT2G42840.2   Symbol: PDF1   protodermal factor 1 (PDF1), identical to protodermal factor 1 ( <i>Arabidopsis thaliana</i> ) gi:4929130:gb:AAD33869   chr2:17833078-17834560 REVERSE   Aliases: F7D19.16, F7D19_16, PROTODERMAL FACTOR 1	3.0	2.9	0.0	0.2	100.0%	-5.4
17774	AT2G34110.1   expressed protein   chr2:14409579-14410396 FORWARD   Aliases: T14G11.23, T14G11_23	3.7	3.6	0.0	0.2	100.0%	-5.3
17775	AT1G51790.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase ( <i>Arabidopsis thaliana</i> ) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069	2.3	2.4	-0.1	-0.2	100.0%	-4.6
17776	AT1G69526.2   similar to UbiE/COQ5 methyltransferase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g69523.1); similar to COG0500: SAM-dependent methyltransferases [ <i>Nostoc punctiforme</i> PCC 73102] (GB:ZP_00110216.1); contains InterPro domain Generic methyltransferase (InterPro:IPR001601); contains InterPro domain SAM (and some other nucleotide) binding motif (InterPro:IPR000051); contains InterPro domain UbiE/COQ5 methyltransferase (InterPro:IPR004033)	3.0	2.9	0.1	0.2	100.0%	-4.6
17777	AT4G30790.1   expressed protein   chr4:14993092-14997791 REVERSE   Aliases: T10C21.140, T10C21_140	6.0	5.9	0.1	0.2	100.0%	-4.7
17778	AT4G38390.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator protein -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from ( <i>Nicotiana tabacum</i> ), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.   chr4:17975770-17978374 FORWARD   Aliases: F22I13.160, F22I13_160	2.8	2.9	-0.1	-0.2	100.0%	-4.5
17779	AT2G28120.1   nodulin family protein, similar to nodulin-like protein ( <i>Arabidopsis thaliana</i> ) GI:3329368, nodule-specific protein Nlj70 ( <i>Lotus japonicus</i> ) GI:3329366   chr2:11992764-11994815 FORWARD   Aliases: F24D13.9, F24D13_9	4.5	4.4	0.0	0.2	100.0%	-5.0
17780	AT1G28327.1   expressed protein   chr1:9931921-9933438 FORWARD   Aliases: F3H9.2, F3H9_2	2.9	2.9	-0.0	-0.2	100.0%	-5.8
17781	AT3G47700.1   chromosome structural maintenance protein-related, contains weak similarity to RAD50-interacting protein 1 ( <i>Homo sapiens</i> ) gi:11967435:gb:AAG42101   chr3:17594586-17597609 REVERSE   Aliases: T23J7.30	6.3	6.4	-0.1	-0.2	100.0%	-4.9
17782	AT4G19740.1   glycosyl hydrolase family 18 protein, similar to chitinase, class V GI:899342 from ( <i>Nicotiana tabacum</i> )   chr4:10739577-10740630 REVERSE   Aliases: T16H5.100, T16H5_100	3.0	3.0	0.0	0.2	100.0%	-5.4
17783	AT1G32780.1   alcohol dehydrogenase, putative, similar to alcohol dehydrogenase GB:CAA37333 GI:297178 from ( <i>Solanum tuberosum</i> ); contains Pfam zinc-binding dehydrogenase domain PF00107   chr1:11869809-11872774 REVERSE   Aliases: F6N18.16, F6N18_16	2.5	2.5	-0.0	-0.2	100.0%	-5.4
17784	AT1G08590.1   similar to CLV1-like leucine rich repeat transmembrane receptor-like protein kinase ( <i>Ipomoea nil</i> ) (U77888)   chr1:2718781-2722224 FORWARD   Aliases: F22O13.7, F22O13_7	3.4	3.4	0.0	0.2	100.0%	-4.8
17785	AT1G67790.1   expressed protein   chr1:25421205-25423762 REVERSE   Aliases: F12A21.8, F12A21_8	2.5	2.5	-0.0	-0.2	100.0%	-5.6
17786	AT2G18870.1   expressed protein, contains 1 transmembrane domain; tandem duplication of fibronectin type III domain protein (GI:3004551) (TIGR_Ath1:At2g18880) ( <i>Arabidopsis thaliana</i> )   chr2:8174553-8175750 FORWARD   Aliases: F19F24.7, F19F24_7	3.9	3.8	0.1	0.2	100.0%	-4.2
17787	AT2G26060.2   Symbol: EMB1345   similar to transducin family protein / WD-40 repeat family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g32990.1); similar to GA11817-PA [ <i>Drosophila pseudoobscura</i> ] (GB:EAL24914.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr2:11109379-11112433 FORWARD   Aliases: EMB1345, EMBRYO DEFECTIVE 1345, T19L18.13, T19L18_13	7.4	7.5	-0.1	-0.2	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17788	AT5G25475.2   expressed protein   chr5:8867843-8869824 REVERSE   Aliases: None	6.2	6.3	-0.1	-0.2	100.0%	-4.6
17789	AT3G24506.1   expressed protein   chr3:8928177-8929336 REVERSE   Aliases: None	6.3	6.3	-0.1	-0.2	100.0%	-4.7
17790	AT1G22130.1   MADS-box family protein, similar to MADS-box protein (ZAP1) GI:939784 from (Zea mays)   chr1:7812376-7814248 REVERSE   Aliases: F2E2.20, F2E2_20	2.3	2.2	0.0	0.2	100.0%	-5.6
17791	AT2G02470.1   PHD finger family protein, contains Pfam domain, PF00628: PHD-finger   chr2:652579-654914 FORWARD   Aliases: T16F16.26, T16F16_26	7.1	7.0	0.1	0.2	100.0%	-4.9
17792	AT1G21370.2   expressed protein   chr1:7483772-7486311 FORWARD   Aliases: F24J8.26, F24J8_26	6.9	6.9	0.1	0.2	100.0%	-5.1
17793	AT1G10920.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.6	2.6	0.0	0.2	100.0%	-5.6
17794	AT3G13590.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr3:4435323-4437341 REVERSE   Aliases: K20M4.3	3.1	3.1	0.0	0.2	100.0%	-5.0
17795	AT4G35530.1   phosphatidylinositolglycan-related, contains weak similarity to Swiss-Prot:Q14442 phosphatidylinositol-glycan biosynthesis, class H protein (PIG-H) (Homo sapiens)   chr4:16871779-16873657 REVERSE   Aliases: F8D20.40, F8D20_40	6.5	6.5	0.1	0.2	100.0%	-4.7
17796	AT3G21160.1   mannosyl-oligosaccharide 1,2-alpha-mannosidase, putative, similar to mannosyl-oligosaccharide 1,2-alpha-mannosidase (Glycine max)(GI:6552504)   chr3:7413853-7418416 REVERSE   Aliases: MSA6.31	4.5	4.4	0.0	0.2	100.0%	-5.2
17797	AT1G78050.1   phosphoglycerate/bisphosphoglycerate mutase family protein, similar to SP:P31217 Phosphoglycerate mutase 1 (EC 5.4.2.1) {Escherichia coli O157:H7}; contains Pfam profile PF00300: phosphoglycerate mutase family   chr1:29352475-29355175 FORWARD   Aliases: F28K19.30, F28K19_30	7.5	7.6	-0.1	-0.2	100.0%	-4.8
17798	AT5G55480.1   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor	4.3	4.4	-0.1	-0.2	100.0%	-5.1
17799	AT5G65250.1   expressed protein   chr5:26095759-26097424 REVERSE   Aliases: MQN23.20, MQN23_20	6.1	6.0	0.1	0.2	100.0%	-4.7
17800	AT1G34280.1   expressed protein   chr1:12495120-12495359 REVERSE   Aliases: F23M19.16, F23M19_16	5.6	5.5	0.0	0.2	100.0%	-5.3
17801	AT3G48810.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:18108033-18110012 FORWARD   Aliases: T21J18.80	4.2	4.3	-0.1	-0.2	100.0%	-4.8
17802	AT3G20200.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:7047587-7051266 FORWARD   Aliases: MAL21.21	2.9	2.9	0.0	0.2	100.0%	-5.5
17803	AT1G41860.1   expressed protein   chr1:15642597-15643235 FORWARD   Aliases: F5A13.6, F5A13_6	2.7	2.7	0.0	0.2	100.0%	-5.8
17804	AT5G66320.2   zinc finger (GATA type) family protein   chr5:26513181-26514903 REVERSE   Aliases: K1L20.10, K1L20_10	3.1	3.1	0.0	0.2	100.0%	-5.3
17805	AT2G22760.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.3	2.4	-0.0	-0.2	100.0%	-5.5
17806	AT3G04830.2   expressed protein   chr3:1326255-1329370 FORWARD   Aliases: T9J14.22, T9J14_22	8.6	8.7	-0.1	-0.2	100.0%	-4.7
17807	AT4G32695.1   expressed protein, hypothetical protein yjbl, Bacillus subtilis, PIR2:A69844   chr4:15768353-15769772 FORWARD   Aliases: None	2.5	2.5	0.0	0.2	100.0%	-5.6
17808	AT2G44110.2   Symbol: MLO15   seven transmembrane MLO family protein / MLO-like protein 15 (MLO15), identical to MLO-like protein 15 (AtMlo15) SP:O80580 from (Arabidopsis thaliana); similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr2:18252433-18255405 REVERSE   Aliases: F6E13.24	2.8	2.9	-0.1	-0.2	100.0%	-4.1
17809	AT3G06000.1   leucine-rich repeat family protein, contains Pfam domain PF00560: Leucine Rich Repeat; contains similarity to RAN GTPase activating protein 2 (Arabidopsis thaliana) gi:6708468:gb:AAF25948   chr3:1801452-1802087 FORWARD   Aliases: F2O10.4, F2O10_4	3.1	3.1	-0.0	-0.2	100.0%	-5.7
17810	AT5G53500.1   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP:Q9UGP9) (Homo sapiens)   chr5:21742667-21746526 REVERSE   Aliases: MNC6.4, MNC6_4	2.6	2.5	0.0	0.2	100.0%	-5.5
17811	AT1G05260.1   Symbol: RCI3   peroxidase 3 (PER3) (P3) / rare cold-inducible protein (RCI3A) (PRC), identical to SP:O23044 Peroxidase 3 precursor (EC 1.11.1.7) (Atperox P3) (Rare cold inducible protein) (RCI3A) (ATPRC) {Arabidopsis thaliana}   chr1:1529767-1531438 FORWARD   Aliases: PEROXIDASE PRECURSOR, RARE COLD INDUCIBLE GENE 3, RCI3A, YUP8H12.13, YUP8H12_13	2.9	2.9	0.0	0.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17812	AT3G44760.1   expressed protein   chr3:16316635-16317204 FORWARD   Aliases: T32N15.7	2.7	2.7	-0.0	-0.2	100.0%	-5.5
17813	AT2G35170.1   MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related, low similarity to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profile PF02493: MORN repeat   chr2:14834542-14836881 FORWARD   Aliases: T4C15.16, T4C15_16	4.5	4.6	-0.1	-0.2	100.0%	-4.9
17814	AT2G33880.1   Symbol: WOX9   homeobox-leucine zipper family protein   chr2:14348509-14350835 REVERSE   Aliases: HB 3, STIMPY, STIP, T1B8.31, T1B8_31	3.4	3.5	-0.1	-0.2	100.0%	-5.0
17815	AT2G42810.2   Symbol: PP5   similar to serine/threonine protein phosphatase PP1 isozyme 2 (TOPP2) [Arabidopsis thaliana] (TAIR:At5g59160.1); similar to serine/threonine protein phosphatase PP1 isozyme 8 (TOPP8) [Arabidopsis thaliana] (TAIR:At5g27840.2); similar to serine/threonine protein phosphatase PP1 isozyme 2 (TOPP2) [Arabidopsis thaliana] (TAIR:At5g59160.2); similar to type 5 serine/threonine phosphatase 55 kDa isoform [Lycopersicon esculentum] (GB:AAN64317.1); similar to putative serine/threonine phosphatase [Oryza sativa (japonica cultivar-group)] (GB:AAV44139.1); contains InterPro domain TPR repeat (InterPro:IPR001440); contains InterPro domain Metallo-phosphoesterase (InterPro:IPR004843); contains InterPro domain Serine/threonine-specific protein phosphatase and bis(5-nucleosyl)-tetraphosphatase (InterPro:IPR006186)   chr2:17819012-17823715 REVERSE   Aliases: F7D19.19, F7D19_19, PAPP5, PP5, PROTEIN PHOSPHATASE 5	5.3	5.3	-0.1	-0.2	100.0%	-4.9
17816	AT3G06160.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr3:1864332-1867198 FORWARD   Aliases: F28L1.10, F28L1_10	2.4	2.4	0.0	0.2	100.0%	-6.0
17817	AT5G19360.1   Symbol: CPK34   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Marchantia polymorpha) gi:5162877:dbj:BAA81748   chr5:6521718-6523782 REVERSE   Aliases: F7K24.110, F7K24_110	2.9	2.9	0.0	0.2	100.0%	-5.5
17818	AT3G08730.1   Symbol: ATPK1   serine/threonine protein kinase (PK1) (PK6), identical to serine/threonine-protein kinase AtPK1/AtPK6 (ribosomal-protein S6 kinase ATPK6) (Arabidopsis thaliana) SWISS-PROT:P42818   chr3:2651453-2654189 REVERSE   Aliases: ATPK6, F17O14.20, PROTEIN SERINE KINASE	9.1	9.0	0.1	0.2	100.0%	-4.9
17819	AT4G25100.4   Symbol: FSD1   similar to superoxide dismutase (Fe), putative / iron superoxide dismutase, putative [Arabidopsis thaliana] (TAIR:At5g51100.1); similar to Fe-superoxide dismutase (GB:AAA32791.1); contains InterPro domain Manganese and iron superoxide dismutase (InterPro:IPR001189)   chr4:12884310-12886537 REVERSE   Aliases: F24A6.1, FE SUPEROXIDE DISMUTASE 1	8.7	8.6	0.2	0.2	100.0%	-4.3
17820	AT5G22420.1   acyl CoA reductase, putative, similar to acyl CoA reductase (Simmondsia chinensis) GI:5020215; contains Pfam profile PF03015: Male sterility protein   chr5:7429906-7432589 FORWARD   Aliases: MWD9.22, MWD9_22	2.4	2.5	-0.0	-0.2	100.0%	-5.5
17821	AT2G34810.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr2:14692335-14694141 FORWARD   Aliases: F19I3.4, F19I3_4	2.6	2.7	-0.1	-0.2	100.0%	-4.7
17822	AT3G46460.1   ubiquitin-conjugating enzyme 13 (UBC13), E2; identical to gi:992706   chr3:17106886-17108437 REVERSE   Aliases: F18L15.180	7.4	7.5	-0.1	-0.2	100.0%	-4.7
17823	AT4G35490.1   ribosomal protein L11 family protein, several ribosomal proteins L11   chr4:16855907-16856679 FORWARD   Aliases: F15J1.60, F15J1_60	9.6	9.5	0.1	0.2	100.0%	-4.7
17824	AT1G51270.1   vesicle-associated membrane protein, putative / VAMP, putative, similar to VAP27 GI:6688926 (Nicotiana glauca)   chr1:19011656-19013247 FORWARD   Aliases: F11M15.13, F11M15_13	3.2	3.2	0.0	0.2	100.0%	-5.2
17825	AT5G53010.1   calcium-transporting ATPase, putative   chr5:21505716-21513763 REVERSE   Aliases: MNB8.7, MNB8_7	2.8	2.7	0.1	0.2	100.0%	-4.5
17826	AT1G66380.1   Symbol: MYB114	2.9	2.9	-0.0	-0.2	100.0%	-5.8
17827	AT1G71470.1   hypothetical protein   chr1:26934448-26935075 FORWARD   Aliases: F26A9.15	3.6	3.6	-0.0	-0.2	100.0%	-5.1
17828	AT1G77830.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:29272054-29272646 REVERSE   Aliases: T32E8.18	3.7	3.8	-0.1	-0.2	100.0%	-5.3
17829	AT2G07505.1   hypothetical protein, and genefinder   chr2:3125668-3126170 FORWARD   Aliases: F9A16.18	3.6	3.7	-0.0	-0.2	100.0%	-5.2
17830	AT3G63370.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:23413055-23416966 FORWARD   Aliases: MAA21.7	2.5	2.6	-0.0	-0.2	100.0%	-5.5
17831	AT5G45250.1   Symbol: RPS4   disease resistance protein (TIR-NBS-LRR class), putative (RPS4), domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein. Identical to RPS4 (GI:11357255). False intron created at intron 2 to escape a frameshift in the BAC sequence.   chr5:18339141-18343249 REVERSE   Aliases: DISEASE RESISTANCE PROTEIN RPS4, K9E15.1, K9E15_1, RESISTANT TO P. SYRINGAE 4	5.7	5.6	0.1	0.2	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17832	AT2G42910.1   ribose-phosphate pyrophosphokinase 4 / phosphoribosyl diphosphate synthetase 4 (PRS4), identical to phosphoribosyl diphosphate synthase (prs4) (Arabidopsis thaliana) GI:4902472	8.6	8.8	-0.2	-0.2	100.0%	-4.5
17833	AT2G37440.2   endonuclease/exonuclease/phosphatase family protein, similar to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr2:15726867-15729187 FORWARD   Aliases: F3G5.23, F3G5_23	4.7	4.8	-0.1	-0.2	100.0%	-4.7
17834	AT3G07950.1   rhomboid protein-related, contains 6 transmembrane domains; similar to phosphatidyl inositol glycan class T (GI:14456615) (Homo sapiens)	4.4	4.5	-0.1	-0.2	100.0%	-4.9
17835	AT4G12470.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to pEARLI 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:7401106-7401904 REVERSE   Aliases: T1P17.60, T1P17_60	2.7	2.8	-0.1	-0.2	100.0%	-4.3
17836	AT5G22430.1   expressed protein   chr5:7433794-7434938 FORWARD   Aliases: MWD9.23, MWD9_23	2.2	2.2	-0.0	-0.2	100.0%	-5.8
17837	AT1G29180.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.3	3.2	0.1	0.2	100.0%	-4.5
17838	AT4G33770.1   inositol 1,3,4-trisphosphate 5/6-kinase family protein, contains Pfam domain PF05770 Inositol 1, 3, 4-trisphosphate 5/6-kinase; contains weak similarity to inositol phosphate kinase (GI:27549256) (Zea mays)   chr4:16193472-16196428 REVERSE   Aliases: T16L1.260, T16L1_260	4.7	4.6	0.1	0.2	100.0%	-4.8
17839	AT3G16600.1   SNF2 domain-containing protein / helicase domain-containing protein / RING finger domain-containing protein, similar to SP:P31244 DNA repair protein RAD16 {Saccharomyces cerevisiae}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:5652845-5655676 REVERSE   Aliases: MGL6.6	2.5	2.6	-0.0	-0.2	100.0%	-5.7
17840	AT2G21370.2   xylulose kinase, putative, similar to xylulose kinase (Xylulokinase) (Bacillus subtilis) Swiss-Prot:P39211   chr2:9144553-9147135 REVERSE   Aliases: F3K23.13, F3K23_13	3.2	3.2	0.0	0.2	100.0%	-5.2
17841	AT3G12260.1   complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)   chr3:3908947-3910403 REVERSE   Aliases: F28J15.12	10.4	10.5	-0.1	-0.2	100.0%	-4.8
17842	AT2G04970.1   hypothetical protein, similar to At2g15200, At1g32830, At2g14140, At3g30450, At4g03990, At5g34895, At3g47270, At2g02200   chr2:1745970-1750204 REVERSE   Aliases: F1O13.10, F1O13_10	2.9	2.9	-0.0	-0.2	100.0%	-5.5
17843	AT3G17220.1   invertase/pectin methylesterase inhibitor family protein, similar to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr3:5883334-5883855 REVERSE   Aliases: MGD8.3	2.8	2.8	0.0	0.2	100.0%	-5.4
17844	AT3G26600.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr3:9770981-9773272 FORWARD   Aliases: MFE16.13	5.7	5.6	0.0	0.2	100.0%	-4.9
17845	AT5G56310.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:22819542-22821140 FORWARD   Aliases: MCD7.3, MCD7_3	3.4	3.4	0.0	0.2	100.0%	-5.6
17846	AT1G74530.3   expressed protein   chr1:28013294-28015823 REVERSE   Aliases: F1M20.21, F1M20_21	5.8	5.7	0.1	0.2	100.0%	-4.6
17847	AT2G20250.1   expressed protein   chr2:8741130-8743497 REVERSE   Aliases: F11A3.20, F11A3_20	2.2	2.2	0.0	0.2	100.0%	-5.9
17848	AT2G44525.1   expressed protein   chr2:18389172-18390587 FORWARD   Aliases: None	8.4	8.4	0.1	0.2	100.0%	-4.9
17849	AT1G14350.1   Symbol: MYB124	2.5	2.4	0.0	0.2	100.0%	-5.2
17850	AT2G36930.1   zinc finger (C2H2 type) family protein, contains Prosite PS00028: Zinc finger, C2H2 type, domain; weak similarity to Zinc finger protein T86 (Swiss-Prot:O00488) (Homo sapiens)   chr2:15516981-15518584 REVERSE   Aliases: T1J8.11, T1J8_11	9.0	8.9	0.1	0.2	100.0%	-4.7
17851	AT3G57440.1   expressed protein   chr3:21269657-21271493 FORWARD   Aliases: T8H10.40	3.3	3.3	-0.0	-0.2	100.0%	-5.2
17852	AT1G26090.1   expressed protein   chr1:9020367-9022977 FORWARD   Aliases: F14G11.6	5.7	5.6	0.0	0.2	100.0%	-4.9
17853	AT5G47560.1   Symbol: ATSDAT/ATTDIT   Encodes a tonoplast malate/fumarate transporter.	2.9	2.9	0.1	0.2	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17854	AT4G09030.1   Symbol: AGP10   arabinogalactan-protein (AGP10), identical to gi:10880497:gb:AAG24278; supported by Ceres cDNA 265772   chr4:5792204-5792787 FORWARD   Aliases: F23J3.60, F23J3_60	8.3	8.4	-0.1	-0.2	100.0%	-4.5
17855	AT5G63720.1   hypothetical protein   chr5:25523575-25525243 FORWARD   Aliases: MBK5.20, MBK5_20	3.1	3.1	0.0	0.2	100.0%	-5.4
17856	AT3G06100.1   major intrinsic family protein / MIP family protein, contains Pfam profile: PF00230 major intrinsic protein; contains non-consensus TT acceptor splice site at exon 4   chr3:1841177-1842981 REVERSE   Aliases: F28L1.3, F28L1_3	4.0	4.0	-0.0	-0.2	100.0%	-5.2
17857	AT1G07310.1   C2 domain-containing protein, contains similarity to shock protein SRC2 (Glycine max) gi:2055230:dbj:BAA19769 ; contains Pfam profile PF00168:C2 domain   chr1:2247508-2248960 REVERSE   Aliases: F22G5.35, F22G5_35	4.3	4.4	-0.0	-0.2	100.0%	-4.7
17858	AT2G33350.1   similar to zinc finger CONSTANS-related [Arabidopsis thaliana] (TAIR:At1g04500.1); similar to zinc finger CONSTANS-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73395.1); contains domain ASN_RICH (PS50321)   chr2:14141005-14144217 FORWARD   Aliases: F4P9.12, F4P9_12	2.6	2.6	-0.0	-0.2	100.0%	-5.8
17859	AT2G17265.1   Symbol: HSK   homoserine kinase (HSK), identical to homoserine kinase (Arabidopsis thaliana) gi:4927412:gb:AAD33097   chr2:7515670-7516837 FORWARD   Aliases: F5J6.24, F5J6_24, HOMOSERINE KINASE	9.2	9.1	0.1	0.2	100.0%	-4.7
17860	AT3G45870.1   integral membrane family protein / nodulin MtN21-related, similar to MtN21 GI:2598575 (root nodule development) Medicago truncatula, EMBL:MTY15293   chr3:16878187-16879911 FORWARD   Aliases: F16L2.80	3.1	3.1	-0.0	-0.2	100.0%	-5.1
17861	AT5G43610.1   sucrose transporter-related / sucrose-proton symporter-related, similar to sucrose-proton symporter SUC1 (Arabidopsis thaliana) GI:407094, sucrose transporter (Arabidopsis thaliana) GI:12057172; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:17536306-17538235 FORWARD   Aliases: K9D7.11, K9D7_11	3.4	3.4	0.1	0.2	100.0%	-5.1
17862	AT1G02560.1   Symbol: CLPP5   ATP-dependent Clp protease proteolytic subunit (ClpP1), identical to nClpP1 GB:BAA82065 GI:5360579 from (Arabidopsis thaliana); contains Pfam profile PF00574: Clp protease; contains TIGRfam profile TIGR00493: ATP-dependent Clp protease, proteolytic subunit ClpP   chr1:537888-540109 FORWARD   Aliases: CLP PROTEASE 1 PROTEOLYTIC SUBUNIT, NCLPP1, NCLPP5, NUCLEAR ENCODED CLP PROTEASE 1, T14P4.12, T14P4_12	9.4	9.5	-0.1	-0.2	100.0%	-4.8
17863	AT5G33240.1   expressed protein   chr5:12507395-12508221 REVERSE   Aliases: T29A4.50, T29A4_50	2.5	2.5	-0.0	-0.2	100.0%	-5.9
17864	AT5G03070.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr5:718206-721538 REVERSE   Aliases: F15A17.100, F15A17_100	5.6	5.7	-0.1	-0.2	100.0%	-5.0
17865	AT4G17785.1   myb family transcription factor (MYB39), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr4:9881648-9883445 REVERSE   Aliases: None	2.2	2.3	-0.0	-0.2	100.0%	-5.7
17866	AT2G48110.1   expressed protein   chr2:19680440-19686564 FORWARD   Aliases: F11L15.1, T9J23.25	2.5	2.6	-0.0	-0.2	100.0%	-5.5
17867	AT4G04320.2   malonyl-CoA decarboxylase family protein, contains weak similarity to Malonyl-CoA decarboxylase, mitochondrial precursor (EC 4.1.1.9) (MCD) (Swiss-Prot:O95822) (Homo sapiens); contains Pfam profile PF05292: Malonyl-CoA decarboxylase (MCD)   chr4:2113528-2116682 FORWARD   Aliases: T19B17.4, T19B17_4	5.0	4.8	0.1	0.2	100.0%	-4.6
17868	AT5G15180.1   peroxidase, putative, similar to peroxidase ATP12a (Arabidopsis thaliana) gi:1429217:emb:CAA67311   chr5:4930522-4932345 FORWARD   Aliases: F8M21.70, F8M21_70	3.0	2.9	0.1	0.2	100.0%	-4.6
17869	AT2G38750.1   Symbol: ANNAT4	3.4	3.5	-0.0	-0.2	100.0%	-5.2
17870	AT3G61830.1   Symbol: ARF18   transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-related, contains Pfam profile: PF02309 AUX/IAA family   chr3:22898864-22902410 FORWARD   Aliases: ARF18, AUXIN RESPONSE FACTOR 18, F21F14.12	4.9	4.9	0.0	0.2	100.0%	-5.3
17871	AT3G15190.1   chloroplast 30S ribosomal protein S20, putative, contains Pfam profile: PF01649 ribosomal protein S20   chr3:5116154-5117622 FORWARD   Aliases: F4B12.10	7.1	7.2	-0.0	-0.2	100.0%	-4.7
17872	AT1G33430.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr1:12124343-12126449 REVERSE   Aliases: F10C21.10, F10C21_10	3.4	3.4	-0.0	-0.2	100.0%	-5.2
17873	AT2G44760.1   expressed protein   chr2:18459844-18461882 REVERSE   Aliases: F16B22.25	5.9	5.9	-0.0	-0.2	100.0%	-5.2
17874	AT1G78240.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr1:29437722-29441377 REVERSE   Aliases: F3F9.21, F3F9_21	6.1	6.0	0.1	0.2	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17875	AT4G02620.1   vacuolar ATPase subunit F family protein, contains weak similarity to vacuolar ATP synthase subunit F (EC 3.6.3.14) (V-ATPase F subunit) (Vacuolar proton pump F subunit) (V-ATPase 14 kDa subunit) (Swiss-Prot:P50408) (Rattus norvegicus); contains Pfam PF01990: ATP synthase (F/14-kDa) subunit   chr4:1149248-1151346 REVERSE   Aliases: T10P11.25, T10P11_25	10.4	10.3	0.1	0.2	100.0%	-5.1
17876	AT4G34370.1   IBR domain-containing protein, similar to SP:Q94981 Ariadne-1 protein (Ari-1) {Drosophila melanogaster}; contains Pfam profile PF01485: IBR domain   chr4:16434337-16437313 FORWARD   Aliases: F10M10.140, F10M10_140	7.3	7.4	-0.1	-0.2	100.0%	-4.6
17877	AT1G23080.2   Symbol: PIN7   auxin efflux carrier protein, putative, similar to efflux carrier of polar auxin transport (Brassica juncea) gi:12331173:emb:CAC24691   chr1:8180594-8183559 REVERSE   Aliases: PIN FORMED 7, PIN7, T26J12.14, T26J12_14	3.6	3.6	0.0	0.2	100.0%	-5.3
17878	AT3G51160.1   Symbol: MUR1   GDP-D-mannose-4,6-dehydratase (MUR1), almost identical to GDP-D-mannose-4,6-dehydratase (MUR1) GI:1764100 from (Arabidopsis thaliana)   chr3:19017989-19019406 REVERSE   Aliases: F24M12.200, GDP D MANNOSE 4,6 DEHYDRATASE, GMD2, MURUS 1, MUR_1	6.4	6.3	0.0	0.2	100.0%	-4.9
17879	AT3G57990.1   expressed protein   chr3:21480979-21482463 REVERSE   Aliases: T10K17.200	6.8	6.9	-0.1	-0.2	100.0%	-4.8
17880	AT2G48050.1   expressed protein, ; expression supported by MPSS   chr2:19660284-19664981 REVERSE   Aliases: T9J23.20	2.4	2.5	-0.0	-0.2	100.0%	-5.6
17881	AT1G37150.4   holocarboxylase synthetase 2 (HCS2.d), identical to holocarboxylase synthetase hcs2.d (Arabidopsis thaliana) GI:19698373; contains non-consensus GG acceptor splice sites; contains Pfam profile PF03099: Biotin/lipoate A/B protein ligase family; contains TIGRfam profile TIGR00121: biotin--acetyl-CoA-carboxylase ligase;   chr1:14177422-14180433 REVERSE   Aliases: F28L22.1, F28L22_1	4.5	4.6	-0.1	-0.2	100.0%	-4.7
17882	AT3G46900.1   Symbol: COPT2   copper transporter, putative, similar to SP:Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}; contains Pfam profile PF04145: Ctr copper transporter family   chr3:17279860-17280495 FORWARD   Aliases: T6H20.70	2.8	2.7	0.1	0.2	100.0%	-4.3
17883	AT4G05100.1   myb family transcription factor (MYB74), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA putative transcription factor (MYB74) mRNA, partial cds GI:3941505   chr4:2618452-2619885 FORWARD   Aliases: C17L7.20, C17L7_20	2.7	2.8	-0.1	-0.2	100.0%	-4.8
17884	AT5G24350.1   expressed protein, weak similarity to neuroblastoma-amplified protein (Homo sapiens) GI:4337460   chr5:8301540-8310898 FORWARD   Aliases: K16H17.4, K16H17_4	5.1	5.2	-0.1	-0.2	100.0%	-5.0
17885	AT4G13250.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr4:7684238-7686803 REVERSE   Aliases: F17N18.140, F17N18_140	8.2	8.2	0.1	0.2	100.0%	-4.3
17886	AT2G16230.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum)   chr2:7043103-7045408 REVERSE   Aliases: F16F14.27, F16F14_27	2.2	2.2	-0.0	-0.2	100.0%	-6.0
17887	NA	2.3	2.3	-0.0	-0.2	100.0%	-6.2
17888	AT1G75250.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain   chr1:28248734-28249114 REVERSE   Aliases: F22H5.3, F22H5_3	2.7	2.8	-0.0	-0.2	100.0%	-5.6
17889	AT4G34620.1   Symbol: SSR16   ribosomal protein S16 family protein, ribosomal protein S16, Neurospora crassa, PIR2:A29927   chr4:16534867-16536176 REVERSE   Aliases: RIBOSOMAL PROTEIN S16, T4L20.200, T4L20_200	11.0	11.0	0.1	0.2	100.0%	-4.9
17890	AT3G16710.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:5690245-5691549 FORWARD   Aliases: MGL6.18	2.8	2.8	0.0	0.2	100.0%	-5.4
17891	AT5G43770.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:17606034-17606597 FORWARD   Aliases: MQD19.12, MQD19_12	2.6	2.6	-0.0	-0.2	100.0%	-5.4
17892	AT5G07500.1   Symbol: PEI1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr5:2372620-2373656 FORWARD   Aliases: T2I1.210, T2I1_210	3.1	3.1	-0.0	-0.2	100.0%	-5.6
17893	AT1G53450.2   expressed protein   chr1:19954674-19957776 REVERSE   Aliases: T3F20.23, T3F20_23	5.0	4.9	0.1	0.2	100.0%	-4.9
17894	AT5G60150.1   expressed protein, ; expression supported by MPSS   chr5:24235437-24240471 FORWARD   Aliases: F15L12.4, F15L12_4	3.7	3.7	-0.0	-0.2	100.0%	-5.5
17895	AT4G33530.1   Symbol: KUP5   potassium transporter family protein, similar to K+ transporter HAK5 (Arabidopsis thaliana) GI:7108597; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter   chr4:16126234-16130441 REVERSE   Aliases: T16L1.20, T16L1_20	5.2	5.2	-0.0	-0.2	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17896	AT3G46860.1   serine protease inhibitor, potato inhibitor I-type family protein, similar to SP:P19873 Inhibitor of trypsin and hageman factor (CMTI-V) {Cucurbita maxima}; contains Pfam profile PF00280: Potato inhibitor I family   chr3:17271219-17271584 FORWARD   Aliases: T6H20.110	3.1	3.1	0.0	0.2	100.0%	-5.3
17897	AT4G14815.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:8505046-8505942 FORWARD   Aliases: None	3.1	3.2	-0.1	-0.2	100.0%	-4.8
17898	AT5G60070.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr5:24207666-24209796 REVERSE   Aliases: MGO3.5, MGO3_5	3.5	3.5	0.0	0.2	100.0%	-5.6
17899	AT5G05880.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:1769649-1771516 FORWARD   Aliases: K18J17.3, K18J17_3	3.9	3.8	0.0	0.2	100.0%	-4.9
17900	AT2G05760.1   xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family   chr2:2180916-2183901 FORWARD   Aliases: T25M19.4, T25M19_4	3.1	3.1	0.0	0.2	100.0%	-5.5
17901	AT5G12890.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:4069580-4071230 REVERSE   Aliases: T24H18.60, T24H18_60	6.9	6.9	-0.0	-0.2	100.0%	-5.2
17902	AT3G09490.1   chloroplast lumen common family protein, 2 TPR domains; similar to chloroplast lumen proteins (GI:4056493 (F3G5.19)(At2g37400)) and (GI:7413648 (T22P11.180),(At5g02590)) (Arabidopsis thaliana); +   chr3:2915565-2916679 FORWARD   Aliases: F11F8.6	4.2	4.2	0.1	0.2	100.0%	-4.5
17903	AT2G31510.1   IBR domain-containing protein / ARIADNE-like protein ARI7 (ARI7), identical to ARIADNE-like protein ARI7 (Arabidopsis thaliana) GI:29125028; contains similarity to Swiss-Prot:Q94981 ariadne-1 protein (Ari-1) (Drosophila melanogaster); contains Pfam profile PF01485: IBR domain   chr2:13423764-13428247 REVERSE   Aliases: T9H9.3, T9H9_3	8.8	8.7	0.1	0.2	100.0%	-4.8
17904	AT4G14385.3   expressed protein   chr4:8287892-8288669 REVERSE   Aliases: None	8.4	8.3	0.0	0.2	100.0%	-4.7
17905	AT1G33280.1   Symbol: ANAC015   no apical meristem (NAM) family protein, similar to CUC1 (GP:12060422) {Arabidopsis thaliana} amd to NAM (GP:1279640) {Petunia x hybrida}   chr1:12072721-12073813 FORWARD   Aliases: ANAC015, T16O9.16, T16O9_16	2.3	2.3	-0.0	-0.2	100.0%	-5.9
17906	AT5G55080.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein atran3 GI:2058280 from (Arabidopsis thaliana)   chr5:22368802-22370284 REVERSE   Aliases: MCO15.3, MCO15_3	2.8	2.8	-0.0	-0.2	100.0%	-5.8
17907	AT1G74260.1   AIR synthase-related family protein, contains Pfam profiles: PF00586 AIR synthase related protein, N-terminal domain, PF02769 AIR synthase related protein, C-terminal domain   chr1:27926494-27931107 REVERSE   Aliases: F1O17.7, F1O17_7	7.7	7.8	-0.1	-0.2	100.0%	-5.0
17908	AT1G80610.1   expressed protein   chr1:30305625-30308925 REVERSE   Aliases: T21F11.6, T21F11_6	2.4	2.6	-0.2	-0.2	100.0%	-5.0
17909	AT1G36640.1   expressed protein   chr1:13854388-13854899 REVERSE   Aliases: T15P17.13, T15P17_13	2.5	2.7	-0.2	-0.2	100.0%	-4.4
17910	AT2G29580.1   zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein, similar to SP:O59800 Cell cycle control protein cwf5 {Schizosaccharomyces pombe}; contains Pfam profile: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain)   chr2:12659000-12661413 FORWARD   Aliases: F16P2.4, F16P2_4	4.0	4.1	-0.0	-0.2	100.0%	-5.0
17911	AT3G54920.1   Symbol: PMR6   pectate lyase, putative / powdery mildew susceptibility protein (PMR6), identical to powdery mildew susceptibility protein (Arabidopsis thaliana) GI:22506901; similar to pectate lyase 2 GP:6606534 from (Musa acuminata)   chr3:20356077-20359507 FORWARD   Aliases: F28P10.100, POWDERY MILDEW RESISTANT 6	8.5	8.6	-0.1	-0.2	100.0%	-4.6
17912	AT5G47230.1   Symbol: ATERF 5/ATERF5	3.7	3.8	-0.1	-0.2	100.0%	-4.4
17913	AT2G24150.1   expressed protein, contains Pfam profile PF03006: Uncharacterised protein family (Hly-III / UPF0073)   chr2:10272564-10274466 REVERSE   Aliases: F27D4.6, F27D4_6	4.6	4.7	-0.1	-0.2	100.0%	-4.4
17914	AT4G26190.1   expressed protein   chr4:13262245-13266969 REVERSE   Aliases: T25K17.7	6.0	6.0	0.0	0.2	100.0%	-5.3
17915	AT5G42720.1   glycosyl hydrolase family 17 protein, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum)   chr5:17147712-17150071 FORWARD   Aliases: MJB21.9, MJB21_9	6.4	6.5	-0.1	-0.2	100.0%	-4.6
17916	AT3G62480.1   expressed protein   chr3:23122259-23122849 REVERSE   Aliases: T12C14.180	2.4	2.4	-0.0	-0.2	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17917	AT1G70410.3   carbonic anhydrase, putative / carbonate dehydratase, putative, similar to SP:P42737 Carbonic anhydrase 2 (EC 4.2.1.1) (Carbonate dehydratase 2) {Arabidopsis thaliana}; contains Pfam profile PF00484: Carbonic anhydrase   chr1:26537589-26540336 REVERSE   Aliases: F1707.5, F1707_5	7.7	7.8	-0.1	-0.2	100.0%	-5.0
17918	AT2G25200.1   expressed protein   chr2:10743659-10744723 REVERSE   Aliases: F13D4.4	6.2	6.3	-0.1	-0.2	100.0%	-4.6
17919	AT2G22980.2   Symbol: SCPL13	2.9	2.9	0.0	0.2	100.0%	-5.4
17920	AT5G20030.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr5:6764729-6766671 REVERSE   Aliases: F28I16.180, F28I16_180	5.1	5.2	-0.1	-0.2	100.0%	-4.8
17921	AT3G08690.1   ubiquitin-conjugating enzyme 11 (UBC11), E2; identical to gi:12643427, SP:P35134	10.4	10.3	0.1	0.2	100.0%	-4.6
17922	AT3G10630.1   glycosyl transferase family 1 protein, contains Pfam glycosyl transferase, group 1 family protein domain PF00534; C-terminal portion similar to mannosyltransferase GB:BAA28328 (Escherichia coli)   chr3:3321468-3323216 REVERSE   Aliases: F13M14.8	5.2	5.3	-0.1	-0.2	100.0%	-5.0
17923	AT4G04760.1   sugar transporter family protein, similar to sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein	3.3	3.4	-0.0	-0.2	100.0%	-5.3
17924	AT1G19715.1   jacalin lectin family protein, similar to agglutinin (Castanea crenata) GI:25528883; contains Pfam profile PF01419: Jacalin-like lectin domain   chr1:6816693-6819533 REVERSE   Aliases: None	3.7	3.7	-0.0	-0.2	100.0%	-5.1
17925	AT4G16320.1   expressed protein, ; expression supported by MPSS   chr4:9223705-9225726 FORWARD   Aliases: DL4190W, FCAALL.344	3.4	3.4	-0.0	-0.2	100.0%	-5.1
17926	AT3G19690.1   pathogenesis-related protein, putative, similar to PR-1a protein GI:19944 GB:X06930 from (Nicotiana tabacum); contains Pfam profile PF00188: SCP-like extracellular protein   chr3:6841970-6842856 REVERSE   Aliases: MMB12.18	2.6	2.6	0.0	0.2	100.0%	-5.6
17927	AT5G19600.1   Symbol: SULTR3;5   sulfate transporter, putative, similar to sulfate transporter (Arabidopsis thaliana) GI:2285885; contains Pfam profiles PF00916: Sulfate transporter family, PF01740: STAS domain; supporting cDNA gi:14141683:dbj:AB061739.1   chr5:6612823-6616999 REVERSE   Aliases: T29J13.20, T29J13_20, sulfate transporter 3;5	2.9	2.9	-0.0	-0.2	100.0%	-4.7
17928	AT2G04330.1   hypothetical protein, contains Pfam profile PF03384: Drosophila protein of unknown function, DUF287   chr2:1510447-1513139 REVERSE   Aliases: T23O15.4	2.4	2.4	0.0	0.2	100.0%	-6.1
17929	AT5G47490.1   expressed protein   chr5:19281902-19288027 FORWARD   Aliases: MNJ7.8, MNJ7_8	2.9	2.8	0.0	0.2	100.0%	-5.2
17930	AT3G10890.1   (1-4)-beta-mannan endohydrolase, putative, similar to (1-4)-beta-mannan endohydrolase (Coffea arabica) GI:10178872, (1-4)-beta-mannan endohydrolase GB:AAB87859 (Lycopersicon esculentum); contains Pfam profile PF00150: Cellulase (glycosyl hydrolase family 5)   chr3:3407460-3409005 REVERSE   Aliases: T7M13.3	2.1	2.1	-0.0	-0.2	100.0%	-5.7
17931	AT5G17890.1   LIM domain-containing protein / disease resistance protein-related, low similarity to disease resistance protein RPP4 (Arabidopsis thaliana) GI:20270890; contains Pfam profiles PF00412: LIM domain, PF00931: NB-ARC domain, PF00560: Leucine Rich Repeat   chr5:5916972-5923350 FORWARD   Aliases: MPI7.6, MPI7_6	3.1	3.2	-0.1	-0.2	100.0%	-4.7
17932	AT1G55330.1   Symbol: AGP21   arabinogalactan-protein (AGP21)	9.1	9.2	-0.1	-0.2	100.0%	-5.3
17933	AT2G20020.1   expressed protein   chr2:8651467-8654272 FORWARD   Aliases: T2G17.18, T2G17_18	3.6	3.5	0.0	0.2	100.0%	-5.3
17934	AT5G19870.1   expressed protein, contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)   chr5:6716075-6717014 REVERSE   Aliases: T29J13.1	2.3	2.3	0.0	0.2	100.0%	-5.4
17935	AT3G09500.1   60S ribosomal protein L35 (RPL35A), similar to 60S ribosomal protein L35 GB:AAC27830   chr3:2916986-2918036 FORWARD   Aliases: F11F8.7	11.6	11.6	-0.0	-0.2	100.0%	-5.2
17936	AT3G29770.1   hydrolase, alpha/beta fold family protein, similar to SP:Q40708 PIR7A protein {Oryza sativa}, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile: PF00561 alpha/beta hydrolase fold   chr3:11650820-11653318 FORWARD   Aliases: T26G12.12	5.6	5.6	-0.1	-0.2	100.0%	-4.9
17937	AT1G06140.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:1864795-1866471 FORWARD   Aliases: T21E18.19, T21E18_19	3.3	3.2	0.0	0.2	100.0%	-5.2
17938	AT1G02490.1   hypothetical protein   chr1:516618-516734 FORWARD   Aliases: T14P4.35, T14P4_35	2.7	2.7	0.0	0.2	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17939	AT5G28630.1   glycine-rich protein   chr5:10636635-10637253 FORWARD   Aliases: F4I4.10, F4I4_10	3.4	3.5	-0.2	-0.2	100.0%	-4.6
17940	AT2G05830.3   similar to eukaryotic translation initiation factor 2B family protein / eIF-2B family protein [Arabidopsis thaliana] (TAIR:At3g07300.1); similar to IDI2 [Hordeum vulgare subsp. vulgare] (GB:BAB21393.1); contains InterPro domain Initiation factor 2B (InterPro:IPR000649)   chr2:2229704-2232103 FORWARD   Aliases: T6P5.3, T6P5_3	9.4	9.3	0.1	0.2	100.0%	-5.2
17941	AT5G52060.1   BAG domain-containing protein, contains Pfam:PF02179 BAG domain   chr5:21169454-21170919 REVERSE   Aliases: MSG15.15, MSG15_15	7.2	7.1	0.1	0.2	100.0%	-4.7
17942	AT3G50700.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:18851394-18853912 FORWARD   Aliases: T3A5.80	3.9	3.9	-0.1	-0.2	100.0%	-4.7
17943	AT5G37620.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.8	-0.0	-0.2	100.0%	-5.2
17944	AT5G51130.1   expressed protein, contains similarity to unknown protein (pir::T26512)   chr5:20799122-20801127 FORWARD   Aliases: MWD22.7, MWD22_7	5.3	5.4	-0.1	-0.2	100.0%	-5.0
17945	AT2G15340.1   glycine-rich protein   chr2:6684369-6684901 FORWARD   Aliases: F26H6.14, F26H6_14	2.9	2.9	0.0	0.2	100.0%	-5.4
17946	AT4G23250.1   Symbol: EMB1290   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:12162014-12167036 REVERSE   Aliases: EMB1290, EMBRYO DEFECTIVE 1290, F21P8.140, F21P8_140	3.5	3.5	0.0	0.2	100.0%	-5.5
17947	AT3G45110.1   hypothetical protein   chr3:16519155-16519517 FORWARD   Aliases: T14D3.50	2.8	2.8	-0.0	-0.2	100.0%	-5.6
17948	AT1G02470.1   expressed protein, contains non-consensus splice sites;   chr1:511765-513611 REVERSE   Aliases: T6A9.26	3.3	3.3	0.1	0.2	100.0%	-4.7
17949	AT2G02350.1   Symbol: SKIP3   SKP1 interacting partner 3 (SKIP3), nearly identical to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)   chr2:617799-619090 REVERSE   Aliases: ATPP2 B9, SKP1 INTERACTING PARTNER 3, T16F16.14, T16F16_14	4.7	4.6	0.1	0.2	100.0%	-5.1
17950	AT2G47150.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to stem secoisolariciresinol dehydrogenase GI:13752458 from (Forsythia x intermedia)   chr2:19359394-19360184 REVERSE   Aliases: F14M4.2	2.6	2.5	0.0	0.2	100.0%	-5.3
17951	AT1G08750.3   GPI-anchor transamidase, putative, similar to SP:P49018 GPI-anchor transamidase (EC 3.-.-) (GPI transamidase) {Saccharomyces cerevisiae}; contains Pfam profile PF01650: Peptidase C13 family   chr1:2801078-2804540 FORWARD   Aliases: F22O13.24, F22O13_24	6.3	6.4	-0.1	-0.2	100.0%	-4.7
17952	AT1G62410.1   MIF4G domain-containing protein, similar to SP:Q03387 Eukaryotic initiation factor (iso)4F subunit P82-34 (eIF-(iso)4F P82-34) {Triticum aestivum}; contains Pfam profile PF02854: MIF4G domain   chr1:23096580-23097534 FORWARD   Aliases: F24O1.14, F24O1_14	2.2	2.2	-0.0	-0.2	100.0%	-6.1
17953	AT5G52340.1   exocyst subunit EXO70 family protein, strong similarity to unknown protein (emb:CAB83315.1); contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr5:21268028-21271165 FORWARD   Aliases: K24M7.7, K24M7_7	2.4	2.4	0.0	0.2	100.0%	-5.6
17954	AT1G08340.1   rac GTPase activating protein, putative, similar to rac GTPase activating protein 1 GI:3695059 from (Lotus japonicus); contains Pfam profile PF00620: RhoGAP domain   chr1:2631065-2632666 FORWARD   Aliases: T23G18.20, T23G18_20	3.0	2.9	0.1	0.2	100.0%	-4.2
17955	AT3G56350.1   superoxide dismutase (Mn), putative / manganese superoxide dismutase, putative, similar to manganese superoxide dismutase (MSD1) (Arabidopsis thaliana) gi:3273751:gb:AAC24832   chr3:20904997-20906604 REVERSE   Aliases: T5P19.1	2.3	2.4	-0.0	-0.2	100.0%	-5.6
17956	AT5G33370.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr5:12619698-12621993 REVERSE   Aliases: F19N2.90, F19N2_90	2.9	2.9	0.1	0.2	100.0%	-5.3
17957	AT1G17880.1   nascent polypeptide-associated complex (NAC) domain-containing protein / BTF3b-like transcription factor, putative, similar to SP:P20290 Transcription factor BTF3 (RNA polymerase B transcription factor 3) {Homo sapiens}; contains Pfam profile PF01849: NAC domain; identical to cDNA BTF3b-like factor GI:5912423   chr1:6152420-6153946 REVERSE   Aliases: F2H15.11, F2H15_11	9.9	9.8	0.1	0.2	100.0%	-4.4
17958	AT1G03720.1   cathepsin-related, contains weak similarity to Cathepsin L precursor (EC 3.4.22.15) (Major excreted protein) (MEP) (Cyclic protein-2) (CP-2) (Swiss-Prot:P07154) (Rattus norvegicus)   chr1:924996-926373 REVERSE   Aliases: F21B7.32	3.2	3.3	-0.1	-0.2	100.0%	-4.9
17959	AT1G18480.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.8	6.9	-0.1	-0.2	100.0%	-4.9
17960	AT3G22040.1   receptor-like protein kinase-related, contains Pfam profile: PF01657 Domain of unknown function that is usually associated with protein kinase domain Pfam:PF00069; similar to receptor-like protein kinase 5 (GI:13506747){Arabidopsis thaliana}   chr3:7761814-7762682 FORWARD   Aliases: MZN24.22	2.6	2.7	-0.0	-0.2	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17961	AT5G26270.1   expressed protein, ; expression supported by MPSS   chr5:9206511-9207515 FORWARD   Aliases: T19G15.120, T19G15_120	3.4	3.5	-0.0	-0.2	100.0%	-5.2
17962	AT5G45840.1   leucine-rich repeat transmembrane protein kinase, putative, and genscan+   chr5:18611307-18614448 REVERSE   Aliases: K15I22.4, K15I22_4	2.5	2.4	0.0	0.2	100.0%	-5.0
17963	AT4G16350.1   Symbol: CBL6   calcineurin B-like protein 6 (CBL6), identical to calcineurin B-like protein 6 (GI:11065943) (Arabidopsis thaliana)   chr4:9242522-9243686 REVERSE   Aliases: CALCINEURIN B LIKE PROTEIN 6, DL4205C, FCAALL.89, SCABP2, SOS3 LIKE CALCIUM BINDING PROTEIN 2	3.2	3.3	-0.1	-0.2	100.0%	-4.4
17964	AT5G45630.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr5:18523036-18523550 REVERSE   Aliases: MRA19.3, MRA19_3	2.6	2.6	-0.0	-0.2	100.0%	-5.7
17965	AT5G61470.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr5:24740096-24741209 FORWARD   Aliases: MCI2.3, MCI2_3	2.4	2.5	-0.0	-0.2	100.0%	-5.5
17966	AT1G03300.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr1:811033-813086 REVERSE   Aliases: F15K9.10, F15K9_10	4.0	4.0	0.0	0.2	100.0%	-5.0
17967	AT1G60980.1   gibberellin 20-oxidase, putative, similar to gibberellin 20-oxidase GB:CAA58295 from (Arabidopsis thaliana)   chr1:22456238-22457805 FORWARD   Aliases: T7P1.12, T7P1_12	3.2	3.2	-0.0	-0.2	100.0%	-5.3
17968	AT5G06110.1   DNAJ heat shock N-terminal domain-containing protein / cell division protein-related, similar to GIsA (Volvox carteri f. nagariensis) GI:4633129; contains Pfam profiles PF00226 DnaJ domain, PF00249 Myb-like DNA-binding domain   chr5:1840831-1843001 REVERSE   Aliases: K16F4.7, K16F4_7	8.3	8.2	0.0	0.2	100.0%	-5.0
17969	AT5G23910.1   similar to kinesin motor protein-related [Arabidopsis thaliana] (TAIR:At5g02370.1); similar to OSJNBb0006N15.7 [Oryza sativa (japonica cultivar-group)] (GB:XP_472192.1); contains InterPro domain Kinesin, motor region (InterPro:IPR001752)   chr5:8068443-8072979 FORWARD   Aliases: MRO11.5, MRO11_5	4.1	4.1	0.1	0.2	100.0%	-4.9
17970	AT2G33370.1   60S ribosomal protein L23 (RPL23B)   chr2:14150646-14151797 REVERSE   Aliases: F4P9.14	8.4	8.5	-0.1	-0.2	100.0%	-4.8
17971	AT5G02690.1   expressed protein   chr5:607358-607608 FORWARD   Aliases: F9G14.2	3.8	3.9	-0.1	-0.2	100.0%	-4.8
17972	AT5G52490.1   fibrillar, putative, similar to fibrillar from {Xenopus laevis} SP:P22232, {Mus musculus} SP:P35550, {Homo sapiens} SP:P22087   chr5:21316083-21317465 FORWARD   Aliases: K24M7.24, K24M7_24	3.1	3.1	-0.1	-0.2	100.0%	-5.1
17973	AT4G31280.1   expressed protein   chr4:15185807-15186011 REVERSE   Aliases: F8F16.100, F8F16_100	3.3	3.3	-0.0	-0.2	100.0%	-5.3
17974	AT5G06570.2   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr5:2007601-2011042 REVERSE   Aliases: F15M7.10, F15M7_10	3.4	3.3	0.1	0.2	100.0%	-4.4
17975	AT1G73360.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, protodermal factor2 (GI:14276060) (Arabidopsis thaliana); similar to homeobox protein GI:1173621 from (Phalaenopsis sp.)   chr1:27582357-27586182 REVERSE   Aliases: T9L24.43, T9L24_43	2.3	2.3	-0.0	-0.2	100.0%	-5.6
17976	AT2G35880.1   expressed protein   chr2:15070067-15072930 REVERSE   Aliases: F11F19.21, F11F19_21	8.7	8.6	0.1	0.2	100.0%	-5.2
17977	AT5G60280.1   lectin protein kinase family protein, contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain, and PF00069: Protein kinase domain   chr5:24277789-24279762 FORWARD   Aliases: F15L12.12, F15L12_12	2.6	2.6	0.1	0.2	100.0%	-4.4
17978	AT4G18120.1   RNA recognition motif (RRM)-containing protein, Mei2-like protein, Arabidopsis thaliana, gb:D86122   chr4:10038890-10042023 FORWARD   Aliases: F15J5.90, F15J5_90	5.8	5.9	-0.1	-0.2	100.0%	-5.1
17979	AT5G19040.1   Symbol: ATIPT5	3.9	3.9	-0.1	-0.2	100.0%	-4.6
17980	AT1G14450.1   expressed protein, contains similarity to cytochrome c oxidase subunit I GI:5678701 from (Loligo pealei)	9.2	9.2	0.0	0.2	100.0%	-5.1
17981	AT3G56890.1   F-box family protein-related, predicted proteins - Arabidopsis thaliana; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:21073969-21074696 REVERSE   Aliases: T8M16.220	3.2	3.2	0.0	0.2	100.0%	-5.5
17982	AT4G28140.1   encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.   chr4:13974697-13975914 REVERSE   Aliases: F26K10.20, F26K10_20	2.8	2.8	0.0	0.2	100.0%	-5.2
17983	AT4G37150.1   esterase, putative, similar to ethylene-induced esterase (Citrus sinensis) GI:14279437, polyneuridine aldehyde esterase (Rauvolfia serpentina) GI:6651393; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr4:17492872-17494101 REVERSE   Aliases: AP22.78, AP22_78	3.0	2.9	0.0	0.2	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
17984	AT5G46550.1   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr5:18901536-18904122 REVERSE   Aliases: F10E10.2, F10E10_2	4.9	4.8	0.1	0.2	100.0%	-4.8
17985	AT1G62790.2   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr1:23256003-23257547 FORWARD   Aliases: F23N19.16, F23N19_16	9.9	9.8	0.1	0.2	100.0%	-5.1
17986	AT5G58240.2   bis(5'-adenosyl)-triphosphatase, putative, similar to bis(5'-adenosyl)-triphosphatase (Diadenosine 5',5'''- P1,P3-triphosphate hydrolase, Dinucleosidetriphosphatase, AP3A hydrolase, AP3AASE, Fragile histidine triad protein) (Homo sapiens) Swiss-Prot:P49789	7.5	7.5	-0.1	-0.2	100.0%	-5.0
17987	AT3G19190.1   expressed protein   chr3:6639717-6648242 FORWARD   Aliases: MVI11.11	4.6	4.7	-0.1	-0.2	100.0%	-4.6
17988	AT1G10550.1   Symbol: XTH33   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to endoxyloglucan transferase related protein EXGT-A3 GI:2154609 from (Arabidopsis thaliana)	4.1	4.1	-0.1	-0.2	100.0%	-4.8
17989	AT1G65730.1   oligopeptide transporter OPT family protein, similar to iron-phytosiderophore transporter protein yellow stripe 1 (Zea mays) GI:10770865; contains Pfam profile PF03169: OPT oligopeptide transporter protein   chr1:24446167-24449954 FORWARD   Aliases: F1E22.10, F1E22_10	4.5	4.5	0.0	0.2	100.0%	-5.2
17990	AT4G22610.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:11902116-11902653 REVERSE   Aliases: F7K2.190, F7K2_190	3.0	2.9	0.0	0.2	100.0%	-5.1
17991	AT1G69760.1   expressed protein   chr1:26242923-26244371 REVERSE   Aliases: T6C23.4, T6C23_4	4.0	4.1	-0.1	-0.2	100.0%	-5.0
17992	AT4G32551.1   Symbol: LUG   WD-40 repeat family protein (LEUNIG), contains seven G-protein beta WD-40 repeats; beta transducin-like protein, Podospora anserina, gb:L28125; contains Pfam profiles PF04503: Single-stranded DNA binding protein, SSDP; PF00400:WD domain, G-beta repeat; identical to cDNA LEUNIG (LEUNIG) GI:11141604   chr4:15707516-15713585 FORWARD   Aliases: L23H3.30, L23H3_30, LEUNIG, RON2	5.8	5.8	-0.1	-0.2	100.0%	-5.0
17993	AT3G26610.1   polygalacturonase, putative / pectinase, putative, similar to polygalacturonase (PG1) GI:5669846, (PG2) GI:5669848 (Glycine max); contains PF00295: Glycosyl hydrolases family 28 (polygalacturonases)   chr3:9778197-9781736 FORWARD   Aliases: MFE16.14	3.4	3.3	0.1	0.2	100.0%	-4.4
17994	AT5G07520.1   Symbol: GRP18   glycine-rich protein (GRP18), Oleosin; glycine-rich protein 18 (GRP18) PMID:11431566;   chr5:2380136-2381231 REVERSE   Aliases: ATGRP 8, ATGRP18, T2I1.230, T2I1_230	2.8	2.8	0.0	0.2	100.0%	-5.4
17995	AT1G75760.1   ER lumen protein retaining receptor family protein, similar to SP:P33946 ER lumen protein retaining receptor 1 (KDEL receptor 1) {Bos taurus}; contains Pfam profile PF00810: ER lumen protein retaining receptor   chr1:28450377-28452293 REVERSE   Aliases: F10A5.5, F10A5_5	4.3	4.2	0.1	0.2	100.0%	-4.8
17996	AT1G69800.1   CBS domain-containing protein, low similarity to SP:Q9UGI9 5'-AMP-activated protein kinase, gamma-3 subunit (AMPK gamma-3 chain) (AMPK gamma3) {Homo sapiens}; contains Pfam profile PF00571: CBS domain	7.2	7.1	0.0	0.2	100.0%	-4.9
17997	AT2G30140.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:12879211-12880897 FORWARD   Aliases: T27E13.12, T27E13_12	9.8	9.9	-0.1	-0.2	100.0%	-4.9
17998	AT1G09360.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	2.6	2.6	0.0	0.2	100.0%	-5.5
17999	AT1G11560.1   OST3/OST6 family protein, contains Pfam profile PF04756: OST3 / OST6 family   chr1:3881788-3882819 FORWARD   Aliases: T23J18.22, T23J18_22	2.9	2.9	0.0	0.2	100.0%	-5.4
18000	AT5G19950.3   expressed protein   chr5:6741111-6743775 REVERSE   Aliases: F28I16.100, F28I16_100	3.4	3.4	0.0	0.2	100.0%	-4.9
18001	AT4G14490.1   forkhead-associated domain-containing protein / FHA domain-containing protein, contains Pfam domain, PF00498: forkhead-associated (FHA) domain   chr4:8332093-8333574 REVERSE   Aliases: DL3285C, FCAALL.220	3.9	3.8	0.1	0.2	100.0%	-5.0
18002	AT5G39870.1   expressed protein   chr5:15985850-15987239 REVERSE   Aliases: MYH19.6, MYH19_6	2.4	2.4	-0.0	-0.2	100.0%	-5.6
18003	AT1G27410.1   DNA cross-link repair protein-related, contains weak similarity to Swiss-Prot:P30620 DNA cross-LINK repair protein PSO2/SNM1 (Saccharomyces cerevisiae)   chr1:9517210-9519012 FORWARD   Aliases: F17L21.20, F17L21_20	3.1	3.2	-0.0	-0.2	100.0%	-5.0
18004	AT5G44970.1   hypothetical protein, contains a novel domain with similarity to F-box domain;   chr5:18173064-18174567 FORWARD   Aliases: K21C13.16, K21C13_16	2.4	2.4	0.0	0.2	100.0%	-5.4
18005	ATCG00120.1   Symbol: ATPA   ATPase alpha subunit   chrC:9938-11461 REVERSE   Aliases: ATPA	6.9	7.0	-0.1	-0.2	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18006	AT1G51740.1   Symbol: SYP81   syntaxin 81 (SYP81), identical to SP:P59277 Syntaxin 81 (AtSYP81) {Arabidopsis thaliana}; identified as syntaxin SYP81 by Sanderfoot, A.A., et al in Plant Physiol. 124:1558-69 (2000); similar to Syntaxin 18 (SP:Q9P2W9){Homo sapiens}   chr1:19192523-19194965 FORWARD   Aliases: ATSY81, F19C24.5, F19C24_5	4.0	4.1	-0.1	-0.2	100.0%	-4.9
18007	AT2G14110.1   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAR07078.1)   chr2:5958977-5960237 FORWARD   Aliases: T22C12.4, T22C12_4	4.9	4.9	-0.0	-0.2	100.0%	-5.2
18008	AT5G48490.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:19665061-19665507 REVERSE   Aliases: MJE7.13, MJE7_13	3.8	3.7	0.0	0.2	100.0%	-5.3
18009	AT4G13330.1   expressed protein   chr4:7754244-7755951 REVERSE   Aliases: T9E8.70, T9E8_70	4.0	4.1	-0.0	-0.2	100.0%	-5.3
18010	AT4G30610.1   Symbol: BRS1   serine carboxypeptidase S10 family protein, similar to Serine carboxypeptidase II chains A and B (SP:P08819) (EC 3.4.16.6) (Triticum aestivum (Wheat));   chr4:14944135-14948611 FORWARD   Aliases: BRI1 SUPPRESSOR 1, F17I23.50, F17I23_50, SCPL24	2.8	2.8	-0.0	-0.2	100.0%	-5.4
18011	AT4G16510.1   YbaK/prolyl-tRNA synthetase-related, contains weak hit to Pfam profile PF04073: YbaK/prolyl-tRNA synthetases associated domain   chr4:9302821-9305070 FORWARD   Aliases: DL4280W, FCAALL.85	5.1	5.1	0.0	0.2	100.0%	-5.1
18012	AT1G55040.1   zinc finger (Ran-binding) family protein, contains Pfam PF00641: Zn-finger in Ran binding protein and others; contains Prosite PS00018: EF-hand calcium-binding domain; similar to Zinc finger protein 265 (Zinc finger, splicing) (Fragment). (SP:Q9R020){Mus musculus}	5.9	5.8	0.1	0.2	100.0%	-4.7
18013	AT4G15310.1   Symbol: CYP702A3   similar to cytochrome P450 family protein [Arabidopsis thaliana] (TAIR:At4g15300.1); similar to putative cytochrome P450 [Oryza sativa (japonica cultivar-group)] (GB:CAD30852.1); contains InterPro domain Cytochrome P450 (InterPro:IPR001128); contains InterPro domain E-class P450, group IV (InterPro:IPR002403)   chr4:8736721-8740047 FORWARD   Aliases: DL3700W, FCAALL.266	2.7	2.6	0.0	0.2	100.0%	-5.3
18014	AT3G18120.1   F-box family protein-related, contains TIGRFAM TIGR01640 : F-box protein interaction domain; similar to F-box protein family, AtFBX9 (GI:20197985) (Arabidopsis thaliana)   chr3:6210096-6210578 REVERSE   Aliases: MRC8.10	3.0	3.0	-0.0	-0.2	100.0%	-5.4
18015	AT5G65600.1   legume lectin family protein / protein kinase family protein, contains Pfam domains PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain	4.6	4.5	0.1	0.2	100.0%	-4.6
18016	AT5G50990.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:20756972-20758507 FORWARD   Aliases: K3K7.15, K3K7_15	4.9	5.0	-0.1	-0.2	100.0%	-4.7
18017	ATCG01110.1   Symbol: NDHH   plastid NAD(P)H dehydrogenase subunit H 49KDa protein   chrC:122011-123192 REVERSE   Aliases: NDHH	3.3	3.3	-0.1	-0.2	100.0%	-5.2
18018	AT2G30270.1   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr2:12914918-12916195 REVERSE   Aliases: T9D9.8, T9D9_8	4.9	5.0	-0.0	-0.2	100.0%	-4.9
18019	AT1G25280.2   F-box family protein / tubby family protein, similar to Tubby protein homolog (SP:O88808) (Rattus norvegicus); contains Pfam PF00646: F-box domain and Pfam PF01167: Tub family;	7.0	7.0	0.0	0.2	100.0%	-5.1
18020	AT1G44090.1   gibberellin 20-oxidase family protein, similar to gibberellin 20-oxidase GI:4164141 from (Lactuca sativa); contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily	2.9	2.9	0.0	0.2	100.0%	-5.3
18021	AT2G31150.1   expressed protein   chr2:13279452-13281655 FORWARD   Aliases: T16B12.4, T16B12_4	4.2	4.3	-0.1	-0.2	100.0%	-4.6
18022	AT1G68920.3   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g26260.1); similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At1g26260.2); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_910691.1); similar to putative TA1 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD68029.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)	5.6	5.7	-0.1	-0.2	100.0%	-4.9
18023	AT1G01225.1   NC domain-containing protein-related, contains weak hit to Pfam profile PF04970: NC domain   chr1:95987-97407 FORWARD   Aliases: None	3.3	3.4	-0.0	-0.2	100.0%	-5.1
18024	AT3G50520.1   phosphoglycerate/bisphosphoglycerate mutase family protein, similar to SP:P00950 Phosphoglycerate mutase 1 (EC 5.4.2.1) {Saccharomyces cerevisiae}; contains Pfam profile PF00300: phosphoglycerate mutase family   chr3:18759010-18760552 FORWARD   Aliases: T20E23.120	6.9	7.0	-0.1	-0.2	100.0%	-4.9
18025	AT1G21070.1   transporter-related, low similarity to GDP-Mannose transporter (Arabidopsis thaliana) GI:15487237; contains Pfam profile PF00892: Integral membrane protein   chr1:7375858-7378136 REVERSE   Aliases: T22I11.10, T22I11_10	4.4	4.4	-0.0	-0.2	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18026	AT2G25370.1   zinc finger protein-related, contains weak similarity to zinc fingers and Pfam:PF01485 IBR domain   chr2:10813779-10816873 FORWARD   Aliases: F13B15.3, F13B15_3	2.1	2.1	-0.0	-0.2	100.0%	-5.6
18027	AT5G08090.1   hypothetical protein   chr5:2591712-2592900 FORWARD   Aliases: T22D6.30, T22D6_30	3.5	3.5	0.0	0.2	100.0%	-5.1
18028	AT1G20750.1   helicase-related, similar to BRCA1-binding helicase-like protein BACH1 (GI:13661819) Homo sapiens.;   chr1:7203292-7208988 REVERSE   Aliases: F2D10.24, F2D10_24	2.7	2.7	-0.0	-0.2	100.0%	-5.6
18029	AT5G53970.1   aminotransferase, putative, similar to nicotianamine aminotransferase from Hordeum vulgare (GI:6498122, GI:6469087); contains Pfam profile PF00155 aminotransferase, classes I and II   chr5:21927771-21930003 FORWARD   Aliases: K19P17.14, K19P17_14	3.4	3.4	0.0	0.2	100.0%	-5.0
18030	AT1G67230.1   expressed protein   chr1:25154914-25159942 REVERSE   Aliases: F1N21.5	6.7	6.7	0.0	0.2	100.0%	-5.2
18031	AT1G30070.1   SGS domain-containing protein, similar to calyculin binding protein (Mus musculus) GI:3142331; contains Pfam profile PF05002: SGS domain	8.2	8.3	-0.1	-0.2	100.0%	-4.5
18032	AT5G04400.1   Symbol: ANAC077   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) protein   chr5:1241556-1243359 FORWARD   Aliases: ANAC077, T19N18.130, T19N18_130	3.0	3.0	-0.0	-0.2	100.0%	-5.3
18033	AT5G27630.1   acyl-CoA binding family protein, similar to RING finger rngB protein, cytosolic - Dictyostelium discoideum, PIR:S68824; contains Pfam profiles PF01344: Kelch motif, PF00887: Acyl CoA binding protein (ACBP)   chr5:9776026-9781530 FORWARD   Aliases: F15A18.90, F15A18_90	4.5	4.6	-0.1	-0.2	100.0%	-4.9
18034	AT2G20805.1   expressed protein   chr2:8963450-8963818 FORWARD   Aliases: F5H14.4, F5H14_4	2.4	2.4	0.0	0.2	100.0%	-6.0
18035	AT4G32915.1   expressed protein   chr4:15885523-15886954 FORWARD   Aliases: None	4.7	4.7	-0.0	-0.2	100.0%	-5.3
18036	AT1G13290.1   zinc finger (C2H2 type) family protein, contains Pfam domain PF00096: Zinc finger, C2H2 type   chr1:4550150-4551617 REVERSE   Aliases: T6J4.5, T6J4_5	3.6	3.6	0.0	0.2	100.0%	-5.6
18037	AT1G25580.1   Symbol: ANAC008   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to putative NAM protein (GP:21554371) (Arabidopsis thaliana)	3.6	3.5	0.1	0.2	100.0%	-4.9
18038	AT3G53550.1   expressed protein, various predicted proteins, Arabidopsis thaliana   chr3:19867848-19869286 FORWARD   Aliases: F4P12.250	2.2	2.2	-0.0	-0.2	100.0%	-5.9
18039	AT4G12480.1   Symbol: PEARL1 1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, identical to pEARL1 1 (Accession No. L43080): an Arabidopsis member of a conserved gene family (PGF95-099), Plant Physiol. 109 (4), 1497 (1995); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:7406102-7406934 REVERSE   Aliases: T1P17.70, T1P17_70	2.3	2.3	-0.0	-0.2	100.0%	-4.7
18040	AT3G26935.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr3:9934238-9936455 REVERSE   Aliases: None	2.9	2.9	-0.0	-0.2	100.0%	-5.1
18041	AT1G49900.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr1:18477576-18481311 REVERSE   Aliases: T18C15.3	2.6	2.6	0.0	0.2	100.0%	-5.5
18042	AT5G20960.2   Symbol: AAO1   aldehyde oxidase 1 (AAO1), identical to aldehyde oxidase AAO1 from Arabidopsis thaliana (gi:3172023) isoform contains a GA-donor splice site at intron 10   chr5:7116740-7122776 FORWARD   Aliases: ALDEHYDE OXIDASE, ALDEHYDE OXIDASE 1, AO1, ATAO, ATAO1, F22D1.130, F22D1_130	6.7	6.6	0.1	0.2	100.0%	-4.9
18043	AT5G54000.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to Flavonol synthase (EC 1.14.11.-) (FLS) from Lisianthus russellianus {Eustoma grandiflorum} (SP:Q9M547), Leucoanthocyanidin dioxygenase (LDOX) (Leucoanthocyanidin hydroxylase) (Anthocyanidin synthase) from Malus spp. (SP:P51091); contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr5:21935002-21936290 REVERSE   Aliases: K19P17.17, K19P17_17	2.8	2.8	-0.0	-0.2	100.0%	-5.5
18044	AT3G59845.1   NADP-dependent oxidoreductase, putative, similar to probable NADP-dependent oxidoreductase (zeta-crystallin homolog) P1 (SP:Q39172)(gi:886428) and P2 (SP:Q39173)(gi:886430), Arabidopsis thaliana; allyl alcohol dehydrogenase - Nicotiana tabacum, EMBL:AB036735   chr3:22117222-22118812 REVERSE   Aliases: None	5.1	5.1	-0.1	-0.2	100.0%	-4.7
18045	AT4G13985.1   F-box family protein, contains F-box domain Pfam:PF00646	2.3	2.4	-0.0	-0.2	100.0%	-5.7
18046	AT4G03170.1   hypothetical protein   chr4:1400832-1401584 FORWARD   Aliases: F4C21.9, F4C21_9	2.7	2.7	0.0	0.2	100.0%	-5.6
18047	AT2G40230.1   transferase family protein, similar to taxadienol acetyl transferase from Taxus cuspidata (gi:6978038); contains Pfam transferase family domain PF002458	3.8	3.8	0.1	0.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18048	AT5G43100.1   aspartyl protease family protein, low similarity to CND41, chloroplast nucleoid DNA binding protein (Nicotiana tabacum) GI:2541876; contains Pfam profile PF00026: Eukaryotic aspartyl protease   chr5:17316351-17320286 FORWARD   Aliases: MMG4.12, MMG4_12	6.5	6.5	-0.1	-0.2	100.0%	-4.7
18049	AT4G27540.1   prenylated rab acceptor (PRA1) protein-related, contains Pfam profile PF03208: PRA1 family protein   chr4:13753219-13754751 REVERSE   Aliases: T29A15.30, T29A15_30	5.1	5.0	0.0	0.2	100.0%	-4.8
18050	AT3G59340.1   expressed protein, identical to anthocyanin-related membrane protein 3 (GI:16416387) (Arabidopsis thaliana)   chr3:21939741-21942547 REVERSE   Aliases: F25L23.200	2.2	2.3	-0.0	-0.2	100.0%	-5.5
18051	AT2G21910.1   Symbol: CYP96A5   cytochrome P450, putative   chr2:9348578-9350110 FORWARD   Aliases: F7D8.23, F7D8_23	2.7	2.8	-0.0	-0.2	100.0%	-5.3
18052	AT5G07930.1   RNA recognition motif (RRM)-containing protein, similar to terminal ear1 (Zea mays) GI:3153237, SP:P08965 Meiosis protein mei2 {Schizosaccharomyces pombe}; contains Pfam profile: PF00076 RNA recognition motif (aka RRM, RBD, or RNP domain)   chr5:2530866-2532217 FORWARD   Aliases: F13G24.130	2.2	2.2	0.0	0.2	100.0%	-5.6
18053	AT3G43320.1   expressed protein   chr3:15286449-15287981 REVERSE   Aliases: T5C2.20	3.2	3.2	-0.0	-0.2	100.0%	-5.4
18054	AT5G41760.2   similar to nucleotide-sugar transporter family protein [Arabidopsis thaliana] (TAIR:At3g59360.2); similar to nucleotide-sugar transporter family protein [Arabidopsis thaliana] (TAIR:At3g59360.1); similar to putative CMP-sialic acid transporter [Oryza sativa (japonica cultivar-group)] (GB:XP_478801.1); contains InterPro domain UDP-galactose transporter (InterPro:IPR004689); contains InterPro domain Nucleotide-sugar transporter (InterPro:IPR007271)   chr5:16724121-16727137 FORWARD   Aliases: K16L22.3, K16L22_3	6.3	6.3	-0.1	-0.2	100.0%	-4.8
18055	AT2G19010.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr2:8250171-8252460 FORWARD   Aliases: T20K24.2, T20K24_2	2.8	2.8	0.0	0.2	100.0%	-5.3
18056	AT4G32770.1   Symbol: VTE1   tocopherol cyclase, chloroplast / vitamin E deficient 1 (VTE1) / sucrose export defective 1 (SXD1), identical to SP:Q94FY7 Tocopherol cyclase, chloroplast precursor (Vitamin E deficient 1) (Sucrose export defective 1) {Arabidopsis thaliana}	6.1	6.0	0.1	0.2	100.0%	-4.4
18057	AT3G20910.1   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr3:7326401-7328580 FORWARD   Aliases: MFD22.7	4.2	4.1	0.0	0.2	100.0%	-5.2
18058	AT2G19210.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:8342721-8346389 REVERSE   Aliases: F27F23.1, F27F23_1	3.1	3.1	0.1	0.2	100.0%	-4.5
18059	AT3G13720.1   prenylated rab acceptor (PRA1) family protein, contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr3:4495026-4495963 REVERSE   Aliases: MMM17.14	3.7	3.6	0.1	0.2	100.0%	-4.4
18060	AT2G42720.1   F-box family protein, contains F-box domain Pfam:PF00646	4.0	4.0	0.0	0.2	100.0%	-5.0
18061	AT4G25070.1   expressed protein, ; expression supported by MPSS   chr4:12872492-12876478 FORWARD   Aliases: F24A6.14	4.6	4.8	-0.1	-0.2	100.0%	-4.7
18062	AT1G19440.1   very-long-chain fatty acid condensing enzyme, putative, similar to GB:AAD37122 from (Arabidopsis thaliana)   chr1:6728975-6730922 FORWARD   Aliases: F18O14.21, F18O14_21	3.1	3.2	-0.0	-0.2	100.0%	-5.1
18063	AT2G46040.1   ARID/BRIGHT DNA-binding domain-containing protein / ELM2 domain-containing protein, contains Pfam profiles PF01388: ARID/BRIGHT DNA binding domain, PF01448: ELM2 domain	2.9	2.9	-0.0	-0.2	100.0%	-5.3
18064	AT2G25350.1   phox (PX) domain-containing protein, weak similarity to SP:Q9UTK5 Abnormal long morphology protein 1 (Sp8) {Schizosaccharomyces pombe}; contains Pfam profile PF00787: PX domain	4.4	4.4	0.0	0.2	100.0%	-5.2
18065	AT3G22450.1   expressed protein, ; expression supported by MPSS   chr3:7962450-7963385 FORWARD   Aliases: F16J14.2	3.7	3.7	-0.0	-0.2	100.0%	-5.2
18066	AT1G56560.1   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr1:21196164-21198777 FORWARD   Aliases: F25P12.99, F25P12_99	7.2	7.3	-0.1	-0.2	100.0%	-4.7
18067	AT3G55560.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr3:20615595-20617359 REVERSE   Aliases: T22E16.220	4.3	4.4	-0.0	-0.2	100.0%	-4.9
18068	AT3G01140.1   Symbol: MYB106	3.1	3.1	-0.0	-0.2	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18069	AT1G28650.1   lipase, putative, strong similarity to lipase (Arabidopsis thaliana) GI:1145627   chr1:10069533-10071068 REVERSE   Aliases: F1K23.27, F1K23_27	2.3	2.3	0.0	0.2	100.0%	-5.7
18070	AT1G27940.1   multidrug resistance P-glycoprotein, putative, similar to mdr-like P-glycoprotein atpgp1 GI:3849833 from (Arabidopsis thaliana)   chr1:9733584-9738116 REVERSE   Aliases: F13K9.5, F13K9_5	2.9	2.9	0.0	0.2	100.0%	-5.3
18071	AT1G75720.1   hypothetical protein   chr1:28438309-28438979 REVERSE   Aliases: F10A5.8, F10A5_8	3.6	3.6	0.0	0.2	100.0%	-5.1
18072	AT1G10950.1   endomembrane protein 70, putative   chr1:3659216-3663984 FORWARD   Aliases: T19D16.13, T19D16_13	9.4	9.5	-0.1	-0.2	100.0%	-5.1
18073	AT3G62740.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; similar to hydroxyisourate hydrolase (GI:19569603) (Glycine max)   chr3:23222392-23224864 FORWARD   Aliases: F26K9.170	3.0	3.0	-0.0	-0.2	100.0%	-5.4
18074	AT3G18070.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-mannosidase enzyme (GI:17226270) (Lycopersicon esculentum)   chr3:6187300-6189953 FORWARD   Aliases: MRC8.6	2.4	2.4	-0.0	-0.2	100.0%	-5.7
18075	AT5G04060.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr5:1099119-1101930 FORWARD   Aliases: F21E1.1	4.7	4.7	0.1	0.2	100.0%	-5.0
18076	AT2G27020.1   Symbol: PAG1   20S proteasome alpha subunit G (PAG1) (PRC8), identical to proteasome subunit alpha type 3 SP:O23715, GI:12644056 from (Arabidopsis thaliana); identical to cDNA proteasome subunit prc8 GI:2511591   chr2:11535437-11538054 REVERSE   Aliases: 20S PROTEASOME SUBUNIT PAG1, T20P8.7, T20P8_7	10.6	10.8	-0.1	-0.2	100.0%	-4.8
18077	AT3G42350.1   hypothetical protein   chr3:14500913-14503573 REVERSE   Aliases: T14K23.60	2.7	2.8	-0.0	-0.2	100.0%	-5.9
18078	AT3G54850.1   armadillo/beta-catenin repeat family protein / U-box domain-containing family protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr3:20332409-20334998 FORWARD   Aliases: F28P10.170	6.1	6.1	-0.1	-0.2	100.0%	-4.8
18079	AT4G17040.1   ATP-dependent Clp protease proteolytic subunit, putative, similar to ATP-dependent Clp protease proteolytic subunit GI:7264063 from (Synechococcus sp.PCC 7942)   chr4:9585724-9589381 REVERSE   Aliases: DL4550C, FCAALL.413	9.3	9.2	0.1	0.2	100.0%	-4.7
18080	AT1G27760.3   interferon-related developmental regulator family protein / IFRD protein family, contains Pfam PF05004: Interferon-related developmental regulator (IFRD); similar to IFR1 protein GI:16580630 (Gallus gallus); similar to Interferon-related developmental regulator 1 (TPA induced sequence 7) (TIS7 protein) (SP:P19182) {Mus musculus}   chr1:9668586-9671597 FORWARD   Aliases: T22C5.22, T22C5_22	6.9	6.8	0.1	0.2	100.0%	-4.9
18081	AT2G17680.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function; expression supported by MPSS   chr2:7686323-7687201 FORWARD   Aliases: T17A5.19, T17A5_19	2.9	3.0	-0.0	-0.2	100.0%	-5.4
18082	AT5G14240.1   expressed protein   chr5:4595607-4597657 REVERSE   Aliases: F18O22.30, F18O22_30	6.7	6.6	0.1	0.2	100.0%	-4.8
18083	AT2G48080.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam domain PF03171 2OG-Fe(II) oxygenase superfamily   chr2:19672060-19674162 REVERSE   Aliases: T9J23.23	3.2	3.1	0.1	0.2	100.0%	-4.3
18084	AT3G50170.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr3:18612840-18614721 REVERSE   Aliases: F11C1.10	2.4	2.5	-0.0	-0.2	100.0%	-5.8
18085	AT1G15030.1   expressed protein   chr1:5177524-5180339 FORWARD   Aliases: T15D22.8, T15D22_8	3.0	3.0	0.0	0.2	100.0%	-5.4
18086	AT2G25670.2   expressed protein   chr2:10935742-10938135 REVERSE   Aliases: F3N11.12, F3N11_12	10.2	10.2	-0.1	-0.2	100.0%	-5.3
18087	AT2G30480.2   expressed protein   chr2:12995344-12999804 REVERSE   Aliases: T6B20.25, T6B20_25	3.2	3.2	-0.0	-0.2	100.0%	-5.4
18088	AT1G80970.1   XH domain-containing protein, contains Pfam profile: PF03469 XH domain   chr1:30425042-30426878 FORWARD   Aliases: F23A5.33, F23A5_33	4.5	4.4	0.0	0.2	100.0%	-4.9
18089	AT3G23580.1   Symbol: RNR2A   ribonucleoside-diphosphate reductase small chain / ribonucleotide reductase, nearly identical to SP:P50651 Ribonucleoside-diphosphate reductase small chain (EC 1.17.4.1) (Ribonucleotide reductase) (R2 subunit) {Arabidopsis thaliana}   chr3:8460059-8462822 FORWARD   Aliases: MDB19.1, R2, RNR2	7.8	7.9	-0.1	-0.2	100.0%	-4.8
18090	AT2G14610.1   Symbol: PR1   pathogenesis-related protein 1 (PR-1), identical to GB:M90508 SP:P33154   chr2:6248786-6249545 REVERSE   Aliases: PATHOGENESIS RELATED GENE 1, PATHOGENESIS RELATED PROTEIN 1, PR 1, T6B13.15, T6B13_15	3.3	3.4	-0.0	-0.2	100.0%	-5.2
18091	AT3G44900.1   Symbol: ATCHX4	2.0	2.1	-0.0	-0.2	100.0%	-6.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18092	AT4G05370.1   expressed protein   chr4:2736132-2736581 FORWARD   Aliases: C6L9.50, C6L9_50	2.3	2.3	-0.0	-0.2	100.0%	-5.7
18093	AT5G44910.1   Toll-Interleukin-Resistance (TIR) domain-containing protein, domain signature TIR exists, suggestive of a disease resistance protein.   chr5:18154581-18155462 FORWARD   Aliases: K21C13.9, K21C13_9	3.3	3.3	0.1	0.2	100.0%	-4.4
18094	AT4G14730.1   transmembrane protein-related, low similarity to transmembrane protein OTMP (Ovis aries) GI:9965379   chr4:8448544-8450068 FORWARD   Aliases: DL3405W, FCAALL.300	4.4	4.4	-0.0	-0.2	100.0%	-5.1
18095	AT5G34895.1   hypothetical protein, similar to At2g04970, At2g15200, At1g32830, At2g14140, At3g30450, At4g03990, At3g47270, At2g02200   chr5:13227044-13229129 REVERSE   Aliases: T2L5.4, T2L5_4	2.0	2.0	0.0	0.2	100.0%	-6.2
18096	AT2G46830.2   Symbol: CCA1   myb-related transcription factor (CCA1), identical to myb-related transcription factor (CCA1) GI:4090569 from (Arabidopsis thaliana)   chr2:19253750-19255983 FORWARD   Aliases: CIRCADIAN CLOCK ASSOCIATED 1, F19D11.11, MYB RELATED DNA BINDING PROTEIN	7.7	7.6	0.1	0.2	100.0%	-4.7
18097	AT3G45710.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:16793629-16795720 FORWARD   Aliases: T6D9.40	3.1	3.0	0.1	0.2	100.0%	-4.6
18098	AT1G70100.3   expressed protein   chr1:26406746-26409751 FORWARD   Aliases: F20P5.17, F20P5_17	2.7	2.7	0.0	0.2	100.0%	-5.9
18099	AT1G47620.1   Symbol: CYP96A8   cytochrome P450, putative, similar to cytochrome P450 GI:4688670 from (Catharanthus roseus)   chr1:17510556-17512118 REVERSE   Aliases: F16N3.8, F16N3_8	2.5	2.5	0.0	0.2	100.0%	-5.9
18100	AT3G14000.2   expressed protein   chr3:4630879-4633923 REVERSE   Aliases: MDC16.13	3.6	3.5	0.0	0.2	100.0%	-5.0
18101	AT4G18370.1   Symbol: HHOA   protease HhoA, chloroplast (SPPA) (HHOA), identical to SP:Q9SEL7 Protease HhoA, chloroplast precursor (EC 3.4.21.-) {Arabidopsis thaliana}   chr4:10149203-10151722 FORWARD   Aliases: F28J12.30, F28J12_30	8.1	8.1	0.1	0.2	100.0%	-4.6
18102	AT5G62460.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:25092134-25094510 FORWARD   Aliases: K19B1.7, K19B1_7	5.0	5.1	-0.1	-0.2	100.0%	-4.6
18103	AT4G10880.1   hypothetical protein, predicted proteins, Arabidopsis thaliana   chr4:6685825-6686343 REVERSE   Aliases: F25I24.90, F25I24_90	2.6	2.6	-0.0	-0.2	100.0%	-5.9
18104	AT5G58410.1   expressed protein, contains similarity to hypothetical proteins   chr5:23626889-23634612 FORWARD   Aliases: MCK7.28, MCK7_28	6.3	6.3	-0.0	-0.2	100.0%	-4.9
18105	AT4G17070.1   expressed protein   chr4:9595404-9598191 REVERSE   Aliases: DL4565C, FCAALL.192	7.4	7.4	0.1	0.2	100.0%	-4.7
18106	AT1G13200.1   F-box family protein, contains F-box domain Pfam:PF00646; contains TIGRFAM TIGR01640: F-box protein interaction domain   chr1:4507218-4508525 REVERSE   Aliases: F3F19.23, F3F19_23	3.0	2.9	0.0	0.2	100.0%	-5.7
18107	AT3G25440.1   similar to group II intron splicing factor CRS1-related [Arabidopsis thaliana] (TAIR:At4g13070.1); similar to group II intron splicing factor CRS1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87110.1); similar to OJ1294_F06.20 [Oryza sativa (japonica cultivar-group)] (GB:NP_914225.1); similar to group II intron splicing factor CRS1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87109.1); similar to group II intron splicing factor CRS1-like [Oryza sativa (japonica cultivar-group)] (GB:BAD87111.1); contains InterPro domain Protein of unknown function UPF0044 (InterPro:IPR001890)   chr3:9225210-9226947 FORWARD   Aliases: MWL2.5	4.1	4.1	0.0	0.2	100.0%	-5.2
18108	AT4G05580.1   hypothetical protein   chr4:2841645-2841995 FORWARD   Aliases: T1J24.6, T1J24_6	2.4	2.4	0.0	0.2	100.0%	-6.0
18109	AT5G66770.1   scarecrow transcription factor family protein   chr5:26677826-26680120 FORWARD   Aliases: MUD21.1, MUD21_1	2.7	2.7	0.0	0.2	100.0%	-5.2
18110	AT5G51860.1   MADS-box protein (AGL72), contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain);   chr5:21099070-21101352 REVERSE   Aliases: MIO24.20, MIO24_20	2.6	2.6	0.0	0.2	100.0%	-5.4
18111	AT4G32910.1   expressed protein   chr4:15881259-15885390 FORWARD   Aliases: F26P21.30, F26P21_30	8.7	8.7	-0.1	-0.2	100.0%	-4.9
18112	AT4G03630.1   root nodule development protein-related, similar to N7 protein (Medicago truncatula) gi:3273101:emb:CAA76808; contains similarity to SKP1 interacting partner 1 GI:10716947 from (Arabidopsis thaliana), PMID:11387208   chr4:1608748-1610035 FORWARD   Aliases: T5L23.12, T5L23_12	2.6	2.6	0.0	0.2	100.0%	-5.4
18113	AT5G18870.1   inosine-uridine preferring nucleoside hydrolase-related   chr5:6298388-6300291 FORWARD   Aliases: F17K4.120, F17K4_120	2.4	2.4	-0.0	-0.2	100.0%	-6.0
18114	AT4G01130.1   acetyltransferase, putative, similar to lanatoside 15'-O-acetyltransferase (Digitalis lanata) GI:3688284; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr4:485857-488007 FORWARD   Aliases: F2N1.17, F2N1_17	2.2	2.2	0.0	0.2	100.0%	-5.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18115	AT4G02310.1   kelch repeat-containing F-box family protein, contains Pfam PF00646: F-box domain; contains Pfam PF01344 : Kelch motif;   chr4:1014680-1015729 REVERSE   Aliases: T2H3.7, T2H3_7	4.3	4.3	0.0	0.2	100.0%	-5.2
18116	AT1G20090.1   Symbol: ROP2   Rac-like GTP-binding protein (ARAC4) / Rho-like GTP-binding protein (ROP2), identical to SP:Q38919 RAC-like GTP binding protein ARAC4 (GTP binding protein ROP2) (Arabidopsis thaliana), Rho-like GTP binding protein (Arabidopsis thaliana) GI:2654009   chr1:6966944-6968924 FORWARD   Aliases: ARAC4, ATRAC4, GTP BINDING PROTEIN ARAC4, ROP2AT, T20H2.12, T20H2_12	7.8	7.9	-0.1	-0.2	100.0%	-4.8
18117	AT1G64440.1   Symbol: RHD1   UDP-glucose 4-epimerase, putative / UDP-galactose 4-epimerase, putative / Galactowaldenase, putative, similar to UDP-galactose 4-epimerase from Arabidopsis thaliana SP:Q42605, Cyamopsis tetragonoloba GI:3021357 (AJ005082) (Plant Sci. 142, 147-154 (1999))   chr1:23940706-23943562 FORWARD   Aliases: F15H21.11, F15H21_11, REB1, ROOT HAIR DEFECTIVE 1	4.5	4.5	-0.0	-0.2	100.0%	-5.3
18118	AT1G53300.1   thioredoxin family protein, contains Pfam profiles PF00085: Thioredoxin, PF00515: TPR Domain; similar to tetratricopeptide repeat protein 2 (GI:7248701) (Drosophila melanogaster); similar to DnaJ homolog subfamily C member 7 (Tetratricopeptide repeat protein 2) (TPR repeat protein 2) (Swiss-Prot:Q99615) (Homo sapiens)   chr1:19883090-19886043 FORWARD   Aliases: F12M16.20, F12M16_20	2.6	2.7	-0.0	-0.2	100.0%	-5.0
18119	AT2G24780.1   expressed protein   chr2:10572701-10573025 REVERSE   Aliases: F27A10.9, F27A10_9	2.3	2.3	0.0	0.2	100.0%	-5.7
18120	AT4G13390.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:7783814-7785322 FORWARD   Aliases: T9E8.130, T9E8_130	2.8	3.0	-0.1	-0.2	100.0%	-4.0
18121	AT1G10940.2   Symbol: ASK1   similar to serine/threonine protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g60940.1); similar to serine/threonine protein kinase, putative [Arabidopsis thaliana] (TAIR:At1g60940.2); similar to probable serine/threonine-specific protein kinase (EC 2.7.1.-) BSK2 - rape (GB:S60611); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:3655777-3658578 REVERSE   Aliases: ARABIDOPSIS SERINE/THREONINE KINASE 1	3.5	3.4	0.1	0.2	100.0%	-4.8
18122	AT2G27920.3   Symbol: SCPL51	3.7	3.8	-0.1	-0.2	100.0%	-4.4
18123	AT1G30990.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:20810); similar to ESTs gb:W43264, gb:H36765, gb:R30617, gb:AA042095, and emb:Z27272 ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:11052111-11053044 FORWARD   Aliases: F17F8.9	2.6	2.7	-0.0	-0.2	100.0%	-5.0
18124	AT1G80620.1   ribosomal protein S15 family protein, similar to ribosomal protein S15 GB:AAD36415 from (Thermotoga maritima)   chr1:30310256-30312308 FORWARD   Aliases: None	5.3	5.4	-0.1	-0.2	100.0%	-4.7
18125	AT1G26820.1   Symbol: RNS3   ribonuclease 3 (RNS3), identical to ribonuclease SP:P42815 Ribonuclease 3 precursor (EC 3.1.27.1) {Arabidopsis thaliana}	3.8	3.7	0.1	0.2	100.0%	-4.7
18126	AT1G64610.2   WD-40 repeat family protein, contains Pfam PF00400: WD domain, G-beta repeat; similar to WD-repeat protein 5 (WD repeat protein BIG-3) (SP:Q9UGP9) (Homo sapiens)   chr1:24002388-24004991 REVERSE   Aliases: F1N19.18, F1N19_18	4.4	4.4	0.0	0.2	100.0%	-5.4
18127	AT3G26300.1   Symbol: CYP71B34   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr3:9640436-9642103 REVERSE   Aliases: F20C19.2	3.4	3.3	0.1	0.2	100.0%	-4.2
18128	AT3G05980.1   expressed protein   chr3:1795345-1796453 FORWARD   Aliases: F2O10.6, F2O10_6	3.5	3.4	0.0	0.2	100.0%	-5.5
18129	AT3G52230.1   expressed protein   chr3:19382265-19383653 FORWARD   Aliases: T25B15.4	7.9	7.8	0.2	0.2	100.0%	-4.6
18130	AT2G26260.2   similar to 3-beta hydroxysteroid dehydrogenase/isomerase family protein [Arabidopsis thaliana] (TAIR:At1g47290.2); similar to putative 3-beta hydroxysteroid dehydrogenase/isomerase [Oryza sativa (japonica cultivar-group)] (GB:AAP50920.1); contains InterPro domain 3-beta hydroxysteroid dehydrogenase/isomerase (InterPro:IPR002225); contains InterPro domain Reticulon (InterPro:IPR003388)   chr2:11185188-11190054 FORWARD   Aliases: T1D16.10, T1D16_10	2.7	2.7	0.0	0.2	100.0%	-5.6
18131	AT1G13050.1   expressed protein   chr1:4450566-4451519 FORWARD   Aliases: F3F19.7, F3F19_7	2.6	2.6	-0.0	-0.2	100.0%	-5.7
18132	AT4G33250.1   Symbol: EIF3K   eukaryotic translation initiation factor 3 subunit 11 / eIF-3 p25 / eIF3k (TIF3K1), identical to Swiss-Prot:Q9SZA3 eukaryotic translation initiation factor 3 subunit 11 (eIF-3 p25) (eIF3k) (Arabidopsis thaliana); identical to cDNA initiation factor 3k GI:12407752	10.2	10.2	-0.1	-0.2	100.0%	-4.9
18133	AT1G36020.1   hypothetical protein   chr1:13435131-13435552 REVERSE   Aliases: T22A15.6, T22A15_6	3.5	3.4	0.0	0.2	100.0%	-5.2
18134	AT5G51500.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:20935155-20937064 REVERSE   Aliases: K17N15.5, K17N15_5	2.5	2.5	0.0	0.2	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18135	AT3G02050.1   Symbol: KUP3   potassium transporter (KUP3), nearly identical to potassium transporter KUP3p (Arabidopsis thaliana) gi:6742169:gb:AAF19432; similar to tiny root hair 1 protein (Arabidopsis thaliana) gi:11181958:emb:CAC16137; KUP/HAK/KT Transporter family member, PMID:11500563   chr3:350705-354311 FORWARD   Aliases: ATKT4, ATKUP3, F1C9.17, F1C9_17, KUP3P	5.3	5.4	-0.0	-0.2	100.0%	-5.1
18136	AT5G65910.1   BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	5.5	5.5	0.0	0.2	100.0%	-4.8
18137	AT1G63500.1   protein kinase-related, low similarity to protein kinase (Arabidopsis thaliana); contains Pfam profile: PF00069 Eukaryotic protein kinase domain	3.5	3.5	0.0	0.2	100.0%	-5.0
18138	AT4G37210.2   tetratricopeptide repeat (TPR)-containing protein, low similarity to SP:Q02508 Protein HGV2 Halocynthia roretzi; contains Pfam profile PF00515 TPR Domain   chr4:17512265-17514619 FORWARD   Aliases: AP22.13, AP22_13	5.7	5.7	0.1	0.2	100.0%	-5.0
18139	AT3G07340.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	3.0	3.0	-0.0	-0.2	100.0%	-5.4
18140	AT4G11720.1   expressed protein   chr4:7063285-7066778 FORWARD   Aliases: T5C23.150, T5C23_150	2.7	2.7	-0.0	-0.2	100.0%	-5.4
18141	AT5G35490.1   expressed protein (MRU1), contains Pfam domain, PF04827: Protein of unknown function (DUF635)   chr5:13707047-13707778 FORWARD   Aliases: MOK9.8, MOK9_8	3.4	3.3	0.0	0.2	100.0%	-5.1
18142	AT3G20630.1   Symbol: UBP14   ubiquitin-specific protease 14, putative (UBP14), similar to ubiquitin-specific protease 14 GI:11993473 (Arabidopsis thaliana)   chr3:7203007-7208346 REVERSE   Aliases: ATUBP14, TITAN6, TTN6, UBIQUITIN SPECIFIC PROTEASE 14	2.2	2.1	0.0	0.2	100.0%	-5.9
18143	AT1G37140.1   RNA-binding protein, putative, similar to terminal ear1 GI:3153237 from (Zea mays)   chr1:14172792-14174481 REVERSE   Aliases: F28L22.10, F28L22_10	2.6	2.7	-0.0	-0.2	100.0%	-5.4
18144	AT2G45810.1   DEAD/DEAH box helicase, putative	4.2	4.3	-0.1	-0.2	100.0%	-5.0
18145	AT2G34740.1   protein phosphatase 2C, putative / PP2C, putative, contains PF00481: Protein phosphatase 2C domain; similar to protein phosphatase type 2C (GI:4336436) (Lotus japonicus)   chr2:14666400-14667384 FORWARD   Aliases: T29F13.5, T29F13_5	3.9	4.0	-0.0	-0.2	100.0%	-5.5
18146	AT5G58750.1   wound-responsive protein-related, similar to induced upon wounding stress (Arabidopsis thaliana) GI:1483218   chr5:23746014-23747348 FORWARD   Aliases: MZN1.13, MZN1_13	3.0	3.0	0.1	0.2	100.0%	-4.4
18147	AT1G78620.2   integral membrane family protein, contains Pfam domain PF01940: Integral membrane protein   chr1:29577764-29580687 REVERSE   Aliases: T30F21.5, T30F21_5	6.5	6.6	-0.1	-0.2	100.0%	-5.1
18148	AT2G01320.4   ABC transporter family protein   chr2:154427-158181 REVERSE   Aliases: F10A8.20, F10A8_20	5.1	5.1	0.1	0.2	100.0%	-4.6
18149	AT2G45800.2   similar to LIM domain-containing protein [Arabidopsis thaliana] (TAIR:At3g61230.1); similar to putative LIM domain protein PLIM-2 [Oryza sativa (japonica cultivar-group)] (GB:XP_466988.1); similar to LIM-domain SF3 protein [Nicotiana tabacum] (GB:CAA71891.1); contains InterPro domain Zn-binding protein, LIM (InterPro:IPR001781)   chr2:18864795-18866263 REVERSE   Aliases: F4I18.22	2.9	2.9	-0.0	-0.2	100.0%	-5.4
18150	AT2G19040.1   Symbol: RALFL12   rapid alkalinization factor (RALF) family protein   chr2:8257005-8258974 FORWARD   Aliases: RALF LIKE 12, RALF LIKE 13, T20K24.5, T20K24_5	3.8	3.8	-0.1	-0.2	100.0%	-4.8
18151	AT5G17140.1   cysteine proteinase-related, low similarity to cysteine proteinase (Sitophilus zeamais) GI:2804262   chr5:5637833-5638276 FORWARD   Aliases: F2K13.290, F2K13_290	2.8	2.9	-0.0	-0.2	100.0%	-5.3
18152	AT1G48930.1   endo-1,4-beta-glucanase, putative / cellulase, putative, similar to endo-beta-1,4-glucanase GI:4972236 from (Fragaria x ananassa)   chr1:18105311-18108329 REVERSE   Aliases: F27K7.5	2.8	2.8	0.0	0.2	100.0%	-4.7
18153	AT1G20830.1   expressed protein   chr1:7242909-7244893 FORWARD   Aliases: F2D10.35, F2D10_35	5.9	5.8	0.1	0.2	100.0%	-4.8
18154	AT2G07190.1   hypothetical protein   chr2:2987364-2988942 FORWARD   Aliases: T25N22.15, T25N22_15	3.4	3.4	-0.0	-0.2	100.0%	-5.5
18155	AT3G49260.2   calmodulin-binding family protein, low similarity to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:18273496-18276965 FORWARD   Aliases: F2K15.120	2.6	2.6	0.0	0.2	100.0%	-5.7
18156	AT5G57070.1   hydroxyproline-rich glycoprotein family protein, Common family members: At5g26070, At5g19800, At1g72790 (Arabidopsis thaliana)   chr5:23113400-23115677 FORWARD   Aliases: MUL3.1, MUL3_1	2.5	2.5	-0.0	-0.2	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18157	AT1G68930.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr1:25921977-25924208 FORWARD   Aliases: T6L1.11, T6L1_11	2.5	2.5	-0.0	-0.2	100.0%	-5.6
18158	AT5G08070.1   TCP family transcription factor, putative, similar to TFPD (GI:6681577) (Arabidopsis thaliana) ; putative basic helix-loop-helix DNA binding protein TCP2 - Arabidopsis thaliana, EMBL:AF072691   chr5:2584886-2585614 FORWARD   Aliases: T22D6.10, T22D6_10	2.6	2.6	-0.0	-0.2	100.0%	-5.7
18159	AT1G47770.1   expressed protein   chr1:17592706-17593701 FORWARD   Aliases: T2E6.25, T2E6_25	2.3	2.3	0.0	0.2	100.0%	-5.6
18160	AT5G13130.1   expressed protein, low similarity to microrchidia (Mus musculus) GI:5410255   chr5:4166758-4170327 FORWARD   Aliases: T19L5.90, T19L5_90	2.4	2.4	0.0	0.2	100.0%	-5.9
18161	AT1G65450.1   transferase family protein, low similarity to anthranilate N-hydroxycinnamoyl/benzoyltransferase Dianthus caryophyllus GI:3288180, GI:2239091; contains Pfam profile PF02458 transferase family   chr1:24321527-24322727 FORWARD   Aliases: T8F5.23, T8F5_23	3.2	3.1	0.0	0.2	100.0%	-5.2
18162	AT2G22050.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:9383764-9384813 FORWARD   Aliases: T16B14.10, T16B14_10	3.8	3.8	-0.0	-0.2	100.0%	-5.1
18163	AT1G56330.1   Symbol: SAR1   GTP-binding protein (SAR1B), identical to GTP-binding protein (SAR1B) (Arabidopsis thaliana) SP:Q01474   chr1:21090220-21092214 REVERSE   Aliases: ATSAR1, ATSARA1B, F14G9.6, F14G9_6, SAR LIKE, SARL, SECRETION ASSOCIATED RAS	9.4	9.5	-0.1	-0.2	100.0%	-4.9
18164	AT5G67580.2   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:26972361-26974868 REVERSE   Aliases: K9I9.15, K9I9_15	4.7	4.7	0.0	0.2	100.0%	-5.1
18165	AT4G20235.1   Symbol: CYP71A28   similar to cytochrome P450 71A20, putative (CYP71A20) [Arabidopsis thaliana] (TAIR:At4g13310.1); similar to cytochrome P450 71A20, putative (CYP71A20) [Arabidopsis thaliana] (TAIR:At4g13310.2); similar to C71AR_ARATH Cytochrome P450 71A27 (GB:O65438)   chr4:10928847-10931287 REVERSE   Aliases: F1C12.160B	2.4	2.4	0.0	0.2	100.0%	-5.6
18166	AT2G36450.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr2:15301382-15301936 REVERSE   Aliases: F1O11.8, F1O11_8	3.0	3.0	0.0	0.2	100.0%	-5.6
18167	AT5G34830.1   expressed protein, ; expression supported by MPSS   chr5:12998875-12999727 FORWARD   Aliases: T3J11.1	2.6	2.6	0.0	0.2	100.0%	-5.3
18168	AT3G55700.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, glucuronosyl transferase homolog, Lycopersicon esculentum, PIR:S39507 ;contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:20682094-20684351 FORWARD   Aliases: F1I16.110	2.8	2.8	-0.0	-0.2	100.0%	-5.1
18169	AT1G29150.1   Symbol: ATS9   26S proteasome regulatory subunit, putative (RPN6), similar to 19S proteasome subunit 9 GB:AAC34120 GI:3450889 from (Arabidopsis thaliana)   chr1:10180505-10182689 FORWARD   Aliases: 19S PROTEOSOME SUBUNIT 9, F28N24.15, F28N24_15, RPN6	10.7	10.6	0.1	0.2	100.0%	-5.2
18170	AT2G33430.1   plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	6.2	6.3	-0.0	-0.2	100.0%	-4.6
18171	AT1G32810.1   expressed protein   chr1:11883495-11885823 FORWARD   Aliases: F9L11.1, F9L11_1	7.8	7.9	-0.1	-0.2	100.0%	-5.0
18172	AT4G19690.2   Symbol: IRT1   similar to metal transporter, putative (ZIP8) [Arabidopsis thaliana] (TAIR:At5g45105.1); similar to iron-regulated transporter 1 [Lycopersicon esculentum] (GB:AAD30548.1); contains InterPro domain ZIP zinc/iron transport (InterPro:IPR004698); contains InterPro domain Zinc transporter ZIP (InterPro:IPR003689)   chr4:10707456-10709025 FORWARD   Aliases: T16H5.50, T16H5_50	2.6	2.7	-0.1	-0.2	100.0%	-4.1
18173	AT4G23270.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr4:12171113-12173935 FORWARD   Aliases: F21P8.160, F21P8_160	6.8	6.9	-0.0	-0.2	100.0%	-5.0
18174	AT2G19520.1   Symbol: FVE   WD-40 repeat protein (MSI4), contains 6 (4 significant) WD-40 repeats (PF0400); identical to WD-40 repeat protein MSI4 (SP:O22607) (Arabidopsis thaliana)	6.2	6.3	-0.1	-0.2	100.0%	-4.7
18175	AT4G29730.1   Symbol: MSI5   similar to WD-40 repeat protein (MSI4) [Arabidopsis thaliana] (TAIR:At2g19520.1); similar to putative WD-repeat protein RBAP1 [Oryza sativa (japonica cultivar-group)] (GB:NP_916585.1); similar to nucleosome/chromatin assembly factor C [Zea mays] (GB:AAK67147.1); similar to WD-repeat protein RBAP1 [Zea mays] (GB:AAF97517.1); similar to putative Y1 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81520.1); similar to nucleosome/chromatin assembly factor group C [Zea mays] (GB:AAM77039.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr4:14558991-14562544 REVERSE   Aliases: T16L4.240, T16L4_240	6.2	6.3	-0.1	-0.2	100.0%	-4.7
18176	AT4G18790.1   Symbol: NRAMP5	3.9	3.9	0.0	0.2	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18177	AT1G02180.1   ferredoxin-related, similar to Ferredoxin. (SP:O78510) (Cryptomonas phi) {Guillardia theta}   chr1:413522-414645 REVERSE   Aliases: T6A9.14	4.4	4.5	-0.0	-0.2	100.0%	-4.8
18178	AT4G29950.2   microtubule-associated protein, identical to microtubule-associated protein GI:5032258 from (Arabidopsis thaliana); similar to TBC1 domain family member 5 (Swiss-Prot:Q92609) (Homo sapiens); contains Pfam profile PF00566: TBC domain	5.7	5.7	-0.1	-0.2	100.0%	-4.5
18179	AT1G17700.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr1:6089581-6090219 FORWARD   Aliases: F11A6.4, F11A6_4	2.4	2.4	0.0	0.2	100.0%	-5.6
18180	AT1G03700.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr1:920950-921901 FORWARD   Aliases: F21B7.30	2.6	2.7	-0.1	-0.2	100.0%	-4.7
18181	AT4G01470.1   Symbol: GAMMA TIP3/TIP1;3   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr4:625092-625850 REVERSE   Aliases: F11O4.1, F11O4_1, GAMMA TIP3, TIP1;3	4.7	4.7	-0.0	-0.2	100.0%	-5.2
18182	AT4G33790.1   acyl CoA reductase, putative, similar to acyl CoA reductase (Simmondsia chinensis) GI:5020215; contains Pfam profile PF03015: Male sterility protein; No start codon identified, may contain anomalous splicing at 5' end.   chr4:16204159-16207947 REVERSE   Aliases: T16L1.280	2.7	2.8	-0.1	-0.2	100.0%	-4.5
18183	AT3G17690.1   Symbol: ATCNGC19   cyclic nucleotide-binding transporter 2 / CNBT2 (CNGC19), identical to cyclic nucleotide-binding transporter 2 (CNBT2) GI:8131900 from (Arabidopsis thaliana); member of the cyclic nucleotide-gated channel family (CNGC)- see PMID:11500563   chr3:6045008-6048494 FORWARD   Aliases: CNGC19, MKP6.6	3.8	3.8	0.1	0.2	100.0%	-5.0
18184	AT2G38020.1   Symbol: VCL1   vacuoleless1 (VCL1), contains Pfam profiles: PF04841 Vps16, N-terminal region, PF04840: Vps16, C-terminal region; identical to cDNA VCL1 (VCL1) GI:13877132   chr2:15916432-15921788 REVERSE   Aliases: MAN, MANGLED, T8P21.7, T8P21_7, VACUOLELESS 1	6.0	6.1	-0.1	-0.2	100.0%	-4.4
18185	AT5G15340.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:4982276-4984147 REVERSE   Aliases: F8M21.230, F8M21_230	3.7	3.7	0.0	0.2	100.0%	-5.2
18186	AT3G07100.1   protein transport protein Sec24, putative, similar to protein transport protein Sec24A (SEC24-related protein) (Homo sapiens) SWISS-PROT:O95486   chr3:2245170-2250700 REVERSE   Aliases: T1B9.25	5.9	5.8	0.1	0.2	100.0%	-4.9
18187	AT5G55450.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:22484716-22485489 FORWARD   Aliases: MTE17.16, MTE17_16	2.2	2.2	-0.0	-0.2	100.0%	-5.7
18188	AT4G29020.1   glycine-rich protein, supporting cDNA gi:20465684:gb:AY096677.1:	6.3	6.3	-0.1	-0.2	100.0%	-5.0
18189	AT2G39480.1   ABC transporter family protein, related to multi drug resistance proteins and P-glycoproteins   chr2:16484870-16492117 REVERSE   Aliases: F12L6.14, F12L6_14	3.3	3.4	-0.0	-0.2	100.0%	-5.0
18190	AT2G14700.1   expressed protein   chr2:6299548-6302808 FORWARD   Aliases: T6B13.6, T6B13_6	3.9	4.0	-0.0	-0.2	100.0%	-5.1
18191	AT2G28380.1   double-stranded RNA-binding domain (DsRBD)-containing protein, contains Pfam profile PF00035: Double-stranded RNA binding motif   chr2:12140888-12143257 REVERSE   Aliases: T1B3.10, T1B3_10	3.5	3.5	-0.1	-0.2	100.0%	-5.3
18192	AT5G64813.1   GTP-binding protein-related, contains weak similarity to Ras-related protein Rab-27A (Rab-27) (GTP-binding protein Ram) (Swiss-Prot:P51159) (Homo sapiens)   chr5:25927567-25930122 FORWARD   Aliases: None	4.6	4.7	-0.1	-0.2	100.0%	-4.6
18193	AT2G04570.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr2:1594701-1596333 FORWARD   Aliases: T1O3.2, T1O3_2	3.3	3.3	0.0	0.2	100.0%	-5.3
18194	AT2G47270.1   expressed protein   chr2:19418630-19419221 REVERSE   Aliases: T8I13.11	2.6	2.5	0.0	0.2	100.0%	-5.3
18195	AT3G05210.1   Symbol: ERCC1   nucleotide repair protein, putative, similar to nucleotide repair protein (Lilium longiflorum) GI:3297891, SP:P07992 DNA excision repair protein ERCC-1 {Homo sapiens}; contains Pfam profile PF00633: Helix-hairpin-helix motif   chr3:1479560-1482048 FORWARD   Aliases: T12H1.18, T12H1_18	5.4	5.4	0.0	0.2	100.0%	-5.1
18196	AT3G16960.1   expressed protein   chr3:5791818-5792270 REVERSE   Aliases: K14A17.5	2.6	2.7	-0.0	-0.2	100.0%	-5.5
18197	AT3G19530.1   expressed protein   chr3:6775271-6775555 REVERSE   Aliases: T31J18.3	2.8	2.8	-0.0	-0.2	100.0%	-5.4
18198	AT1G76770.1   heat shock protein-related, contains similarity to 17.9 kDa heat-shock protein (Helianthus annuus) gi:11990130:emb:CAB55634   chr1:28818463-28819272 FORWARD   Aliases: F28O16.14, F28O16_14	2.6	2.6	0.0	0.2	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18199	AT1G48690.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr1:18012773-18013636 REVERSE   Aliases: F11I4.13, F11I4_13	2.4	2.6	-0.1	-0.2	100.0%	-4.2
18200	ATCG00300.1   Symbol: YCF9   encodes PsbZ, which is a subunit of photosystem II. In Chlamydomonas, this protein has been shown to be essential in the interaction between PS II and the light harvesting complex II.   chrC:35751-35939 FORWARD   Aliases: YCF9	10.4	10.5	-0.1	-0.2	100.0%	-5.5
18201	AT5G65510.1   similar to ovule development protein, putative [Arabidopsis thaliana] (TAIR:At5g10510.1); similar to AP2/EREBP transcription factor BABY BOOM1 [Brassica napus] (GB:AAM33802.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr5:26203542-26206639 FORWARD   Aliases: K21L13.1, K21L13_1	2.6	2.6	-0.0	-0.2	100.0%	-5.4
18202	AT2G47570.1   60S ribosomal protein L18 (RPL18A)   chr2:19522968-19523787 REVERSE   Aliases: T30B22.13	3.0	2.9	0.0	0.2	100.0%	-5.1
18203	AT2G05810.2   armadillo/beta-catenin repeat family protein, weak similarity to CCLS 65 (Silene latifolia) GI:2570102; contains Pfam profile PF00514: Armadillo/beta-catenin-like repeat   chr2:2215142-2217156 REVERSE   Aliases: T17C22.4, T17C22_4	4.1	4.0	0.1	0.2	100.0%	-4.7
18204	AT1G14680.1   expressed protein   chr1:5040856-5041728 FORWARD   Aliases: F10B6.4, F10B6_4	4.2	4.3	-0.1	-0.2	100.0%	-4.9
18205	AT5G02790.1   In2-1 protein, putative, similar to In2-1, Zea mays, EMBL:X58573	10.2	10.1	0.1	0.2	100.0%	-4.6
18206	AT3G55350.1   expressed protein   chr3:20529450-20531792 FORWARD   Aliases: T22E16.10	3.9	4.0	-0.0	-0.2	100.0%	-5.2
18207	AT1G48390.1   syntaxin-related family protein, contains a novel domain similar to F-box that is shared among other proteins in Arabidopsis; similar to proteins At3g54160, At1g47920 (syntaxin SYP81), At5g41830, At3g44180, At3g58890, At1g56610, At1g48390, At3g59270 (Arabidopsis thaliana)	2.6	2.5	0.0	0.2	100.0%	-5.8
18208	AT5G62920.1   Symbol: ARR6   two-component responsive regulator / response regulator 6 (ARR6), identical to response regulator 6 (Arabidopsis thaliana) GI:3953601   chr5:25269612-25271438 REVERSE   Aliases: MQB2.220, MQB2_220, RESPONSE REGULATOR 6	3.3	3.2	0.0	0.2	100.0%	-5.0
18209	AT1G78930.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr1:29682994-29685650 REVERSE   Aliases: YUP8H12R.46, YUP8H12R_46	2.9	2.9	0.0	0.2	100.0%	-5.2
18210	AT4G30550.1   glutamine amidotransferase class-I domain-containing protein, similar to defense-related protein (Brassica carinata) GI:14009290, component of aniline dioxygenase (GMP synthase like protein) - Acinetobacter sp.,PID:d1013698; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr4:14925416-14926864 FORWARD   Aliases: F17I23.110, F17I23_110	8.3	8.4	-0.1	-0.2	100.0%	-5.0
18211	AT3G07330.1   Symbol: ATCSLC06   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	2.9	2.9	-0.0	-0.2	100.0%	-5.2
18212	AT2G29800.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:12730435-12731679 REVERSE   Aliases: T27A16.10, T27A16_10	3.2	3.2	0.0	0.2	100.0%	-5.5
18213	AT5G64270.1   splicing factor, putative, similar to splicing factor 3B subunit 1 (Spliceosome associated protein 155) (SAP 155) (SF3b155) (Pre-mRNA splicing factor SF3b 155 kDa subunit) (146 kDa nuclear protein) SP:O57683 from (Xenopus laevis)   chr5:25723885-25728151 FORWARD   Aliases: MSJ1.11, MSJ1_11	5.7	5.6	0.1	0.2	100.0%	-4.8
18214	AT1G68980.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:25936686-25938545 FORWARD   Aliases: T6L1.16, T6L1_16	4.4	4.4	0.0	0.2	100.0%	-5.0
18215	AT5G06710.2   Symbol: HAT14   homeobox-leucine zipper protein 14 (HAT14) / HD-ZIP protein 14, contains similarity to homeodomain leucine zipper protein   chr5:2068083-2070357 REVERSE   Aliases: HD ZIP PROTEIN 14, MPH15.6, MPH15_6	3.5	3.4	0.0	0.2	100.0%	-5.2
18216	AT2G18650.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 finger protein RHX1a (Arabidopsis thaliana) GI:3790591; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr2:8093942-8095213 REVERSE   Aliases: MSF3.3, MSF3_3	2.9	2.8	0.0	0.2	100.0%	-5.1
18217	AT2G35330.1   zinc finger (C3HC4-type RING finger) protein-related, contains weak hit to Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger); weak similarity to RING finger protein 8 (Swiss-Prot:O76064) (Homo sapiens)   chr2:14876068-14879019 FORWARD   Aliases: T32F12.29, T32F12_29	4.9	5.0	-0.1	-0.2	100.0%	-4.8
18218	AT5G62090.2   expressed protein   chr5:24952189-24956335 REVERSE   Aliases: MTG10.12, MTG10_12	3.5	3.5	-0.0	-0.2	100.0%	-5.2
18219	AT1G79170.1   hypothetical protein   chr1:29787166-29787515 FORWARD   Aliases: YUP8H12R.22, YUP8H12R_22	5.1	5.2	-0.1	-0.2	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18220	AT3G07170.1   sterile alpha motif (SAM) domain-containing protein, contains Pfam profile PF00536: SAM domain (Sterile alpha motif)   chr3:2280207-2282344 FORWARD   Aliases: T1B9.17	8.4	8.4	-0.1	-0.2	100.0%	-4.9
18221	AT1G47380.1   protein phosphatase 2C-related / PP2C-related, contains similarity to protein phosphatase 2C GB:AAD25933 GI:4587992 from (Arabidopsis thaliana)   chr1:17374977-17378515 REVERSE   Aliases: T3F24.2, T3F24_2	5.0	5.1	-0.1	-0.2	100.0%	-4.7
18222	AT5G01270.1   Symbol: CPL2   similar to double-stranded RNA-binding domain (DsRBD)-containing protein [Arabidopsis thaliana] (TAIR:At4g21670.1); similar to OSJNBa0074L08.12 [Oryza sativa (japonica cultivar-group)] (GB:XP_473264.1); contains InterPro domain NLI interacting factor (InterPro:IPR004274); contains InterPro domain Double-stranded RNA binding (DsRBD) domain (InterPro:IPR001159)   chr5:107741-112294 REVERSE   Aliases: F7J8.250, F7J8_250	4.3	4.4	-0.1	-0.2	100.0%	-4.9
18223	AT4G08040.1   Symbol: ACS11   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to ACC synthase from Malus sylvestris (SP:P37821), Solanum tuberosum (GI:520914)	2.9	2.8	0.0	0.2	100.0%	-4.8
18224	AT2G03500.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:1059707-1062407 FORWARD   Aliases: T4M8.7, T4M8_7	2.9	2.9	0.0	0.2	100.0%	-5.1
18225	AT5G03240.3   Symbol: UBQ3   similar to polyubiquitin (UBQ10) (SEN3) [Arabidopsis thaliana] (TAIR:At4g05320.2); similar to polyubiquitin (UBQ10) (SEN3) [Arabidopsis thaliana] (TAIR:At4g05320.4); similar to polyubiquitin (UBQ10) (SEN3) [Arabidopsis thaliana] (TAIR:At4g05320.3); similar to polyubiquitin (UBQ10) (SEN3) [Arabidopsis thaliana] (TAIR:At4g05320.1); similar to polyubiquitin (UBQ14) [Arabidopsis thaliana] (TAIR:At4g02890.3); similar to polyubiquitin [Oryza sativa (japonica cultivar-group)] (GB:BAD45891.1); similar to hexaubiquitin protein [Helianthus annuus] (GB:CAA40325.1); similar to PREDICTED OJ9003_G05.28 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_506723.1); similar to tetraubiquitin [Avena fatua] (GB:CAA49200.1); similar to pentameric polyubiquitin [Nicotiana tabacum] (GB:CAA54603.1); contains InterPro domain Ubiquitin domain (InterPro:IPR000626)   chr5:771724-773514 REVERSE   Aliases: F15A17.270, F15A17_270, POLYUBIQUITIN 3, POLYUBIQUITIN 3 PROTEIN	5.6	5.7	-0.1	-0.2	100.0%	-4.9
18226	AT1G30230.1   elongation factor 1-beta / EF-1-beta, identical to SP:P48006 Elongation factor 1-beta (EF-1-beta) {Arabidopsis thaliana}	9.8	9.9	-0.1	-0.2	100.0%	-4.7
18227	AT2G18110.1   elongation factor 1-beta, putative / EF-1-beta, putative, nearly identical to eEF-1beta (Arabidopsis thaliana) GI:398606	9.8	9.9	-0.1	-0.2	100.0%	-4.7
18228	AT2G21320.1   zinc finger (B-box type) family protein   chr2:9133344-9134924 FORWARD   Aliases: F3K23.8, F3K23_8	6.8	6.7	0.1	0.2	100.0%	-4.4
18229	AT5G42420.1   transporter-related, low similarity to phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275, glucose-6-phosphate/phosphate-translocator precursor (Solanum tuberosum) GI:2997593   chr5:16985894-16987657 FORWARD   Aliases: MDH9.11, MDH9_11	6.0	6.0	0.0	0.2	100.0%	-5.1
18230	AT1G69640.1   acid phosphatase, putative, similar to GI:5360721 from (Lupinus albus)   chr1:26197322-26199319 REVERSE   Aliases: F24J1.22	3.7	3.7	0.1	0.2	100.0%	-5.3
18231	AT5G51360.1   hypothetical protein   chr5:20889144-20889503 FORWARD   Aliases: MFG13.7, MFG13_7	2.4	2.4	-0.0	-0.2	100.0%	-5.4
18232	AT1G64030.1   serpin family protein / serine protease inhibitor family protein, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311, serpin (Triticum aestivum) GI:871551; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr1:23756536-23758011 REVERSE   Aliases: F22C12.22, F22C12_22	3.3	3.2	0.0	0.2	100.0%	-5.5
18233	AT2G27120.1   DNA-directed DNA polymerase epsilon catalytic subunit, putative, similar to SP:Q07864 DNA polymerase epsilon, catalytic subunit A (EC 2.7.7.7) (DNA polymerase II subunit A) {Homo sapiens}; contains Pfam profiles: PF03175 DNA polymerase type B, organellar and viral, PF00136 DNA polymerase family B, PF03104 DNA polymerase family B, exonuclease domain   chr2:11588301-11601424 FORWARD   Aliases: T20P8.17, T20P8_17	2.6	2.6	-0.0	-0.2	100.0%	-5.6
18234	AT1G12730.2   cell division cycle protein-related, contains 10 transmembrane domains; similar to PIG-U (GI:27372215) (Rattus norvegicus); similar to Cell division cycle protein 91-like 1 (CDC91-like 1 protein) (PIG-U) (Swiss-Prot:Q9H490) (Homo sapiens)   chr1:4334613-4337771 FORWARD   Aliases: T12C24.26, T12C24_26	3.3	3.4	-0.0	-0.2	100.0%	-5.2
18235	AT1G61040.1   plus-3 domain-containing protein, contains Pfam profile PF03126: Plus-3 domain   chr1:22486872-22489634 FORWARD   Aliases: T7P1.17, T7P1_17	6.2	6.1	0.1	0.2	100.0%	-5.0
18236	AT3G58060.1   cation efflux family protein / metal tolerance protein, putative (MTPc3), member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr3:21508755-21510653 REVERSE   Aliases: T10K17.270	3.2	3.1	0.1	0.2	100.0%	-4.3
18237	AT3G19890.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.6	-0.0	-0.2	100.0%	-5.8
18238	AT4G28710.1   Symbol: XIH   myosin heavy chain, putative, similar to myosin (Arabidopsis thaliana) gi:499047:emb:CAA84066.   chr4:14172004-14178054 FORWARD   Aliases: ATXIH, F16A16.180, F16A16_180	3.8	3.9	-0.1	-0.2	100.0%	-4.8
18239	AT2G42500.2   Symbol: PP2A 4	6.5	6.2	0.2	0.2	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18240	AT3G58500.1   Symbol: PP2A 3	6.5	6.2	0.2	0.2	100.0%	-4.4
18241	AT5G42690.1   expressed protein, contains Pfam profile PF04784: Protein of unknown function, DUF547; expression supported by MPSS   chr5:17133858-17136351 REVERSE   Aliases: MJB21.6, MJB21_6	3.7	3.8	-0.1	-0.2	100.0%	-4.9
18242	AT5G37040.1   F-box family protein, contains Pfam profile: PF00646 F-box domain   chr5:14656365-14657164 FORWARD   Aliases: MJG14.2, MJG14_2	3.8	3.8	-0.1	-0.2	100.0%	-4.9
18243	AT4G33430.1   Symbol: BAK1   brassinosteroid insensitive 1-associated receptor kinase 1 (BAK1) / somatic embryogenesis receptor-like kinase 3 (SERK3), identical to SP:Q94F62 BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1 precursor (EC 2.7.1.37) (BR1-associated receptor kinase 1) (Somatic embryogenesis receptor-like kinase 3) {Arabidopsis thaliana}; contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain; identical to cDNA somatic embryogenesis receptor-like kinase 3 (SERK3) GI:14573458	6.3	6.4	-0.1	-0.2	100.0%	-4.7
18244	AT1G65510.1   expressed protein   chr1:24363116-24363532 FORWARD   Aliases: F5I14.24, F5I14_24	3.0	3.0	-0.1	-0.2	100.0%	-4.7
18245	AT4G33700.1   CBS domain-containing protein, contains Pfam profiles PF00571: CBS domain, PF01595: Domain of unknown function   chr4:16176403-16179482 REVERSE   Aliases: T16L1.190, T16L1_190	8.0	8.1	-0.0	-0.2	100.0%	-5.1
18246	AT3G42830.1   ring-box protein Roc1/Rbx1/Hrt1, putative, E3 ubiquitin ligase, SCF complex subunit; contains similarity to ring-box protein 1 RBX1 GI:4769004 from (Homo sapiens)   chr3:14940702-14941666 REVERSE   Aliases: T21C14.50	3.0	3.0	0.0	0.2	100.0%	-5.4
18247	AT5G63800.1   Symbol: BGAL6   glycosyl hydrolase family 35 protein, similar to beta-galactosidase GI:7939621 from (Lycopersicon esculentum); contains Pfam profile PF01301: Glycosyl hydrolases family 35   chr5:25547359-25553062 FORWARD   Aliases: MBK5.28, MBK5_28	3.6	3.6	0.0	0.2	100.0%	-4.7
18248	AT5G19240.1   expressed protein   chr5:6470131-6471064 FORWARD   Aliases: T24G5.140, T24G5_140	2.7	2.8	-0.1	-0.2	100.0%	-4.4
18249	AT3G16270.1   expressed protein, gene model   chr3:5513331-5516942 FORWARD   Aliases: MYA6.8	2.7	2.8	-0.0	-0.2	100.0%	-5.1
18250	AT1G11340.1   S-locus lectin protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:3814116-3817420 REVERSE   Aliases: T28P6.1, T28P6_1	3.0	3.0	0.0	0.2	100.0%	-5.3
18251	AT5G47540.1   Mo25 family protein, similar to MO25 protein (early mouse development protein family) (Mouse) SWISS-PROT:Q06138   chr5:19300492-19302554 REVERSE   Aliases: MNJ7.13, MNJ7_13	7.1	7.0	0.1	0.2	100.0%	-4.6
18252	AT5G52960.1   expressed protein, similar to unknown protein (pir :S77140)   chr5:21494372-21495662 FORWARD   Aliases: MNB8.2, MNB8_2	4.8	4.8	-0.1	-0.2	100.0%	-4.4
18253	AT1G15420.1   expressed protein   chr1:5301608-5303372 REVERSE   Aliases: None	6.0	6.0	-0.1	-0.2	100.0%	-4.6
18254	AT2G36810.1   expressed protein   chr2:15432818-15443960 REVERSE   Aliases: F13K3.21, F13K3_21	3.3	3.4	-0.1	-0.2	100.0%	-4.8
18255	AT5G60020.1   laccase, putative / diphenol oxidase, putative, similar to laccase LAC2-4, Liriodendron tulipifera, EMBL:LTU73106 (GI:1621467)   chr5:24185222-24187688 FORWARD   Aliases: MMN10.20, MMN10_20	3.7	3.8	-0.1	-0.2	100.0%	-4.5
18256	AT3G44970.1   cytochrome P450 family protein, similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum}; contains Pfam profile: PF00067 cytochrome P450   chr3:16443428-16445833 FORWARD   Aliases: F14D17.40	2.4	2.3	0.0	0.2	100.0%	-5.7
18257	AT1G01410.1   hypothetical protein   chr1:153113-154198 FORWARD   Aliases: F6F3.21, F6F3_21	2.8	2.8	-0.0	-0.2	100.0%	-5.6
18258	AT5G23480.1   expressed protein   chr5:7918338-7919276 FORWARD   Aliases: K19M13.11, K19M13_11	2.9	3.0	-0.0	-0.2	100.0%	-5.5
18259	AT1G28080.1   expressed protein   chr1:9789813-9791533 FORWARD   Aliases: F13K9.18, F13K9_18	3.4	3.5	-0.0	-0.2	100.0%	-5.1
18260	AT4G00430.2   Symbol: TMP C   plasma membrane intrinsic protein, putative, identical to transmembrane protein GI:535780 from (Arabidopsis thaliana); very strong similarity to SP:Q08733 Plasma membrane intrinsic protein 1C (Transmembrane protein B) (TMP-B) {Arabidopsis thaliana}; contains Pfam profile PF00230: Major intrinsic protein;   chr4:185854-187617 REVERSE   Aliases: A_IG005I10.2, A_IG005I10_2, F5I10.2, F5I10_2, PIP1;4, PIP1E	4.9	5.1	-0.1	-0.2	100.0%	-4.2
18261	AT5G12110.1   elongation factor 1B alpha-subunit 1 (eEF1Balpha1), identical to elongation factor 1B alpha-subunit (Arabidopsis thaliana) GI:6686819   chr5:3914482-3915936 FORWARD   Aliases: MXC9.7, MXC9_7	7.6	7.6	0.0	0.2	100.0%	-5.0
18262	AT3G42140.1   expressed protein   chr3:14313046-14314004 REVERSE   Aliases: T27B3.10	3.0	3.0	0.0	0.2	100.0%	-5.5
18263	AT1G19010.2   expressed protein   chr1:6565774-6567515 FORWARD   Aliases: F14D16.16, F14D16_16	4.4	4.4	-0.0	-0.2	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18264	AT1G28360.1   Symbol: ATERF12/ERF12   encodes a member of the ERF (ethylene response factor) subfamily B-1 of ERF/AP2 transcription factor family (ERF12). The protein contains one AP2 domain. There are 15 members in this subfamily including ATERF-3, ATERF-4, ATERF-7, and leafy petiole.   chr1:9951835-9952726 FORWARD   Aliases: ATERF12, ERF12, F3M18.21, F3M18_21	2.8	2.8	0.0	0.2	100.0%	-5.2
18265	AT1G08940.1   phosphoglycerate/bisphosphoglycerate mutase family protein, contains Pfam profile PF00300: phosphoglycerate mutase family   chr1:2877695-2879172 FORWARD   Aliases: F7G19.18, F7G19_18	7.8	7.9	-0.1	-0.2	100.0%	-5.2
18266	AT1G35570.1   hypothetical protein   chr1:13119597-13120417 REVERSE   Aliases: F15O4.34	3.4	3.4	0.0	0.2	100.0%	-5.5
18267	AT4G24600.1   hypothetical protein   chr4:12699996-12700488 FORWARD   Aliases: F22K18.200, F22K18_200	3.0	3.0	0.0	0.2	100.0%	-5.5
18268	AT1G16210.1   expressed protein, ESTs gb:T04357 and gb:AA595092 come from this gene   chr1:5546127-5547546 REVERSE   Aliases: F3O9.2, F3O9_2	10.0	9.9	0.1	0.2	100.0%	-5.0
18269	AT4G31460.1   ribosomal protein L28 family protein, ribosomal protein YmL14 precursor, mitochondrial - Saccharomyces cerevisiae, PIR2:S50921   chr4:15259475-15261197 REVERSE   Aliases: F3L17.30, F3L17_30	6.2	6.1	0.1	0.2	100.0%	-4.8
18270	AT1G11220.1   expressed protein, contains similarity to cotton fiber expressed protein 1 (Gossypium hirsutum) gi:3264828:gb:AAC33276   chr1:3759867-3761165 REVERSE   Aliases: T28P6.12, T28P6_12	2.7	2.7	0.0	0.2	100.0%	-5.5
18271	AT3G07420.1   Symbol: NS2   asparaginyl-tRNA synthetase 2, cytoplasmic / asparagine-tRNA ligase 2 (SYNC2), nearly identical to SP:Q9SW95; HMM hit: tRNA synthetases class II   chr3:2373983-2376748 REVERSE   Aliases: ATNS2, F21O3.13, SYNC2, SYNC2_ARATH	3.9	4.0	-0.1	-0.2	100.0%	-4.4
18272	AT5G04110.1   DNA topoisomerase II family protein, similar to DNA topoisomerase II subunit B (Thermotoga maritima) GI:1622792; contains Pfam profiles PF00204: DNA topoisomerase II (N-terminal region), PF00249: Myb-like DNA-binding domain	3.8	3.7	0.0	0.2	100.0%	-5.8
18273	AT3G43600.1   Symbol: AAO2   aldehyde oxidase, putative, identical to gi: 3172025; identical to cDNA putative aldehyde oxidase (AO3) mRNA, partial cds GI:2792303   chr3:15523595-15528494 REVERSE   Aliases: ALDEHYDE OXIDASE 2, F22J12.40	5.3	5.4	-0.1	-0.2	100.0%	-5.0
18274	AT4G21050.1   Dof-type zinc finger domain-containing protein, PBF protein, Triticum aestivum, EMBL:AJ012284   chr4:11238452-11239084 FORWARD   Aliases: T13K14.210, T13K14_210	2.5	2.5	0.0	0.2	100.0%	-5.7
18275	AT1G76890.2   Symbol: GT2   trihelix DNA-binding protein / GT-2 factor (GT2), identical to GT2 factor (Arabidopsis thaliana) GI:416490, GI:2664202 (DNA binding factor GT-2 from Arabidopsis)	3.7	3.7	0.1	0.2	100.0%	-4.2
18276	AT3G45690.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:16787253-16789135 FORWARD   Aliases: T6D9.20	2.4	2.4	-0.0	-0.2	100.0%	-5.4
18277	AT4G03080.1   kelch repeat-containing serine/threonine phosphoesterase family protein, contains Pfam profiles: PF00149 calcineurin-like phosphoesterase, PF01344 kelch motif   chr4:1359349-1365451 REVERSE   Aliases: T4I9.4, T4I9_4	5.6	5.7	-0.1	-0.2	100.0%	-4.9
18278	AT5G37280.1   zinc finger (C3HC4-type RING finger) family protein, low similarity to RING-H2 finger protein RHA1b (Arabidopsis thaliana) GI:3790567; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:14778505-14779155 REVERSE   Aliases: MNJ8.7, MNJ8_7	3.0	3.0	-0.0	-0.2	100.0%	-5.7
18279	AT3G45290.1   Symbol: MLO3   seven transmembrane MLO family protein / MLO-like protein 3 (MLO3), membrane protein Mlo3 (Arabidopsis thaliana) gi:14091576:gb:AAK53796; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr3:16628529-16632355 FORWARD   Aliases: F18N11.50	2.4	2.4	0.0	0.2	100.0%	-5.6
18280	AT3G19980.1   Symbol: ATFYPP3   serine/threonine protein phosphatase (STPP), identical to serine/threonine protein phosphatase (Arabidopsis thaliana) GI:14582206; very similar to serine/threonine protein phosphatase GB:Z47076 GI:1143510 (Malus domestica); contains Pfam profile PF00149: Ser/Thr protein phosphatase   chr3:6961831-6965114 FORWARD   Aliases: EMB2736, EMBRYO DEFECTIVE 2736, MZE19.9, SERINE/THREONINE PROTEIN PHOSPHATASE, STPP	6.6	6.5	0.1	0.2	100.0%	-5.0
18281	AT1G70140.1   Symbol: ATFH8   Encodes a group I formin. Binds to F-actin barbed ends. Has severing actin filaments activity. Binds profilin. Involved in the initiation and tip growth of root hairs through regulation of actin cytoskeleton.   chr1:26416351-26418893 REVERSE   Aliases: ATFH8, F20P5.14, F20P5_14, FORMIN 8	6.7	6.6	0.1	0.2	100.0%	-4.8
18282	AT3G13100.1   Symbol: ATMRP7	3.6	3.7	-0.1	-0.2	100.0%	-4.5
18283	AT2G31760.1   zinc finger protein-related, contains low similarity to zinc finger proteins and Pfam PF01485: IBR domain   chr2:13515570-13517467 FORWARD   Aliases: F20M17.20, F20M17_20	2.6	2.6	-0.0	-0.2	100.0%	-6.0
18284	AT3G29570.1   expressed protein   chr3:11366285-11367268 REVERSE   Aliases: MWE13.1	2.7	2.7	-0.0	-0.2	100.0%	-5.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18285	AT2G39560.1   expressed protein   chr2:16511924-16513086 REVERSE   Aliases: F12L6.22, F12L6_22	3.1	3.1	0.0	0.1	100.0%	-5.8
18286	AT1G51510.1   RNA-binding protein, putative, similar to RNA-binding protein 8 (Ribonucleoprotein RBM8) SP:Q9Y5S9 from (Homo sapiens), RNA-binding protein Y14 (Xenopus laevis) GI:11034807; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:19106475-19108518 REVERSE   Aliases: F5D21.5, F5D21_5	7.4	7.4	0.1	0.1	100.0%	-4.8
18287	AT1G78680.1   gamma-glutamyl hydrolase (GGH1) / gamma-Glu-X carboxypeptidase / conjugase, identical to SP:O65355 Gamma-glutamyl hydrolase precursor (EC 3.4.19.9) (Gamma-Glu-X carboxypeptidase) (Conjugase) (GH) {Arabidopsis thaliana}   chr1:29598758-29601163 FORWARD   Aliases: F9K20.28, F9K20_28	5.3	5.3	-0.1	-0.1	100.0%	-4.6
18288	AT5G37900.1   seven in absentia (SINA) family protein, similar to SIAH1 protein (Brassica napus var. napus) GI:7657876; contains Pfam profile PF03145: Seven in absentia protein family   chr5:15111133-15112032 REVERSE   Aliases: K18L3.10, K18L3_10	2.1	2.1	-0.0	-0.1	100.0%	-6.1
18289	AT2G41720.2   Symbol: EMB2654   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:17410681-17413800 REVERSE   Aliases: EMB2654, EMBRYO DEFECTIVE 2654, T11A7.18, T11A7_18	6.8	6.9	-0.1	-0.1	100.0%	-4.4
18290	AT1G56220.3   dormancy/auxin associated family protein, similar to Auxin-repressed 12.5 kDa protein (Swiss-Prot:Q05349) (Fragaria ananassa); similar to auxin-repressed protein (GI:927034) (Fragaria x ananassa); similar to dormancy-associated protein (GI:2605887) (Pisum sativum)	5.9	6.0	-0.1	-0.1	100.0%	-4.8
18291	AT4G26000.1   KH domain-containing protein, single-stranded nucleic acid-binding protein CBP - mouse, PIR2:S78515   chr4:13197255-13199837 FORWARD   Aliases: F20B18.110, F20B18_110	2.9	3.0	-0.0	-0.1	100.0%	-5.5
18292	AT1G19880.1   regulator of chromosome condensation (RCC1) family protein, low similarity to UVB-resistance protein UVR8 (Arabidopsis thaliana) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)   chr1:6900406-6904060 REVERSE   Aliases: F6F9.7, F6F9_7	4.3	4.4	-0.0	-0.1	100.0%	-4.7
18293	AT3G20800.1   rcd1-like cell differentiation protein, putative, similar to protein involved in sexual development (Schizosaccharomyces pombe) GI:1620896; contains Pfam profile PF04078: Cell differentiation family, Rcd1-like   chr3:7271143-7273950 REVERSE   Aliases: MOE17.9	5.7	5.8	-0.1	-0.1	100.0%	-4.9
18294	AT4G16460.1   expressed protein   chr4:9285651-9286168 FORWARD   Aliases: DL4255W, FCAALL.371	2.7	2.7	0.0	0.1	100.0%	-5.7
18295	AT4G37445.1   expressed protein   chr4:17604088-17604926 REVERSE   Aliases: None	3.1	3.0	0.0	0.1	100.0%	-4.6
18296	AT5G44030.1   Symbol: CESA4   cellulose synthase, catalytic subunit (IRX5), nearly identical to cellulose synthase (Arabidopsis thaliana) GI:27462651; contains Pfam profile PF03552: Cellulose synthase   chr5:17731872-17737318 FORWARD   Aliases: CELLULASE SYNTHASE 4, IRREGULAR XYLEM5, IRX5, MRH10.14, MRH10_14	3.0	2.9	0.1	0.1	100.0%	-4.1
18297	AT1G23320.1   alliinase family protein, contains Pfam profiles: PF04864 alliinase C-terminal domain, PF04863 alliinase EGF-like domain   chr1:8273412-8275339 REVERSE   Aliases: F26F24.17, F26F24_17	2.8	2.8	0.0	0.1	100.0%	-5.7
18298	AT3G02680.1   expressed protein   chr3:578335-578920 FORWARD   Aliases: F16B3.31, F16B3_31	3.6	3.6	0.1	0.1	100.0%	-5.0
18299	AT5G10230.1   Symbol: ANN7   annexin 7 (ANN7), nearly identical to calcium-binding protein annexin 7 (Arabidopsis thaliana) GI:12667522   chr5:3209541-3211424 REVERSE   Aliases: F18D22.4, annexin 7	2.6	2.6	0.0	0.1	100.0%	-5.1
18300	AT3G50180.1   expressed protein   chr3:18615926-18618145 REVERSE   Aliases: F11C1.20	2.5	2.6	-0.0	-0.1	100.0%	-5.6
18301	AT4G11290.1   peroxidase, putative, identical to peroxidase ATP19a (Arabidopsis thaliana) gi:1546692:emb:CAA67337   chr4:6869959-6871657 FORWARD   Aliases: F8L21.80, F8L21_80	1.9	2.0	-0.1	-0.1	100.0%	-4.6
18302	AT3G50280.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus, PIR:T10717 (gi:2239091); contains Pfam transferase family domain PF002458   chr3:18648836-18650167 FORWARD   Aliases: F11C1.120	3.4	3.4	0.0	0.1	100.0%	-5.1
18303	AT1G54730.3   sugar transporter, putative, similar to ERD6 protein (Arabidopsis thaliana) GI:3123712, sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:20428077-20433790 FORWARD   Aliases: T22H22.15, T22H22_15	3.4	3.4	0.0	0.1	100.0%	-4.8
18304	AT5G07100.2   Symbol: WRKY26	3.2	3.1	0.1	0.1	100.0%	-5.0
18305	AT2G44010.1   expressed protein   chr2:18223760-18224514 FORWARD   Aliases: F6E13.14	3.5	3.6	-0.2	-0.1	100.0%	-4.4
18306	AT4G01440.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr4:596399-598718 FORWARD   Aliases: F3D13.3, F3D13_3	4.3	4.3	-0.1	-0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18307	AT2G33760.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:14282876-14284627 FORWARD   Aliases: T1B8.7, T1B8_7	3.7	3.8	-0.0	-0.1	100.0%	-5.0
18308	AT5G17450.2   heavy-metal-associated domain-containing protein / copper chaperone (CCH)-related, similar to copper homeostasis factor (Arabidopsis thaliana)(GI:3168840), and farnesylated proteins GMFP7 (Glycine max)(GI:4097573), ATFP7 (GI:4097555), and ATFP6 (GI:4097553); contains heavy-metal-associated domain PF00403   chr5:5755350-5756880 FORWARD   Aliases: K3M16.20, K3M16_20	2.8	2.8	-0.1	-0.1	100.0%	-5.0
18309	AT3G10750.1   hypothetical protein   chr3:3366932-3368274 FORWARD   Aliases: T7M13.17	3.1	3.0	0.0	0.1	100.0%	-5.4
18310	AT1G77570.1   similar to heat shock transcription factor family protein [Arabidopsis thaliana] (TAIR:At4g13980.1); similar to heat shock factor protein hsf8-related [Glycine max] (GB:AAS15800.1); contains InterPro domain Heat shock factor (HSF)-type DNA-binding domain (InterPro:IPR000232); contains InterPro domain HSF/ETS DNA-binding (InterPro:IPR002341)   chr1:29148244-29148897 FORWARD   Aliases: T5M16.16, T5M16_16	3.5	3.5	0.0	0.1	100.0%	-5.4
18311	AT3G21270.1   Symbol: ADOF2   Dof-type zinc finger domain-containing protein (ADOF2), identical to Dof zinc finger protein ADOF2 GI:3608263 from (Arabidopsis thaliana); identical to cDNA adof2 mRNA for Dof zinc finger protein GI:3608262; contains Pfam profile PF02701: Dof domain, zinc finger   chr3:7474685-7475762 FORWARD   Aliases: MXL8.14	6.0	6.0	0.1	0.1	100.0%	-5.0
18312	AT1G50560.1   Symbol: CYP705A25   cytochrome P450, putative, similar to CYTOCHROME P450 93A3 (P450 CP5) (SP:O81973) (Glycine max)   chr1:18727875-18731215 FORWARD   Aliases: F11F12.12, F11F12_12	2.5	2.6	-0.1	-0.1	100.0%	-4.3
18313	AT2G35730.1   heavy-metal-associated domain-containing protein, contains PS1047 Heavy-metal-associated domain contains Pfam profile PF00403: Heavy-metal-associated domain   chr2:15027579-15028635 REVERSE   Aliases: T20F21.3	2.4	2.5	-0.1	-0.1	100.0%	-4.4
18314	AT2G20270.1   glutaredoxin family protein, contains glutaredoxin domain, Pfam:PF00462   chr2:8744786-8746741 REVERSE   Aliases: F11A3.18, F11A3_18	7.6	7.7	-0.1	-0.1	100.0%	-4.5
18315	AT1G33810.1   expressed protein   chr1:12265050-12266827 FORWARD   Aliases: F14M2.27	9.2	9.3	-0.1	-0.1	100.0%	-4.6
18316	AT4G18330.2   eukaryotic translation initiation factor 2 subunit 3, putative / eIF2S3, putative / eIF-2-gamma, putative, similar to SP:Q09130 Eukaryotic translation initiation factor 2 gamma subunit (eIF-2-gamma) {Schizosaccharomyces pombe}; contains Pfam profile PF00009: Elongation factor Tu GTP binding domain; isoform predicted to contain a TG non-consensus acceptor splice site.   chr4:10126590-10128745 FORWARD   Aliases: T9A21.180, T9A21_180	3.5	3.4	0.0	0.1	100.0%	-5.2
18317	AT1G74780.1   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr1:28099476-28101845 FORWARD   Aliases: F25A4.25, F25A4_25	6.3	6.3	0.1	0.1	100.0%	-5.0
18318	AT2G42250.1   Symbol: CYP712A1   cytochrome P450 family protein, similar to cytochrome P450 93A1 (SP:Q42798) (Glycine max)   chr2:17607153-17608927 REVERSE   Aliases: T24P15.16, T24P15_16	3.3	3.3	-0.0	-0.1	100.0%	-5.5
18319	ATCG01120.1   Symbol: RPS15   encodes a chloroplast ribosomal protein S15, a constituent of the small subunit of the ribosomal complex   chrC:123296-123562 REVERSE   Aliases: RPS15	6.4	6.6	-0.2	-0.1	100.0%	-4.6
18320	AT5G60760.1   2-phosphoglycerate kinase-related, contains weak similarity to 2-phosphoglycerate kinase (GI:467751) (Methanothermus fervidus)   chr5:24455497-24459513 FORWARD   Aliases: MAE1.1, MAE1_1	4.7	4.6	0.1	0.1	100.0%	-4.7
18321	AT5G22810.1   GDSL-motif lipase, putative, similar to EXL3 (GP:15054386) (Arabidopsis thaliana)   chr5:7621571-7623370 FORWARD   Aliases: MRN17.4, MRN17_4	2.6	2.6	0.0	0.1	100.0%	-5.6
18322	AT2G02300.1   Symbol: ATPP2 B5   F-box family protein / SKP1 interacting partner 3-related, contains similarity to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)	2.7	2.6	0.0	0.1	100.0%	-5.0
18323	AT5G17880.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:5908876-5913101 REVERSE   Aliases: MPI7.20, MPI7_20	3.8	3.9	-0.1	-0.1	100.0%	-4.2
18324	AT5G67190.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr5:26826361-26826915 REVERSE   Aliases: K21H1.15, K21H1_15	4.6	4.7	-0.2	-0.1	100.0%	-4.6
18325	AT4G05270.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:2694937-2695326 FORWARD   Aliases: C17L7.190, C17L7_190	2.4	2.4	-0.0	-0.1	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18326	AT1G14330.1   kelch repeat-containing F-box family protein, contains Pfam profile PF01344: Kelch motif; contains weak Pfam PF00646: F-box domain; weak similarity to Kelch-like protein 1 (Swiss-Prot:Q9NR64) (Homo sapiens)   chr1:4890113-4892246 REVERSE   Aliases: F14L17.10, F14L17_10	5.1	5.1	0.0	0.1	100.0%	-5.2
18327	NA	8.3	8.2	0.2	0.1	100.0%	-4.7
18328	AT2G24950.1   expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr2:10620184-10622642 FORWARD   Aliases: F27C12.13, F27C12_13	3.8	3.9	-0.0	-0.1	100.0%	-5.0
18329	AT3G58390.1   eukaryotic release factor 1 family protein / eRF1 family protein, contains Pfam profiles: PF03463 eRF1 domain 1, PF03464 eRF1 domain 2, PF03465 eRF1 domain 3   chr3:21611007-21612194 REVERSE   Aliases: F9D24.300	2.7	2.7	-0.0	-0.1	100.0%	-5.5
18330	AT2G27160.1   expressed protein   chr2:11614723-11615281 REVERSE   Aliases: F20F1.3, F20F1_3	2.4	2.5	-0.0	-0.1	100.0%	-5.5
18331	AT3G26350.1   expressed protein, ; expression supported by MPSS   chr3:9654897-9655967 REVERSE   Aliases: F20C19.7	2.7	2.7	0.0	0.1	100.0%	-5.2
18332	AT1G17455.1   expressed protein   chr1:5997173-5998468 FORWARD   Aliases: None	5.8	5.7	0.1	0.1	100.0%	-5.0
18333	AT2G37870.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr2:15866317-15866985 FORWARD   Aliases: T8P21.22, T8P21_22	10.3	10.2	0.1	0.1	100.0%	-4.7
18334	AT2G42300.2   similar to basic helix-loop-helix (bHLH) family protein [Arabidopsis thaliana] (TAIR:At3g57800.2); similar to bHLH transcription factor GBOF-1 [Tulipa gesneriana] (GB:AAD56411.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_469986.1)   chr2:17628235-17631916 FORWARD   Aliases: MHK10.2, MHK10_2	4.8	4.8	0.1	0.1	100.0%	-4.7
18335	AT5G45480.1   expressed protein, contains Pfam domain, PF04578: Protein of unknown function, DUF594   chr5:18443331-18446317 REVERSE   Aliases: MFC19.15, MFC19_15	2.8	2.8	0.1	0.1	100.0%	-4.4
18336	AT5G65410.1   zinc finger homeobox family protein / ZF-HD homeobox family protein, similar to hypothetical proteins (GP:4220524)(GP:3184285:)(Arabidopsis); ZP-HD homeobox family protein GP:13374061 (Flaveria bidentis);GP:5091602 {Oryza sativa}   chr5:26153320-26154409 FORWARD   Aliases: MNA5.14, MNA5_14	3.0	2.9	0.0	0.1	100.0%	-5.2
18337	AT2G39970.1   peroxisomal membrane protein (PMP36), identical to 36kDa-peroxisomal membrane protein (PMP36) GI:15146342 from (Arabidopsis thaliana)   chr2:16690910-16693740 REVERSE   Aliases: T28M21.13, T28M21_13	8.4	8.3	0.1	0.1	100.0%	-4.9
18338	AT3G45410.1   lectin protein kinase family protein, contains Pfam profiles: PF00069 protein kinase domain, PF00138 legume lectins alpha domain, PF00139 legume lectins beta domain   chr3:16664884-16666998 REVERSE   Aliases: F18N11.170	3.6	3.7	-0.1	-0.1	100.0%	-4.2
18339	AT5G24290.2   integral membrane family protein, contains Pfam domain PF01988: Integral membrane protein   chr5:8263135-8265658 REVERSE   Aliases: MOP9.11, MOP9_11	3.8	3.8	0.0	0.1	100.0%	-4.9
18340	AT1G05450.2   protease inhibitor/seed storage/lipid transfer protein (LTP)-related, similar to geranyl diphosphate synthase large subunit (Mentha x piperita) GI:6449052   chr1:1599955-1601624 FORWARD   Aliases: T25N20.10, T25N20_10	2.7	2.7	-0.0	-0.1	100.0%	-5.6
18341	AT1G76220.1   hypothetical protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr1:28602424-28603194 REVERSE   Aliases: T23E18.15, T23E18_15	3.0	3.0	0.0	0.1	100.0%	-5.3
18342	AT3G27370.1   expressed protein   chr3:10131661-10131993 REVERSE   Aliases: K1G2.16	3.0	3.0	-0.0	-0.1	100.0%	-5.2
18343	ATCG00500.1   Symbol: ACCD   carboxytransferase beta subunit   chrC:57075-58541 FORWARD   Aliases: ACCD	6.7	6.8	-0.1	-0.1	100.0%	-4.9
18344	AT3G14990.3   similar to DJ-1 family protein [Arabidopsis thaliana] (TAIR:At1g53280.1); similar to putative 4-methyl-5(B-hydroxyethyl)-thiazol monophosphate biosynthesis enzyme [Oryza sativa (japonica cultivar-group)] (GB:BAD54224.1); contains InterPro domain Protein of unknown function Thij/Pfpl (InterPro:IPR002818); contains InterPro domain DJ-1 protein (InterPro:IPR006287)   chr3:5047407-5049884 FORWARD   Aliases: K15M2.13, K15M2_13	12.7	12.7	-0.1	-0.1	100.0%	-5.2
18345	AT2G17040.1   Symbol: ANAC036   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; similar to petunia NAM (X92205) and A. thaliana sequences ATAF1 (X74755) and ATAF2 (X74756); probable DNA-binding protein   chr2:7414207-7415352 FORWARD   Aliases: ANAC036, F6P23.7, F6P23_7	3.0	3.0	-0.0	-0.1	100.0%	-5.7
18346	AT4G38710.1   glycine-rich protein, cylicin II - bovine, PIR2:I46014   chr4:18077784-18080077 REVERSE   Aliases: T9A14.5	7.7	7.8	-0.1	-0.1	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18347	AT1G63600.1   protein kinase-related, low similarity to receptor-like protein kinase 5 (Arabidopsis thaliana) GI:13506747; contains Pfam profile: PF01657 Domain of unknown function DUF26   chr1:23585375-23586287 FORWARD   Aliases: F2K11.4, F2K11_4	2.3	2.3	-0.0	-0.1	100.0%	-5.7
18348	AT3G11560.3   expressed protein   chr3:3639447-3646054 FORWARD   Aliases: F24K9.23	6.0	6.1	-0.0	-0.1	100.0%	-4.8
18349	AT3G09810.1   Symbol: AT3G09805   isocitrate dehydrogenase, putative / NAD+ isocitrate dehydrogenase, putative, strong similarity to isocitrate dehydrogenase (NAD+) GB:CAA65502 GI:3021506 (Nicotiana tabacum)   chr3:3008699-3011442 FORWARD   Aliases: AT3G09805, F8A24.14, F8A24_14	9.7	9.5	0.1	0.1	100.0%	-4.6
18350	AT5G08620.1   DEAD box RNA helicase (RH25), identical to RNA helicase (Arabidopsis thaliana) GI:3776023; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain	6.3	6.4	-0.0	-0.1	100.0%	-5.0
18351	AT3G59900.1   expressed protein, hypothetical protein At2g44080 - Arabidopsis thaliana, EMBL:AC004005   chr3:22140703-22141434 FORWARD   Aliases: F24G16.170	6.1	6.0	0.1	0.1	100.0%	-4.6
18352	AT4G26390.1   pyruvate kinase, putative, identical to probable pyruvate kinase, cytosolic isozyme (EC 2.7.1.40) (Arabidopsis thaliana) SWISS-PROT:O65595   chr4:13342216-13344427 FORWARD   Aliases: T25K17.3	3.0	3.0	0.0	0.1	100.0%	-5.2
18353	AT3G44070.1   expressed protein, ; expression supported by MPSS   chr3:15839164-15840075 REVERSE   Aliases: F26G5.20	3.0	3.0	0.0	0.1	100.0%	-5.3
18354	AT1G52290.1   protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr1:19473733-19476031 REVERSE   Aliases: F19K6.9, F19K6_9	4.3	4.3	0.0	0.1	100.0%	-4.9
18355	AT1G29870.1   tRNA synthetase class II (G, H, P and S) family protein, similar to SP:O23627 Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine--tRNA ligase) (GlyRS) {Arabidopsis thaliana}; contains Pfam profile PF00587: tRNA synthetase class II core domain (G, H, P, S and T); contains non-consensus TA acceptor splice site at intron 4   chr1:10456886-10458766 REVERSE   Aliases: F1N18.9, F1N18_9	2.2	2.2	0.0	0.1	100.0%	-5.9
18356	AT4G39320.1   microtubule-associated protein-related, contains weak similarity to microtubule-associated protein 1B (MAP 1B) (Swiss-Prot:P46821) (Homo sapiens)   chr4:18289049-18289851 FORWARD   Aliases: T22F8.220, T22F8_220	3.7	3.7	-0.0	-0.1	100.0%	-5.3
18357	AT3G57020.2   similar to strictosidine synthase family protein [Arabidopsis thaliana] (TAIR:At3g57010.1); similar to putative strictosidine synthase [Lycopersicon esculentum] (GB:AAF75751.1); contains InterPro domain Strictosidine synthase (InterPro:IPR004141)   chr3:21109294-21111338 REVERSE   Aliases: F24I3.100	4.3	4.4	-0.1	-0.1	100.0%	-4.5
18358	AT1G33850.1   40S ribosomal protein S15, putative, similar to SP:Q08112 40S ribosomal protein S15 {Arabidopsis thaliana}   chr1:12287893-12288190 REVERSE   Aliases: T3M13.13	2.3	2.4	-0.0	-0.1	100.0%	-6.0
18359	AT2G35075.1   expressed protein   chr2:14793761-14796102 FORWARD   Aliases: None	3.0	3.0	-0.0	-0.1	100.0%	-5.5
18360	AT3G27560.1   Symbol: ATN1   protein kinase (ATN1), almost identical (1 amino acid difference) to protein kinase ATN1 (Arabidopsis thaliana) gi:1054633;emb:CAA63387   chr3:10211668-10214241 REVERSE   Aliases: ATN, MMJ24.11	7.4	7.4	-0.0	-0.1	100.0%	-4.7
18361	AT4G05630.1   expressed protein   chr4:2988445-2988819 REVERSE   Aliases: F21I2.20, F21I2_20	2.8	2.8	-0.0	-0.1	100.0%	-5.4
18362	AT1G61410.1   tolA protein-related, contains weak similarity to Swiss-Prot:P19934 TolA protein (Escherichia coli)   chr1:22662217-22663126 REVERSE   Aliases: T1F9.10, T1F9_10	4.5	4.5	-0.0	-0.1	100.0%	-5.1
18363	AT4G20140.1   leucine-rich repeat transmembrane protein kinase, putative, Cf-2.2, Lycopersicon pimpinellifolium, PIR:T10515   chr4:10884207-10888280 FORWARD   Aliases: F1C12.60, F1C12_60	3.6	3.7	-0.1	-0.1	100.0%	-4.5
18364	AT1G53090.2   Symbol: SPA4   WD-40 repeat family protein / phytochrome A-related, contains 7 WD-40 repeats (PF00400) (1 below cutoff); similar to phytochrome A supressor spa1 (GI:4809171) (Arabidopsis thaliana)   chr1:19787020-19790565 FORWARD   Aliases: F8L10.5, F8L10_5, SPA1 RELATED 4	4.6	4.6	-0.1	-0.1	100.0%	-4.4
18365	AT3G43950.1   expressed protein   chr3:15777348-15778001 FORWARD   Aliases: T15B3.90	2.9	2.9	0.0	0.1	100.0%	-5.6
18366	AT4G09090.1   glycosyl hydrolase family protein 17, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum)   chr4:5807285-5807707 REVERSE   Aliases: T8A17.3	2.6	2.6	-0.0	-0.1	100.0%	-5.7
18367	AT5G56110.1   myb family transcription factor, contains PFAM profile: Myb DNA binding domain PF00249   chr5:22736417-22737890 FORWARD   Aliases: MDA7.17, MDA7_17	3.8	3.8	0.0	0.1	100.0%	-5.2
18368	AT5G48340.1   expressed protein   chr5:19607765-19610115 FORWARD   Aliases: K23F3.6, K23F3_6	8.9	8.8	0.1	0.1	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18369	AT3G47110.1   leucine-rich repeat transmembrane protein kinase, putative, protein kinase Xa21 receptor type precursor, <i>Oryza sativa</i> , PIR:A57676   chr3:17358088-17361281 REVERSE   Aliases: F13I12.160	3.3	3.2	0.0	0.1	100.0%	-5.0
18370	AT4G38360.2   expressed protein, contains Pfam profile PF03619: Domain of unknown function   chr4:17967101-17969952 FORWARD   Aliases: F22I13.130, F22I13_130	3.8	3.7	0.1	0.1	100.0%	-4.9
18371	AT5G19640.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:6636462-6638592 FORWARD   Aliases: T29J13.60, T29J13_60	3.6	3.6	0.0	0.1	100.0%	-5.3
18372	AT1G26310.1   Symbol: CAL   MADS-box protein, putative, strong similarity to DNA-binding protein ( <i>Brassica rapa</i> subsp. <i>pekinensis</i> ) GI:6469345, SP:Q41276 Floral homeotic protein APETALA1 (MADS C) { <i>Sinapis alba</i> }; contains InterPro accession IPR002100: Transcription factor, MADS-box   chr1:9100145-9103590 REVERSE   Aliases: AGL10, CAL1, CAULIFLOWER, F28B23.25, F28B23_25, MADS3	2.3	2.2	0.0	0.1	100.0%	-5.6
18373	AT1G19030.1   expressed protein   chr1:6571175-6572928 FORWARD   Aliases: F14D16.18, F14D16_18	2.2	2.1	0.0	0.1	100.0%	-5.9
18374	AT1G44050.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	2.4	-0.1	-0.1	100.0%	-5.1
18375	AT4G15560.1   Symbol: CLA1   1-deoxy-D-xylulose 5-phosphate synthase, putative / 1-deoxyxylulose-5-phosphate synthase, putative / DXP-synthase, putative (DEF) (CLA1), identical to SP:Q38854 Probable 1-deoxy-D-xylulose 5-phosphate synthase, chloroplast precursor (EC 4.1.3.37) (1-deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS). (Mouse-ear cress) { <i>Arabidopsis thaliana</i> }, DEF (deficient in photosynthesis) protein ( <i>Arabidopsis thaliana</i> ) GI:1399261   chr4:8883905-8887563 FORWARD   Aliases: 1 DEOXY D XYLULOSE 5 PHOSPHATE SYNTHASE, CHLOROPLASTOS ALTERADOS, CLA, CLOROPLASTOS ALTERADOS 1, DEF, DL3821W, DXS, FCAALL.24	8.6	8.6	0.1	0.1	100.0%	-5.1
18376	AT2G19640.2   SET domain-containing protein, contains Pfam profile PF00856: SET domain	3.7	3.7	0.0	0.1	100.0%	-5.0
18377	AT3G48410.1   hydrolase, alpha/beta fold family protein, low similarity to 2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrolase ( <i>Rhodococcus</i> sp. RHA1) GI:8978311, SP:Q59695:ACOC_PSEPU Dihydrolipoamide acetyltransferase component of acetoin cleaving system (EC 2.3.1.12) (Acetoin dehydrogenase E2 component) { <i>Pseudomonas putida</i> }; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr3:17936687-17939173 REVERSE   Aliases: T29H11.70	4.7	4.7	0.1	0.1	100.0%	-4.9
18378	AT5G55250.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:jasmonic acid carboxyl methyltransferase (JMT)(GI:13676829) and to SAM:benzoic acid carboxyl methyltransferase (BAMT)(GI:9789277)( <i>Antirrhinum majus</i> )   chr5:22424775-22428170 REVERSE   Aliases: MCO15.20, MCO15_20	2.8	2.8	0.1	0.1	100.0%	-4.4
18379	AT4G24510.1   Symbol: CER2   eceriferum protein (CER2), identical to (CER2) ( <i>Arabidopsis thaliana</i> ) GI:1213594; contains Pfam profile PF02458: Transferase family   chr4:12660759-12662666 FORWARD   Aliases: ECERIFERUM 2, F22K18.290, F22K18_290, VC 2, VC2	2.3	2.3	0.0	0.1	100.0%	-5.8
18380	AT3G57750.2   similar to protein kinase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g57700.1); similar to OSJNBa0083N12.1 [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:CAE03464.2); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:21404956-21406221 FORWARD   Aliases: F15B8.60	5.8	5.8	0.0	0.1	100.0%	-4.9
18381	AT1G14280.1   Symbol: PKS2   phytochrome kinase, putative, contains similarity to Swiss-Prot:Q9SWI1 phytochrome kinase substrate 1 ( <i>Arabidopsis thaliana</i> )   chr1:4877622-4879144 FORWARD   Aliases: F14L17.4, F14L17_4, PHYTOCHROME KINASE SUBSTRATE 2	2.3	2.3	-0.0	-0.1	100.0%	-5.9
18382	AT2G17210.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:7492480-7494684 REVERSE   Aliases: T23A1.7, T23A1_7	3.4	3.4	0.0	0.1	100.0%	-5.5
18383	AT3G53040.1   late embryogenesis abundant protein, putative / LEA protein, putative, similar to LEA protein in group 3 ( <i>Arabidopsis thaliana</i> ) GI:1526424; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr3:19675652-19677465 REVERSE   Aliases: F8J2.210	3.4	3.3	0.0	0.1	100.0%	-5.3
18384	AT1G34420.1   leucine-rich repeat family protein / protein kinase family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:12584565-12587548 FORWARD   Aliases: F12K21.25, F12K21_25	2.9	2.9	0.0	0.1	100.0%	-4.7
18385	AT1G53325.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; similar to suppressor of nim1-1 (GI:22023774) ( <i>Arabidopsis thaliana</i> )   chr1:19898895-19899401 REVERSE   Aliases: None	2.2	2.2	-0.0	-0.1	100.0%	-6.2
18386	AT5G19350.1   RNA-binding protein 45 (RBP45), putative	8.9	8.9	0.0	0.1	100.0%	-5.1
18387	AT5G26140.1   lysine decarboxylase family protein, contains Pfam profile PF03641: decarboxylase family protein	2.4	2.4	-0.0	-0.1	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18388	AT2G47900.2   similar to F-box family protein / tubby family protein [Arabidopsis thaliana] (TAIR:At1g25280.1); similar to putative tubby protein [Oryza sativa (japonica cultivar-group)] (GB:AAV59313.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Tubby (InterPro:IPR000007)   chr2:19618013-19620289 REVERSE   Aliases: F17A22.29	4.0	4.0	0.0	0.1	100.0%	-4.8
18389	AT4G40090.1   Symbol: AGP3   arabinogalactan-protein (AGP3), InDels between the genome sequence and the cDNA prevent identical translations from being annotated; the basis for this is under investigation.	1.9	2.0	-0.1	-0.1	100.0%	-4.1
18390	AT2G06390.1   expressed protein   chr2:2516583-2516709 REVERSE   Aliases: F18P14.18, F18P14_18	1.4	1.5	-0.1	-0.1	100.0%	-4.6
18391	AT5G45120.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr5:18258230-18259705 FORWARD   Aliases: K17O22.14, K17O22_14	3.2	3.2	0.0	0.1	100.0%	-5.3
18392	AT5G10800.1   RNA recognition motif (RRM)-containing protein, KIAA0332 gene, Homo sapiens, EMBL:HSAB2330   chr5:3412759-3418383 REVERSE   Aliases: T30N20.70, T30N20_70	3.0	3.0	0.0	0.1	100.0%	-5.6
18393	AT3G09310.1   expressed protein   chr3:2860246-2861338 REVERSE   Aliases: F3L24.18	3.9	3.9	0.0	0.1	100.0%	-5.2
18394	AT4G10340.1   Symbol: LHCB5   chlorophyll A-B binding protein CP26, chloroplast / light-harvesting complex II protein 5 / LHCIIC (LHCB5), identical to SP:Q9XF89 Chlorophyll A/B-binding protein CP26, chloroplast precursor (Light-harvesting complex II protein 5) (LHCB5) (LHCIIC) {Arabidopsis thaliana}; contains Pfam profile: PF00504 chlorophyll A-B binding protein; chlorophyll a/b-binding protein CP26 in PS II, Brassica juncea, gb:X95727   chr4:6408012-6409673 FORWARD   Aliases: CP 26, CP26, F24G24.140, F24G24_140, LIGHT HARVESTING COMPLEX OF PHOTOSYSTEM II 5	12.8	12.7	0.1	0.1	100.0%	-4.7
18395	AT5G37240.1   expressed protein   chr5:14754975-14760710 REVERSE   Aliases: MNJ8.30, MNJ8_30	2.9	2.9	0.0	0.1	100.0%	-5.1
18396	AT5G40270.1   metal-dependent phosphohydrolase HD domain-containing protein, similar to SP:Q60710 Interferon-gamma inducible protein MG11 {Mus musculus}; contains Pfam profile PF01966: HD domain   chr5:16110400-16114447 REVERSE   Aliases: MSN9.18, MSN9_18	4.9	4.9	0.1	0.1	100.0%	-4.9
18397	AT5G61220.1   complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)   chr5:24642802-24644149 REVERSE   Aliases: MAF19.16, MAF19_16	10.6	10.7	-0.1	-0.1	100.0%	-4.9
18398	AT4G21230.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:11319196-11321689 REVERSE   Aliases: F7J7.170, F7J7_170	3.3	3.4	-0.1	-0.1	100.0%	-4.2
18399	AT1G64100.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:23795248-23797304 FORWARD   Aliases: F22C12.14	3.5	3.5	0.0	0.1	100.0%	-5.5
18400	AT4G23310.1   receptor-like protein kinase, putative, similar to receptor-like protein kinase 4 (gi:13506745), 5 (gi:13506747), and 6 (gi:13506749) from Arabidopsis thaliana; contains Pfam protein kinase domain PF00069   chr4:12185747-12188773 FORWARD   Aliases: F21P8.200, F21P8_200	3.7	3.6	0.0	0.1	100.0%	-5.0
18401	AT1G50050.1   pathogenesis-related protein, putative, similar to pathogenesis-related protein 1b precursor (pr-1b) GB:X03465 GI:19977 from (Nicotiana tabacum); contains Pfam profile PF00188: SCP-like extracellular protein   chr1:18549833-18552714 FORWARD   Aliases: F2J10.7, F2J10_7	3.1	3.1	0.0	0.1	100.0%	-5.4
18402	AT4G08450.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:5365607-5371098 FORWARD   Aliases: C18G5.30, C18G5_30	2.9	2.9	-0.0	-0.1	100.0%	-5.7
18403	AT5G13070.1   MSF1-like family protein, similar to px19 (Gallus gallus) GI:969170; contains Pfam profile PF04707: MSF1-like conserved region   chr5:4148219-4149215 FORWARD   Aliases: T19L5.30, T19L5_30	8.1	8.2	-0.1	-0.1	100.0%	-4.6
18404	AT4G39690.1   expressed protein   chr4:18417664-18421965 FORWARD   Aliases: T19P19.80, T19P19_80	7.6	7.7	-0.1	-0.1	100.0%	-4.6
18405	AT4G26510.2   uracil phosphoribosyltransferase / UMP pyrophosphorylase (UPT1), nearly identical to SP:O65583 Uracil phosphoribosyltransferase (EC 2.4.2.9) (UMP pyrophosphorylase) (UPRTase) {Arabidopsis thaliana}   chr4:13384070-13388297 FORWARD   Aliases: M3E9.60, M3E9_60	4.4	4.4	-0.0	-0.1	100.0%	-5.2
18406	AT4G39930.1   expressed protein   chr4:18518337-18518977 REVERSE   Aliases: T5J17.100, T5J17_100	2.4	2.5	-0.0	-0.1	100.0%	-5.5
18407	AT2G36920.1   expressed protein   chr2:15515877-15516926 FORWARD   Aliases: T1J8.10, T1J8_10	3.1	3.1	0.0	0.1	100.0%	-5.5
18408	AT5G14050.1   transducin family protein / WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400); similar to unknown protein (ref:NP_057085.1)   chr5:4533292-4535303 FORWARD   Aliases: MUA22.5, MUA22_5	8.1	8.1	-0.0	-0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18409	AT1G12090.1   Symbol: ELP   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to 14 kDa polypeptide (Catharanthus roseus) GI:407410; contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr1:4089845-4090723 REVERSE   Aliases: EXTENSIN LIKE PROTEIN, F12F1.3, F12F1_3	2.5	2.5	-0.0	-0.1	100.0%	-4.6
18410	AT4G22960.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g11860.1); similar to hypothetical protein LOC75007 [Mus musculus] (GB:NP_598619.2); similar to PREDICTED: hypothetical protein XP_524866 [Pan troglodytes] (GB:XP_524866.1); similar to LOC310665 protein [Rattus norvegicus] (GB:AAH91386.1); similar to PREDICTED: similar to hypothetical protein FLJ11280 [Canis familiaris] (GB:XP_540306.1); similar to NF-E2 inducible protein [Mus musculus] (GB:BAD06451.1); contains InterPro domain Protein of unknown function DUF544 (InterPro:IPR007518)   chr4:12030031-12033148 FORWARD   Aliases: F7H19.140, F7H19_140	3.8	3.9	-0.1	-0.1	100.0%	-5.0
18411	AT3G42980.1   hypothetical protein   chr3:15038577-15040097 FORWARD   Aliases: F18P9.140	2.8	2.8	-0.0	-0.1	100.0%	-5.5
18412	AT1G47680.1   hypothetical protein   chr1:17543215-17543529 FORWARD   Aliases: F16N3.39, F16N3_39	3.2	3.3	-0.0	-0.1	100.0%	-5.4
18413	AT1G02540.1   expressed protein   chr1:534827-535699 REVERSE   Aliases: T14P4.13, T14P4_13	2.6	2.7	-0.0	-0.1	100.0%	-5.6
18414	AT1G07680.1   hypothetical protein   chr1:2376059-2376990 FORWARD   Aliases: F24B9.23, F24B9_23	3.5	3.4	0.0	0.1	100.0%	-4.8
18415	AT3G57510.1   Symbol: ADPG1   endo-polygalacturonase (ADPG1), identical to endo-polygalacturonase (Arabidopsis thaliana) GI:2597824   chr3:21294315-21296918 REVERSE   Aliases: T8H10.110	3.4	3.4	0.0	0.1	100.0%	-5.3
18416	AT1G78900.2   Symbol: VHA A   similar to ATP synthase beta chain 2, mitochondrial [Arabidopsis thaliana] (TAIR:At5g08690.1); similar to ATP synthase beta chain, mitochondrial, putative [Arabidopsis thaliana] (TAIR:At5g08680.1); similar to ATP synthase beta chain 1, mitochondrial [Arabidopsis thaliana] (TAIR:At5g08670.1); similar to vacuolar H+-ATPase catalytic subunit [Pyrus communis] (GB:BAD90912.1); similar to vacuolar H+-ATPase catalytic subunit [Pyrus communis] (GB:BAD90911.1); similar to H+-exporting ATPase (EC 3.6.3.6), vacuolar, 69K chain - carrot (GB:PXPZV9); similar to V-ATPase catalytic subunit A [Prunus persica] (GB:AAL11505.1); similar to VATA_CITUN Vacuolar ATP synthase catalytic subunit A (V-ATPase A subunit) (Vacuolar proton pump alpha subunit) (V-ATPase 69 kDa subunit) (GB:Q9SM09); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, C-terminal (InterPro:IPR000793); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, N-terminal (InterPro:IPR004100); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, central region (InterPro:IPR000194); contains InterPro domain ATP synthase V-type, A subunit (InterPro:IPR005725)   chr1:29665091-29669843 FORWARD   Aliases: F9K20.5, F9K20_5, VHA A	7.9	7.7	0.2	0.1	100.0%	-4.6
18417	AT4G08160.2   similar to glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein [Arabidopsis thaliana] (TAIR:At1g10050.1); similar to glycosyl hydrolase family 10 protein / carbohydrate-binding domain-containing protein [Arabidopsis thaliana] (TAIR:At1g58370.1); similar to putative 1,4-beta-D xylan xylanohydrolase [Oryza sativa (japonica cultivar-group)] (GB:XP_477949.1); similar to putative xylan xylanohydrolase isoenzyme [Oryza sativa (japonica cultivar-group)] (GB:XP_469240.1); contains InterPro domain Glycoside hydrolase, family 10 (InterPro:IPR001000); contains InterPro domain Carbohydrate-binding, CenC-like (InterPro:IPR003305)   chr4:5159031-5162771 REVERSE   Aliases: F9M13.1, F9M13_1	3.2	3.3	-0.1	-0.1	100.0%	-4.1
18418	AT5G07110.1   prenylated rab acceptor (PRA1) family protein, weak similarity to prenylated Rab acceptor 1 (PRA1) (Homo sapiens) GI:4877285; contains Pfam profile PF03208: Prenylated rab acceptor (PRA1)   chr5:2206001-2207153 FORWARD   Aliases: T28J14.50	4.9	4.8	0.1	0.1	100.0%	-4.7
18419	AT1G80340.1   Symbol: GA4H   gibberellin 3-beta-dioxygenase / gibberellin 3 beta-hydroxylase (GA4H), nearly identical to gibberellin 3 beta-hydroxylase GI:3982753 GB:AAC83647 (Arabidopsis thaliana)	2.8	2.7	0.0	0.1	100.0%	-5.2
18420	AT5G37860.1   copper-binding family protein, similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam profile PF00403: Heavy-metal-associated domain   chr5:15086808-15087785 REVERSE   Aliases: K18L3.3, K18L3_3	3.0	2.9	0.0	0.1	100.0%	-5.4
18421	AT5G66650.1   expressed protein, contains Pfam domain, PF04678: Protein of unknown function, DUF607   chr5:26620229-26621602 REVERSE   Aliases: MSN2.3, MSN2_3	3.5	3.5	0.0	0.1	100.0%	-4.7
18422	AT3G51330.1   aspartyl protease family protein, contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141   chr3:19064347-19067203 REVERSE   Aliases: F24M12.370, F24M12_370	2.6	2.7	-0.1	-0.1	100.0%	-4.1
18423	AT1G65350.1   Symbol: UBIQ13   polyubiquitin, putative, similar to polyubiquitin GI:248337 from (Zea mays)   chr1:24280054-24280938 REVERSE   Aliases: T8F5.13, T8F5_13	4.9	4.8	0.0	0.1	100.0%	-4.8
18424	AT1G53530.1   signal peptidase I family protein, contains similarity to SP:P28627 Mitochondrial inner membrane protease subunit 1 (EC 3.4.99.-) {Saccharomyces cerevisiae}; contains Pfam profile PF00461: Signal peptidase I   chr1:19981821-19983751 FORWARD   Aliases: F22G10.30	4.9	4.9	-0.1	-0.1	100.0%	-4.8
18425	AT1G30515.1   expressed protein   chr1:10809271-10809897 REVERSE   Aliases: None	3.0	3.0	0.0	0.1	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18426	AT3G59830.1   ankyrin protein kinase, putative, similar to ankyrin-kinase (Medicago truncatula) gi:18700701:gb:AAL78674   chr3:22113780-22116357 REVERSE   Aliases: F24G16.100	3.0	3.0	0.0	0.1	100.0%	-5.6
18427	AT5G54040.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.6	-0.1	-0.1	100.0%	-5.2
18428	AT4G17270.1   Mo25 family protein, similar to MO25 protein (early mouse development protein family) (Mouse) SWISS-PROT:Q06138   chr4:9676140-9679153 FORWARD   Aliases: DL4670W, FCAALL.22	8.2	8.1	0.1	0.1	100.0%	-4.5
18429	AT1G30530.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:10814641-10816565 FORWARD   Aliases: F26G16.15, F26G16_15	5.6	5.5	0.1	0.1	100.0%	-4.5
18430	AT5G01015.1   expressed protein   chr5:5261-5890 REVERSE   Aliases: None	3.4	3.5	-0.1	-0.1	100.0%	-5.0
18431	AT4G15750.1   invertase/pectin methylesterase inhibitor family protein, nearly identical to gi:3426058 novel gene of unknown function; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor; identical to cDNA IB1P8-4 protein GI:3426057   chr4:8967555-8968602 REVERSE   Aliases: DL3915C, FCAALL.95	2.8	2.8	0.0	0.1	100.0%	-5.4
18432	AT3G23230.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr3:8289654-8290073 REVERSE   Aliases: K14B15.1	2.9	2.9	0.0	0.1	100.0%	-5.2
18433	AT1G64430.2   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_481689.1)   chr1:23937043-23940509 FORWARD   Aliases: F15H21.10, F15H21_10	5.1	5.1	0.0	0.1	100.0%	-4.8
18434	AT3G24160.1   Symbol: PMP   expressed protein, identical to cDNA putative type 1 membrane protein (PMP)GI:4206764   chr3:8726138-8729396 FORWARD   Aliases: MUJ8.6, PUTATIVE TYPE 1 MEMBRANE PROTEIN	9.3	9.2	0.1	0.1	100.0%	-5.1
18435	AT2G27370.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr2:11715532-11716983 REVERSE   Aliases: F12K2.5, F12K2_5	2.5	2.6	-0.1	-0.1	100.0%	-4.2
18436	AT4G29980.1   expressed protein   chr4:14664960-14665589 REVERSE   Aliases: F6G3.10, F6G3_10	3.5	3.6	-0.0	-0.1	100.0%	-4.9
18437	AT2G03830.1   expressed protein   chr2:1171169-1172349 FORWARD   Aliases: T18C20.3, T18C20_3	2.0	2.0	0.0	0.1	100.0%	-6.0
18438	AT4G29440.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g19710.1); similar to MAPK activating protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD82253.1); contains InterPro domain Eukaryotic protein of unknown function DUF292 (InterPro:IPR005061)   chr4:14473763-14477941 REVERSE   Aliases: F17A13.260, F17A13_260	3.9	3.8	0.1	0.1	100.0%	-4.9
18439	AT1G65880.1   AMP-dependent synthetase and ligase family protein, similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501   chr1:24512296-24514405 REVERSE   Aliases: F12P19.5, F12P19_5	2.7	2.7	-0.0	-0.1	100.0%	-5.7
18440	AT5G42810.1   Symbol: ATIPK1	7.3	7.4	-0.1	-0.1	100.0%	-4.7
18441	AT3G49820.1   expressed protein   chr3:18492222-18492707 FORWARD   Aliases: T16K5.170	2.2	2.2	0.0	0.1	100.0%	-5.4
18442	AT3G12900.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to SP:P10967 1-aminocyclopropane-1-carboxylate oxidase homolog (Protein E8) {Lycopersicon esculentum}, desacetoxvindoline-4-hydroxylase (Catharanthus roseus) GI:2352812; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr3:4104583-4106119 FORWARD   Aliases: MJM20.4	3.4	3.5	-0.1	-0.1	100.0%	-4.3
18443	AT1G17520.1   DNA-binding protein, putative, contains similarity to DNA-binding protein PcMYB1 (Petroselinum crispum) gi:2224899:gb:AAB61699   chr1:6024632-6027378 REVERSE   Aliases: F1L3.23, F1L3_23	4.2	4.2	0.0	0.1	100.0%	-5.3
18444	AT3G15660.2   similar to thioredoxin family protein [Arabidopsis thaliana] (TAIR:At4g04950.1); similar to glutaredoxin-related protein -like [Oryza sativa (japonica cultivar-group)] (GB:XP_550301.1); contains InterPro domain Glutaredoxin (InterPro:IPR002109); contains InterPro domain Glutaredoxin-related protein (InterPro:IPR004480)	10.8	11.0	-0.1	-0.1	100.0%	-4.8
18445	AT1G49940.1   expressed protein, contains similarity to putative beta-9 tubulin protein GB:AAF40459 GI:7211988 from (Arabidopsis thaliana)   chr1:18492185-18494488 REVERSE   Aliases: F2J10.17, F2J10_17	3.0	3.0	-0.0	-0.1	100.0%	-5.5
18446	AT1G29630.1   exonuclease, putative, similar to Swiss-Prot:P53695 exonuclease I (EXO I) (Schizosaccharomyces pombe)   chr1:10349458-10351431 FORWARD   Aliases: F15D2.37, F15D2_37	2.3	2.3	-0.0	-0.1	100.0%	-5.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18447	AT1G19160.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain   chr1:6614153-6614815 REVERSE   Aliases: T29M8.3, T29M8_3	3.2	3.2	-0.0	-0.1	100.0%	-5.3
18448	AT5G14740.4   Symbol: CA2   similar to carbonic anhydrase 1, chloroplast / carbonate dehydratase 1 (CA1) [Arabidopsis thaliana] (TAIR:At3g01500.1); similar to carbonic anhydrase 1, chloroplast / carbonate dehydratase 1 (CA1) [Arabidopsis thaliana] (TAIR:At3g01500.3); similar to carbonic anhydrase 1, chloroplast / carbonate dehydratase 1 (CA1) [Arabidopsis thaliana] (TAIR:At3g01500.2); similar to chloroplast carbonic anhydrase precursor [Thlaspi caerulescens] (GB:AAS65454.1); contains InterPro domain Carbonic anhydrase, prokaryotic (InterPro:IPR001765)	2.9	3.0	-0.0	-0.1	100.0%	-5.0
18449	AT3G09290.1   zinc finger (C2H2 type) family protein, ; contains Pfam profile: PF00096 Zinc finger, C2H2 type   chr3:2856147-2856665 FORWARD   Aliases: F3L24.16	3.1	3.2	-0.1	-0.1	100.0%	-4.3
18450	AT4G28200.1   expressed protein   chr4:13987608-13990456 REVERSE   Aliases: F26K10.80, F26K10_80	6.6	6.5	0.1	0.1	100.0%	-5.0
18451	AT2G30320.1   tRNA pseudouridine synthase family protein, similar to pseudouridine synthase (Schizosaccharomyces pombe) GI:6469502; contains Pfam profile PF01416: tRNA pseudouridine synthase	5.8	5.7	0.1	0.1	100.0%	-4.5
18452	AT5G66220.1   chalcone-flavanone isomerase, putative / chalcone isomerase, putative (CHI), similar to SP:P41088   chr5:26478403-26479400 FORWARD   Aliases: K2A18.30, K2A18_30	2.7	2.7	0.0	0.1	100.0%	-5.9
18453	AT3G12840.1   expressed protein   chr3:4085812-4086090 REVERSE   Aliases: MBK21.20	2.6	2.6	0.0	0.1	100.0%	-5.6
18454	AT5G11470.1   bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain   chr5:3663366-3667042 REVERSE   Aliases: F15N18.60, F15N18_60	2.9	2.9	0.0	0.1	100.0%	-5.5
18455	AT4G15230.1   ABC transporter family protein, similar to pleiotropic drug resistance like protein (Nicotiana tabacum) GI:20522008, PDR5-like ABC transporter (Spirodela polyrhiza) GI:1514643; contains Pfam profile PF00005: ABC transporter   chr4:8680182-8686880 FORWARD   Aliases: DL3660W, FCAALL.241	3.1	3.1	-0.0	-0.1	100.0%	-5.1
18456	AT4G27170.1   2S seed storage protein 4 / 2S albumin storage protein / NWMU2-2S albumin 4, identical to SP:P15460   chr4:13613602-13614289 FORWARD   Aliases: T24A18.120, T24A18_120	2.3	2.3	0.0	0.1	100.0%	-6.1
18457	AT4G35870.1   expressed protein   chr4:16990176-16992891 FORWARD   Aliases: F4B14.140, F4B14_140	4.4	4.4	-0.0	-0.1	100.0%	-4.7
18458	AT1G01970.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to 67 kD chloroplastic RNA-binding protein RSP67.2 (Raphanus sativus) GI:9755888; contains Pfam profile PF01535: PPR repeat   chr1:338292-340074 FORWARD   Aliases: F22M8.10, F22M8_10	6.2	6.1	0.0	0.1	100.0%	-4.6
18459	AT2G25980.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.2	3.1	0.0	0.1	100.0%	-4.9
18460	AT3G51050.1   FG-GAP repeat-containing protein	6.0	5.9	0.1	0.1	100.0%	-4.9
18461	AT5G15290.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588) contains plant integral membrane protein domain, TIGR01569	2.4	2.4	0.1	0.1	100.0%	-4.2
18462	ATMG00680.1   Symbol: ORF122C   hypothetical protein   chrM:201729-202097 FORWARD   Aliases: ORF122C	2.6	2.6	0.0	0.1	100.0%	-5.3
18463	AT2G44520.1   UbiA prenyltransferase family protein, similar to SP:Q12887 Protoheme IX farnesyltransferase, mitochondrial precursor (EC 2.5.1.-) (Heme O synthase) {Homo sapiens}, SP:P21592 COX10 {Saccharomyces cerevisiae}   chr2:18386651-18389018 FORWARD   Aliases: F4I1.50, F4I1_50	8.4	8.5	-0.1	-0.1	100.0%	-4.7
18464	AT1G29230.1   Symbol: CIPK18	3.9	3.9	-0.0	-0.1	100.0%	-4.8
18465	AT4G27710.1   Symbol: CYP709B3   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr4:13828468-13830602 FORWARD   Aliases: T29A15.200, T29A15_200	2.9	2.9	0.1	0.1	100.0%	-4.8
18466	AT1G34575.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:12657127-12658710 REVERSE   Aliases: None	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18467	AT3G16870.1   zinc finger (GATA type) family protein, contains Pfam profile:PF00320 GATA:GATA zinc finger   chr3:5763592-5764660 REVERSE   Aliases: MUH15.3	4.3	4.4	-0.0	-0.1	100.0%	-4.9
18468	AT1G15520.1   Symbol: PDR12   ABC transporter family involved in resistant to lead. Localizes to plasma membrane. Upregulated by lead. Expressed in leaves, flowers. Not expressed in roots.   chr1:5331988-5338170 REVERSE   Aliases: PDR12, PLEIOTROPIC DRUG RESISTANCE 12, T16N11.3, T16N11_3	3.8	3.8	0.0	0.1	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18469	AT2G46020.2   transcription regulatory protein SNF2, putative, similar to SP:P22082 Transcription regulatory protein SNF2 (SWI/SNF complex component SNF2) {Saccharomyces cerevisiae}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr2:18930377-18938842 FORWARD   Aliases: T3F17.33	5.5	5.5	-0.0	-0.1	100.0%	-5.3
18470	AT2G26350.1   Symbol: PEX10   zinc-binding peroxisomal integral membrane protein (PEX10), identical to zinc-binding peroxisomal integral membrane protein Gl:4337011 from (Arabidopsis thaliana)   chr2:11224570-11227511 REVERSE   Aliases: PEX10, T9J22.2	4.1	4.0	0.0	0.1	100.0%	-5.0
18471	AT4G26700.3   Symbol: ATFIM1	6.5	6.4	0.1	0.1	100.0%	-4.6
18472	AT4G26290.1   expressed protein   chr4:13307604-13307831 REVERSE   Aliases: T25K17.100, T25K17_100	2.6	2.6	0.0	0.1	100.0%	-5.6
18473	AT1G30250.1   expressed protein   chr1:10646971-10647495 REVERSE   Aliases: F12P21.5, F12P21_5	3.5	3.6	-0.0	-0.1	100.0%	-4.9
18474	AT1G72600.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:27341787-27342341 FORWARD   Aliases: F28P22.21, F28P22_21	3.8	3.8	0.0	0.1	100.0%	-5.4
18475	AT3G59220.1   Symbol: PRN   pirin, putative, similar to SP:O00625 Pirin {Homo sapiens}; contains Pfam profile PF02678: Pirin   chr3:21905111-21906600 FORWARD   Aliases: ATPIRIN1, F25L23.80, PIRIN, PRN1	3.4	3.4	0.0	0.1	100.0%	-5.1
18476	AT2G23660.1   LOB domain family protein / lateral organ boundaries domain family protein (LBD10), identical to SP:O64836 Putative LOB domain protein 10 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis thaliana	3.8	3.8	0.0	0.1	100.0%	-5.7
18477	AT5G37090.1   replication protein-related, weak similarity to Replication Protein A 70	2.6	2.6	-0.0	-0.1	100.0%	-5.7
18478	AT5G18710.1   expressed protein, predicted proteins - Arabidopsis thaliana   chr5:6241632-6243481 FORWARD   Aliases: T1A4.90, T1A4_90	3.6	3.5	0.0	0.1	100.0%	-5.2
18479	AT1G17760.1   suppressor of forked protein family protein / SUF family protein, Contains Pfam PF05843: Suppressor of forked protein (Suf); identical to cleavage stimulation factor 77 (Gl:21591637) (Arabidopsis thaliana); similar to suppressor of forked protein; Su(f) protein (Drosophila virilis) Gl:4092534   chr1:6110100-6116610 REVERSE   Aliases: F11A6.10, F11A6_10	6.1	6.1	-0.0	-0.1	100.0%	-4.9
18480	AT2G37700.1   CER1 protein, putative, similar to CER1 Gl:1199467 and maize gl1 homolog (glossy1 locus) Gl:1209703 from (Arabidopsis thaliana); may be involved in wax biosynthesis; contains a SUR2-type hydroxylase/desaturase catalytic domain (PS50242)   chr2:15818706-15821286 REVERSE   Aliases: F13M22.20, F13M22_20	3.9	3.8	0.1	0.1	100.0%	-4.5
18481	AT1G14130.1   2-oxoglutarate-dependent dioxygenase, putative, similar to adventitious rooting related oxygenase ARRO-1 from Malus x domestica, gi:3492806; contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr1:4835721-4837588 REVERSE   Aliases: F7A19.21, F7A19_21	5.7	5.6	0.1	0.1	100.0%	-4.8
18482	AT5G05740.2   peptidase M50 family protein / sterol-regulatory element binding protein (SREBP) site 2 protease family protein, contains Pfam PF02163: Sterol-regulatory element binding protein (SREBP) site 2 protease   chr5:1723837-1726860 REVERSE   Aliases: ATEGY2, MJJ3.15, MJJ3_15	6.4	6.5	-0.1	-0.1	100.0%	-4.3
18483	AT2G30660.1   3-hydroxyisobutyryl-coenzyme A hydrolase, putative / CoA-thioester hydrolase, putative, strong similarity to gi:8572760; contains Pfam profile PF00388 enoyl-CoA hydratase/isomerase family protein   chr2:13065577-13068742 REVERSE   Aliases: T11J7.5, T11J7_5	2.7	2.7	0.0	0.1	100.0%	-5.5
18484	AT5G46670.1   CHP-rich zinc finger protein, putative, contains similarity to CHP-rich zinc finger protein   chr5:18956268-18957266 FORWARD   Aliases: MZA15.8, MZA15_8	3.5	3.5	-0.1	-0.1	100.0%	-4.8
18485	AT1G05530.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr1:1636495-1637862 REVERSE   Aliases: T25N20.18	3.5	3.5	0.0	0.1	100.0%	-4.9
18486	AT3G43330.1   hypothetical protein, putative proteins - Arabidopsis thaliana   chr3:15290335-15292896 FORWARD   Aliases: T5C2.30	2.3	2.3	0.0	0.1	100.0%	-5.3
18487	AT5G29070.1   expressed protein   chr5:11132179-11133520 REVERSE   Aliases: F23C8.40, F23C8_40	2.2	2.2	-0.0	-0.1	100.0%	-5.8
18488	AT3G56260.1   expressed protein   chr3:20878950-20880003 REVERSE   Aliases: F18O21.220	3.1	3.2	-0.0	-0.1	100.0%	-5.3
18489	AT5G48300.1   Symbol: ADG1   glucose-1-phosphate adenylyltransferase small subunit 1 (APS1) / ADP-glucose pyrophosphorylase (ADG1), identical to SP:P55228   chr5:19587472-19590030 FORWARD   Aliases: ADP GLUCOSE PYROPHOSPHORYLASE SMALL SUBUNIT, ADP GLUCOSE PYROPHOSPHORYLASE SMALL SUBUNIT 1, APS1, K23F3.2, K23F3_2	8.3	8.4	-0.1	-0.1	100.0%	-4.6
18490	AT1G53640.1   expressed protein, ; expression supported by MPSS   chr1:20024553-20029129 REVERSE   Aliases: F22G10.8	5.7	5.7	0.0	0.1	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18491	AT3G42380.1   hypothetical protein   chr3:14514596-14514903 FORWARD   Aliases: T14K23.90	2.5	2.5	0.0	0.1	100.0%	-5.7
18492	AT1G05330.1   expressed protein, ; expression supported by MPSS   chr1:1558169-1558582 FORWARD   Aliases: YUP8H12.5, YUP8H12_5	2.4	2.4	-0.0	-0.1	100.0%	-5.8
18493	ATCG00360.1   Symbol: YCF3   hypothetical protein   chrC:42584-43751 REVERSE   Aliases: YCF3	7.0	7.2	-0.2	-0.1	100.0%	-4.4
18494	AT5G01930.1   (1-4)-beta-mannan endohydrolase, putative, similar to (1-4)-beta-mannan endohydrolase (Coffea arabica) GI:10178872; contains Pfam profile PF00150: Cellulase (glycosyl hydrolase family 5)   chr5:361085-362895 REVERSE   Aliases: T20L15.200, T20L15_200	3.3	3.2	0.1	0.1	100.0%	-4.5
18495	AT3G04120.1   Symbol: GAPC   glyceraldehyde-3-phosphate dehydrogenase, cytosolic (GAPC) / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, identical to SP:P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}   chr3:1080960-1083537 FORWARD   Aliases: GLYCERALDEHYDE 3 PHOSPHATE DEHYDROGENASE C SUBUNIT, T6K12.26, T6K12_26	11.1	11.2	-0.1	-0.1	100.0%	-5.2
18496	AT1G67590.2   similar to remorin family protein [Arabidopsis thaliana] (TAIR:At2g02170.1); similar to Unknown protein [Oryza sativa (japonica cultivar-group)] (GB:NP_912455.1); contains InterPro domain Remorin, C-terminal region (InterPro:IPR005516)   chr1:25336721-25338310 REVERSE   Aliases: F12B7.14, F12B7_14	4.6	4.5	0.0	0.1	100.0%	-5.0
18497	AT4G17615.2   Symbol: CBL1   calcineurin B-like protein 1 (CBL1), identical to calcineurin B-like protein 1 (GI:3309082) (Arabidopsis thaliana)   chr4:9816579-9819325 FORWARD   Aliases: ATCBL1, CALCINEURIN B LIKE PROTEIN 1, FCAALL.122	6.9	7.0	-0.0	-0.1	100.0%	-5.1
18498	AT1G73960.2   similar to TATA box binding protein (TBP)-associated factor 150kDa [Danio rerio] (GB:AAT68099.1)	6.6	6.7	-0.1	-0.1	100.0%	-4.5
18499	AT5G62620.1   galactosyltransferase family protein, contains Pfam profile: PF01762 galactosyltransferase   chr5:25153977-25157148 FORWARD   Aliases: MRG21.3, MRG21_3	6.0	6.0	0.0	0.1	100.0%	-4.6
18500	AT5G58050.1   glycerophosphoryl diester phosphodiesterase family protein, contains Pfam PF03009 : Glycerophosphoryl diester phosphodiesterase family; similar to Glycerophosphoryl diester phosphodiesterase precursor	2.3	2.2	0.0	0.1	100.0%	-5.7
18501	AT3G27750.1   expressed protein   chr3:10286057-10286728 FORWARD   Aliases: None	2.4	2.4	0.0	0.1	100.0%	-5.4
18502	AT3G19500.1   ethylene-responsive protein -related, contains similarity to ethylene-inducible ER33 protein (Lycopersicon esculentum) gi:5669656:gb:AAD46413   chr3:6759022-6760945 REVERSE   Aliases: MLD14.24	3.3	3.3	-0.0	-0.1	100.0%	-5.0
18503	AT1G48180.1   expressed protein, ; expression supported by MPSS   chr1:17796118-17797386 REVERSE   Aliases: F21D18.8, F21D18_8	3.1	3.1	-0.0	-0.1	100.0%	-5.4
18504	AT2G33540.1   Symbol: CPL3   CTD phosphatase-like protein 3 (CPL3), identical to CTD phosphatase-like 3 (CPL3) (Arabidopsis thaliana) GI:22212705; contains Pfam profile PF03031: NLI interacting factor   chr2:14210581-14215873 REVERSE   Aliases: C TERMINAL DOMAIN PHOSPHATASE LIKE 3, CPL3, F4P9.31, F4P9_31	2.6	2.6	0.0	0.1	100.0%	-5.5
18505	AT1G05550.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr1:1641228-1643747 REVERSE   Aliases: T25N20.20	3.7	3.7	0.0	0.1	100.0%	-5.3
18506	AT3G01680.1   expressed protein   chr3:251988-255520 FORWARD   Aliases: F4P13.22, F4P13_22	3.3	3.4	-0.1	-0.1	100.0%	-4.5
18507	AT5G11010.3   pre-mRNA cleavage complex-related, low similarity to SP:Q92989 Pre-mRNA cleavage complex II protein Clp1 {Homo sapiens}   chr5:3483773-3486268 FORWARD   Aliases: T30N20.280, T30N20_280	4.3	4.3	-0.0	-0.1	100.0%	-5.1
18508	AT5G46830.1   basic helix-loop-helix (bHLH) family protein   chr5:19019946-19021481 FORWARD   Aliases: MZA15.1	2.4	2.4	-0.0	-0.1	100.0%	-6.0
18509	AT4G29620.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase 2 (CDA2) (Arabidopsis thaliana) GI:5080713, cytidine deaminase homolog DesE (Arabidopsis thaliana) GI:4836447; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14519869-14521093 FORWARD   Aliases: T16L4.130, T16L4_130	3.0	3.0	0.0	0.1	100.0%	-4.9
18510	AT3G01260.1   aldose 1-epimerase family protein, similar to non-cell-autonomous protein pathway2, plasmodesmal receptor (Nicotiana tabacum) GI:15824567; contains Pfam profile PF01263: Aldose 1-epimerase   chr3:80183-81958 REVERSE   Aliases: T4P13.5, T4P13_5	3.0	3.1	-0.1	-0.1	100.0%	-4.5
18511	AT4G38990.1   glycosyl hydrolase family 9 protein, endo-1,4-beta-glucanase precursor - Fragaria ananassa, PID:g3549291 A short intron was annotated between exons 4 and 5 to circumvent a frameshift.	3.0	3.0	0.0	0.1	100.0%	-5.4
18512	AT2G15600.1   hypothetical protein   chr2:6812268-6812540 REVERSE   Aliases: F9O13.15	2.9	2.9	0.0	0.1	100.0%	-5.7
18513	AT1G04400.2   Symbol: CRY2   cryptochrome 2 apoprotein (CRY2) / blue light photoreceptor (PHH1), 97% identical to photolysase (PHH1)	6.8	6.8	-0.1	-0.1	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18514	AT2G37450.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr2:15729647-15732141 REVERSE   Aliases: F3G5.24, F3G5_24	6.5	6.6	-0.1	-0.1	100.0%	-4.4
18515	AT1G03090.2   Symbol: MCCA   methylcrotonyl-CoA carboxylase alpha chain, mitochondrial / 3-methylcrotonyl-CoA carboxylase 1 (MCCA), nearly identical to SP:Q42523 Methylcrotonyl-CoA carboxylase alpha chain, mitochondrial precursor (EC 6.4.1.4) (3-Methylcrotonyl-CoA carboxylase 1) (MCCase alpha subunit) (3-methylcrotonyl-CoA:carbon dioxide ligase alpha subunit) {Arabidopsis thaliana}   chr1:739687-744184 FORWARD   Aliases: None	8.5	8.5	-0.0	-0.1	100.0%	-5.2
18516	AT5G37170.1   O-methyltransferase family 2 protein, similar to caffeic acid 3-O-methyltransferase (Populus tremuloides)(SP:Q00763)   chr5:14730041-14731533 FORWARD   Aliases: MJG14.10, MJG14_10	3.1	3.0	0.0	0.1	100.0%	-5.5
18517	AT3G54100.1   expressed protein, similar to axi 1 (Nicotiana tabacum) GI:559921; contains Pfam profile PF03138: Plant protein family   chr3:20045049-20048929 REVERSE   Aliases: F24B22.60	3.0	3.0	-0.0	-0.1	100.0%	-4.7
18518	AT3G12050.2   Aha1 domain-containing protein, contains Pfam PF05146: Aha1 domain; similar to Protein C14orf3 (HSPC322) (Swiss-Prot:O95433) (Homo sapiens)   chr3:3839108-3841472 FORWARD   Aliases: MEC18.18	11.4	11.4	0.0	0.1	100.0%	-5.4
18519	AT3G59790.1   Symbol: ATMPK10   mitogen-activated protein kinase, putative / MAPK, putative (MPK10), mitogen-activated protein kinase (MAPK)(AtMPK10), PMID:12119167   chr3:22103425-22105217 FORWARD   Aliases: F24G16.60	2.7	2.7	-0.0	-0.1	100.0%	-5.2
18520	AT1G14070.1   Symbol: FUT7   xyloglucan fucosyltransferase, putative (FUT7), nearly identical to SP:Q9XI81 Probable fucosyltransferase 7 (EC 2.4.1.-) (AtFUT7) {Arabidopsis thaliana}; similar to xyloglucan fucosyltransferase GI:5231145 from (Arabidopsis thaliana)   chr1:4818545-4820147 FORWARD   Aliases: F7A19.15, F7A19_15	2.6	2.5	0.0	0.1	100.0%	-4.7
18521	AT2G45900.1   expressed protein   chr2:18893142-18895747 REVERSE   Aliases: F4I18.12	2.3	2.3	-0.0	-0.1	100.0%	-6.1
18522	AT2G47590.1   Symbol: PHR2   photolyase/blue light photoreceptor (PHR2), identical to photolyase/blue light photoreceptor PHR2 (Arabidopsis thaliana) GI:3319288; contains Pfam domain, PF00875: deoxyribodipyrimidine photolyase   chr2:19528867-19531133 FORWARD   Aliases: PHOTOLYASE/BLUE LIGHT RECEPTOR 2, T30B22.11	6.0	6.1	-0.1	-0.1	100.0%	-4.5
18523	AT5G17420.1   Symbol: IRX3   cellulose synthase, catalytic subunit (IRX3), identical to gi:5230423   chr5:5736294-5741454 REVERSE   Aliases: ATCESA7, CELLULASE SYNTHASE 7, CELLULOSE SYNTHASE CATALYTIC SUBUNIT, CESA7, IRREGULAR XYLEM 3, T10B6.80, T10B6_80	3.3	3.4	-0.1	-0.1	100.0%	-4.3
18524	AT1G33220.1   beta-1,3-glucanase, putative, similar to plant beta-1,3-glucanase bg4 GI:2808438 from (Arabidopsis thaliana)   chr1:12044852-12045859 FORWARD   Aliases: T9L6.8, T9L6_8	2.6	2.6	0.0	0.1	100.0%	-5.7
18525	AT5G35080.1   expressed protein   chr5:13371503-13374047 REVERSE   Aliases: F7N22.4, F7N22_4	7.2	7.2	0.0	0.1	100.0%	-4.7
18526	AT2G15830.1   expressed protein   chr2:6901200-6901633 FORWARD   Aliases: F19G14.17, F19G14_17	3.3	3.1	0.1	0.1	100.0%	-4.0
18527	AT5G24410.1   glucosamine/galactosamine-6-phosphate isomerase-related, contains weak similarity to Swiss-Prot:O95336 6-phosphogluconolactonase (EC 3.1.1.31) (6PGL) (Homo sapiens)   chr5:8332476-8333987 REVERSE   Aliases: K16H17.12, K16H17_12	3.0	3.1	-0.1	-0.1	100.0%	-4.2
18528	AT1G54740.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g22110.1); similar to hypothetical protein [Plasmodium falciparum 3D7] (GB:NP_704767.1)   chr1:20434478-20435653 FORWARD   Aliases: T22H22.16, T22H22_16	2.2	2.2	-0.0	-0.1	100.0%	-4.7
18529	AT1G61740.1   expressed protein, contains Pfam profile: PF01925 domain of unknown function DUF81; identical to cDNA hypothetical protein, partial GI:4079631   chr1:22801734-22804738 REVERSE   Aliases: T13M11.10, T13M11_10	5.1	5.2	-0.1	-0.1	100.0%	-4.5
18530	AT5G49020.2   protein arginine N-methyltransferase family protein, similar to protein arginine methyltransferase (Mus musculus) GI:5257221   chr5:19888504-19892146 FORWARD   Aliases: K19E20.17, K19E20_17	6.9	7.0	-0.0	-0.1	100.0%	-4.9
18531	AT1G02120.1   similar to C2 domain-containing protein / GRAM domain-containing protein [Arabidopsis thaliana] (TAIR:At3g59660.1); similar to unnamed protein product [Homo sapiens] (GB:BAC11289.1); contains InterPro domain GRAM domain (InterPro:IPR004182)	7.5	7.6	-0.1	-0.1	100.0%	-4.9
18532	AT2G14020.1   expressed protein   chr2:5900869-5901354 REVERSE   Aliases: F9B22.13, F9B22_13	3.6	3.7	-0.0	-0.1	100.0%	-5.1
18533	AT2G23350.1   Symbol: PAB4   polyadenylate-binding protein, putative / PABP, putative. Member of the Class II family of PABP proteins. Highly and ubiquitously expressed.   chr2:9950133-9953347 FORWARD   Aliases: PAB4, POLY(A) BINDING PROTEIN 4, T20D16.2, T20D16_2	7.2	7.1	0.1	0.1	100.0%	-4.8
18534	AT3G42190.1   expressed protein   chr3:14375912-14382054 FORWARD   Aliases: F26B15.2	2.8	2.9	-0.0	-0.1	100.0%	-5.4
18535	AT3G04650.1   expressed protein   chr3:1262018-1264628 FORWARD   Aliases: F7O18.13, F7O18_13	4.9	5.0	-0.0	-0.1	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18536	AT1G03990.1   alcohol oxidase-related, low similarity to long chain fatty alcohol oxidase from <i>Candida cloacae</i> (GI:6983581), <i>Candida tropicalis</i> (GI:6983594); Location of EST 248L9T7, gb:AA713296   chr1:1024846-1027615 FORWARD   Aliases: F21M11.7, F21M11_7	3.3	3.4	-0.0	-0.1	100.0%	-5.0
18537	AT2G18340.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to SP:P20075 Embryonic protein DC-8 { <i>Daucus carota</i> }; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr2:7976482-7978107 FORWARD   Aliases: T30D6.15, T30D6_15	2.9	2.9	-0.0	-0.1	100.0%	-5.6
18538	AT3G04220.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr3:1109125-1112195 REVERSE   Aliases: T6K12.16, T6K12_16	3.3	3.2	0.0	0.1	100.0%	-5.2
18539	AT2G36890.1   myb family transcription factor (MYB38), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:15492858-15494356 FORWARD   Aliases: T1J8.7, T1J8_7	2.6	2.6	-0.1	-0.1	100.0%	-4.4
18540	AT5G49380.1   expressed protein, contains Pfam domain, PF04802: Protein of unknown function (DUF625)   chr5:20042791-20044304 FORWARD   Aliases: K7J8.5, K7J8_5	3.0	3.0	0.0	0.1	100.0%	-5.3
18541	AT5G08480.2   VQ motif-containing protein, contains PF05678: VQ motif   chr5:2743621-2745112 FORWARD   Aliases: F8L15.9	2.1	2.1	-0.0	-0.1	100.0%	-5.5
18542	AT2G40990.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr2:17112175-17114258 REVERSE   Aliases: T3K9.24, T3K9_24	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18543	AT3G03550.1   zinc finger (C3HC4-type RING finger) family protein, contains zinc finger domain, C3HC4 type (RING finger) 152633.   chr3:850115-851597 REVERSE   Aliases: T12J13.17, T12J13_17	6.6	6.6	-0.1	-0.1	100.0%	-4.9
18544	AT3G45840.1   similar to DC1 domain-containing protein / UV-B light-insensitive protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g59940.1); contains InterPro domain Zn-finger-like, PHD finger (InterPro:IPR001965); contains InterPro domain Cytochrome c heme-binding site (InterPro:IPR000345); contains InterPro domain DC1 domain (InterPro:IPR004146)	2.9	3.1	-0.1	-0.1	100.0%	-4.6
18545	AT2G25810.1   tonoplast intrinsic protein, putative, similar to tonoplast intrinsic protein GI:4584429 from ( <i>Nicotiana tabacum</i> )   chr2:11019679-11021071 FORWARD   Aliases: F17H15.16, F17H15_16	2.7	2.8	-0.0	-0.1	100.0%	-4.9
18546	AT3G44690.1   expressed protein   chr3:16241672-16245202 REVERSE   Aliases: T18B22.90	2.9	2.9	-0.0	-0.1	100.0%	-5.8
18547	AT5G63930.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:25600232-25603725 FORWARD   Aliases: MBM17.3, MBM17_3	6.3	6.2	0.0	0.1	100.0%	-4.8
18548	AT3G50160.1   hypothetical protein, contains Pfam profile PF03140: Plant protein of unknown function   chr3:18609642-18611886 REVERSE   Aliases: F3A4.240	2.7	2.7	-0.0	-0.1	100.0%	-5.6
18549	AT1G27520.1   glycoside hydrolase family 47 protein, Similar to gb:U04299 mannosyl-oligosaccharide alpha-1,2-mannosidase from <i>Mus musculus</i> . ESTs gb:R84145 and gb:AA394707 come from this gene	5.2	5.3	-0.0	-0.1	100.0%	-5.0
18550	AT1G18370.1   Symbol: HIK   kinesin motor family protein (NACK1), similar to kinesin heavy chain isolog GB:AAB63609 GI:2262101 from ( <i>Arabidopsis thaliana</i> )   chr1:6319643-6323813 REVERSE   Aliases: F15H18.12, F15H18_12, HINKEL	3.6	3.7	-0.0	-0.1	100.0%	-5.0
18551	AT2G46180.1   intracellular protein transport protein USO1-related, similar to Intracellular protein transport protein USO1 (Swiss-Prot:P25386) ( <i>Saccharomyces cerevisiae</i> )   chr2:18974432-18978423 REVERSE   Aliases: T3F17.17	8.3	8.2	0.1	0.1	100.0%	-4.9
18552	AT4G27410.2   Symbol: RD26   no apical meristem (NAM) family protein (RD26), contains Pfam PF02365: No apical meristem (NAM) domain; <i>Arabidopsis thaliana</i> nap gene,PID:e1234813; identical to cDNA RD26 mRNA for NAM-like protein GI:15375403	7.3	7.2	0.1	0.1	100.0%	-4.5
18553	AT5G28090.1   hypothetical protein   chr5:10101046-10102278 FORWARD   Aliases: T24G3.20, T24G3_20	2.7	2.7	0.0	0.1	100.0%	-5.5
18554	AT1G69240.1   hydrolase, alpha/beta fold family protein, low similarity to SP:Q40708 PIR7A protein { <i>Oryza sativa</i> }, polyneuridine aldehyde esterase GI:6651393 from ( <i>Rauvolfia serpentina</i> ), ethylene-induced esterase ( <i>Citrus sinensis</i> ) GI:14279437; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:26031639-26033897 REVERSE   Aliases: F4N2.19, F4N2_19	2.4	2.3	0.0	0.1	100.0%	-5.0
18555	AT1G36550.1   hypothetical protein, weak similarity to gag-pol polyprotein ( <i>Zea mays</i> ) GI:22296822   chr1:13796743-13798497 FORWARD   Aliases: F28J9.18, F28J9_18	2.8	2.8	0.0	0.1	100.0%	-5.3
18556	AT4G13430.1   aconitase family protein / aconitate hydratase family protein, contains Pfam profile PF00330: Aconitase family (aconitate hydratase   chr4:7803929-7807865 REVERSE   Aliases: T9E8.170, T9E8_170	11.8	11.9	-0.1	-0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18557	AT3G10240.1   F-box protein-related, contains weak Pfam:PF00646 F-box domain   chr3:3166703-3167872 FORWARD   Aliases: F14P13.16	2.9	2.9	-0.0	-0.1	100.0%	-5.4
18558	AT4G04510.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:2242120-2244654 FORWARD   Aliases: F4H6.1	3.2	3.2	-0.0	-0.1	100.0%	-5.2
18559	AT3G22380.1   expressed protein   chr3:7913126-7919491 FORWARD   Aliases: None	5.9	6.0	-0.0	-0.1	100.0%	-4.8
18560	AT1G48330.1   expressed protein, similar to hypothetical protein GI:9294146 from (Arabidopsis thaliana)   chr1:17867513-17868054 FORWARD   Aliases: F11A17.11, F11A17_11	3.1	3.1	0.0	0.1	100.0%	-5.8
18561	AT1G72440.1   CCAAT-box-binding transcription factor-related, similar to CCAAT-box-binding transcription factor (CCAAT-binding factor) (CBF) (Swiss-Prot:Q03701) (Homo sapiens), GB:P53569 (Mus musculus)   chr1:27271827-27277258 REVERSE   Aliases: T10D10.9, T10D10_9	8.7	8.8	-0.1	-0.1	100.0%	-5.2
18562	AT1G09090.2   Symbol: ATRBOHB   respiratory burst oxidase protein B (RbohB) / NADPH oxidase, identical to respiratory burst oxidase protein B from Arabidopsis thaliana (gi:3242783)   chr1:2932741-2936588 FORWARD   Aliases: ATRBOHB, F7G19.4, F7G19_4, RESPIRATORY BURST OXIDASE HOMOLOG B	1.9	1.9	-0.0	-0.1	100.0%	-4.9
18563	AT5G11460.1   senescence-associated protein-related, similar to senescence-associated protein SAG102 (GI:22331931) (Arabidopsis thaliana)   chr5:3656812-3658932 REVERSE   Aliases: F15N18.50, F15N18_50	6.0	5.9	0.0	0.1	100.0%	-4.8
18564	AT3G16020.1   hypothetical protein   chr3:5438293-5438657 FORWARD   Aliases: MSL1.23	2.6	2.5	0.0	0.1	100.0%	-5.8
18565	AT2G25090.1   Symbol: CIPK16	3.1	3.0	0.1	0.1	100.0%	-4.1
18566	AT2G31100.1   lipase, putative, similar to lipase (Dianthus caryophyllus) GI:4103627; contains Pfam profile PF01764: Lipase (class 3)   chr2:13263815-13265251 REVERSE   Aliases: T16B12.9, T16B12_9	2.4	2.4	0.0	0.1	100.0%	-5.8
18567	AT4G26470.1   calcium-binding EF hand family protein, low similarity to SP:P06787 Calmodulin {Saccharomyces cerevisiae}; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:13371078-13372351 FORWARD   Aliases: M3E9.100, M3E9_100	3.2	3.1	0.1	0.1	100.0%	-4.5
18568	AT1G73000.1   expressed protein   chr1:27466753-27467382 FORWARD   Aliases: F3N23.20, F3N23_20	2.9	2.9	-0.0	-0.1	100.0%	-5.6
18569	AT3G08970.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to PIR:A47079:A47079 heat shock protein dnaJ - Lactococcus lactis; contains Pfam profile PF00226 DnaJ domain   chr3:2737542-2740535 FORWARD   Aliases: T16O11.7	2.7	2.6	0.0	0.1	100.0%	-5.6
18570	AT5G66590.1   allergen V5/Tpx-1-related family protein, contains similarity to SP:Q41495 STS14 protein precursor {Solanum tuberosum}; contains Pfam profile PF00188: SCP-like extracellular protein   chr5:26591407-26592098 FORWARD   Aliases: K1F13.27, K1F13_27	3.0	3.0	-0.0	-0.1	100.0%	-5.2
18571	AT4G13410.1   Symbol: ATCSLA15   glycosyl transferase family 2 protein, similar to beta-(1-3)-glucosyl transferase GB:AAC62210 GI:3687658 from (Bradyrhizobium japonicum), cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	2.2	2.2	-0.0	-0.1	100.0%	-5.7
18572	AT4G15650.1   protein kinase-related, contains weak similarity to protein kinase (Dictyostelium discoideum) gi:551446:emb:CAA86053   chr4:8922630-8923663 FORWARD   Aliases: DL3865W, FCAALL.351	3.2	3.2	0.0	0.1	100.0%	-5.5
18573	AT4G11110.1   Symbol: SPA2   WD-40 repeat family protein / phytochrome A-related, contains 7 WD-40 repeats (PF00400); similar to phytochrome A supressor spa1	2.9	2.9	0.0	0.1	100.0%	-5.3
18574	AT3G18450.1   expressed protein, similar to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr3:6331040-6332124 REVERSE   Aliases: MYF24.17	1.9	1.9	0.0	0.1	100.0%	-4.6
18575	AT1G69500.1   cytochrome P450 family protein, similar to Cytochrome P450 86A2 (SP:O23066) (Arabidopsis thaliana) contains Pfam profile: PF00067: Cytochrome P450   chr1:26127652-26129720 FORWARD   Aliases: F10D13.15, F10D13_15	2.8	2.8	-0.0	-0.1	100.0%	-5.7
18576	AT5G16430.1   hypothetical protein   chr5:5370353-5370610 FORWARD   Aliases: MQK4.16, MQK4_16	3.0	3.0	-0.0	-0.1	100.0%	-5.7
18577	AT4G08320.2   similar to serine/threonine protein phosphatase, putative [Arabidopsis thaliana] (TAIR:At2g42810.1); similar to CAA30373.1 protein [Oryza sativa] (GB:CAB53476.1); contains InterPro domain TPR repeat (InterPro:IPR001440)   chr4:5252808-5255516 FORWARD   Aliases: T28D5.10, T28D5_10	6.1	6.0	0.0	0.1	100.0%	-5.0
18578	AT5G65860.2   expressed protein, similar to hypothetical protein SPAC26A3.17c - fission yeast (Schizosaccharomyces pombe) (GB:T38405); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr5:26364860-26366282 REVERSE   Aliases: K14B20.3, K14B20_3	6.3	6.3	0.0	0.1	100.0%	-4.7
18579	AT5G22910.1   Symbol: ATCHX9	3.1	3.1	-0.0	-0.1	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18580	AT3G57220.1   UDP-GlcNAc:dolichol phosphate N-acetylglucosamine-1-phosphate transferase, putative, strong similarity to Gl:5804772   chr3:21185438-21188080 FORWARD   Aliases: F28O9.70, F28O9_70	6.6	6.6	-0.1	-0.1	100.0%	-4.5
18581	AT1G78360.1   Symbol: ATGSTU21   glutathione S-transferase, putative, similar to glutathione transferase Gl:2853219 from (Carica papaya)   chr1:29486963-29487859 REVERSE   Aliases: F3F9.24, F3F9_24	2.7	2.7	-0.0	-0.1	100.0%	-5.4
18582	AT1G29610.1   hypothetical protein   chr1:10345749-10346229 FORWARD   Aliases: F15D2.18, F15D2_18	2.4	2.4	0.0	0.1	100.0%	-5.6
18583	AT5G45180.1   flavin-containing monooxygenase family protein / FMO family protein, low similarity to SP:P31513 Dimethylaniline monooxygenase (N-oxide forming) 3 (EC 1.14.13.8) (Hepatic flavin-containing monooxygenase 3) (FMO 3) {Homo sapiens}; contains Pfam profile PF00743: Flavin-binding monooxygenase-like   chr5:18291406-18293795 REVERSE   Aliases: K18C1.6, K18C1_6	2.9	2.9	0.0	0.1	100.0%	-5.4
18584	AT2G05030.1   hypothetical protein   chr2:1781883-1782500 FORWARD   Aliases: F1O13.16, F1O13_16	2.2	2.2	-0.0	-0.1	100.0%	-5.9
18585	AT3G59140.1   Symbol: ATMRP14   ABC transporter family protein, putative multi resistance protein mrp - Arabidopsis thaliana, EMBL:ATMRPPROT   chr3:21874496-21879678 REVERSE   Aliases: F17J16.190	6.3	6.4	-0.1	-0.1	100.0%	-4.3
18586	AT5G13740.1   sugar transporter family protein, contains Pfam profile PF00083: major facilitator superfamily protein   chr5:4432309-4436671 FORWARD   Aliases: MSH12.21, MSH12_21	7.8	7.8	-0.1	-0.1	100.0%	-5.0
18587	AT5G04900.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 Short-chain dehydrogenase/reductase (SDR) superfamily   chr5:1434816-1437326 FORWARD   Aliases: MUG13.25, MUG13_25	5.2	5.1	0.0	0.1	100.0%	-4.5
18588	AT5G35260.1   replication protein-related, weak similarity to Replication Protein A 70	3.2	3.2	-0.0	-0.1	100.0%	-5.8
18589	AT5G35280.1   expressed protein, similar to At2g10840, At2g10500, At2g05860, At4g07310, At4g07430, At1g39270   chr5:13526852-13527760 FORWARD   Aliases: T26D22.1, T26D22_1	2.7	2.7	0.0	0.1	100.0%	-6.0
18590	AT5G07920.1   Symbol: ATDGK1/DGK1   diacylglycerol kinase 1 (DGK1), identical to diacylglycerol kinase 1 (Diglyceride kinase 1, DGK 1, DAG kinase 1) (Arabidopsis thaliana) SWISS-PROT:Q39017	8.4	8.3	0.1	0.1	100.0%	-5.1
18591	AT3G53300.1   Symbol: CYP71B31   cytochrome P450 family protein, CYTOCHROME P450 71B5, Arabidopsis thaliana, SWISSPROT:C7B5_ARATH   chr3:19771453-19773335 FORWARD   Aliases: F4P12.1	2.3	2.3	-0.0	-0.1	100.0%	-5.9
18592	AT2G33110.1   Symbol: ATVAMP723   synaptobrevin family protein, similar to Vesicle-associated membrane protein 722 (AtVAMP722) Synaptobrevin-related protein 1 (SP:P47192) {Arabidopsis thaliana}   chr2:14048115-14050370 REVERSE   Aliases: F25I18.15, F25I18_15, VAMP723	3.9	4.0	-0.1	-0.1	100.0%	-4.5
18593	AT2G33120.2   Symbol: SAR1   similar to synaptobrevin family protein [Arabidopsis thaliana] (TAIR:At1g04750.1); similar to synaptobrevin 1 [Oryza sativa (japonica cultivar-group)] (GB:CAD70274.1); contains InterPro domain Synaptobrevin (InterPro:IPR001388)   chr2:14050536-14052620 REVERSE   Aliases: ATVAMP722, F25I18.14, F25I18_14, SYNAPTOBREVIN RELATED PROTEIN 1, VAMP722	3.9	4.0	-0.1	-0.1	100.0%	-4.5
18594	AT5G35270.1   cytochrome P-450 aromatase-related, similar to minor outer capsid protein VP4 (Gl:13446784) (Human rotavirus C); similar to cytochrome P-450 aromatase (Gl:21170) (Gallus gallus);   chr5:13524678-13525611 FORWARD   Aliases: T25C13.150, T25C13_150	3.3	3.4	-0.0	-0.1	100.0%	-5.0
18595	AT2G32700.6   similar to WD-40 repeat family protein (LEUNIG) [Arabidopsis thaliana] (TAIR:At4g32551.1); similar to putative LEUNIG [Oryza sativa (japonica cultivar-group)] (GB:XP_468366.1); similar to OSJNBb0065L13.11 [Oryza sativa (japonica cultivar-group)] (GB:XP_473135.1); contains InterPro domain Lissencephaly type-1-like homology motif (InterPro:IPR006594); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr2:13873894-13879217 FORWARD   Aliases: F24L7.16, F24L7_16	7.5	7.6	-0.1	-0.1	100.0%	-5.0
18596	AT1G64930.1   Symbol: CYP89A7   cytochrome P450, putative, similar to cytochrome P450 CYP89 (SP:Q42602)(Arabidopsis thaliana); similar to cytochrome p450 Gl:438242 from (Solanum melongena)   chr1:24124589-24126124 FORWARD   Aliases: F13O11.23, F13O11_23	3.0	3.0	0.1	0.1	100.0%	-4.7
18597	AT1G12290.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.7	2.6	0.0	0.1	100.0%	-5.0
18598	AT1G61570.1   Symbol: TIM13   mitochondrial import inner membrane translocase (TIM13), identical to mitochondrial import inner membrane translocase subunit Tim13 (Arabidopsis thaliana) Swiss-Prot:Q9XH48; contains Pfam domain, PF02953: Tim10/DDP family zinc finger   chr1:22722370-22723181 REVERSE   Aliases: T25B24.8, T25B24_8, TIM13, translocase of the inner membrane 13	11.3	11.3	-0.0	-0.1	100.0%	-5.0
18599	AT4G11640.1   serine racemase, putative, similar to serine racemase (Mus musculus) Gl:6448865; contains Pfam profile PF00291: Pyridoxal-phosphate dependent enzyme   chr4:7021764-7023246 FORWARD   Aliases: T5C23.70, T5C23_70	4.8	4.8	0.0	0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18600	AT2G16660.1   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr2:7225788-7228707 REVERSE   Aliases: T24I21.7, T24I21_7	7.6	7.5	0.1	0.1	100.0%	-4.8
18601	AT2G28355.1   Symbol: LCR5   expressed protein, contains similarity to anther-specific protein GI:1448935 from (Brassica rapa)   chr2:12126397-12127331 FORWARD   Aliases: LCR5, Low molecular weight cysteine rich 5	3.0	3.0	0.0	0.1	100.0%	-5.1
18602	AT5G17030.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, similar to UDP glucose:flavonoid 3-o-glucosyltransferase from Vitis vinifera, EMBL:AF000372   chr5:5603136-5604741 REVERSE   Aliases: F2K13.180, F2K13_180	3.4	3.4	0.0	0.1	100.0%	-5.4
18603	AT2G20030.1   zinc finger (C3HC4-type RING finger) family protein, similar to RING-H2 zinc finger protein ATL6 (Arabidopsis thaliana) GI:4928403; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)	3.5	3.4	0.1	0.1	100.0%	-4.4
18604	AT1G50940.1   electron transfer flavoprotein alpha subunit family protein, contains Pfam profile: PF00766 electron transfer flavoprotein, alpha subunit   chr1:18881480-18883638 REVERSE   Aliases: F8A12.16, F8A12_16	6.8	6.9	-0.1	-0.1	100.0%	-5.2
18605	AT4G35350.2   Symbol: XCP1   cysteine endopeptidase, papain-type (XCP1), identical to papain-type cysteine endopeptidase XCP1 GI:6708181 from (Arabidopsis thaliana)   chr4:16810487-16812009 FORWARD   Aliases: F23E12.90, F23E12_90, XYLEM CYSTEINE PEPTIDASE 1	3.5	3.7	-0.1	-0.1	100.0%	-4.6
18606	AT2G33590.1   cinnamoyl-CoA reductase family, similar to cinnamoyl-CoA reductase from Pinus taeda (GI:17978649), Eucalyptus gunnii (GI:2058311)   chr2:14231344-14233678 FORWARD   Aliases: F4P9.36, F4P9_36	8.8	8.7	0.1	0.1	100.0%	-4.8
18607	AT5G57420.1   Symbol: IAA33   auxin-responsive factor-related, contains weak similarity to Swiss-Prot:P33078 auxin-responsive protein IAA5 (Indoleacetic acid-induced protein 5) (Auxin-induced protein AUX2-27) (Arabidopsis thaliana)   chr5:23287250-23288185 FORWARD   Aliases: MUA2.1, MUA2_1	2.4	2.4	0.0	0.1	100.0%	-5.7
18608	AT2G44260.2   expressed protein   chr2:18302914-18304943 FORWARD   Aliases: F4I1.7	3.0	3.0	-0.0	-0.1	100.0%	-4.9
18609	AT3G44660.1   histone deacetylase-related / HD-related, similar to SP:O09106 Histone deacetylase 1 (HD1) {Mus musculus}   chr3:16225951-16226772 REVERSE   Aliases: T18B22.60	8.4	8.4	-0.0	-0.1	100.0%	-4.9
18610	AT1G23780.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to SP:Q9Y311 F-box only protein 7 {Homo sapiens}; similar to SKP1 interacting partner 2 (SKIP2) TIGR_Ath1:At5g67250   chr1:8406675-8408514 REVERSE   Aliases: F5O8.33, F5O8_33	7.0	6.9	0.0	0.1	100.0%	-5.2
18611	AT5G10960.1   CCR4-NOT transcription complex protein, putative, similar to SWISS-PROT:Q9UFF9 CCR4-NOT transcription complex, subunit 8 (CAF1-like protein, CALIFp) (Homo sapiens)   chr5:3464249-3465688 FORWARD   Aliases: T30N20.230, T30N20_230	7.5	7.4	0.1	0.1	100.0%	-4.7
18612	AT5G22890.1   zinc finger (C2H2 type) family protein, contains Pfam domain PF00096: Zinc finger, C2H2 type   chr5:7653264-7654727 REVERSE   Aliases: MRN17.12, MRN17_12	2.9	2.9	0.0	0.1	100.0%	-5.4
18613	AT3G26200.1   Symbol: CYP71B22   cytochrome P450 71B22, putative (CYP71B22), identical to cytochrome P450 71B22 (SP:Q9LTM1)(Arabidopsis thaliana);contains Pfam profile: PF00067 cytochrome P450   chr3:9590519-9592416 FORWARD   Aliases: MTC11.11	3.2	3.2	-0.0	-0.1	100.0%	-5.1
18614	AT1G80880.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:30400086-30401813 REVERSE   Aliases: F23A5.24, F23A5_24	2.7	2.7	0.0	0.1	100.0%	-5.3
18615	AT5G41310.1   kinesin motor protein-related   chr5:16533862-16539620 REVERSE   Aliases: K1O13.11, K1O13_11	2.9	2.9	-0.0	-0.1	100.0%	-5.4
18616	AT3G20460.1   sugar transporter, putative, similar to ERD6 protein (Arabidopsis thaliana) GI:3123712, sugar-porter family proteins 1 and 2 (Arabidopsis thaliana) GI:14585699, GI:14585701; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:7135056-7139478 FORWARD   Aliases: MQC12.5	3.5	3.5	0.1	0.1	100.0%	-4.3
18617	AT3G42080.1   hypothetical protein, hypothetical proteins - Arabidopsis thaliana   chr3:14271580-14272153 FORWARD   Aliases: F4M19.40	2.6	2.6	0.0	0.1	100.0%	-5.9
18618	AT4G13345.2   TMS membrane family protein / tumour differentially expressed (TDE) family protein, contains Pfam domain, PF03348: TMS membrane protein/tumour differentially expressed protein (TDE)   chr4:7765117-7769677 FORWARD   Aliases: None	3.8	3.8	-0.0	-0.1	100.0%	-5.3
18619	AT3G02390.1   expressed protein   chr3:489066-489478 FORWARD   Aliases: F11A12.8, F11A12_8	3.3	3.4	-0.1	-0.1	100.0%	-5.0
18620	AT1G50720.1   stigma-specific Stig1 family protein, similar to stigma-specific protein STIG1 (Nicotiana tabacum) GI:496647; contains Pfam profile PF04885: Stigma-specific protein, Stig1   chr1:18792848-18793312 REVERSE   Aliases: F17J6.24, F17J6_24	3.2	3.2	-0.0	-0.1	100.0%	-5.3
18621	AT3G55070.1   expressed protein   chr3:20419263-20422117 FORWARD   Aliases: T15C9.70	5.8	5.9	-0.1	-0.1	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18622	AT5G02600.2   heavy-metal-associated domain-containing protein, low similarity to gi:3168840 copper homeostasis factor; contains Pfam heavy-metal-associated domain PF00403; predicted proteins, Arabidopsis thaliana   chr5:584160-586895 REVERSE   Aliases: T22P11.190, T22P11_190	3.2	3.2	-0.0	-0.1	100.0%	-5.2
18623	AT2G05530.1   glycine-rich protein   chr2:2029709-2030541 FORWARD   Aliases: T20G20.12, T20G20_12	5.5	5.4	0.1	0.1	100.0%	-4.7
18624	AT4G11880.1   Symbol: AGL14   MADS-box protein (AGL14), nearly identical to MADS-box protein AGL14 GI:862644   chr4:7143506-7147216 FORWARD   Aliases: AGAMOUS LIKE 14, T26M18.90, T26M18_90	5.9	5.9	-0.1	-0.1	100.0%	-4.8
18625	AT2G04870.1   expressed protein   chr2:1716165-1716383 REVERSE   Aliases: F28I8.6, F28I8_6	3.5	3.6	-0.0	-0.1	100.0%	-5.2
18626	AT1G51690.2   Symbol: ATB ALPHA   serine/threonine protein phosphatase 2A (PP2A) 55 kDa regulatory subunit B, identical to 55 kDa B regulatory subunit of phosphatase 2A (GI:710330) (Arabidopsis thaliana); similar to type 2A protein serine/threonine phosphatase 55 kDa B regulatory GI:1408460 (Arabidopsis thaliana); contains Pfam PF00400: WD domain, G-beta repeat (5 copies, 3 weak)   chr1:19169643-19174114 FORWARD   Aliases: F19C24.10, F19C24_10	4.5	4.5	-0.0	-0.1	100.0%	-4.9
18627	AT3G21370.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to beta-glucosidase (GI:757740) (Brassica napus); similar to beta-glucosidase GB:AAB64244 from (Arabidopsis thaliana), (Plant Mol. Biol. 34 (1), 57-68 (1997))	2.9	2.9	0.0	0.1	100.0%	-5.1
18628	AT5G62380.1   Symbol: ANAC101   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain; OsNAC7, Oryza sativa, EMBL:AB028186   chr5:25067910-25069084 FORWARD   Aliases: ANAC101, MMI9.6, MMI9_6	2.5	2.5	0.0	0.1	100.0%	-5.9
18629	AT4G30090.1   Symbol: EMB1353   expressed protein   chr4:14708723-14711618 REVERSE   Aliases: EMB1353, EMBRYO DEFECTIVE 1353, F6G3.120, F6G3_120	3.0	3.0	-0.0	-0.1	100.0%	-5.5
18630	AT3G46970.1   Encodes a cytosolic alpha-glucan phosphorylase.   chr3:17312379-17317431 REVERSE   Aliases: F13I12.20	8.2	8.3	-0.0	-0.1	100.0%	-4.7
18631	AT5G19150.2   carbohydrate kinase family, contains Pfam profile PF01256: Carbohydrate kinase   chr5:6423307-6428456 REVERSE   Aliases: T24G5.50, T24G5_50	8.1	8.1	-0.0	-0.1	100.0%	-5.0
18632	AT5G34850.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	8.1	8.0	0.1	0.1	100.0%	-4.8
18633	AT1G07210.1   30S ribosomal protein S18 family, contains Pfam profile: PF01084 ribosomal protein S18; similar to 30S ribosomal protein S18 (SP:P80382) {Thermus thermophilus}   chr1:2215235-2217391 FORWARD   Aliases: F10K1.8, F10K1_8	5.8	5.8	0.0	0.1	100.0%	-4.7
18634	AT5G61260.1   chromosome scaffold protein-related, contains weak similarity to chromosome scaffold protein p85 (Moneuplotes crassus) gi:25990101:gb:AAN75020   chr5:24654335-24655825 FORWARD   Aliases: MFB13.3, MFB13_3	2.7	2.8	-0.1	-0.1	100.0%	-4.2
18635	AT4G19320.1   expressed protein, similar to At5g28170, At1g35110, At1g44880, At3g42530, At5g36020, At4g03970, At3g43010, At2g10350   chr4:10549359-10552983 REVERSE   Aliases: T5K18.100, T5K18_100	2.1	2.1	-0.0	-0.1	100.0%	-5.8
18636	AT5G36020.1   hypothetical protein, similar to At5g28170, At1g35110, At1g44880, At3g42530, At4g19320, At4g03970, At3g43010, At2g10350   chr5:14176551-14180178 FORWARD   Aliases: MEE13.17, MEE13_17	2.1	2.1	-0.0	-0.1	100.0%	-5.8
18637	AT3G49790.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:18479036-18480748 REVERSE   Aliases: T16K5.140	3.4	3.3	0.0	0.1	100.0%	-5.3
18638	AT3G04500.1   RNA recognition motif (RRM)-containing protein, similar to ssRNA-binding protein (Dictyostelium discoideum) GI:1546894; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr3:1211768-1213854 REVERSE   Aliases: T27C4.15, T27C4_15	4.2	4.3	-0.0	-0.1	100.0%	-5.1
18639	AT2G32160.2   expressed protein   chr2:13669296-13673346 FORWARD   Aliases: F22D22.9, F22D22_9	2.8	2.8	-0.0	-0.1	100.0%	-5.5
18640	AT5G22960.1   serine carboxypeptidase S10 family protein, similar to serine carboxypeptidase III (Precursor) (SP:P37891) (Oryza sativa)   chr5:7684017-7685055 REVERSE   Aliases: MRN17.19, MRN17_19	2.1	2.1	0.0	0.1	100.0%	-5.5
18641	AT5G08630.1   DDT domain-containing protein, low similarity to SP:Q9NRL2 Bromodomain adjacent to zinc finger domain protein 1A (ATP-utilizing chromatin assembly and remodeling factor 1) (ATP-dependent chromatin remodelling protein) (Williams syndrome transcription factor-related chromatin remodeling factor 180) {Homo sapiens}; contains Pfam profile PF02791: DDT domain   chr5:2798392-2803172 REVERSE   Aliases: MAH20.19, MAH20_19	6.1	6.1	-0.1	-0.1	100.0%	-4.9
18642	AT1G12470.1   Pep3/Vps18/deep orange family protein, contains Pfam profile PF05131: Pep3/Vps18/deep orange family; similar to Vacuolar protein sorting 18 (hVPS18) (SP:Q9P253) {Homo sapiens}   chr1:4251357-4257663 FORWARD   Aliases: F5O11.22, F5O11_22	5.9	6.0	-0.1	-0.1	100.0%	-4.8
18643	AT3G25040.1   ER lumen protein retaining receptor, putative / HDEL receptor, putative, similar to SP:P35402 ER lumen protein retaining receptor (HDEL receptor) {Arabidopsis thaliana}; contains Pfam profile PF00810: ER lumen protein retaining receptor   chr3:9124313-9126301 FORWARD   Aliases: K3G3.1	6.7	6.7	-0.1	-0.1	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18644	AT1G42393.1   expressed protein   chr1:15864058-15864714 REVERSE   Aliases: None	2.4	2.4	0.0	0.1	100.0%	-5.8
18645	AT1G48650.1   helicase domain-containing protein, contains similarity to DEIH-box RNA/DNA helicase (Arabidopsis thaliana) GI:5881579; contains Pfam profiles PF04408: Helicase associated domain (HA2), PF00271: Helicase conserved C-terminal domain, PF00035: Double-stranded RNA binding motif   chr1:17992826-17998994 REVERSE   Aliases: F11I4.16, F11I4_16	4.5	4.5	-0.1	-0.1	100.0%	-4.8
18646	AT3G02670.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr3:573787-574633 REVERSE   Aliases: F16B3.30, F16B3_30	2.7	2.7	0.0	0.1	100.0%	-5.6
18647	AT1G10610.1   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	5.4	5.4	-0.1	-0.1	100.0%	-4.7
18648	AT5G54090.1   DNA mismatch repair MutS family protein, low similarity to SP:Q56239 DNA mismatch repair protein mutS {Thermus aquaticus; contains Pfam profile PF00488: MutS domain V   chr5:21965109-21969776 REVERSE   Aliases: MJP23.7, MJP23_7	4.2	4.2	-0.0	-0.1	100.0%	-5.1
18649	AT1G31330.1   photosystem I reaction center subunit III family protein, contains Pfam profile: PF02507: photosystem I reaction center subunit III   chr1:11214805-11215992 REVERSE   Aliases: T19E23.12, T19E23_12	7.3	7.3	0.0	0.1	100.0%	-5.0
18650	AT5G62730.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr5:25214720-25217259 FORWARD   Aliases: MQB2.30, MQB2_30	2.7	2.7	0.0	0.1	100.0%	-5.3
18651	AT3G16860.1   phytochelatin synthetase-related, contains Pfam PF04833: Phytochelatin synthetase-like conserved region   chr3:5759381-5762241 REVERSE   Aliases: MUH15.2	3.6	3.6	-0.0	-0.1	100.0%	-5.1
18652	AT5G15680.1   expressed protein   chr5:5101191-5110796 REVERSE   Aliases: F14F8.60, F14F8_60	3.7	3.8	-0.0	-0.1	100.0%	-5.1
18653	AT4G21620.1   glycine-rich protein   chr4:11491495-11492179 FORWARD   Aliases: F17L22.80, F17L22_80	10.2	10.3	-0.1	-0.1	100.0%	-4.3
18654	AT1G28350.1   similar to tRNA synthetase class I (W and Y) family protein [Arabidopsis thaliana] (TAIR:At2g33840.1); similar to putative tyrosyl-tRNA synthetase [Oryza sativa (japonica cultivar-group)] (GB:XP_480120.1); contains InterPro domain Aminoacyl-tRNA synthetase, class Ib (InterPro:IPR002305)   chr1:9944470-9949786 FORWARD   Aliases: F3M18.22, F3M18_22	10.0	10.0	-0.1	-0.1	100.0%	-4.7
18655	AT2G33840.1   tRNA synthetase class I (W and Y) family protein, similar to SP:P54577 Tyrosyl-tRNA synthetase (EC 6.1.1.1) (Tyrosyl--tRNA ligase) (TyrRS) {Homo sapiens}; contains Pfam profile PF00579: tRNA synthetases class I (W and Y)   chr2:14322044-14324575 FORWARD   Aliases: T1B8.14, T1B8_14	10.0	10.0	-0.1	-0.1	100.0%	-4.7
18656	AT4G38820.1   expressed protein   chr4:18121537-18121969 REVERSE   Aliases: T9A14.100, T9A14_100	2.7	2.7	0.0	0.1	100.0%	-5.6
18657	AT3G57370.1   transcription factor IIB (TFIIB) family protein, contains Pfam profile: PF00382 transcription factor TFIIB repeat   chr3:21237816-21239452 REVERSE   Aliases: F28O9.220	3.1	3.1	-0.0	-0.1	100.0%	-5.4
18658	AT4G10820.1   F-box family protein, similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)   chr4:6648005-6648905 REVERSE   Aliases: F25I24.30, F25I24_30	3.6	3.6	-0.0	-0.1	100.0%	-5.6
18659	AT5G35620.2   Symbol: LSP1   eukaryotic translation initiation factor 4E 2 / eIF-4E2 / mRNA cap-binding protein 2 (EIF4E2), identical to SP:O04663 Eukaryotic translation initiation factor 4E (eIF-4E) (eIF4E) (mRNA cap-binding protein) (eIF-(iso)4F 25 kDa subunit) (eIF-(ISO)4F P28 subunit) (eIF4Eiso protein) {Arabidopsis thaliana}   chr5:13841959-13843598 REVERSE   Aliases: EIF(ISO)4E, LOSS OF SUSCEPTIBILITY TO POTYVIRUSES, LSP, MJE4.8, MJE4_8	7.8	7.8	0.1	0.1	100.0%	-4.7
18660	AT5G53130.1   Symbol: CNGC1   cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC1), almost identical to cyclic nucleotide-regulated ion channel 1 pir:T51354, GI:11357236 from (Arabidopsis thaliana)   chr5:21554811-21558255 REVERSE   Aliases: ATCNGC1, CYCLIC NUCLEOTIDE GATED CHANNEL 1, MFH8.6, MFH8_6	7.5	7.5	0.0	0.1	100.0%	-5.3
18661	AT1G73910.1   Symbol: ATARP4A   Encodes a gene similar to actin-related proteins in other organisms. Member of nuclear ARP family of genes. Component	2.1	2.1	-0.0	-0.1	100.0%	-6.0
18662	AT2G39930.1   Symbol: ATISA1/ISA1   isoamylase, putative / starch debranching enzyme, putative, similar to isoamylase from (Solanum tuberosum) GI:27728145, (Triticum aestivum) GI:17932898, (Hordeum vulgare) GI:21314275, (Oryza sativa) GI:3252794; contains Pfam profiles PF00128: Alpha amylase catalytic domain, PF02922: Isoamylase N-terminal domain. Mutants have reduced starch content and abnormally structured amylopectins and phytoglycogens.   chr2:16673125-16680012 FORWARD   Aliases: ATISA1, ISA1, T28M21.9, T28M21_9	7.3	7.2	0.1	0.1	100.0%	-4.6
18663	AT3G21830.1   Symbol: ASK8   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At8), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1b GI:3068809, UIP2 GI:3719211 from (Arabidopsis thaliana)   chr3:7693488-7693946 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 8, ASK8, MSD21.20	2.2	2.2	-0.0	-0.1	100.0%	-6.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18664	AT3G55940.1   phosphoinositide-specific phospholipase C, putative, similar to phosphoinositide specific phospholipase C GI:857374 from (Arabidopsis thaliana)   chr3:20758766-20761163 FORWARD   Aliases: F27K19.120	3.1	3.1	-0.0	-0.1	100.0%	-5.1
18665	AT5G55990.1   Symbol: CBL2   calcineurin B-like protein 2 (CBL2), identical to calcineurin B-like protein 2 GI:3309084 from (Arabidopsis thaliana)   chr5:22688678-22691081 FORWARD   Aliases: ATCBL2, MDA7.3, MDA7_3	7.5	7.5	0.0	0.1	100.0%	-4.9
18666	AT5G21010.1   Symbol: ATBPM5	5.0	5.0	0.0	0.1	100.0%	-5.2
18667	AT1G56160.1   myb family transcription factor (MYB72), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA putative transcription factor (MYB72) mRNA, partial cds GI:3941501   chr1:21026049-21027252 FORWARD   Aliases: F14G9.22	2.9	3.0	-0.1	-0.1	100.0%	-4.8
18668	AT2G10850.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g43970.1); similar to envelope-like protein [Glycine max] (GB:AAO73530.1)   chr2:4283406-4284587 REVERSE   Aliases: F16G22.9, F16G22_9	3.4	3.4	0.0	0.1	100.0%	-5.5
18669	AT2G34490.1   Symbol: CYP710A2   cytochrome P450 family protein, similar to Cytochrome P450 61 (C-22 sterol desaturase) (SP:P54781) {Saccharomyces cerevisiae}; contains Pfam profile: PF00067 cytochrome P450; supported by full-length cDNA: Ceres:158108.   chr2:14542724-14544511 REVERSE   Aliases: F13P17.22	2.3	2.3	0.0	0.1	100.0%	-5.9
18670	AT3G53700.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr3:19911258-19913862 FORWARD   Aliases: F5K20.2	5.4	5.4	-0.0	-0.1	100.0%	-4.8
18671	AT2G10500.1   hypothetical protein, similar to At2g10840, At5g35280, At2g05860, At4g07310, At4g07430, At1g39270   chr2:4051809-4052829 FORWARD   Aliases: T4D8.9, T4D8_9	2.4	2.4	0.0	0.1	100.0%	-6.0
18672	AT2G21040.1   C2 domain-containing protein, low similarity to phloem protein (Cucurbita maxima) GI:4164541; contains Pfam profile PF00168: C2 domain   chr2:9033238-9034391 FORWARD   Aliases: F26H11.20, F26H11_20	3.6	3.6	0.0	0.1	100.0%	-5.1
18673	AT3G13230.1   expressed protein   chr3:4269985-4271211 FORWARD   Aliases: MDC11.5	6.3	6.2	0.1	0.1	100.0%	-4.9
18674	AT1G07120.1   expressed protein   chr1:2184758-2186579 REVERSE   Aliases: F10K1.18, F10K1_18	2.9	2.9	-0.0	-0.1	100.0%	-5.3
18675	AT4G22440.1   expressed protein   chr4:11831036-11832280 FORWARD   Aliases: F7K2.20, F7K2_20	2.9	2.9	-0.0	-0.1	100.0%	-5.5
18676	AT3G04210.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr3:1105976-1108076 REVERSE   Aliases: T6K12.17, T6K12_17	3.0	3.0	-0.0	-0.1	100.0%	-5.7
18677	AT5G40010.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr5:16037446-16038990 REVERSE   Aliases: MYH19.21, MYH19_21	3.1	3.0	0.1	0.1	100.0%	-4.8
18678	AT2G23970.1   defense-related protein, putative, similar to defense-related protein (Brassica carinata) GI:14009290   chr2:10206778-10208161 FORWARD   Aliases: T29E15.17, T29E15_17	4.8	4.8	0.0	0.1	100.0%	-4.6
18679	AT2G23390.1   expressed protein   chr2:9967452-9970699 REVERSE   Aliases: F26B6.4, F26B6_4	6.2	6.3	-0.0	-0.1	100.0%	-4.7
18680	AT3G48680.1   bacterial transferase hexapeptide repeat-containing protein, contains Pfam profile PF00132: Bacterial transferase hexapeptide (four repeats); ferripyochelin binding protein - Methanobacterium thermoautotrophicum, EMBL:AE000918.1   chr3:18046092-18047789 FORWARD   Aliases: T8P19.190	11.0	11.1	-0.1	-0.1	100.0%	-5.3
18681	AT1G64570.1   expressed protein   chr1:23982531-23987588 FORWARD   Aliases: F1N19.14, F1N19_14	3.2	3.2	0.0	0.1	100.0%	-5.5
18682	AT4G12650.1   endomembrane protein 70, putative, TM4 family;   chr4:7467975-7469787 REVERSE   Aliases: T1P17.240, T1P17_240	7.3	7.2	0.1	0.1	100.0%	-5.0
18683	AT1G52660.1   disease resistance protein, putative, similar to NBS/LRR disease resistance protein GI:9758302 from (Arabidopsis thaliana)   chr1:19617143-19618354 FORWARD   Aliases: F6D8.12, F6D8_12	3.5	3.5	0.0	0.1	100.0%	-5.1
18684	AT1G58210.1   Symbol: EMB1674   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) {Petunia integrifolia}   chr1:21557286-21561721 FORWARD   Aliases: EMB1674, EMBRYO DEFECTIVE 1674, F16M22.3, F16M22_3	2.5	2.6	-0.0	-0.1	100.0%	-5.7
18685	AT2G43840.2   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:18164715-18166252 FORWARD   Aliases: F18O19.5	5.7	5.8	-0.0	-0.1	100.0%	-5.1
18686	AT1G66850.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to GP:3062791 Lipid transfer protein {Brassica rapa}; contains Pfam profile: PF00234: protease inhibitor/seed storage/LTP family   chr1:24940621-24941097 FORWARD   Aliases: F4N21.4, F4N21_4	2.4	2.4	-0.0	-0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18687	AT1G13090.1   Symbol: CYP71B28   cytochrome P450 71B28, putative (CYP71B28), Identical to Cytochrome P450 (SP:Q9SAE3) (Arabidopsis thaliana); strong similarity to gb:X97864 cytochrome P450 from Arabidopsis thaliana and is a member of the PF:00067 Cytochrome P450 family. ESTs gb:N65665, gb:T14112, gb:T76255, gb:T20906 and gb:AI100027 come from this gene   chr1:4461804-4463541 FORWARD   Aliases: F3F19.11, F3F19_11	7.0	7.1	-0.0	-0.1	100.0%	-4.9
18688	AT3G53080.1   galactose-binding lectin family protein, contains Pfam domain PF02140: Galactose binding lectin domain   chr3:19688974-19689717 FORWARD   Aliases: T4D2.10	2.3	2.3	-0.0	-0.1	100.0%	-5.7
18689	AT5G37570.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:14941724-14943376 REVERSE   Aliases: K12B20.3, K12B20_3	3.3	3.3	-0.0	-0.1	100.0%	-5.2
18690	AT2G25510.1   expressed protein   chr2:10863505-10864234 FORWARD   Aliases: F13B15.17, F13B15_17	2.6	2.5	0.0	0.1	100.0%	-5.7
18691	AT3G32160.1   expressed protein   chr3:13149153-13149666 FORWARD   Aliases: F1M23.1	2.7	2.7	0.0	0.1	100.0%	-5.4
18692	AT1G75460.1   ATP-dependent protease La (LON) domain-containing protein, weak similarity to SP:P36774 ATP-dependent protease La 2 (EC 3.4.21.53) {Myxococcus xanthus}; contains Pfam profile PF02190: ATP-dependent protease La (LON) domain   chr1:28331547-28333425 FORWARD   Aliases: F1B16.1, F1B16_1	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18693	AT5G59040.1   Symbol: COPT3   copper transporter family protein, similar to SP:Q39065 Copper transporter 1 (COPT1) {Arabidopsis thaliana}; contains Pfam profile PF04145: Ctr copper transporter family   chr5:23853912-23854485 FORWARD   Aliases: K18B18.3, K18B18_3	3.7	3.6	0.0	0.1	100.0%	-5.4
18694	AT4G13130.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr4:7647385-7649827 FORWARD   Aliases: F17N18.20, F17N18_20	3.1	3.2	-0.1	-0.1	100.0%	-4.5
18695	AT4G34290.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr4:16410836-16412389 FORWARD   Aliases: F10M10.60, F10M10_60	3.9	4.0	-0.1	-0.1	100.0%	-4.8
18696	AT1G13560.2   Symbol: AAPT1   aminoalcoholphosphotransferase (AAPT1), identical to aminoalcoholphosphotransferase GI:3661593 from (Arabidopsis thaliana)   chr1:4638511-4642041 REVERSE   Aliases: AMINOALCOHOLPHOSPHOTRANSFERASE, AMINOALCOHOLPHOSPHOTRANSFERASE 1, F13B4.5, F13B4_5	8.5	8.4	0.1	0.1	100.0%	-4.7
18697	AT1G79880.3   La domain-containing protein, contains Pfam profile PF05383: La domain; similar to putative protein GB:CAA18589 (Arabidopsis thaliana)   chr1:30050954-30053254 REVERSE   Aliases: F19K16.16, F19K16_16	6.1	6.0	0.1	0.1	100.0%	-4.6
18698	AT5G16490.1   Symbol: RIC4   p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	3.2	3.1	0.1	0.1	100.0%	-4.5
18699	AT4G10140.1   expressed protein   chr4:6322453-6324660 FORWARD   Aliases: F28M11.60, F28M11_60	6.7	6.7	-0.1	-0.1	100.0%	-4.7
18700	AT1G27970.1   nuclear transport factor 2 (NTF2), putative, similar to Swiss-Prot:P33331 nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10) (Saccharomyces cerevisiae)   chr1:9746798-9748006 FORWARD   Aliases: F13K9.26, F13K9_26	9.1	9.2	-0.1	-0.1	100.0%	-4.5
18701	AT3G47130.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain;	2.4	2.4	0.0	0.1	100.0%	-5.6
18702	AT5G04960.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:1461911-1463970 FORWARD   Aliases: MUG13.18, MUG13_18	2.8	2.9	-0.1	-0.1	100.0%	-4.5
18703	AT4G03380.1   expressed protein   chr4:1485048-1490227 REVERSE   Aliases: F4C21.34, F4C21_34	3.2	3.2	0.0	0.1	100.0%	-5.5
18704	AT4G16620.1   integral membrane family protein / nodulin MtN21-related, low similarity to MtN21 (Medicago truncatula) GI:2598575   chr4:9358139-9360082 REVERSE   Aliases: DL4335C, FCAALL.421	3.2	3.3	-0.0	-0.1	100.0%	-5.0
18705	AT5G14130.1   peroxidase, putative, identical to peroxidase ATP20a (Arabidopsis thaliana) gi:1546694:emb:CAA67338   chr5:4558101-4560069 REVERSE   Aliases: MUA22.13, MUA22_13	3.5	3.6	-0.1	-0.1	100.0%	-5.0
18706	AT5G04930.1   Symbol: ALA1   phospholipid-transporting ATPase 1 / aminophospholipid flippase 1 / magnesium-ATPase 1 (ALA1), nearly identical to SP:P98204 Phospholipid-transporting ATPase 1 (EC 3.6.3.1) (Aminophospholipid flippase 1) {Arabidopsis thaliana}; contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr5:1444871-1449818 FORWARD   Aliases: None	5.7	5.8	-0.0	-0.1	100.0%	-5.1
18707	AT5G39020.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:15634147-15636588 FORWARD   Aliases: MXF12.30, MXF12_30	2.7	2.6	0.0	0.1	100.0%	-4.9
18708	AT3G19430.1   late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (Picea glauca) GI:1350543   chr3:6736190-6738336 REVERSE   Aliases: MLD14.16	2.2	2.3	-0.0	-0.1	100.0%	-5.9



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18709	AT5G63660.1   Symbol: LCR74/PDF2.5   plant defensin-fusion protein, putative (PDF2.5), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be)   chr5:25502918-25503288 FORWARD   Aliases: LCR74, Low molecular weight cysteine rich 74, MBK5.14, MBK5_14, PDF2.5	2.3	2.3	-0.1	-0.1	100.0%	-5.1
18710	AT4G15150.1   glycine-rich protein   chr4:8641673-8642279 REVERSE   Aliases: DL3620C, FCAALL.210	4.1	4.1	0.0	0.1	100.0%	-5.0
18711	AT2G19940.2   semialdehyde dehydrogenase family protein, similar to N-acetyl-glutamyl-phosphate reductase (Campylobacter jejuni) GI:6650362; contains Pfam profiles PF02774: Semialdehyde dehydrogenase dimerisation domain, PF01118: Semialdehyde dehydrogenase NAD binding domain   chr2:8620116-8623099 FORWARD   Aliases: F6F22.3, F6F22_3	9.3	9.3	-0.1	-0.1	100.0%	-4.5
18712	AT3G09020.1   alpha 1,4-glycosyltransferase family protein / glycosyltransferase sugar-binding DXD motif-containing protein, low similarity to alpha-1,4-N-acetylglucosaminyltransferase, Homo sapiens (gi:5726306), Gb3 synthase, Rattus norvegicus (gi:9082162) ; contains Pfam profiles PF04572: Alpha 1,4-glycosyltransferase conserved region, PF04488: Glycosyltransferase sugar-binding region containing DXD motif   chr3:2753312-2754626 FORWARD   Aliases: T16O11.2	2.3	2.2	0.1	0.1	100.0%	-4.4
18713	AT4G17880.1   basic helix-loop-helix (bHLH) family protein, bHLH protein, Arabidopsis thaliana, PATCHX:E255557	4.8	4.8	-0.0	-0.1	100.0%	-4.9
18714	AT3G58460.1   rhomboid family protein / ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profiles PF01694: Rhomboid family, PF00627: UBA/TS-N domain   chr3:21634160-21637420 REVERSE   Aliases: F14P22.50	5.4	5.3	0.1	0.1	100.0%	-4.8
18715	AT3G10770.2   expressed protein   chr3:3372275-3374276 REVERSE   Aliases: T7M13.15	10.1	10.1	-0.0	-0.1	100.0%	-5.0
18716	AT1G08670.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain;similar to epsin 2b (GI:3894397) (Homo sapiens)   chr1:2760349-2761554 REVERSE   Aliases: F22O13.15, F22O13_15	3.3	3.5	-0.1	-0.1	100.0%	-4.3
18717	AT1G66170.1   Symbol: MMD1   PHD finger family protein (MMD1), contains Pfam profile: PF00628: PHD-finger   chr1:24642348-24645157 REVERSE   Aliases: F15E12.11, F15E12_11, MALE MEIOCYTE DEATH 1	2.9	2.9	-0.0	-0.1	100.0%	-6.0
18718	AT1G11990.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown; previously annotated as 'growth regulator protein -related' based on similarity to axi 1 protein (GB:X80301) (GI:559920) from (Nicotiana tabacum), which, due to scientific fraud was retracted. Retraction in: Schell J. EMBO J 1999 May 17;18(10):2908. PMID:10400497.; expression supported by MPSS   chr1:4046244-4049058 REVERSE   Aliases: F12F1.14, F12F1_14	2.0	2.0	0.0	0.1	100.0%	-6.2
18719	AT3G28470.1   myb family transcription factor (MYB35), similar to Atmyb103 GB:AAD40692 from (Arabidopsis thaliana); contains PFAM profile: myb DNA binding domain PF00249   chr3:10675745-10676961 REVERSE   Aliases: MFJ20.19	2.0	2.0	-0.0	-0.1	100.0%	-6.1
18720	AT3G04450.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:1184308-1186270 FORWARD   Aliases: T27C4.10, T27C4_10	3.1	3.0	0.0	0.1	100.0%	-5.3
18721	AT3G55030.1   phosphatidylglycerolphosphate synthase, putative, similar to phosphatidylglycerolphosphate synthase GI:13365519 from (Arabidopsis thaliana); contains non-consensus CG acceptor splice site at exon 4   chr3:20407737-20409630 FORWARD   Aliases: T15C9.30	7.0	7.1	-0.0	-0.1	100.0%	-4.7
18722	AT5G18910.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:6306830-6309421 REVERSE   Aliases: F17K4.160, F17K4_160	2.9	2.9	-0.0	-0.1	100.0%	-5.9
18723	AT3G07490.1   calcium-binding protein, putative, similar to calcium-binding protein GI:6580549 from (Lotus japonicus)   chr3:2391195-2391656 FORWARD   Aliases: F21O3.20	3.0	3.0	0.1	0.1	100.0%	-4.3
18724	AT4G39740.1   electron transport SCO1/SenC family protein, similar to SP:P23833 SCO1 protein, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF02630: SCO1/SenC   chr4:18435288-18437118 REVERSE   Aliases: T19P19.130, T19P19_130	4.1	4.1	0.0	0.1	100.0%	-5.0
18725	AT4G15610.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:8909098-8910906 FORWARD   Aliases: DL3845W, FCAALL.139	5.0	5.0	0.0	0.1	100.0%	-4.6
18726	AT2G34890.1   CTP synthase, putative / UTP--ammonia ligase, putative, similar to SP:P17812 CTP synthase (EC 6.3.4.2) (UTP--ammonia ligase) {Homo sapiens}; contains Pfam profile PF00117: glutamine amidotransferase class-I   chr2:14725274-14728350 REVERSE   Aliases: F19I3.12, F19I3_12	3.1	3.1	0.0	0.1	100.0%	-5.6
18727	AT2G16270.1   expressed protein, and genefinder; expression supported by MPSS	4.3	4.2	0.0	0.1	100.0%	-5.1
18728	AT1G01060.3   Symbol: LHY   similar to myb-related transcription factor (CCA1) [Arabidopsis thaliana] (TAIR:At2g46830.1); similar to LHY protein [Phaseolus vulgaris] (GB:CAD12767.2); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005); contains InterPro domain Myb-like DNA-binding domain, SHAQKYF class (InterPro:IPR006447)	4.1	4.1	0.1	0.1	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18729	AT4G30120.1   Symbol: HMA3   ATPase E1-E2 type family protein / heavy-metal-associated domain-containing protein, similar to cadmium efflux ATPase (Streptococcus thermophilus) GI:22416341; contains Pfam profile PF00122: E1-E2 ATPase   chr4:14730407-14733508 REVERSE   Aliases: F6G3.150, F6G3_150	3.7	3.7	-0.1	-0.1	100.0%	-4.3
18730	AT2G36970.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:15536085-15537828 FORWARD   Aliases: T1J8.15, T1J8_15	6.1	6.1	0.1	0.1	100.0%	-4.5
18731	AT2G47380.1   cytochrome c oxidase subunit Vc family protein / COX5C family protein, contains Pfam profile: PF05799 cytochrome c oxidase subunit Vc (COX5C)   chr2:19448025-19449123 FORWARD   Aliases: T8I13.22	12.2	12.2	-0.0	-0.1	100.0%	-5.6
18732	AT5G61880.2   signaling molecule-related, contains similarity to mitochondria-associated granulocyte macrophage CSF signaling molecule, mitochondrial precursor (CGI-136) (Mus musculus) SWISS-PROT:Q9CQV1   chr5:24867542-24868997 FORWARD   Aliases: MAC9.20, MAC9_20	7.3	7.2	0.1	0.1	100.0%	-4.5
18733	AT1G55910.1   Symbol: ZIP11   metal transporter, putative (ZIP11), similar to putative zinc transporter ZIP2 (Arabidopsis thaliana) gi:3252868:gb:AAC24198; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563   chr1:20909799-20911078 FORWARD   Aliases: F14J16.16	4.1	4.1	-0.0	-0.1	100.0%	-5.2
18734	AT5G09890.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At4g14350.1); similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At4g14350.2); similar to protein kinase [Triticum aestivum] (GB:BAD19068.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719); contains InterPro domain Protein kinase C-terminal domain (InterPro:IPR000961)   chr5:3085546-3089011 REVERSE   Aliases: MYH9.10, MYH9_10	5.0	5.0	0.0	0.1	100.0%	-4.8
18735	AT1G50750.1   expressed protein   chr1:18812852-18815958 REVERSE   Aliases: F4M15.2, F4M15_2	3.3	3.3	-0.0	-0.1	100.0%	-5.4
18736	AT2G04690.1   cellular repressor of E1A-stimulated genes (CREG) family, contains 1 transmembrane domain; similar to CREG2 (GI:24371079) (Homo sapiens) and (GI:24371081) (Mus musculus); similar to cellular repressor of E1A-stimulated genes CREG (GI:3550343) (Homo sapiens)   chr2:1644494-1646348 FORWARD   Aliases: F28I8.27, F28I8_27	6.1	6.2	-0.1	-0.1	100.0%	-4.6
18737	AT3G28030.1   Symbol: UVH3   UV hypersensitive protein (UVH3) / DNA-repair protein, putative, identical to UV hypersensitive protein (Arabidopsis thaliana) gi:13649704:gb:AAK37472; similar to Swiss-Prot:P14629 DNA-repair protein complementing XP-G cells homolog (Xeroderma pigmentosum group G complementing protein homolog) (Xenopus laevis)   chr3:10425490-10432441 FORWARD   Aliases: MMG15.7, ULTRAVIOLET HYPERSENSITIVE 3	5.0	4.9	0.1	0.1	100.0%	-4.8
18738	AT1G68420.1   asparaginyl-tRNA synthetase-related, similar to asparaginyl-tRNA synthetase SP:Q9SW96 from (Arabidopsis thaliana)   chr1:25657556-25657819 FORWARD   Aliases: T2E12.3, T2E12_3	2.8	2.8	-0.0	-0.1	100.0%	-5.7
18739	AT3G09370.1   Symbol: MYB3R 3   myb family transcription factor (MYB3R3), contains Pfam profile: Myb DNA-binding proteins; identical to cDNA putative c-myb-like transcription factor (MYB3R3) GI:15375285   chr3:2879372-2882273 FORWARD   Aliases: F3L24.24	2.9	2.9	0.0	0.1	100.0%	-5.8
18740	AT3G15970.1   Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein, similar to Ran binding protein (Homo sapiens) GI:624232; contains Pfam profile PF00638: RanBP1 domain   chr3:5408803-5411114 REVERSE   Aliases: MSL1.1	6.5	6.5	0.0	0.1	100.0%	-5.2
18741	AT5G11950.2   expressed protein, contains Pfam profile PF03641: decarboxylase family protein   chr5:3854917-3856977 FORWARD   Aliases: F14F18.120, F14F18_120	7.6	7.5	0.0	0.1	100.0%	-5.1
18742	AT4G11600.1   Symbol: ATGPX6	11.1	11.1	0.1	0.1	100.0%	-5.1
18743	AT1G67350.1   expressed protein, contains similarity to MHC class II antigen GI:9502037 from (Aotus nancymaae)	11.9	11.8	0.0	0.1	100.0%	-5.8
18744	AT3G12850.1   COP9 signalosome complex-related / CSN complex-related, low similarity to SP:P45432 COP9 signalosome complex subunit 1 (CSN complex subunit 1) (COP11 protein) (FUSCA protein FUS6) {Arabidopsis thaliana}   chr3:4088381-4090310 REVERSE   Aliases: MBK21.21	3.0	3.0	-0.0	-0.1	100.0%	-5.3
18745	AT3G53380.1   lectin protein kinase family protein, contains Pfam domains, PF00069: Protein kinase domain, PF00138: Legume lectins alpha domain, and PF00139: Legume lectins beta domain   chr3:19800072-19802329 REVERSE   Aliases: F4P12.80	3.6	3.6	0.0	0.1	100.0%	-5.1
18746	AT2G23210.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:9889087-9890477 REVERSE   Aliases: T20D16.16, T20D16_16	3.1	3.0	0.0	0.1	100.0%	-5.6
18747	AT2G43200.1   dehydration-responsive family protein, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr2:17965307-17967613 FORWARD   Aliases: F14B2.14	4.7	4.7	0.0	0.1	100.0%	-5.3
18748	AT1G69260.1   expressed protein   chr1:26042825-26044751 FORWARD   Aliases: F4N2.22, F4N2_22	7.6	7.6	-0.1	-0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18749	AT2G24300.2   calmodulin-binding protein, similar to calmodulin-binding protein TCB60 GI:1698548 from (Nicotiana tabacum)   chr2:10347988-10350816 FORWARD   Aliases: T28I24.3, T28I24_3	3.2	3.2	0.0	0.1	100.0%	-5.1
18750	AT5G25520.2   transcription elongation factor-related, contains weak similarity to transcription elongation factors   chr5:8885091-8889623 FORWARD   Aliases: T14C9.60, T14C9_60	5.0	5.1	-0.1	-0.1	100.0%	-4.8
18751	AT5G66430.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri) and to SAM:benzoic acid carboxyl methyltransferase (BAMT)(GI:9789277)(Antirrhinum majus)   chr5:26542636-26544025 REVERSE   Aliases: K1F13.8, K1F13_8	2.1	2.1	0.0	0.1	100.0%	-6.0
18752	AT1G73050.1   (R)-mandelonitrile lyase, putative / (R)-oxynitrilase, putative, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:52707); contains Pfam profile PF00732 GMC oxidoreductase   chr1:27480226-27482195 REVERSE   Aliases: F3N23.25, F3N23_25	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18753	AT1G01110.1   expressed protein, contains Prosite PS00165: Serine/threonine dehydratases pyridoxal-phosphate attachment site   chr1:52869-54685 FORWARD   Aliases: T25K16.10, T25K16_10	2.9	3.0	-0.0	-0.1	100.0%	-5.4
18754	AT4G15755.1   C2 domain-containing protein, similar to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain   chr4:8970652-8971521 REVERSE   Aliases: None	2.3	2.3	-0.0	-0.1	100.0%	-5.8
18755	AT4G24240.1   Symbol: WRKY7   WRKY family transcription factor, contains Pfam profile: PF03106 WRKY DNA -binding domain   chr4:12571776-12573735 FORWARD   Aliases: ATWRKY7, T22A6.70, T22A6_70	3.6	3.6	0.0	0.1	100.0%	-4.9
18756	AT5G52140.1   zinc finger protein-related   chr5:21201748-21204098 REVERSE   Aliases: F17P19.3, F17P19_3	2.2	2.3	-0.0	-0.1	100.0%	-5.5
18757	AT3G20680.1   expressed protein   chr3:7230078-7231200 REVERSE   Aliases: F3H11.7	4.4	4.4	-0.0	-0.1	100.0%	-4.8
18758	AT1G02620.1   GTP-binding protein (SAR1A), identical to GTP-binding protein Sar1 (SP:O04834) (Arabidopsis thaliana); contains domain PF00025: ADP-ribosylation factor family   chr1:557092-557986 FORWARD   Aliases: T14P4.21, T14P4_21	3.4	3.5	-0.0	-0.1	100.0%	-5.2
18759	AT5G36260.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr5:14302185-14305563 REVERSE   Aliases: T30G6.12, T30G6_12	2.8	2.8	-0.0	-0.1	100.0%	-4.8
18760	AT3G19700.1   leucine-rich repeat transmembrane protein kinase, putative, similar to leucine-rich receptor-like protein kinase GB:AAC36318 from (Malus domestica); contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr3:6843668-6847281 FORWARD   Aliases: MMB12.19	3.7	3.7	0.0	0.1	100.0%	-5.1
18761	AT5G17430.1   Encodes an AP2-domain containing protein similar to ANT. Expressed in embryos and lateral root primordium.   chr5:5742544-5745570 REVERSE   Aliases: T10B6.90, T10B6_90	2.8	2.8	0.0	0.1	100.0%	-4.9
18762	AT3G28360.1   ABC transporter family protein, similar to P-glycoprotein homologue GI:2292907 from (Hordeum vulgare subsp. vulgare)   chr3:10612308-10616236 REVERSE   Aliases: MFJ20.1	2.5	2.5	0.0	0.1	100.0%	-5.4
18763	AT3G13410.1   expressed protein   chr3:4361889-4364242 REVERSE   Aliases: MRP15.4	9.7	9.6	0.1	0.1	100.0%	-4.9
18764	AT1G71840.1   transducin family protein / WD-40 repeat family protein, contains Pfam profile:PF00560 Leucine Rich Repeat (4 copies); Pfam profile:PF00069 Eukaryotic protein kinase domain; Pfam profile:PF00400 WD domain, G-beta repeat (7 copies)   chr1:27025880-27028213 FORWARD   Aliases: F14O23.22, F14O23_22	6.8	6.9	-0.1	-0.1	100.0%	-5.0
18765	AT1G55700.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.8	-0.0	-0.1	100.0%	-5.2
18766	AT4G33520.3   Symbol: PAA1   metal-transporting P-type ATPase, putative (PAA1), nearly identical to gi:2668492; contains Pfam heavy-metal-associated domain PF00403   chr4:16118899-16126153 FORWARD   Aliases: F17M5.280, F17M5_280	6.7	6.7	-0.0	-0.1	100.0%	-4.9
18767	AT5G52240.1   Symbol: MSBP1   cytochrome b5 domain-containing protein, similar to SP:P70580 Membrane associated progesterone receptor component 1 {Rattus norvegicus}; contains Pfam profile PF00173: Heme/Steroid binding domain   chr5:21230286-21231965 FORWARD   Aliases: ATMP1, F17P19.14, F17P19_14	8.8	8.8	-0.1	-0.1	100.0%	-4.8
18768	AT5G49180.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr5:19957904-19960233 REVERSE   Aliases: K21P3.5, K21P3_5	2.4	2.5	-0.0	-0.1	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18769	AT1G28420.1   Symbol: HB 1   homeobox transcription factor, putative, similar to homeobox transcription factor Hox7 GI:19486 (Lycopersicon peruvianum)   chr1:9979928-9987624 FORWARD   Aliases: F3M18.14, F3M18_14, HB 1	7.1	7.0	0.1	0.1	100.0%	-4.8
18770	AT5G01360.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g55990.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAV43889.1)   chr5:147947-149366 REVERSE   Aliases: T10O8.70, T10O8_70	3.7	3.6	0.1	0.1	100.0%	-4.3
18771	AT2G17380.1   Symbol: AP19   clathrin assembly protein AP19, identical to clathrin assembly protein AP19 GI:2231698 from (Arabidopsis thaliana)   chr2:7560084-7562127 FORWARD   Aliases: CLATHRIN ASSEMBLY PROTEIN AP19, F5J6.14, F5J6_14	8.5	8.4	0.1	0.1	100.0%	-4.7
18772	AT1G17210.1   expressed protein, distantly related to dentin phosphoryn (Homo sapiens) (GI:4322670)   chr1:5880123-5884749 REVERSE   Aliases: F20D23.9, F20D23_9	7.9	7.9	0.0	0.1	100.0%	-5.0
18773	AT3G26290.1   Symbol: CYP71B26   cytochrome P450 71B26, putative (CYP71B26), identical to cytochrome P450 71B26 (SP:Q9LTL0) (Arabidopsis thaliana); contains Pfam profile: PF00067 cytochrome P450   chr3:9633919-9635703 REVERSE   Aliases: MTC11.20	3.9	4.0	-0.1	-0.1	100.0%	-4.4
18774	AT3G43840.1   expressed protein   chr3:15711339-15711842 FORWARD   Aliases: T28A8.130	2.3	2.2	0.0	0.1	100.0%	-6.1
18775	AT4G10010.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:6263594-6266242 REVERSE   Aliases: T5L19.140, T5L19_140	3.0	3.0	0.0	0.1	100.0%	-5.5
18776	AT4G00970.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:418437-421694 FORWARD   Aliases: A_TM018A10.18, A_TM018A10_18, T18A10.9, T18A10_9	3.1	3.1	-0.0	-0.1	100.0%	-5.8
18777	AT4G32880.1   Symbol: ATHB 8	6.0	6.0	-0.0	-0.1	100.0%	-4.8
18778	AT3G20700.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:7233531-7234511 REVERSE   Aliases: F3H11.9	4.0	3.9	0.1	0.1	100.0%	-5.0
18779	AT1G16380.1   Symbol: ATCHX1	2.8	2.8	-0.0	-0.1	100.0%	-5.5
18780	AT2G29790.1   expressed protein   chr2:12727961-12729532 REVERSE   Aliases: T27A16.11, T27A16_11	2.4	2.4	0.0	0.1	100.0%	-5.6
18781	AT1G47660.1   expressed protein   chr1:17536381-17537991 REVERSE   Aliases: F16N3.35, F16N3_35	2.3	2.2	0.0	0.1	100.0%	-5.5
18782	AT4G29040.1   Symbol: RPT2A   26S proteasome AAA-ATPase subunit (RPT2a), almost identical to 26S proteasome AAA-ATPase subunit RPT2a (GI:6652880) {Arabidopsis thaliana}; Drosophila melanogaster 26S proteasome subunit 4 ATPase, PID:g1066065   chr4:14312309-14314568 FORWARD   Aliases: 26S PROTEASOME AAA ATPASE SUBUNIT RPT2A, F19B15.70, F19B15_70	10.6	10.6	-0.0	-0.1	100.0%	-5.0
18783	AT2G17540.2   expressed protein   chr2:7637502-7638980 REVERSE   Aliases: MJB20.10, MJB20_10	4.3	4.2	0.0	0.1	100.0%	-5.1
18784	AT1G56380.1   mitochondrial transcription termination factor family protein / mTERF family protein, weak similarity to mtDBP protein (Paracentrotus lividus) GI:4584695; contains Pfam profile PF02536: mTERF   chr1:21105039-21106366 FORWARD   Aliases: F14G9.1, F14G9_1	2.8	2.8	0.0	0.1	100.0%	-5.4
18785	AT2G43190.3   ribonuclease P family protein, similar to Ribonuclease P protein subunit p29 (EC 3.1.26.5) (hPOP4) (Swiss-Prot:O95707) (Homo sapiens)   chr2:17963066-17965118 FORWARD   Aliases: F14B2.13	7.5	7.5	0.0	0.1	100.0%	-5.0
18786	AT5G64050.1   glutamate-tRNA ligase family protein / glutamyl-tRNA synthetase family protein, similar to SP:P22250 from Bacillus subtilis, SP:P22249 from Bacillus stearothermophilus; contains Pfam tRNA synthetases class I (E and Q), catalytic domain PF00749   chr5:25647189-25650434 REVERSE   Aliases: MHJ24.3, MHJ24_3	3.6	3.6	-0.0	-0.1	100.0%	-5.1
18787	AT5G22950.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr5:7681308-7682906 FORWARD   Aliases: MRN17.18, MRN17_18	7.6	7.5	0.0	0.1	100.0%	-4.8
18788	AT2G33640.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr2:14246339-14249441 FORWARD   Aliases: F4P9.41, F4P9_41	3.4	3.4	-0.0	-0.1	100.0%	-5.0
18789	AT5G50380.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr5:20533338-20535799 REVERSE   Aliases: MXI22.10, MXI22_10	6.4	6.3	0.1	0.1	100.0%	-4.6
18790	AT4G37130.1   hydroxyproline-rich glycoprotein family protein   chr4:17489461-17492004 FORWARD   Aliases: AP22.15, AP22_15	6.6	6.7	-0.0	-0.1	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18791	AT2G34290.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:14479712-14480509 REVERSE   Aliases: F13P17.13, F13P17_13	3.6	3.6	-0.0	-0.1	100.0%	-4.9
18792	AT1G12570.1   glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:P52707); contains Pfam profile PF00732 GMC oxidoreductase   chr1:4278000-4280860 REVERSE   Aliases: F5O11.31, F5O11_31	2.6	2.6	0.0	0.1	100.0%	-5.8
18793	AT4G21690.1   gibberellin 3 beta-hydroxylase family protein, similar to gibberellin 3 beta-hydroxylase (GI:4164145)(Lactuca sativa), 3b-hydroxylase, Solanum lycopersicum, AB010992; contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr4:11527241-11529072 FORWARD   Aliases: F17L22.150, F17L22_150	2.4	2.4	0.0	0.1	100.0%	-5.5
18794	AT5G57300.1   UbiE/COQ5 methyltransferase family protein, similar to ubiquinone biosynthesis methyltransferase COQ5 (Saccharomyces cerevisiae)(SP:P49017), ubiquinone/menaquinone biosynthesis methyltransferase ubiE (Escherichia coli)(SP:P27851); contains Pfam profile PF01209: methlytransferase, UbiE/COQ5 family   chr5:23225809-23228316 REVERSE   Aliases: MJB24.11, MJB24_11	9.1	9.1	0.1	0.1	100.0%	-4.7
18795	AT5G64210.1   Symbol: AOX2   alternative oxidase 2, mitochondrial (AOX2), nearly identical to SP:O22049   chr5:25701191-25702890 REVERSE   Aliases: ALTERNATIVE OXIDASE, MSJ1.5, MSJ1_5	2.7	2.7	-0.0	-0.1	100.0%	-5.3
18796	AT5G63620.2   oxidoreductase, zinc-binding dehydrogenase family protein, contains PFAM zinc-binding dehydrogenase domain PF00107   chr5:25483354-25485619 REVERSE   Aliases: MBK5.9, MBK5_9	8.9	8.9	0.0	0.1	100.0%	-5.2
18797	AT3G47180.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr3:17383785-17384438 REVERSE   Aliases: F13I12.230	3.6	3.7	-0.0	-0.1	100.0%	-4.8
18798	AT3G23070.1   expressed protein, contains Pfam domain, PF04581: Protein of unknown function (DUF578)   chr3:8203476-8208003 FORWARD   Aliases: MXC7.10	4.8	4.9	-0.0	-0.1	100.0%	-4.8
18799	AT2G16835.1   water channel protein, putative, similar to MipC (Mesembryanthemum crystallinum) gi:1657948:gb:AAB18227   chr2:7302933-7303400 FORWARD   Aliases: F12A24.1	3.1	3.1	0.0	0.1	100.0%	-5.7
18800	AT3G48970.1   copper-binding family protein, similar to copper homeostasis factor gi:3168840 from Arabidopsis thaliana; contains Pfam heavy-metal-associated domain PF00403   chr3:18163273-18164360 REVERSE   Aliases: T2J13.190	3.1	3.2	-0.1	-0.1	100.0%	-4.4
18801	AT5G22900.1   Symbol: ATCHX3	2.4	2.3	0.0	0.1	100.0%	-5.7
18802	ATCG00130.1   Symbol: ATPF   ATPase F subunit.   chrC:11529-12798 REVERSE   Aliases: ATPF	8.6	8.4	0.1	0.1	100.0%	-4.7
18803	AT1G17900.1   expressed protein   chr1:6157361-6158123 REVERSE   Aliases: F2H15.23, F2H15_23	3.0	3.0	0.0	0.1	100.0%	-6.0
18804	AT3G09050.1   expressed protein   chr3:2764656-2766092 FORWARD   Aliases: MZB10.8	3.5	3.6	-0.0	-0.1	100.0%	-5.2
18805	AT2G44100.1   Symbol: ATGDI1	11.0	11.1	-0.1	-0.1	100.0%	-5.3
18806	AT3G51810.1   Symbol: ATEM1   Em-like protein GEA1 (EM1), identical to SP:Q07187 Em-like protein GEA1 (EM1) {Arabidopsis thaliana}; contains Pfam profile PF00477: Small hydrophilic plant seed protein   chr3:19225725-19226808 FORWARD   Aliases: AT3, ATEM1.6, EM1, EM1 PROTEIN, GEA1	3.8	3.7	0.0	0.1	100.0%	-5.4
18807	AT3G20570.1   plastocyanin-like domain-containing protein   chr3:7186312-7187527 REVERSE   Aliases: K10D20.11	4.2	4.2	-0.0	-0.1	100.0%	-4.6
18808	AT1G53800.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g53250.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAP52650.1)   chr1:20085367-20088168 FORWARD   Aliases: T18A20.4, T18A20_4	2.8	2.8	0.0	0.1	100.0%	-5.3
18809	AT4G35380.1   guanine nucleotide exchange family protein, similar to guanine nucleotide exchange factor (Homo sapiens) GI:5456754; contains Pfam profile PF01369: Sec7 domain   chr4:16819888-16826066 FORWARD   Aliases: F23E12.60, F23E12_60	3.7	3.8	-0.1	-0.1	100.0%	-4.6
18810	AT1G50020.1   expressed protein   chr1:18522758-18525363 REVERSE   Aliases: F2J10.10, F2J10_10	6.6	6.7	-0.1	-0.1	100.0%	-4.7
18811	AT5G39230.1   transcription initiation factor-related, contains weak similarity to Transcription initiation factor IIB (General transcription factor TFIIB) (Swiss-Prot:Q8W0W3) (Oryza sativa)	2.5	2.5	-0.0	-0.1	100.0%	-5.4
18812	AT4G16930.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr4:9529583-9530134 REVERSE   Aliases: DL4495C, FCAALL.312	2.9	2.9	-0.0	-0.1	100.0%	-5.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18813	AT2G43220.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	4.3	4.3	0.0	0.1	100.0%	-5.2
18814	AT4G34230.2   Symbol: CAD5   similar to cinnamyl-alcohol dehydrogenase (CAD) [Arabidopsis thaliana] (TAIR:At3g19450.1); similar to cinnamyl alcohol dehydrogenase [Aralia cordata] (GB:BAA03099.1); contains InterPro domain Zinc-containing alcohol dehydrogenase superfamily (InterPro:IPR002085); contains InterPro domain Zinc-containing alcohol dehydrogenase (InterPro:IPR002328)   chr4:16386723-16388723 REVERSE   Aliases: ATCAD5, CAD 5, CINNAMYL ALCOHOL DEHYDROGENASE 5, F10M10.11	10.2	10.3	-0.1	-0.1	100.0%	-4.8
18815	AT3G53620.1   inorganic pyrophosphatase, putative (soluble) / pyrophosphate phospho-hydrolase, putative / PPase, putative, similar to magnesium dependent soluble inorganic pyrophosphatase (Solanum tuberosum) GI:2706450; contains Pfam profile PF00719: inorganic pyrophosphatase   chr3:19891482-19894648 FORWARD   Aliases: F4P12.320	7.2	7.1	0.1	0.1	100.0%	-4.5
18816	AT3G12200.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	7.4	7.4	0.0	0.1	100.0%	-4.8
18817	AT4G26920.1   expressed protein   chr4:13525037-13527178 FORWARD   Aliases: F10M23.260, F10M23_260	4.2	4.2	0.0	0.1	100.0%	-5.6
18818	AT1G44478.1   hypothetical protein   chr1:16854781-16855678 REVERSE   Aliases: T18F15.6, T18F15_6	2.5	2.5	0.0	0.1	100.0%	-5.0
18819	AT4G34580.1   similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At4g39180.1); similar to SEC14 cytosolic factor family protein / phosphoglyceride transfer family protein [Arabidopsis thaliana] (TAIR:At2g16380.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [Arabidopsis thaliana] (TAIR:At2g21540.1); similar to putative phosphatidylinositol/phosphatidylcholine transfer protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464026.1); similar to putative SEC14 cytosolic factor [Oryza sativa (japonica cultivar-group)] (GB:XP_465384.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251); contains InterPro domain Cellular retinaldehyde binding/alpha-tocopherol transport (InterPro:IPR001071); contains InterPro domain Cellular retinaldehyde-binding/triple function, N-terminal (InterPro:IPR008273)   chr4:16515332-16519539 FORWARD   Aliases: T4L20.160, T4L20_160	3.2	3.2	0.1	0.1	100.0%	-4.4
18820	AT1G12970.1   leucine-rich repeat family protein   chr1:4423638-4425787 FORWARD   Aliases: F13K23.23, F13K23_23	3.8	3.7	0.0	0.1	100.0%	-5.4
18821	AT3G50740.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:18866142-18867865 REVERSE   Aliases: F18B3.20	3.1	3.2	-0.1	-0.1	100.0%	-4.3
18822	AT3G02150.2   Symbol: PTF1   TCP family transcription factor, putative, similar to transcription factor PCF6 (Oryza sativa (japonica cultivar-group)) GI:20975255; contains Pfam profile PF03634: TCP family transcription factor   chr3:391098-392748 FORWARD   Aliases: F1C9.6, PLASTID TRANSCRIPTION FACTOR 1, TFPD	2.3	2.3	0.0	0.1	100.0%	-5.8
18823	AT3G62020.2   Symbol: GLP10   germin-like protein (GLP10), identical to germin-like protein subfamily 2 member 4 (SP:Q9M263)   chr3:22982333-22983214 REVERSE   Aliases: F21F14.190, GERMIN LIKE PROTEIN 10	3.7	3.8	-0.1	-0.1	100.0%	-4.4
18824	AT2G25990.1   hypothetical protein   chr2:11087664-11087784 FORWARD   Aliases: T19L18.20, T19L18_20	3.4	3.4	-0.0	-0.1	100.0%	-5.5
18825	AT4G26100.3   Symbol: CK1   casein kinase, putative, similar to casein kinase I, delta isoform (Arabidopsis thaliana) SWISS-PROT:P42158; contains protein kinase domain, Pfam:PF00069	7.8	7.9	-0.1	-0.1	100.0%	-4.6
18826	AT5G51580.1   expressed protein   chr5:20969668-20970619 REVERSE   Aliases: K17N15.13, K17N15_13	2.8	2.7	0.0	0.1	100.0%	-5.8
18827	AT3G11210.1   GDSL-motif lipase/hydrolase family protein, contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr3:3510669-3513066 REVERSE   Aliases: F11B9.13	4.3	4.3	-0.0	-0.1	100.0%	-4.5
18828	AT3G52840.1   beta-galactosidase, putative / lactase, putative, similar to beta-galactosidase precursor GI:3869280 from (Carica papaya)   chr3:19592132-19597277 FORWARD   Aliases: F8J2.10	3.8	3.7	0.0	0.1	100.0%	-5.1
18829	AT4G09990.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr4:6258877-6260061 REVERSE   Aliases: T5L19.120, T5L19_120	3.1	3.0	0.1	0.1	100.0%	-4.5
18830	AT1G51980.1   mitochondrial processing peptidase alpha subunit, putative, similar to mitochondrial processing peptidase alpha subunit, mitochondrial precursor, Alpha-MPP (Ubiquinol-cytochrome C reductase subunit II) (Potato) SWISS-PROT:P29677   chr1:19327071-19330551 REVERSE   Aliases: F5F19.4, F5F19_4	10.3	10.4	-0.1	-0.1	100.0%	-5.0
18831	AT3G16920.1   glycoside hydrolase family 19 protein, similar to class I chitinase GI:7798670 from (Arabis microphylla)	2.9	2.8	0.1	0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18832	AT5G61090.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965; contains similarity to vegetative cell wall protein gp1 (Chlamydomonas reinhardtii) gi:12018147:gb:AAG45420; common family members: At4g18570, At3g25690, At4g04980 (Arabidopsis thaliana)   chr5:24593552-24594940 REVERSE   Aliases: MAF19.21, MAF19_21	2.5	2.5	-0.0	-0.1	100.0%	-5.5
18833	AT3G08770.1   Symbol: LTP6   lipid transfer protein 6 (LTP6), identical to GI:8571927	3.4	3.4	-0.0	-0.1	100.0%	-5.4
18834	AT1G07110.1   Symbol: F2KP   fructose-6-phosphate 2-kinase / fructose-2,6-bisphosphatase (F2KP), identical to fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase (F2KP) (Arabidopsis thaliana) GI:13096098   chr1:2178103-2184135 REVERSE   Aliases: ATF2KP, F10K1.19, F10K1_19, FKFBP, FRUCTOSE 2,6-BISPHOSPHATASE, FRUCTOSE 6 PHOSPHATE 2 KINASE	7.2	7.2	-0.1	-0.1	100.0%	-4.7
18835	AT5G25415.1   expressed protein, several hypothetical proteins - Arabidopsis thaliana   chr5:8834209-8837179 FORWARD   Aliases: None	2.8	2.8	-0.0	-0.1	100.0%	-5.1
18836	AT3G15240.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g53900.2); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD37771.1)   chr3:5134551-5135909 FORWARD   Aliases: K7L4.4	2.3	2.3	-0.0	-0.1	100.0%	-5.5
18837	AT2G39050.1   hydroxyproline-rich glycoprotein family protein, contains QXW lectin repeat domain, Pfam:PF00652	7.3	7.3	-0.0	-0.1	100.0%	-4.6
18838	AT2G28870.1   expressed protein   chr2:12401333-12401992 REVERSE   Aliases: F8N16.16, F8N16_16	2.7	2.8	-0.0	-0.1	100.0%	-5.5
18839	AT4G10510.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr4:6495951-6499006 FORWARD   Aliases: F7L13.90, F7L13_90	2.5	2.6	-0.0	-0.1	100.0%	-5.1
18840	AT3G21680.1   expressed protein   chr3:7633501-7633860 REVERSE   Aliases: MIL23.24	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18841	AT3G47040.1   glycosyl hydrolase family 3 protein, beta-D-glucan exohydrolase, Nicotiana tabacum, TREMBL:AB017502_1   chr3:17335216-17338090 REVERSE   Aliases: F13I12.90	4.7	4.6	0.1	0.1	100.0%	-4.5
18842	AT2G31160.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr2:13284888-13285822 FORWARD   Aliases: T16B12.3, T16B12_3	2.6	2.7	-0.0	-0.1	100.0%	-5.2
18843	AT5G07570.1   glycine/proline-rich protein, contains similarity to flagelliform silk protein (Nephila clavipes) gi:7106224:gb:AAF36090	2.3	2.3	0.0	0.1	100.0%	-5.7
18844	AT1G29400.2   Symbol: AML5   RNA recognition motif (RRM)-containing protein, similar to GI:6650523 from (Arabidopsis thaliana)   chr1:10290026-10294508 REVERSE   Aliases: ARABIDOPSIS MEI2 LIKE PROTEIN 5, F15D2.30, F15D2_30	3.4	3.4	0.0	0.1	100.0%	-5.1
18845	AT1G29310.1   protein transport protein sec61, putative, similar to PfSec61 (Plasmodium falciparum) GI:3057044; contains Pfam profile PF00344: eubacterial secY protein   chr1:10252292-10254676 FORWARD   Aliases: F28N24.2, F28N24_2	5.6	5.7	-0.0	-0.1	100.0%	-4.6
18846	AT5G46880.1   Symbol: HB 7   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to HD-Zip homeo domain OCL4 protein GI:8920425 from (Zea mays); contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain   chr5:19048767-19052615 FORWARD   Aliases: HB 7, MQD22.1, MQD22_1	2.5	2.5	-0.0	-0.1	100.0%	-5.4
18847	AT4G16770.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, low similarity to flavonol synthase from Petunia hybrida (SP:Q07512), Citrus unshiu (GI:4126403); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily; non-consensus GG acceptor splice site at exon 8   chr4:9434376-9437187 REVERSE   Aliases: DL4410C, FCAALL.233	6.4	6.5	-0.0	-0.1	100.0%	-4.7
18848	AT2G35960.1   Symbol: NHL12   harpin-induced family protein / HIN1 family protein / harpin-responsive family protein, similar to harpin-induced protein hin1 (GI:1619321) (Nicotiana tabacum)   chr2:15114019-15114966 FORWARD   Aliases: F11F19.13, F11F19_13	3.2	3.2	-0.0	-0.1	100.0%	-5.5
18849	AT3G17130.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	3.5	3.4	0.0	0.1	100.0%	-5.0
18850	AT2G28270.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.7	-0.0	-0.1	100.0%	-5.8
18851	AT5G35370.1   similar to lectin protein kinase family protein [Arabidopsis thaliana] (TAIR:At4g32300.1); similar to putative S-receptor kinase, homolog precursor [Oryza sativa (japonica cultivar-group)] (GB:BAD38273.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Curculin-like (mannose-binding) lectin (InterPro:IPR001480); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:13605794-13608501 REVERSE   Aliases: T26D22.12, T26D22_12	5.3	5.4	-0.0	-0.1	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18852	AT5G67440.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr5:26929933-26933306 REVERSE   Aliases: K8K14.18, K8K14_18	5.1	5.0	0.0	0.1	100.0%	-5.0
18853	AT3G49300.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:18287802-18288590 REVERSE   Aliases: F2K15.160	3.8	3.8	0.0	0.1	100.0%	-5.3
18854	AT2G05950.1   hypothetical protein   chr2:2297813-2298718 FORWARD   Aliases: T6P5.15, T6P5_15	2.8	2.7	0.0	0.1	100.0%	-5.5
18855	AT5G59930.1   DC1 domain-containing protein / UV-B light-insensitive protein, putative, similar to ULI3 (UV-B light insensitive) (Arabidopsis thaliana) GI:17225050; contains Pfam profile PF03107: DC1 domain	2.6	2.6	-0.1	-0.1	100.0%	-4.6
18856	AT1G05770.1   jacalin lectin family protein, similar to gi:6503088 (GB:AAF14583) from (Arabidopsis thaliana) (Proc. Natl. Acad. Sci. U.S.A. 97 (1), 489-494 (2000)); contains Pfam profile PF01419 jacalin-like lectin domain   chr1:1725387-1726270 REVERSE   Aliases: T20M3.3, T20M3_3	2.5	2.5	0.0	0.1	100.0%	-5.0
18857	AT1G71910.1   expressed protein   chr1:27068594-27069609 FORWARD   Aliases: F17M19.6, F17M19_6	4.4	4.4	-0.0	-0.1	100.0%	-4.9
18858	AT1G50960.1   gibberellin 20-oxidase-related, similar to gibberellin 20-oxidase from Pisum sativum (GI:1848146), Phaseolus vulgaris (GI:2262201); contains Pfam domain PF03171, 2OG-Fe(II) oxygenase superfamily   chr1:18893217-18895387 FORWARD   Aliases: F8A12.18, F8A12_18	3.3	3.3	0.0	0.1	100.0%	-5.6
18859	AT1G14740.1   expressed protein   chr1:5075208-5077786 REVERSE   Aliases: F10B6.14, F10B6_14	4.6	4.6	-0.0	-0.1	100.0%	-5.2
18860	AT4G01760.1   DC1 domain-containing protein, similar to T15B16.10 similar to A. thaliana CHP-rich proteins encoded by T10M13, GenBank accession number AF001308   chr4:759131-761134 REVERSE   Aliases: T7B11.2	2.9	2.9	-0.0	-0.1	100.0%	-5.3
18861	AT5G05300.1   expressed protein, similar to unknown protein (gb:AAF01528.1); expression supported by MPSS   chr5:1570103-1570411 REVERSE   Aliases: K18I23.10, K18I23_10	4.1	4.1	-0.0	-0.1	100.0%	-5.0
18862	AT5G15000.1   expressed protein   chr5:4853467-4855174 FORWARD   Aliases: F2G14.120, F2G14_120	2.4	2.3	0.0	0.1	100.0%	-5.8
18863	AT3G18820.1   Ras-related GTP-binding protein, putative, similar to Ras-related protein RAB7 GI:1370186 from (Pisum sativum), Plant Mol. Biol. 21 (6), 1195-1199 (1993); contains Pfam profile: PF00071 Ras family   chr3:6484107-6486252 FORWARD   Aliases: MVE11.21	9.1	9.0	0.1	0.1	100.0%	-4.8
18864	AT2G33820.1   mitochondrial substrate carrier family protein (BAC1), contains Pfam profile: PF00153 mitochondrial carrier protein   chr2:14313369-14315369 REVERSE   Aliases: T1B8.12, T1B8_12	5.9	5.9	0.0	0.1	100.0%	-5.0
18865	AT4G24175.1   expressed protein   chr4:12546979-12548968 FORWARD   Aliases: None	4.9	4.9	-0.0	-0.1	100.0%	-4.7
18866	AT1G59560.1   Symbol: ZCF61   expressed protein, contains similarity to apoptosis inhibitors   chr1:21885264-21887443 FORWARD   Aliases: T30E16.12, T30E16_12, ZCF61	5.1	5.1	0.0	0.1	100.0%	-4.9
18867	AT4G20080.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr4:10865305-10867629 FORWARD   Aliases: F18F4.180, F18F4_180	2.6	2.6	0.0	0.1	100.0%	-5.4
18868	AT2G16860.1   GCIP-interacting family protein, similar to GCIP-interacting protein mp29 (GI:27372623) (Mus musculus); similar to GCIP-interacting protein P29 (GI:11967379) (Homo sapiens)   chr2:7311002-7313735 REVERSE   Aliases: F12A24.4, F12A24_4	9.9	9.8	0.0	0.1	100.0%	-4.9
18869	AT3G11750.1   dihydroneopterin aldolase, putative, similar to SP:P28823 Dihydroneopterin aldolase (EC 4.1.2.25) (DHNA) {Bacillus subtilis}; contains Pfam profile PF02152: dihydroneopterin aldolase   chr3:3715077-3715910 REVERSE   Aliases: F26K24.4	4.0	4.0	0.0	0.1	100.0%	-5.1
18870	AT1G50080.1   hypothetical protein   chr1:18557669-18557944 REVERSE   Aliases: F2J10.18, F2J10_18	2.7	2.7	-0.0	-0.1	100.0%	-5.5
18871	AT3G46530.1   Symbol: RPP13   disease resistance protein, RPP13-like (CC-NBS class), putative, domain signature CC-NBS exists, suggestive of a disease resistance protein. Closest homolog in Col-0 to RPP13.	2.9	2.9	0.0	0.1	100.0%	-5.3
18872	AT2G34880.1   transcription factor jumonji (jmj) family protein / zinc finger (C5HC2 type) family protein, contains Pfam domains, PF02375: jmjN domain, PF02373: jmjC domain and PF02928: C5HC2 zinc finger   chr2:14718959-14723713 REVERSE   Aliases: F19I3.11, F19I3_11	3.4	3.3	0.0	0.1	100.0%	-5.4
18873	AT1G29520.1   AWPM-19-like membrane family protein, contains Pfam profile: PF05512 AWPM-19-like family	2.5	2.6	-0.0	-0.1	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18874	AT2G20890.1   Symbol: THF1   Chloroplast-localized Thylakoid formation1 gene product involved in vesicle-mediated formation of thylakoid membranes. Thf1 antisense lines contain abnormal chloroplasts early in leaf development (chloroplasts have loosely stacked thylakoid membranes). Expression was induced in the light and decreased under dark conditions.   chr2:8994749-8996494 FORWARD   Aliases: F5H14.14, F5H14_14, THF1, THYLAKOID FORMATION1	9.3	9.4	-0.0	-0.1	100.0%	-4.9
18875	AT5G19380.1   expressed protein   chr5:6526830-6530594 REVERSE   Aliases: F7K24.130, F7K24_130	6.1	6.1	-0.0	-0.1	100.0%	-4.7
18876	AT1G72560.1   Symbol: PSD   tRNA export mediator exportin-t, putative (PAUSED), contains Pfam profile: PF04150 exportin-t, identical to PAUSED gi:30909318   chr1:27328051-27333129 REVERSE   Aliases: F28P22.25, F28P22_25, PAUSED	3.9	3.9	0.0	0.1	100.0%	-4.9
18877	AT2G43600.1   glycoside hydrolase family 19 protein, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus)   chr2:18093126-18094095 REVERSE   Aliases: F18O19.29	3.2	3.2	0.0	0.1	100.0%	-5.4
18878	AT2G40580.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:16950942-16952081 FORWARD   Aliases: T2P4.7, T2P4_7	3.0	3.0	-0.0	-0.1	100.0%	-5.2
18879	AT3G03480.1   transferase family protein, similar to hypersensitivity-related gene GB:CAA64636 (Nicotiana tabacum); contains Pfam transferase family domain PF00248   chr3:828303-829903 REVERSE   Aliases: T21P5.10, T21P5_10	2.1	2.0	0.0	0.1	100.0%	-6.0
18880	AT1G33880.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to AIG1 protein SP:P54120 (Arabidopsis thaliana); contains Pfam PF04548: AIG1 family;   chr1:12303842-12304891 REVERSE   Aliases: T3M13.10, T3M13_10	3.0	3.0	-0.0	-0.1	100.0%	-5.5
18881	AT1G76530.1   auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547   chr1:28723273-28725265 FORWARD   Aliases: F14G6.13, F14G6_13	2.6	2.6	0.0	0.1	100.0%	-5.5
18882	AT5G35940.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	2.7	2.7	-0.0	-0.1	100.0%	-5.4
18883	AT1G48010.1   invertase/pectin methylesterase inhibitor family protein, low similarity to SP:P83326 Pectinesterase inhibitor (Pectin methylesterase inhibitor) (PMEI) {Actinidia chinensis}; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:17715160-17716329 REVERSE   Aliases: T2J15.8, T2J15_8	2.3	2.3	0.0	0.1	100.0%	-6.1
18884	AT5G38340.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:15337737-15341291 FORWARD   Aliases: MSI17.60, MSI17_60	3.5	3.5	0.0	0.1	100.0%	-5.5
18885	AT5G40810.1   cytochrome c1, putative, cytochrome c1, heme protein, mitochondrial precursor (Clone PC13III) (Solanum tuberosum) SWISS-PROT:P25076   chr5:16357135-16359872 FORWARD   Aliases: MHK7.4, MHK7_4	8.0	8.1	-0.1	-0.1	100.0%	-4.4
18886	AT1G16890.2   ubiquitin-conjugating enzyme, putative, nearly identical to ubiquitin-conjugating enzyme E2 (Catharanthus roseus) GI:5381319; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr1:5776339-5778448 REVERSE   Aliases: F17F16.19	10.1	10.2	-0.1	-0.1	100.0%	-5.1
18887	AT1G78870.3   similar to ubiquitin-conjugating enzyme, putative [Arabidopsis thaliana] (TAIR:At1g16890.2); similar to ubiquitin-conjugating enzyme E2 [Catharanthus roseus] (GB:AAD42941.1); contains InterPro domain Ubiquitin-conjugating enzymes (InterPro:IPR000608)   chr1:29655348-29657410 FORWARD   Aliases: F9K20.8, F9K20_8	10.1	10.2	-0.1	-0.1	100.0%	-5.1
18888	AT1G73280.1   Symbol: SCPL3   serine carboxypeptidase S10 family protein, similar to serine carboxypeptidase I precursor (SP:P07519) (Hordeum vulgare); glucose acyltransferase GB:AAD01263 (Solanum berthaultii); contains Pfam profile: PF00450 Serine carboxypeptidase;   chr1:27556631-27558983 REVERSE   Aliases: SCPL3, T18K17.5, T18K17_5	2.7	2.8	-0.0	-0.1	100.0%	-5.1
18889	AT5G28210.1   mRNA capping enzyme family protein, similar to mRNA capping enzyme (Xenopus laevis) GI:7239232; contains Pfam profiles PF01331: mRNA capping enzyme catalytic domain, PF03919: mRNA capping enzyme C-terminal domain   chr5:10188590-10190467 FORWARD   Aliases: F26C17.2, F26C17_2	2.8	2.8	-0.0	-0.1	100.0%	-5.5
18890	AT3G02570.1   phosphomannose isomerase type I family protein, contains Pfam profile: PF01238 phosphomannose isomerase type I   chr3:543356-545602 REVERSE   Aliases: F16B3.20, F16B3_20	5.8	5.8	-0.1	-0.1	100.0%	-4.7
18891	AT1G13380.1   expressed protein   chr1:4589068-4590408 REVERSE   Aliases: T6J4.13, T6J4_13	8.2	8.2	-0.0	-0.1	100.0%	-4.8
18892	AT5G15160.1   bHLH family protein   chr5:4921269-4922638 REVERSE   Aliases: F8M21.50, F8M21_50	2.1	2.1	-0.0	-0.1	100.0%	-6.1
18893	AT3G29035.1   Symbol: ANAC059   no apical meristem (NAM) family protein, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (GI:1944132) (Arabidopsis thaliana)   chr3:11035069-11036467 FORWARD   Aliases: ANAC059, MRI12.1	3.5	3.4	0.0	0.1	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18894	AT5G01160.1   e-cadherin binding protein-related, contains weak similarity to E-cadherin binding protein E7 (Mus musculus GP:9622093:gb:AAF89617   chr5:54009-55854 FORWARD   Aliases: F7J8.140, F7J8_140	5.3	5.3	0.0	0.1	100.0%	-5.3
18895	AT4G13440.1   calcium-binding EF hand family protein, low similarity to Polcalcin (Calcium-binding pollen allergen) from {Phleum pratense} SP:O82040, {Cynodon dactylon} SP:P94092; contains INTERPRO:IPR002048 calcium-binding EF-hand domain	2.4	2.4	0.0	0.1	100.0%	-5.2
18896	AT5G07070.1   Symbol: CIPK2   CBL-interacting protein kinase 2 (CIPK2), identical to CBL-interacting protein kinase 2 (Arabidopsis thaliana) gi:9280636:gb:AAF86506   chr5:2196435-2198115 REVERSE   Aliases: CBL INTERACTING PROTEIN KINASE 2, T28J14.10, T28J14_10	3.8	3.8	0.0	0.1	100.0%	-5.1
18897	AT1G64380.1   encodes a member of the DREB subfamily A-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 8 members in this subfamily including RAP2.4.   chr1:23894309-23895836 REVERSE   Aliases: F15H21.12, F15H21_12	2.4	2.5	-0.0	-0.1	100.0%	-4.7
18898	AT1G67220.1   zinc finger protein-related, similar to SP:Q09472 E1A-associated protein p300 {Homo sapiens}, SP:Q92793 CREB-binding protein {Homo sapiens}; contains Pfam profiles PF00569: Zinc finger ZZ type, PF00628: PHD-finger, PF02135: TAZ zinc finger   chr1:25149250-25153993 FORWARD   Aliases: F1N21.4	2.4	2.4	0.0	0.1	100.0%	-5.5
18899	AT2G30890.1   membrane protein, putative, similar to membrane protein SDR2 (GI:1747306) (Mus musculus)	2.5	2.6	-0.0	-0.1	100.0%	-5.3
18900	AT2G21600.1   Symbol: ATRER1B   RER1B protein, identical to SP:O48671 RER1B protein (AtRER1B) {Arabidopsis thaliana}   chr2:9249881-9251913 FORWARD   Aliases: ATRER1B, F2G1.13, F2G1_13	7.3	7.4	-0.1	-0.1	100.0%	-4.7
18901	AT2G38300.1   similar to myb family transcription factor [Arabidopsis thaliana] (TAIR:At2g40260.1); similar to myb family transcription factor-like [Oryza sativa (japonica cultivar-group)] (GB:BAD28879.1); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005); contains InterPro domain Myb-like DNA-binding domain, SHAQKYF class (InterPro:IPR006447)   chr2:16051038-16053070 REVERSE   Aliases: F16M14.25	2.4	2.4	-0.0	-0.1	100.0%	-5.8
18902	ATMG01360.1   Symbol: COX1   cytochrome c oxidase subunit 1   chrM:349830-351413 REVERSE   Aliases: COX1	7.9	7.7	0.1	0.1	100.0%	-5.0
18903	AT1G07990.1   SIT4 phosphatase-associated family protein, contains Pfam profile: PF04499 SIT4 phosphatase-associated protein   chr1:2477155-2483135 FORWARD   Aliases: T6D22.8, T6D22_8	3.7	3.8	-0.0	-0.1	100.0%	-4.9
18904	AT3G61220.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to carbonyl reductase GI:1049108 from (Mus musculus)   chr3:22673962-22675468 FORWARD   Aliases: T20K12.120	10.3	10.2	0.0	0.1	100.0%	-5.0
18905	AT2G14560.2   expressed protein, contains Pfam profile PF04525: Protein of unknown function (DUF567)   chr2:6221054-6221870 FORWARD   Aliases: T13P21.6, T13P21_6	3.1	3.1	0.0	0.1	100.0%	-5.4
18906	AT5G44570.1   expressed protein   chr5:17981666-17982841 FORWARD   Aliases: K15C23.1, K15C23_1	2.4	2.4	-0.0	-0.1	100.0%	-5.8
18907	AT2G24550.1   expressed protein, weak similarity to MTD1 (Medicago truncatula) GI:9294810   chr2:10434936-10436301 REVERSE   Aliases: F25P17.15, F25P17_15	5.8	5.9	-0.1	-0.1	100.0%	-4.8
18908	AT1G74620.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:28031913-28032662 FORWARD   Aliases: F1M20.30, F1M20_30	2.4	2.4	-0.0	-0.1	100.0%	-5.7
18909	AT2G13570.1   CCAAT-box binding transcription factor, putative, similar to CAAT-box DNA binding protein subunit B (NF-YB) (SP:P25209) (GI:22380) (Zea mays); contains Pfam PF00808 : Histone-like transcription factor (CBF/NF-Y) and archaeal histone	2.3	2.3	-0.0	-0.1	100.0%	-5.6
18910	AT4G12380.1   expressed protein   chr4:7333508-7334466 REVERSE   Aliases: T1P17.1	2.8	2.8	-0.0	-0.1	100.0%	-5.3
18911	AT5G07150.1   leucine-rich repeat family protein, contains weak similarity to LRR receptor-like protein kinase (Nicotiana tabacum) gi:7672732:gb:AAF66615; contains Pfam PF00560 domain Leucine Rich Repeat   chr5:2215821-2217984 FORWARD   Aliases: T28J14.90, T28J14_90	2.7	2.8	-0.0	-0.1	100.0%	-5.5
18912	AT2G41210.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF02493: MORN repeat   chr2:17180491-17183885 FORWARD   Aliases: T3K9.2, T3K9_2	3.1	3.1	0.0	0.1	100.0%	-5.3
18913	AT3G57690.1   arabinogalactan-protein, putative (AGP23), similar to arabinogalactan protein (Arabidopsis thaliana) gi:10880503:gb:AAG24281   chr3:21395181-21395549 FORWARD   Aliases: F15B8.120	5.1	5.1	0.0	0.1	100.0%	-5.4
18914	AT2G30940.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:13175610-13177264 FORWARD   Aliases: F7F1.15, F7F1_15	3.4	3.4	-0.0	-0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18915	AT2G27730.1   expressed protein, contains 1 transmembrane domain; similar to Unknown mitochondrial protein At2g27730 (Swiss-Prot:Q9ZUX4) (Arabidopsis thaliana) similar to F1F0-ATPase inhibitor protein (GI:5821432) (Oryza sativa)   chr2:11826906-11828955 REVERSE   Aliases: F15K20.17, F15K20_17	11.0	11.0	-0.0	-0.1	100.0%	-5.1
18916	AT3G13660.1   disease resistance response protein-related/ dirigent protein-related, similar to dirigent protein (Forsythia x intermedia) gi:6694695:gb:AAF25358; similar to disease resistance response protein 206-d (Pisum sativum) gi:508844:gb:AAB18669	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18917	AT5G64680.2   expressed protein   chr5:25871408-25872710 FORWARD   Aliases: MUB3.20, MUB3_20	5.8	5.8	0.0	0.1	100.0%	-4.9
18918	AT5G11790.1   Ndr family protein, similar to SP:O23969 Pollen specific protein SF21 {Helianthus annuus}; contains Pfam profile PF03096: Ndr family   chr5:3799551-3802793 FORWARD   Aliases: T22P22.180, T22P22_180	5.4	5.4	0.0	0.1	100.0%	-4.6
18919	AT5G24230.1   expressed protein   chr5:8228895-8230967 FORWARD   Aliases: MOP9.4, MOP9_4	2.4	2.4	-0.0	-0.1	100.0%	-4.8
18920	AT5G48380.1   leucine-rich repeat family protein / protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains leucine-rich repeats, Pfam:PF00560   chr5:19621315-19624235 REVERSE   Aliases: K23F3.10	5.2	5.2	-0.0	-0.1	100.0%	-4.5
18921	AT1G79700.1   ovule development protein, putative, similar to ovule development protein AINTEGUMENTA (GI:1209099) (Arabidopsis thaliana)   chr1:29995164-29998617 REVERSE   Aliases: F20B17.12, F20B17_12	3.0	3.0	0.0	0.1	100.0%	-4.8
18922	AT5G14540.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr5:4687150-4689677 REVERSE   Aliases: T15N1.30, T15N1_30	4.7	4.8	-0.1	-0.1	100.0%	-4.6
18923	AT5G42910.1   basic leucine zipper transcription factor (BZIP15), identical to cDNA basic leucine zipper transcription factor (atbzip15 gene) GI:18656050, basic leucine zipper transcription factor (Arabidopsis thaliana) GI:18656051; contains Pfam profile PF00170: bZIP transcription factor   chr5:17220970-17222608 FORWARD   Aliases: MBD2.11, MBD2_11	2.8	2.8	-0.0	-0.1	100.0%	-5.6
18924	AT1G32375.1   F-box family protein, contains F-box domain Pfam:PF00646	4.1	4.1	-0.0	-0.1	100.0%	-5.1
18925	AT1G50610.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor-like protein kinase GB:AAC12254 GI:3015488 from (Lycopersicon esculentum)   chr1:18745803-18748393 FORWARD   Aliases: F11F12.7, F11F12_7	3.7	3.7	-0.0	-0.1	100.0%	-5.3
18926	AT3G03340.1   LUC7 N_terminus domain-containing protein, contains Pfam domain PF03194: LUC7 N_terminus	7.1	7.0	0.0	0.1	100.0%	-5.4
18927	AT5G23900.1   60S ribosomal protein L13 (RPL13D)   chr5:8064016-8065520 REVERSE   Aliases: MRO11.6, MRO11_6	9.8	9.9	-0.0	-0.1	100.0%	-4.6
18928	AT4G00870.1   basic helix-loop-helix (bHLH) family protein, similar to the myc family of helix-loop-helix transcription factors; contains Pfam profile PF00010: Helix-loop-helix DNA-binding domain; PMID: 12679534   chr4:362169-363691 REVERSE   Aliases: A_TM018A10.7, A_TM018A10_7, T18A10.17, T18A10_17	2.7	2.7	-0.0	-0.1	100.0%	-5.5
18929	AT1G19780.1   Symbol: ATCNGC8   cyclic nucleotide-regulated ion channel, putative (CNGC8), similar to cyclic nucleotide and calmodulin-regulated ion channel GI:4581207 from (Arabidopsis thaliana)   chr1:6833876-6836396 REVERSE   Aliases: CNGC8, CYCLIC NUCLEOTIDE GATED CHANNEL 8, F14P1.12, F14P1_12	2.1	2.1	-0.0	-0.1	100.0%	-5.9
18930	AT4G32330.2   expressed protein   chr4:15608918-15612291 FORWARD   Aliases: F8B4.30	7.4	7.4	0.0	0.1	100.0%	-4.7
18931	AT2G22670.2   Symbol: IAA8   auxin-responsive protein / indoleacetic acid-induced protein 8 (IAA8), identical to SP:Q38826 Auxin-responsive protein IAA8 (Indoleacetic acid-induced protein 8) {Arabidopsis thaliana}	10.7	10.8	-0.0	-0.1	100.0%	-5.1
18932	AT2G31440.1   expressed protein, identical to cDNA endonuclease III homologue (nth1 gene) GI:11181951   chr2:13406386-13408048 REVERSE   Aliases: T28P16.7, T28P16_7	5.1	5.2	-0.1	-0.1	100.0%	-4.9
18933	AT3G60430.1   expressed protein   chr3:22347088-22348305 FORWARD   Aliases: T8B10.90	2.3	2.3	0.0	0.1	100.0%	-5.9
18934	AT2G06630.1   hypothetical protein, similar to At2g12120, At1g45090, At2g05470, At5g28482   chr2:2645685-2646380 REVERSE   Aliases: T14A4.21, T14A4_21	2.9	2.9	0.0	0.1	100.0%	-6.0
18935	AT2G07728.1   expressed protein, ; expression supported by MPSS   chr2:3453683-3456124 FORWARD   Aliases: T5E7.16, T5E7_16	2.2	2.2	0.0	0.1	100.0%	-5.6
18936	AT3G20400.1   Symbol: EMB2743   hypothetical protein   chr3:7114409-7114720 FORWARD   Aliases: EMB2743, EMBRYO DEFECTIVE 2743, MQC12.19	2.6	2.6	0.0	0.1	100.0%	-5.6
18937	AT2G42150.1   DNA-binding bromodomain-containing protein, contains Pfam domains, PF00439: Bromodomain and PF00249: Myb-like DNA-binding domain	4.0	4.0	-0.0	-0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18938	AT1G23590.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8359120-8360634 REVERSE   Aliases: F28C11.29	3.1	3.1	0.0	0.1	100.0%	-5.7
18939	AT5G54390.1   Symbol: AHL   inositol monophosphatase family protein, similar to SP:Q42546 3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7) {Arabidopsis thaliana}; contains Pfam profile PF00459: Inositol monophosphatase family; supporting cDNA gi:1354509:gb:U55205.1:ATU55205   chr5:22103224-22105243 FORWARD   Aliases: AT AHL, F24B18.1, F24B18_1, HAL2 LIKE	7.2	7.3	-0.1	-0.1	100.0%	-4.8
18940	AT2G26410.1   calmodulin-binding family protein, similar to SF16 protein (Helianthus annuus) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr2:11241729-11243829 REVERSE   Aliases: T9J22.8, T9J22_8	3.3	3.2	0.1	0.1	100.0%	-4.6
18941	AT3G28380.1   P-glycoprotein, putative, similar to P-glycoprotein homologue GI:2292907 from (Hordeum vulgare subsp. vulgare)   chr3:10624979-10629438 REVERSE   Aliases: MFJ20.4	2.4	2.4	-0.0	-0.1	100.0%	-5.8
18942	AT3G27473.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.3	2.3	0.0	0.1	100.0%	-6.0
18943	AT5G40430.1   Symbol: MYB22   myb family transcription factor (MYB22), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:16193655-16194959 REVERSE   Aliases: MPO12.140, MPO12_140	2.6	2.6	-0.0	-0.1	100.0%	-5.8
18944	AT3G21660.1   UBX domain-containing protein, contains Pfam profile: PF00789 UBX domain	3.2	3.2	0.0	0.1	100.0%	-5.4
18945	AT4G36590.1   MADS-box protein (AGL40), contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr4:17260942-17262232 REVERSE   Aliases: AP22.88, AP22_88	3.1	3.1	0.0	0.1	100.0%	-5.6
18946	AT5G05990.1   mitochondrial glycoprotein family protein / MAM33 family protein, low similarity to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein	9.0	9.0	0.0	0.1	100.0%	-4.7
18947	AT5G52540.1   expressed protein, contains PF05684: Protein of unknown function (DUF819)   chr5:21338654-21341006 REVERSE   Aliases: F6N7.1, F6N7_1	9.6	9.5	0.1	0.1	100.0%	-4.9
18948	AT2G30560.1   glycine-rich protein   chr2:13024424-13025934 FORWARD   Aliases: T6B20.9, T6B20_9	6.3	6.2	0.1	0.1	100.0%	-4.7
18949	AT5G13750.3   similar to sugar transporter family protein [Arabidopsis thaliana] (TAIR:At5g13740.1); similar to putative major facilitator superfamily antiporter [Oryza sativa (japonica cultivar-group)] (GB:BAD81140.1); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain Tetracycline resistance protein (InterPro:IPR001958)   chr5:4438203-4441570 FORWARD   Aliases: MXE10.2, MXE10_2	6.1	6.1	-0.0	-0.1	100.0%	-4.9
18950	AT5G05640.1   nucleoprotein-related, contains weak similarity to Swiss-Prot:P03515 nucleocapsid protein (Nucleoprotein) (Punta toro phlebovirus)   chr5:1684607-1685578 FORWARD   Aliases: MJJ3.3, MJJ3_3	5.1	5.1	-0.0	-0.1	100.0%	-5.1
18951	AT1G77770.2   expressed protein   chr1:29251099-29252921 REVERSE   Aliases: T32E8.10, T32E8_10	6.4	6.4	0.0	0.1	100.0%	-5.1
18952	AT1G23205.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Phaseolus vulgaris SP:Q43111, Lycopersicon esculentum SP:Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr1:8233986-8234882 REVERSE   Aliases: F26F24.4, F26F24_4	4.3	4.3	-0.0	-0.1	100.0%	-5.4
18953	AT3G54900.1   Symbol: CXIP1   CAX-interacting protein 1 (CAXIP1), identical to cDNA CAXIP1 protein (CAXIP1) GI:27752304, CAXIP1 protein (Arabidopsis thaliana) GI:27752305   chr3:20352566-20353371 REVERSE   Aliases: CAX INTERACTING PROTEIN 1, F28P10.120	5.0	5.0	0.1	0.1	100.0%	-4.8
18954	AT1G27600.2   glycosyl transferase family 43 protein, similar to Galactosylgalactosylxylosylprotein 3-beta-glucuronosyltransferase 1, Rattus norvegicus (SP:O35789), Homo sapiens (SP:Q9P2W7); contains Pfam domain Glycosyltransferase family 43 (PF03360)   chr1:9603165-9606088 REVERSE   Aliases: T22C5.4	3.7	3.8	-0.0	-0.1	100.0%	-5.0
18955	AT4G15940.1   fumarylacetoacetate hydrolase family protein, contains Pfam domain, PF01557: fumarylacetoacetate hydrolase family protein   chr4:9038304-9040758 FORWARD   Aliases: DL4011W, FCAALL.203	9.5	9.5	0.1	0.1	100.0%	-5.0
18956	AT5G45090.1   Symbol: ATPP2 A7   lectin-related, low similarity to PP2 lectin polypeptide (Cucurbita maxima) GI:410437; contains Pfam profile PF01582: TIR domain   chr5:18219980-18222227 REVERSE   Aliases: ATPP2 A7, K17O22.8, K17O22_8	3.8	3.9	-0.1	-0.1	100.0%	-4.6
18957	AT3G16540.1   DegP protease, putative, contains similarity to DegP2 protease GI:13172275 from (Arabidopsis thaliana)   chr3:5626296-5628863 REVERSE   Aliases: MDC8.17	3.4	3.4	-0.0	-0.1	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18958	AT2G02060.1   calcium-dependent protein kinase-related / CDPK-related, contains TIGRFAM TIGR01557: myb-like DNA-binding domain, SHAQKYF class; contains Pfam PF00249: Myb-like DNA-binding domain; similar to CDPK substrate protein 1; CSP1 (GI:6942190) (Mesembryanthemum crystallinum).   chr2:495690-499558 FORWARD   Aliases: F14H20.13	2.5	2.5	-0.0	-0.1	100.0%	-5.5
18959	AT1G80320.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to GS-AOP loci (GI:16118889, GI:16118887, GI:16118891, GI:16118893); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:30201674-30202788 FORWARD   Aliases: F5I6.7, F5I6_7	2.5	2.6	-0.1	-0.1	100.0%	-5.0
18960	AT2G34590.1   transketolase family protein, similar to SP:O66113 Pyruvate dehydrogenase E1 component, beta subunit (EC 1.2.4.1). {Zymomonas mobilis}; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain   chr2:14575890-14578048 REVERSE   Aliases: T31E10.7, T31E10_7	8.7	8.7	0.0	0.1	100.0%	-5.0
18961	AT4G00890.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr4:373960-375350 REVERSE   Aliases: A_TM018A10.5, A_TM018A10_5, T18A10.19, T18A10_19	2.4	2.4	0.0	0.1	100.0%	-5.8
18962	AT4G31710.1   Symbol: ATGLR2.4   glutamate receptor family protein (GLR2.4), plant glutamate receptor family, PMID:11379626   chr4:15349127-15352968 FORWARD   Aliases: F28M20.100, F28M20_100, GLR2.4	4.0	3.9	0.1	0.1	100.0%	-4.4
18963	AT1G67840.2   ATP-binding region, ATPase-like domain-containing protein, contains Pfam profile PF02518: ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like domain protein; similar to ESTs gb:AI995396.1, dbj:AV557393.1, and dbj:AV557055.1   chr1:25437765-25440738 FORWARD   Aliases: F12A21.3, F12A21_3	5.6	5.6	-0.0	-0.1	100.0%	-4.6
18964	AT2G34450.2   similar to high mobility group protein beta1 (HMGbeta1) / HMG protein beta1 [Arabidopsis thaliana] (TAIR:At1g20693.1); similar to high mobility group protein beta2 (HMGbeta2) / HMG protein beta2 [Arabidopsis thaliana] (TAIR:At1g20696.1); similar to OSJNBb0063G05.2 [Oryza sativa (japonica cultivar-group)] (GB:NP_916804.1); contains InterPro domain HMG1/2 (high mobility group) box (InterPro:IPR000910)   chr2:14534815-14536571 REVERSE   Aliases: F13P17.25	3.7	3.8	-0.0	-0.1	100.0%	-4.9
18965	AT1G69430.1   expressed protein   chr1:26101688-26102740 FORWARD   Aliases: F10D13.10, F10D13_10	3.9	3.9	0.0	0.1	100.0%	-5.1
18966	AT1G12840.1   Symbol: DET3   vacuolar ATP synthase subunit C (VATC) / V-ATPase C subunit / vacuolar proton pump C subunit (DET3), identical to vacuolar ATP synthase subunit C SP:Q9SDS7 from (Arabidopsis thaliana)   chr1:4375517-4378509 FORWARD   Aliases: DE ETIOLATED 3, F13K23.9, F13K23_9, VACUOLAR ATP SYNTHASE SUBUNIT C	9.4	9.3	0.0	0.1	100.0%	-5.0
18967	AT1G20050.1   Symbol: HYD1   C-8,7 sterol isomerase, identical to C-8,7 sterol isomerase GI:11279073 from (Arabidopsis thaliana) (Plant Mol. Biol. 38 (5), 807-815 (1998))   chr1:6949060-6950310 FORWARD   Aliases: HYDRA1	8.7	8.6	0.1	0.1	100.0%	-4.9
18968	AT4G26210.2   mitochondrial ATP synthase g subunit family protein, contains Pfam profile: PF04718 mitochondrial ATP synthase g subunit	8.0	8.0	-0.1	-0.1	100.0%	-4.7
18969	AT1G26160.1   metal-dependent phosphohydrolase HD domain-containing protein, contains Pfam profile PF01966: HD domain   chr1:9044428-9046966 REVERSE   Aliases: F28B23.16, F28B23_16	6.4	6.3	0.1	0.1	100.0%	-4.6
18970	AT3G16580.1   F-box family protein, contains F-box domain Pfam:PF00646	4.3	4.3	-0.0	-0.1	100.0%	-5.6
18971	AT4G30000.1   dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative, similar to dihydropterin pyrophosphokinase /dihydropteroate synthase (Pisum sativum) gi:1934972:emb:CAA69903   chr4:14670162-14672675 REVERSE   Aliases: F6G3.30, F6G3_30	2.8	2.8	0.0	0.1	100.0%	-5.4
18972	AT5G37310.1   endomembrane protein 70, putative, multispreading membrane protein, Homo sapiens, EMBL:HSU94831   chr5:14790059-14793436 REVERSE   Aliases: MNJ8.100, MNJ8_100	4.5	4.5	-0.0	-0.1	100.0%	-4.8
18973	AT1G32880.1   importin alpha-1 subunit, putative, similar to importin alpha-1 subunit (Karyopherin alpha-1 subunit, KAP alpha) (Arabidopsis thaliana) SWISS-PROT:Q96321   chr1:11913908-11914715 REVERSE   Aliases: F9L11.34, F9L11_34	3.0	3.0	0.0	0.1	100.0%	-5.5
18974	AT5G46320.1   hypothetical protein   chr5:18805473-18806115 REVERSE   Aliases: MPL12.11, MPL12_11	3.9	3.9	-0.0	-0.1	100.0%	-5.2
18975	AT1G01610.1   Symbol: ATGPAT4/GPAT4   Encodes a protein with glycerol-3-phosphate acyltransferase activity.   chr1:221691-224315 REVERSE   Aliases: ATGPAT4, F22L4.15, F22L4_15, GPAT4	2.4	2.3	0.1	0.1	100.0%	-4.4
18976	AT3G18035.1   Symbol: HON4   histone H1/H5 family protein, contains Pfam domain, PF00538: linker histone H1 and H5 family;similar to HMG I/Y like protein (GI:15706274) (Glycine max);similar to HMR1 protein (GI:4218141) (Antirrhinum majus); similar to high mobility group protein (GI:1483173) (Canavalia gladiata)   chr3:6169096-6171730 REVERSE   Aliases: HISTONE H1, MRC8.1	8.5	8.5	0.0	0.1	100.0%	-4.8
18977	AT3G26440.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g13000.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAU44134.1); contains InterPro domain Protein of unknown function DUF707 (InterPro:IPR007877)	4.6	4.7	-0.1	-0.1	100.0%	-4.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
18978	AT4G00770.1   expressed protein   chr4:331157-333477 FORWARD   Aliases: A_TM018A10.11, A_TM018A10_11, T18A10.2, T18A10_2	2.8	2.8	0.0	0.1	100.0%	-5.3
18979	AT3G59190.1   F-box family protein, contains F-box domain Pfam:PF00646	2.8	2.8	-0.0	-0.1	100.0%	-5.6
18980	AT2G21210.1   auxin-responsive protein, putative, similar to small auxin-up regulated protein SAUR (GI:3043536) (Raphanus sativus)   chr2:9092291-9092957 REVERSE   Aliases: F26H11.3, F26H11_3	2.5	2.5	-0.0	-0.1	100.0%	-5.7
18981	AT2G05080.1   expressed protein, low similarity to SP:Q9UUA2 DNA repair and recombination protein pif1, mitochondrial precursor {Schizosaccharomyces pombe}   chr2:1805748-1809972 REVERSE   Aliases: F1O13.21, F1O13_21	3.0	3.0	-0.0	-0.1	100.0%	-5.6
18982	AT3G46820.1   Symbol: TOPP5   serine/threonine protein phosphatase PP1 isozyme 5 (TOPP5) / phosphoprotein phosphatase 1, identical to SP:P48485 Serine/threonine protein phosphatase PP1 isozyme 5 (EC 3.1.3.16) {Arabidopsis thaliana}, phosphoprotein phosphatase 1 GI:166803 {Arabidopsis thaliana}   chr3:17252768-17255262 REVERSE   Aliases: T6H20.150	5.3	5.3	-0.0	-0.1	100.0%	-4.8
18983	AT3G53370.1   DNA-binding S1FA family protein, contains Pfam profile: PF04689 DNA binding protein S1FA	7.0	7.1	-0.1	-0.1	100.0%	-4.3
18984	AT3G22490.1   late embryogenesis abundant protein, putative / LEA protein, putative, similar to LEA protein in group 5 (AtECP31) (Arabidopsis thaliana) GI:1526422; contains Pfam profile PF04927: Seed maturation protein   chr3:7969688-7970850 REVERSE   Aliases: F16J14.21	2.1	2.1	-0.0	-0.1	100.0%	-5.7
18985	AT1G48270.1   Symbol: GCR1   G protein coupled receptor-related, identical to putative G protein coupled receptor GI:2104224 from (Arabidopsis thaliana)   chr1:17831621-17834088 REVERSE   Aliases: F11A17.17, F11A17_17, G PROTEIN COUPLED RECEPTOR 1, GCR1	4.3	4.3	-0.0	-0.1	100.0%	-4.9
18986	AT5G20935.1   expressed protein   chr5:7103473-7104023 FORWARD   Aliases: None	2.4	2.4	0.0	0.1	100.0%	-5.7
18987	AT1G17920.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to A20 (GI:1881536) (Arabidopsis thaliana); similar to homeobox protein GI:1173622 from (Phalaenopsis sp. SM9108)   chr1:6161865-6165375 REVERSE   Aliases: F2H15.14, F2H15_14	2.8	2.8	-0.0	-0.1	100.0%	-5.5
18988	AT5G04980.1   endonuclease/exonuclease/phosphatase family protein, contains similarity to inositol polyphosphate 5-phosphatase I (GI:10444261) and II (GI:10444263) (Arabidopsis thaliana); contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family	3.6	3.5	0.0	0.1	100.0%	-5.1
18989	AT5G12100.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:3911364-3914076 FORWARD   Aliases: MXC9.6, MXC9_6	4.3	4.3	-0.0	-0.1	100.0%	-5.3
18990	AT2G37610.1   hypothetical protein   chr2:15783947-15784751 REVERSE   Aliases: F13M22.11, F13M22_11	2.5	2.5	-0.0	-0.1	100.0%	-5.8
18991	AT1G43920.1   expressed protein   chr1:16662523-16663065 FORWARD   Aliases: F9C16.8, F9C16_8	4.0	4.0	0.0	0.1	100.0%	-4.9
18992	AT1G55780.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr1:20856351-20856846 REVERSE   Aliases: F20N2.22	2.7	2.7	0.0	0.1	100.0%	-5.5
18993	AT5G66880.1   serine/threonine protein kinase, putative, similar to serine-threonine protein kinase (Triticum aestivum) gi:2055374:gb:AAB58348	6.2	6.1	0.1	0.1	100.0%	-4.8
18994	AT5G05400.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	3.4	3.3	0.0	0.1	100.0%	-4.4
18995	AT5G37030.1   tRNA-splicing endonuclease positive effector-related, contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease (Saccharomyces cerevisiae) gi:172574:gb:AAB63976   chr5:14651844-14654169 REVERSE   Aliases: K15O15.6, K15O15_6	3.1	3.1	0.0	0.1	100.0%	-5.6
18996	AT3G59570.1   RabGAP/TBC domain-containing protein, similar to GTPase activating protein (Yarrowia lipolytica) GI:2370595; contains Pfam profile PF00566: TBC domain   chr3:22011809-22017033 REVERSE   Aliases: T16L24.120	4.1	4.1	0.0	0.1	100.0%	-5.4
18997	AT2G22425.1   expressed protein, weak similarity to Swiss-Prot:Q9Y6A9 microsomal signal peptidase 12 kDa subunit (SPase 12 kDa subunit, SPC12, HSPC033) (Homo sapiens)	10.6	10.7	-0.0	-0.1	100.0%	-5.6
18998	AT2G05870.1   cytochrome P-450 aromatase-related, similar to minor outer capsid protein VP4 (GI:13446784) (Human rotavirus C); similar to cytochrome P-450 aromatase (GI:21170) (Gallus gallus);   chr2:2249078-2249996 REVERSE   Aliases: T6P5.7, T6P5_7	2.2	2.1	0.0	0.1	100.0%	-5.6
18999	AT2G04420.1   expressed protein   chr2:1535486-1536247 FORWARD   Aliases: T1O3.17, T1O3_17	2.1	2.1	-0.0	-0.1	100.0%	-6.1
19000	AT4G37480.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to J-Domain (Residues 2-76) In The Escherichia coli N-Terminal Fragment (Residues 2-108) Of The Molecular Chaperone Dnaj GI:1942570; contains Pfam profile PF00226 Dnaj domain   chr4:17619255-17621396 FORWARD   Aliases: F6G17.130, F6G17_130	3.6	3.6	-0.0	-0.1	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19001	AT5G07770.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr5:2474643-2479338 FORWARD   Aliases: MBK20.23, MBK20_23	2.0	2.0	-0.0	-0.1	100.0%	-5.5
19002	AT1G22940.1   Symbol: TH1   thiamin biosynthesis protein, putative, strong similarity to hydroxymethylpyrimidine kinase/thiamin-phosphate pyrophosphorylase (BTH1) GI:7488455 from (Brassica napus)   chr1:8122340-8125057 FORWARD   Aliases: F19G10.10, F19G10_10, THIAMINE REQUIRING 1	5.9	6.0	-0.0	-0.1	100.0%	-4.8
19003	AT5G17540.1   transferase family protein, similar to hypersensitivity-related gene product HSR201 - Nicotiana tabacum, EMBL:X95343; contains Pfam transferase family domain PF00248   chr5:5781989-5783708 REVERSE   Aliases: K10A8.20, K10A8_20	3.4	3.3	0.0	0.1	100.0%	-5.4
19004	AT2G26135.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile PF01485:IBR domain   chr2:11137197-11138592 FORWARD   Aliases: None	3.2	3.2	0.0	0.1	100.0%	-5.4
19005	AT3G25260.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:9200675-9203237 FORWARD   Aliases: MJL12.27	3.0	3.0	0.0	0.1	100.0%	-5.2
19006	AT5G63330.2   similar to DNA-binding bromodomain-containing protein [Arabidopsis thaliana] (TAIR:At5g14270.1); similar to global transcription factor group E [Zea mays] (GB:AAO84020.1); contains InterPro domain Bromodomain (InterPro:IPR001487)   chr5:25394322-25396500 REVERSE   Aliases: K9H21.1, K9H21_1	4.7	4.7	0.1	0.1	100.0%	-4.6
19007	AT2G01460.1   phosphoribulokinase/uridine kinase family protein, contains Pfam profile PF00485: Phosphoribulokinase / Uridine kinase family   chr2:206135-210974 FORWARD   Aliases: F2I9.8, F2I9_8	3.3	3.3	0.0	0.1	100.0%	-5.2
19008	AT1G23700.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:8379443-8381954 REVERSE   Aliases: F5O8.25, F5O8_25	2.9	2.9	0.0	0.1	100.0%	-5.3
19009	AT5G50480.1   CCAAT-box binding transcription factor Hap5a, putative, GI:14577940 CCAAT-binding protein subunit HAP5 {Hypocrea jecorina} similar to Transcription factor GB:CAA74053 GI:2398533 from (Arabidopsis thaliana) similarity to transcription factor Hap5a similar to transcription factor Hap5a (Arabidopsis thaliana)(GI:6523090)   chr5:20574800-20575690 REVERSE   Aliases: MBA10.3, MBA10_3	3.1	3.1	0.0	0.1	100.0%	-5.2
19010	AT1G44130.1   nucellin protein, putative, similar to nucellin GI:2290202 from (Hordeum vulgare)   chr1:16789948-16791758 REVERSE   Aliases: T7O23.17, T7O23_17	2.9	2.8	0.0	0.1	100.0%	-5.6
19011	AT2G35150.1   phosphate-responsive 1 family protein, similar to phi-1 (phosphate-induced gene) (Nicotiana tabacum) GI:3759184; contains Pfam profile PF04674: Phosphate-induced protein 1 conserved region   chr2:14824126-14825290 REVERSE   Aliases: T4C15.11	3.5	3.6	-0.0	-0.1	100.0%	-4.7
19012	AT1G29040.3   expressed protein, similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD61226.1)   chr1:10134055-10135342 FORWARD   Aliases: F28N24.25, F28N24_25	6.6	6.6	-0.0	-0.1	100.0%	-4.7
19013	AT3G45010.1   Symbol: SCPL48	9.2	9.2	-0.1	-0.1	100.0%	-5.6
19014	AT2G16010.1   hypothetical protein   chr2:6972692-6973081 FORWARD   Aliases: F7H1.3, F7H1_3	3.0	3.0	-0.0	-0.1	100.0%	-5.4
19015	AT5G56340.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:22834937-22836883 FORWARD   Aliases: MCD7.7, MCD7_7	5.2	5.3	-0.0	-0.1	100.0%	-4.9
19016	AT2G26050.1   expressed protein   chr2:11105730-11106458 REVERSE   Aliases: T19L18.14, T19L18_14	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19017	AT3G13784.1   beta-fructosidase, putative / beta-fructofuranosidase, putative / cell wall invertase, putative, similar to beta-fructofuranosidase GI:402740 from (Arabidopsis thaliana)   chr3:4528536-4530676 REVERSE   Aliases: MMM17.25	3.3	3.2	0.0	0.1	100.0%	-5.3
19018	AT3G50750.1   brassinosteroid signalling positive regulator-related, contains similarity to BZR1 protein (Arabidopsis thaliana) gi:20270971:gb:AAM18490   chr3:18872820-18874215 REVERSE   Aliases: F18B3.30	2.4	2.4	0.0	0.1	100.0%	-6.0
19019	AT2G04840.1   F-box family protein, similar to F-box protein family, AtFBX7 (GI:20197899) (Arabidopsis thaliana)   chr2:1697006-1698237 FORWARD   Aliases: F28I8.12, F28I8_12	3.4	3.4	0.0	0.1	100.0%	-5.7
19020	AT1G78470.1   hypothetical protein   chr1:29526663-29527889 FORWARD   Aliases: F3F9.2	2.8	2.8	0.0	0.1	100.0%	-5.2
19021	AT4G28580.1   magnesium transporter CorA-like family protein (MRS2-6), weak similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg2+ transporter protein   chr4:14123495-14125058 FORWARD   Aliases: T5F17.30, T5F17_30	3.9	4.0	-0.0	-0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19022	AT4G10390.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:6441689-6443385 REVERSE   Aliases: F7L13.4	4.2	4.2	-0.0	-0.1	100.0%	-4.7
19023	AT2G03680.1   Symbol: SPR1   expressed protein, Alternative splicing exists based on EST evidence   chr2:1120797-1122004 FORWARD   Aliases: F19B11.13, F19B11_13, SKU6, SPIRAL1	11.7	11.8	-0.0	-0.1	100.0%	-5.6
19024	AT2G18170.1   Symbol: ATMPK7	2.7	2.8	-0.0	-0.1	100.0%	-5.1
19025	AT4G25835.1   AAA-type ATPase family protein, contains Pfam profile: PF00004 ATPase family   chr4:13136116-13137739 FORWARD   Aliases: None	3.1	3.1	-0.1	-0.1	100.0%	-4.5
19026	AT3G50360.1   Symbol: ATCEN2	8.8	8.8	-0.0	-0.1	100.0%	-4.9
19027	AT3G58350.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, similar to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471; contains Pfam profile PF00917: MATH domain   chr3:21602429-21603939 REVERSE   Aliases: F9D24.260	3.0	2.9	0.0	0.1	100.0%	-4.5
19028	AT4G19200.1   proline-rich family protein, contains proline rich extensin domains, INTERPRO:IPR002965   chr4:10498887-10500733 FORWARD   Aliases: T18B16.170, T18B16_170	8.4	8.3	0.1	0.1	100.0%	-4.5
19029	AT2G35030.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr2:14767948-14770156 REVERSE   Aliases: F19I3.26, F19I3_26	3.2	3.2	-0.0	-0.1	100.0%	-5.4
19030	AT2G32610.1   Symbol: ATCSLB01   cellulose synthase family protein, similar to Zea mays cellulose synthase-3 (gi:9622878), -2 (gi:9622876), -1 (gi:9622874)   chr2:13843311-13846590 FORWARD   Aliases: ATCSLB1, CSLB01, T26B15.17, T26B15_17	3.2	3.2	0.0	0.1	100.0%	-4.7
19031	AT2G05400.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, supported by tandem duplication of meprin and TRAF homology (MATH) domain protein (GI:4914358) (TIGR_Ath1:At2g05420) (Arabidopsis thaliana)	2.8	2.8	0.0	0.1	100.0%	-5.4
19032	AT4G03290.1   calcium-binding protein, putative, similar to calcium-binding protein (Lotus japonicus) GI:18413495; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:1442634-1443499 FORWARD   Aliases: F4C21.22, F4C21_22	2.9	2.9	-0.0	-0.1	100.0%	-5.6
19033	AT2G17470.1   expressed protein, contains Pfam profile PF01027: Uncharacterized protein family UPF0005	3.2	3.2	-0.0	-0.1	100.0%	-5.4
19034	AT1G47920.1   syntaxin-related family protein, contains a novel domain similar to F-box that is shared among other proteins in Arabidopsis;   chr1:17664764-17666063 FORWARD   Aliases: T6B12.5, T6B12_5	2.8	2.8	0.0	0.1	100.0%	-5.4
19035	AT4G22410.1   ubiquitin carboxyl-terminal hydrolase family protein, similar to U4/U6.U5 tri-snRNP-associated 65 kDa protein (Homo sapiens) GI:13926071; contains Pfam profile PF00443: Ubiquitin carboxyl-terminal hydrolase   chr4:11818225-11820147 REVERSE   Aliases: F7K2.7, F7K2_7	2.5	2.4	0.0	0.1	100.0%	-5.0
19036	AT5G61800.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:24847213-24848779 REVERSE   Aliases: MAC9.12, MAC9_12	4.7	4.7	-0.0	-0.1	100.0%	-5.1
19037	AT3G13370.1   hypothetical protein   chr3:4341671-4342237 FORWARD   Aliases: MDC11.21	2.8	2.8	0.0	0.1	100.0%	-5.7
19038	AT3G46280.1   protein kinase-related, contains similarity to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376   chr3:17016498-17019399 REVERSE   Aliases: F12M12.250	3.3	3.3	0.0	0.1	100.0%	-5.1
19039	AT4G11890.3   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:7148242-7149915 FORWARD   Aliases: T26M18.100, T26M18_100	3.3	3.2	0.0	0.1	100.0%	-5.4
19040	AT4G05620.1   F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profile PF00646: F-box domain   chr4:2985048-2985446 REVERSE   Aliases: F21I2.10, F21I2_10	3.1	3.0	0.0	0.1	100.0%	-5.3
19041	AT2G27110.3   similar to far-red impaired responsive protein, putative [Arabidopsis thaliana] (TAIR:At4g38180.1); similar to putative FAR1 protein [Oryza sativa (japonica cultivar-group)] (GB:AAT78829.1); contains InterPro domain SWIM Zn-finger (InterPro:IPR007527); contains InterPro domain Zn-finger, PMZ type (InterPro:IPR006564); contains InterPro domain FAR1 (InterPro:IPR004330)   chr2:11583747-11587869 REVERSE   Aliases: T20P8.16, T20P8_16	4.7	4.7	-0.0	-0.1	100.0%	-5.0
19042	AT4G11590.1   F-box family protein, contains weak hit to Pfam PF00646: F-box domain   chr4:7008597-7009790 FORWARD   Aliases: T5C23.20, T5C23_20	3.0	3.0	-0.0	-0.1	100.0%	-5.5
19043	AT2G43540.1   expressed protein   chr2:18079448-18080040 FORWARD   Aliases: T1O24.28	6.1	6.0	0.0	0.1	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19044	AT1G02860.1   SPX (SYG1/Pho81/XPR1) domain-containing protein / zinc finger (C3HC4-type RING finger) protein-related, weak similarity to tripartite motif protein TRIM13 (Mus musculus) GI:12407427, gpStaf50 (Homo sapiens) GI:899300; contains Pfam profiles PF03105: SPX domain, PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:635144-637262 FORWARD   Aliases: F22D16.14, F22D16_14	6.5	6.5	0.0	0.1	100.0%	-5.0
19045	AT1G69860.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:26313291-26315837 FORWARD   Aliases: T17F3.11, T17F3_11	2.4	2.5	-0.0	-0.1	100.0%	-5.3
19046	AT3G25165.1   Symbol: RALFL25   rapid alkalization factor (RALF) family protein   chr3:9163347-9163900 REVERSE   Aliases: RALF LIKE 25	2.2	2.2	0.0	0.1	100.0%	-6.1
19047	AT3G09780.1   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr3:3000764-3003170 REVERSE   Aliases: F11F8.37	4.2	4.3	-0.0	-0.1	100.0%	-4.7
19048	AT1G14900.1   high-mobility-group protein / HMG-I/Y protein, nearly identical to high-mobility-group protein HMG-I/Y protein (Arabidopsis thaliana) GI:1429211; contains Pfam profiles PF00538: linker histone H1 and H5 family, PF02178: AT hook motif   chr1:5138329-5139419 REVERSE   Aliases: F10B6.31, F10B6_31	4.9	4.9	-0.0	-0.1	100.0%	-4.8
19049	AT1G55060.1   Symbol: UBQ12   polyubiquitin (UBQ12), identical to polyubiquitin (ubq12) gene sequence GI:304121 from (Arabidopsis thaliana)   chr1:20553200-20553892 FORWARD   Aliases: T7N22.10, UBIQUITIN 12	2.3	2.3	0.0	0.1	100.0%	-6.1
19050	AT5G01910.1   expressed protein   chr5:357947-358652 REVERSE   Aliases: T20L15.180, T20L15_180	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19051	AT2G25760.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:10991886-10996002 REVERSE   Aliases: AT2G25750, F17H15.21, F17H15_21	4.9	4.9	-0.0	-0.1	100.0%	-5.5
19052	AT4G13810.1   disease resistance family protein / LRR family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAC78591   chr4:8005058-8007283 REVERSE   Aliases: F18A5.200, F18A5_200	3.1	3.2	-0.0	-0.1	100.0%	-5.4
19053	ATCG01060.1   Symbol: PSAC   Encodes the PsaC subunit of photosystem I.   chrC:117318-117563 REVERSE   Aliases: PSAC	4.7	4.6	0.1	0.1	100.0%	-4.6
19054	AT2G39030.1   GCN5-related N-acetyltransferase (GNAT) family protein, similar to SP:Q9SMB8 Tyramine N-feruloyltransferase 4/11 (EC 2.3.1.110) (Hydroxycinnamoyl-CoA: tyramine N-hydroxycinnamoyltransferase) {Nicotiana tabacum}; contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:16305305-16306280 FORWARD   Aliases: T7F6.20, T7F6_20	3.8	3.8	0.0	0.1	100.0%	-5.2
19055	AT3G63210.1   Symbol: MARD1   expressed protein, identical to senescence-associated protein SAG102 (GI::22331931) (Arabidopsis thaliana) (unpublished); contains Pfam profile PF04570: Protein of unknown function (DUF581)   chr3:23364590-23366135 REVERSE   Aliases: F16M2.60, MEDIATOR OF ABA REGULATED DORMANCY 1	2.6	2.7	-0.1	-0.1	100.0%	-4.6
19056	AT5G01950.1   leucine-rich repeat transmembrane protein kinase, putative, receptor protein kinases   chr5:364899-370079 REVERSE   Aliases: T20L15.220, T20L15_220	5.9	5.9	-0.1	-0.1	100.0%	-5.0
19057	AT2G27340.3   similar to N-acetylglucosaminyl-phosphatidylinositol de-N-acetylase-related [Arabidopsis thaliana] (TAIR:At3g58130.1); similar to N-acetylglucosaminylphosphatidylinositol deacetylase; GlcNAc-PI de-N-acetylase [Leishmania major] (GB:AAN60998.1); contains InterPro domain LmbE-like protein (InterPro:IPR003737)   chr2:11703831-11706302 FORWARD   Aliases: F12K2.8	6.1	6.1	-0.0	-0.1	100.0%	-5.0
19058	AT3G11430.1   Symbol: ATGPAT5/GPAT5   Encodes a protein with glycerol-3-phosphate acyltransferase activity.   chr3:3595771-3597958 FORWARD   Aliases: ATGPAT5, F24K9.10, GPAT5	3.2	3.2	-0.0	-0.1	100.0%	-4.6
19059	AT4G17470.1   palmitoyl protein thioesterase family protein   chr4:9742771-9744859 REVERSE   Aliases: DL4770C, FCAALL.11	2.9	2.9	0.0	0.1	100.0%	-5.4
19060	AT1G18670.1   Symbol: IBS1   Encodes a cyclin-dependent kinase-like protein with a ser/thr protein kinase domain and an N-terminal myristoylation sequence. Mutants in this gene are unable to express female sterility in response to beta-aminobutyric acid, as wild type plants do.   chr1:6426890-6430688 REVERSE   Aliases: F6A14.22, F6A14_22, IBS1, IMPAIRED IN BABA INDUCED STERILITY 1	6.2	6.2	-0.1	-0.1	100.0%	-4.3
19061	AT1G52570.1   Symbol: PLDALPHA2   phospholipase D alpha 2 / PLD alpha 2 (PLDALPHA2) (PLD2) / choline phosphatase 2, identical to phospholipase D alpha 2 ( PLD alpha 2) SP:Q9SSQ9 from (Arabidopsis thaliana)	3.1	3.1	-0.0	-0.1	100.0%	-5.4
19062	AT1G75930.1   Symbol: EXL6   family II extracellular lipase 6 (EXL6), EXL6 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 (Arabidopsis thaliana)   chr1:28511770-28513502 FORWARD   Aliases: T4O12.260, T4O12_260	2.9	2.9	0.0	0.1	100.0%	-5.7
19063	AT5G22410.1   peroxidase, putative, identical to peroxidase ATP14a (Arabidopsis thaliana) gi:1546690:emb:CAA67335   chr5:7426328-7427967 FORWARD   Aliases: MWD9.21, MWD9_21	2.9	2.9	0.0	0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19064	AT1G49800.1   expressed protein   chr1:18442033-18442607 REVERSE   Aliases: F10F5.5, F10F5_5	3.4	3.4	-0.0	-0.1	100.0%	-5.1
19065	AT2G28630.1   beta-ketoacyl-CoA synthase family protein   chr2:12282396-12284322 REVERSE   Aliases: T8O18.8, T8O18_8	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19066	AT5G19960.1   RNA recognition motif (RRM)-containing protein, low similarity to glycine-rich RNA-binding protein (Euphorbia esula) GI:2645699; contains INTERPRO:IPR000504 RNA-binding region RNP-1 (RNA recognition motif) (RRM) domain   chr5:6743928-6746341 FORWARD   Aliases: F28I16.110, F28I16_110	7.6	7.6	0.0	0.1	100.0%	-5.0
19067	AT4G27320.1   universal stress protein (USP) family protein, low similarity to ER6 protein (Lycopersicon esculentum) GI:5669654, early nodulin ENOD18 (Vicia faba) GI:11602747; contains Pfam profile PF00582: universal stress protein family	6.4	6.4	-0.0	-0.1	100.0%	-5.0
19068	AT1G07300.1   josephin protein-related, similar to Josephin-like protein (Swiss-Prot:O82391) (Arabidopsis thaliana)   chr1:2245913-2246299 REVERSE   Aliases: F22G5.36, F22G5_36	4.5	4.5	-0.0	-0.1	100.0%	-5.0
19069	AT1G17240.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-0B (Lycopersicon esculentum) gi:3894387:gb:AAC78593   chr1:5896409-5898710 REVERSE   Aliases: F20D23.6, F20D23_6	2.8	2.8	-0.0	-0.1	100.0%	-5.2
19070	AT5G13300.1   Symbol: VAN3   similar to ARF GTPase-activating domain-containing protein [Arabidopsis thaliana] (TAIR:At5g61980.1); similar to ARF GTPase-activating domain-containing protein [Arabidopsis thaliana] (TAIR:At1g60860.1); similar to ARF GTPase-activating domain-containing protein [Arabidopsis thaliana] (TAIR:At1g10870.1); similar to putative ADP-ribosylation factor-directed GTPase activating protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466898.1); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164); contains InterPro domain BAR (InterPro:IPR006632); contains InterPro domain Pleckstrin-like (InterPro:IPR001849); contains InterPro domain Ankyrin (InterPro:IPR002110)   chr5:4255604-4262317 REVERSE   Aliases: T31B5.120, T31B5_120, VASCULAR NETWORK DEFECTIVE 3	4.3	4.3	0.0	0.1	100.0%	-4.9
19071	AT5G65310.2   Symbol: ATHB5   similar to homeobox-leucine zipper protein 6 (HB-6) / HD-ZIP transcription factor 6 [Arabidopsis thaliana] (TAIR:At2g22430.1); similar to homeodomain protein Hfi22 [Nicotiana tabacum] (GB:AAM48290.1); contains InterPro domain Leucine zipper, homeobox-associated (InterPro:IPR003106); contains InterPro domain Helix-turn-helix motif, lambda-like repressor (InterPro:IPR000047); contains InterPro domain Homeobox (InterPro:IPR001356)	4.6	4.5	0.0	0.1	100.0%	-5.0
19072	AT2G23510.1   transferase family protein, low similarity to EIG-I24 from Nicotiana tabacum (gi:10798748), 10-deacetylbaocatin III-10-O-acetyl transferase from Taxus cuspidata (gi:6746554); contains Pfam transferase family domain PF02458   chr2:10018597-10020613 REVERSE   Aliases: F26B6.16, F26B6_16	2.7	2.6	0.0	0.1	100.0%	-5.1
19073	AT3G12300.1   expressed protein   chr3:3921537-3923162 REVERSE   Aliases: F28J15.10	4.9	4.8	0.0	0.1	100.0%	-5.0
19074	AT5G60450.1   Symbol: ARF4   auxin-responsive factor (ARF4), contains Pfam profile: PF02362 B3 DNA binding domain; identical to cDNA auxin response factor 4 (ARF4) GI:4102597   chr5:24325549-24329924 REVERSE   Aliases: AUXIN RESPONSE FACTOR 4, MUF9.7, MUF9_7	5.6	5.6	0.0	0.1	100.0%	-4.7
19075	AT3G11950.1   UbiA prenyltransferase family protein, contains Pfam profile PF01040: UbiA prenyltransferase family   chr3:3779845-3785104 REVERSE   Aliases: MEC18.6	6.9	6.9	0.1	0.1	100.0%	-4.8
19076	AT5G54220.1   Encodes a defensin-like (DEFL) family protein.   chr5:22028575-22028981 FORWARD   Aliases: MDK4.4, MDK4_4	2.9	3.0	-0.0	-0.1	100.0%	-5.0
19077	AT3G11080.1   disease resistance family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-2.2 (Lycopersicon pimpinellifolium) gi:1184077:gb:AAC15780   chr3:3470446-3473318 FORWARD   Aliases: F11B9.4	3.1	3.1	-0.0	-0.1	100.0%	-5.6
19078	AT1G32700.2   zinc-binding family protein, similar to zinc-binding protein (Pisum sativum) GI:16117799; contains Pfam profile PF04640 : Protein of unknown function, DUF597   chr1:11827447-11829739 FORWARD   Aliases: F6N18.8, F6N18_8	6.0	5.9	0.1	0.1	100.0%	-4.7
19079	AT2G30250.1   Symbol: WRKY25	3.3	3.3	0.0	0.1	100.0%	-4.5
19080	AT2G04450.1   MutT/nudix family protein, similar to SP:P53370 Nucleoside diphosphate-linked moiety X motif 6 {Homo sapiens}; contains Pfam profile PF00293: NUDIX domain   chr2:1543707-1545392 FORWARD   Aliases: T1O3.14, T1O3_14	3.9	3.9	0.0	0.1	100.0%	-5.3
19081	AT2G27630.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr2:11794475-11799681 REVERSE   Aliases: F15K20.27, F15K20_27	3.1	3.1	-0.0	-0.1	100.0%	-5.7
19082	AT2G18750.2   similar to calmodulin-binding protein [Arabidopsis thaliana] (TAIR:At4g25800.1); similar to calmodulin-binding protein [Arabidopsis thaliana] (TAIR:At5g57580.1); similar to putative calmodulin-binding protein [Oryza sativa (japonica cultivar-group)] (GB:XP_466263.1); similar to OSJNBa0058G03.4 [Oryza sativa (japonica cultivar-group)] (GB:XP_472636.1); similar to calmodulin-binding protein (GB:AAB37246.1)   chr2:8132710-8135703 FORWARD   Aliases: MSF3.13, MSF3_13	3.6	3.6	0.0	0.1	100.0%	-5.1
19083	AT5G15130.1   Symbol: WRKY72	2.4	2.5	-0.0	-0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19084	AT2G39020.1   GCN5-related N-acetyltransferase (GNAT) family protein, similar to SP:Q9SMB8 Tyramine N-feruloyltransferase 4/11 (EC 2.3.1.110) (Hydroxycinnamoyl-CoA: tyramine N-hydroxycinnamoyltransferase) {Nicotiana tabacum}; contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:16302393-16303406 FORWARD   Aliases: T7F6.19, T7F6_19	5.8	5.8	-0.0	-0.1	100.0%	-4.4
19085	AT4G28130.1   diacylglycerol kinase accessory domain-containing protein, similar to diacylglycerol kinase (Lycopersicon esculentum) GI:10798892; contains Pfam profile PF00609: Diacylglycerol kinase accessory domain (presumed)   chr4:13971558-13974329 FORWARD   Aliases: AT4G28120, F26K10.10, F26K10_10	2.6	2.6	-0.0	-0.1	100.0%	-5.8
19086	AT2G39040.1   peroxidase, putative, similar to cationic peroxidase isozyme 38K precursor (Nicotiana tabacum) gi:575603:dbj:BAA07663   chr2:16306541-16308251 REVERSE   Aliases: T7F6.21, T7F6_21	2.3	2.3	-0.0	-0.1	100.0%	-5.2
19087	AT4G22570.1   adenine phosphoribosyltransferase, putative, strong similarity to Adenine phosphoribosyltransferase (Hordeum vulgare subsp. vulgare) GI:9711921; contains Pfam profile PF00156: Phosphoribosyl transferase domain   chr4:11882161-11885414 REVERSE   Aliases: F7K2.150, F7K2_150	10.2	10.1	0.1	0.1	100.0%	-4.6
19088	AT3G02830.1   Symbol: ZFN1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr3:613846-616151 FORWARD   Aliases: F13E7.23, F13E7_23, ZINC FINGER PROTEIN 1	4.6	4.7	-0.0	-0.1	100.0%	-4.7
19089	AT2G06925.1   phospholipase A2 family protein, similar to secretory low molecular weight phospholipase A2 beta (Arabidopsis thaliana) GI:25992715; contains INTERPRO domain IPR001211 phospholipase A2	4.0	4.0	-0.0	-0.1	100.0%	-4.5
19090	AT3G23620.1   brix domain-containing protein, contains Pfam domain, PF04427: Brix domain   chr3:8480076-8482164 FORWARD   Aliases: MDB19.11	6.4	6.5	-0.1	-0.1	100.0%	-4.3
19091	AT2G15310.1   Symbol: ATARFB1A   Gene encoding ADP-ribosylation factor and similar to ADP-ribosylation factor (GI:861205) (Chlamydomonas reinhardtii), other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding.   chr2:6660874-6662583 FORWARD   Aliases: ATARFB1A, F27O10.4, F27O10_4	3.0	3.1	-0.0	-0.1	100.0%	-4.8
19092	AT1G08180.1   expressed protein   chr1:2564738-2565073 REVERSE   Aliases: T23G18.4, T23G18_4	3.0	3.0	-0.0	-0.1	100.0%	-5.0
19093	ATCG00590.1   Symbol: ORF31   hypothetical protein   chrC:65712-65807 FORWARD   Aliases: ORF31	4.7	4.6	0.1	0.1	100.0%	-4.6
19094	AT1G04150.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr1:1081207-1084245 REVERSE   Aliases: F20D22.8, F20D22_8	3.5	3.6	-0.0	-0.1	100.0%	-5.1
19095	AT4G17950.1   DNA-binding family protein, contains Pfam PF03479: Domain of unknown function (DUF296); contains Pfam PF02178: AT hook motif;   chr4:9967002-9969244 REVERSE   Aliases: T6K21.130, T6K21_130	6.0	6.0	0.0	0.1	100.0%	-4.7
19096	AT3G22660.1   rRNA processing protein-related, contains weak similarity to rRNA processing protein EBP2 (EBNA1-binding protein homolog) (Swiss-Prot:P36049) (Saccharomyces cerevisiae)	7.1	7.1	-0.0	-0.1	100.0%	-5.0
19097	AT5G43480.1   expressed protein   chr5:17484626-17484871 REVERSE   Aliases: MWF20.20, MWF20_20	3.9	3.9	-0.0	-0.1	100.0%	-5.9
19098	AT2G29130.1   laccase, putative / diphenol oxidase, putative, similar to laccase (Liriodendron tulipifera)(GI:1621467)	2.9	2.9	-0.0	-0.1	100.0%	-5.3
19099	AT3G48140.1   senescence-associated protein, putative, similar to B12D protein (Ipomoea batatas) GB:AAD22104   chr3:17789385-17790534 FORWARD   Aliases: T24C20.20	12.2	12.2	0.0	0.1	100.0%	-5.6
19100	AT1G13680.1   expressed protein   chr1:4690694-4692838 FORWARD   Aliases: F21F23.12, F21F23_12	2.2	2.1	0.0	0.1	100.0%	-6.0
19101	AT3G09980.1   expressed protein, contains Pfam profile PF04949: Family of unknown function (DUF662)   chr3:3069236-3071412 FORWARD   Aliases: T22K18.21	8.2	8.3	-0.1	-0.1	100.0%	-4.6
19102	AT5G20870.1   glycosyl hydrolase family 17 protein, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 (Nicotiana tabacum)   chr5:7079977-7081771 REVERSE   Aliases: F22D1.40, F22D1_40	3.5	3.5	0.0	0.1	100.0%	-5.1
19103	AT3G50200.1   expressed protein, ; expression supported by MPSS   chr3:18623445-18624306 REVERSE   Aliases: F11C1.40	2.8	2.7	0.0	0.1	100.0%	-5.3
19104	AT3G04060.1   Symbol: ANAC046   no apical meristem (NAM) family protein, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (GI:1944132) (Arabidopsis thaliana)   chr3:1053373-1055170 REVERSE   Aliases: ANAC046, T11I18.17, T11I18_17	3.0	3.1	-0.1	-0.1	100.0%	-4.4
19105	AT1G13600.1   bZIP transcription factor family protein, contains Pfam profile: PF00170 bZIP transcription factor   chr1:4650784-4651466 REVERSE   Aliases: F21F23.3	3.7	3.6	0.0	0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19106	AT1G08360.1   60S ribosomal protein L10A (RPL10aA), similar to 60S ribosomal protein L10A GB:AAC73045 GI:3860277 from (Arabidopsis thaliana)   chr1:2636027-2637912 FORWARD   Aliases: T27G7.6, T27G7_6	11.4	11.4	-0.0	-0.1	100.0%	-4.9
19107	AT4G13340.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	4.1	4.1	0.1	0.1	100.0%	-4.6
19108	AT3G61950.2   basic helix-loop-helix (bHLH) family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain	2.4	2.5	-0.0	-0.1	100.0%	-5.6
19109	AT3G57840.1   self-incompatibility protein-related, similar to S1 self-incompatibility protein (Papaver rhoeas) GI:452430   chr3:21433800-21434264 FORWARD   Aliases: T10K17.50	4.4	4.4	-0.0	-0.1	100.0%	-5.2
19110	AT5G61850.1   Symbol: LFY   floral meristem identity control protein LEAFY (LFY), identical to PIR:B38104 LFY floral meristem identity control protein, splice form 2 - Arabidopsis thaliana; contains Pfam profile PF01698: Floricaula / Leafy protein   chr5:24861521-24864159 FORWARD   Aliases: LEAFY, MAC9.13, MAC9_13	2.7	2.7	-0.0	-0.1	100.0%	-5.7
19111	AT3G04170.1   germin-like protein, putative, contains Pfam profile: PF01072 germin family; similar to germin-like protein type2 GB:CAA63023 (SP:P92996), GLP6 (SP:P92997), GLP2A (SP:P92999) (Arabidopsis thaliana)   chr3:1094628-1095672 REVERSE   Aliases: T6K12.21, T6K12_21	2.9	2.9	0.0	0.1	100.0%	-5.4
19112	AT2G32360.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr2:13744096-13744623 REVERSE   Aliases: T32F6.12, T32F6_12	3.4	3.4	0.0	0.1	100.0%	-5.2
19113	AT1G04770.1   male sterility MS5 family protein, similar to male sterility MS5 (Arabidopsis thaliana) GI:3859112; contains Pfam profile PF00515 TPR Domain   chr1:1336370-1337838 REVERSE   Aliases: F13M7.24, F13M7_24	8.5	8.5	-0.1	-0.1	100.0%	-5.3
19114	AT5G19820.1   Symbol: EMB2734   PBS lyase HEAT-like repeat-containing protein, contains Pfam profile: PF03130 PBS lyase HEAT-like repeat   chr5:6695226-6701313 REVERSE   Aliases: EMB2734, EMBRYO DEFECTIVE 2734, T29J13.240, T29J13_240	3.6	3.5	0.0	0.1	100.0%	-4.9
19115	ATCG00660.1   Symbol: RPL20   encodes a chloroplast ribosomal protein L20, a constituent of the large subunit of the ribosomal complex   chrC:68512-68865 REVERSE   Aliases: RPL20	9.0	8.8	0.2	0.1	100.0%	-5.1
19116	AT5G23960.1   Encodes a sesquiterpene synthase involved in generating all of the group A sesquiterpenes found in the Arabidopsis floral volatile blend. Strongly expressed in the stigma.   chr5:8092972-8095131 FORWARD   Aliases: MZF18.16, MZF18_16	2.4	2.4	-0.0	-0.1	100.0%	-5.8
19117	AT1G15870.1   mitochondrial glycoprotein family protein / MAM33 family protein, similar to SUAPRGA1 (Emericella nidulans) GI:6562379; contains Pfam profile PF02330: Mitochondrial glycoprotein   chr1:5457078-5458423 FORWARD   Aliases: F7H2.20, F7H2_20	2.9	2.9	-0.0	-0.1	100.0%	-5.4
19118	AT1G75440.1   ubiquitin-conjugating enzyme 16 (UBC16), E2; identical to gi:2801444, GB:AAC39325 from (Arabidopsis thaliana) (Plant Mol. Biol. 23 (2), 387-396 (1993))   chr1:28317189-28318802 FORWARD   Aliases: F1B16.3, F1B16_3	5.8	5.8	-0.0	-0.1	100.0%	-4.9
19119	AT4G21370.1   S-locus protein kinase, putative, similar to SRKa (Arabidopsis lyrata) gi:13620927:dbj:BAB40986; contains Pfam domains PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain and PF01453: Lectin (probable mannose binding)   chr4:11383895-11387147 REVERSE   Aliases: T6K22.100, T6K22_100	2.4	2.4	-0.0	-0.1	100.0%	-5.2
19120	AT1G74680.1   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr1:28062849-28064872 FORWARD   Aliases: F25A4.34, F25A4_34	7.2	7.2	-0.0	-0.1	100.0%	-5.1
19121	AT3G61300.1   C2 domain-containing protein, anthranilate phosphoribosyltransferase (fragment) - Pisum sativum, PIR:T06460   chr3:22698545-22701978 FORWARD   Aliases: T20K12.200	4.3	4.4	-0.1	-0.1	100.0%	-4.3
19122	AT4G32430.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:15652898-15655480 FORWARD   Aliases: F8B4.130, F8B4_130	3.0	3.0	-0.0	-0.1	100.0%	-5.3
19123	AT4G04540.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr4:2259578-2262136 FORWARD   Aliases: F4H6.4	2.6	2.7	-0.0	-0.1	100.0%	-5.0
19124	AT4G04570.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:2289957-2292753 FORWARD   Aliases: F4H6.9, F4H6_9	2.6	2.7	-0.0	-0.1	100.0%	-5.0
19125	AT5G03150.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:745643-749002 FORWARD   Aliases: F15A17.180, F15A17_180	3.1	3.2	-0.1	-0.1	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19126	AT5G05630.1   amino acid permease family protein, weak similarity to y+LAT1a (amino acid transporter) (Mus musculus) GI:3970791; contains Pfam profile PF00324: Amino acid permease   chr5:1682322-1684192 FORWARD   Aliases: MJJ3.2, MJJ3_2	3.7	3.7	0.0	0.1	100.0%	-5.0
19127	AT1G55540.1   Symbol: EMB1011   proline-rich family protein, contains proline rich extensin domain, INTERPRO:IPR002965   chr1:20738274-20741686 REVERSE   Aliases: EMB1011, EMBRYO DEFECTIVE 1011, T5A14.22	5.0	5.0	0.0	0.1	100.0%	-5.2
19128	AT1G23420.1   Symbol: INO   inner no outer protein (INO), identical to INNER NO OUTER (INO) (Arabidopsis thaliana) GI:6684816	3.1	3.1	0.0	0.1	100.0%	-5.2
19129	AT1G51860.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:19261303-19265148 REVERSE   Aliases: T14L22.7, T14L22_7	2.6	2.7	-0.1	-0.1	100.0%	-4.3
19130	AT5G46200.1   expressed protein, contains similarity to carboxyl-terminal proteinase contains Pfam profile PF03080: Arabidopsis proteins of unknown function; expression supported by MPSS   chr5:18745277-18747474 REVERSE   Aliases: MDE13.2, MDE13_2	3.0	3.0	0.0	0.1	100.0%	-5.3
19131	AT5G63260.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr5:25378976-25381940 FORWARD   Aliases: MDC12.23, MDC12_23	4.9	5.0	-0.0	-0.1	100.0%	-4.9
19132	AT1G50530.1   expressed protein   chr1:18724880-18725397 REVERSE   Aliases: F11F12.27	2.4	2.4	-0.0	-0.1	100.0%	-5.9
19133	AT2G28990.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:12462132-12466618 FORWARD   Aliases: T9I4.7, T9I4_7	2.7	2.7	0.0	0.1	100.0%	-4.7
19134	AT1G52340.1   Symbol: ABA2   short-chain dehydrogenase/reductase (SDR) family protein, similar to stem secoisolariciresinol dehydrogenase GI:13752458 from (Forsythia x intermedia)   chr1:19493468-19495317 REVERSE   Aliases: ABA DEFICIENT 2, F19K6.3, F19K6_3, GIN1, GLUCOSE INSENSITIVE 1, IMPAIRED SUCROSE INDUCTION 4, ISI4, SALT RESISTANT 1, SDR1, SHORT CHAIN DEHYDROGENASE REDUCTASE 1, SIS4, SRE1, SUGAR INSENSITIVE 4	6.5	6.5	-0.1	-0.1	100.0%	-4.8
19135	AT2G20970.1   expressed protein   chr2:9016948-9018148 FORWARD   Aliases: F26H11.27, F26H11_27	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19136	AT5G51890.1   similar to peroxidase 64 (PER64) (P64) (PRXR4) [Arabidopsis thaliana] (TAIR:At5g42180.1); similar to cationic peroxidase [Zinnia elegans] (GB:BAD93164.1); contains InterPro domain Haem peroxidase (InterPro:IPR002016); contains InterPro domain Plant peroxidase (InterPro:IPR000823)	3.8	3.9	-0.1	-0.1	100.0%	-4.5
19137	AT3G08800.1   expressed protein   chr3:2671154-2675202 FORWARD   Aliases: F17O14.27	3.9	4.0	-0.0	-0.1	100.0%	-5.0
19138	AT4G28850.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, contains similarity to xyloglucan endotransglycosylase XET2 GI:8886867 from (Asparagus officinalis)   chr4:14244301-14245963 FORWARD   Aliases: F16A16.40, F16A16_40	2.0	2.0	0.0	0.1	100.0%	-5.0
19139	AT2G22900.1   galactosyl transferase GMA12/MNN10 family protein, very low similarity to alpha-1,2-galactosyltransferase, Schizosaccharomyces pombe (SP:Q09174)	7.3	7.3	-0.0	-0.1	100.0%	-5.0
19140	AT4G00640.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g12150.1); similar to unknown protein [Grouper iridovirus] (GB:YP_195012.1)   chr4:266233-267789 REVERSE   Aliases: F6N23.14, F6N23_14	2.5	2.6	-0.0	-0.1	100.0%	-5.7
19141	AT5G22580.1   expressed protein   chr5:7502681-7503448 FORWARD   Aliases: MQJ16.12, MQJ16_12	2.9	2.9	-0.0	-0.1	100.0%	-5.2
19142	AT1G27380.2   Symbol: RIC2   p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	3.0	3.0	-0.0	-0.1	100.0%	-4.7
19143	AT1G47480.1   expressed protein, similar to PrMC3 (Pinus radiata) GI:5487873   chr1:17420019-17421872 FORWARD   Aliases: F16N3.25, F16N3_25	2.7	2.8	-0.1	-0.1	100.0%	-4.5
19144	AT3G61390.2   U-box domain-containing protein, several hypothetical proteins - Arabidopsis thaliana   chr3:22727328-22729348 FORWARD   Aliases: F2A19.1	2.6	2.6	0.0	0.1	100.0%	-5.2
19145	AT3G06720.2   Symbol: AT IMP	4.4	4.5	-0.0	-0.1	100.0%	-4.9
19146	AT2G44830.1   protein kinase, putative, similar to protein kinase PVPK-1 (Phaseolus vulgaris) SWISS-PROT:P15792   chr2:18497439-18499891 FORWARD   Aliases: T13E15.16	4.6	4.6	-0.0	-0.1	100.0%	-4.6
19147	AT1G54920.2   expressed protein   chr1:20474487-20478819 FORWARD   Aliases: F14C21.46, F14C21_46	3.1	3.0	0.0	0.1	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19148	AT3G01500.4   Symbol: CA1   similar to carbonic anhydrase 2 / carbonate dehydratase 2 (CA2) (CA18) [Arabidopsis thaliana] (TAIR:At5g14740.1); similar to carbonic anhydrase 2 / carbonate dehydratase 2 (CA2) (CA18) [Arabidopsis thaliana] (TAIR:At5g14740.2); similar to carbonic anhydrase (GB:AAB65822.1); contains InterPro domain Carbonic anhydrase, prokaryotic (InterPro:IPR001765)   chr3:194792-198000 REVERSE   Aliases: CARBONIC ANHYDRASE 1, F4P13.5, F4P13_5	3.0	3.1	-0.0	-0.1	100.0%	-4.9
19149	AT4G15490.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase ;simalr to UDP-glucose:sinapate glucosyltransferase GI:9794913 from (Brassica napus)   chr4:8852696-8854543 REVERSE   Aliases: DL3785C, FCAALL.17	3.7	3.7	0.0	0.1	100.0%	-5.5
19150	AT2G03070.1   expressed protein   chr2:905618-908944 FORWARD   Aliases: T17M13.24, T17M13_24	3.9	3.8	0.0	0.1	100.0%	-5.1
19151	AT4G08410.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965;   chr4:5339083-5341206 REVERSE   Aliases: T28D5.100, T28D5_100	3.5	3.7	-0.1	-0.1	100.0%	-4.0
19152	AT3G60750.1   transketolase, putative, strong similarity to transketolase 1 (Capsicum annuum) GI:3559814; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain, PF00456: Transketolase, thiamine diphosphate binding domain   chr3:22464694-22468127 FORWARD   Aliases: T4C21.160	7.1	7.2	-0.1	-0.1	100.0%	-4.6
19153	AT1G43730.1   expressed protein   chr1:16511163-16512224 REVERSE   Aliases: F2J6.21, F2J6_21	2.7	2.7	-0.0	-0.1	100.0%	-5.7
19154	AT5G01960.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:370425-373314 FORWARD   Aliases: T7H20.10, T7H20_10	6.5	6.5	0.0	0.1	100.0%	-4.8
19155	AT4G39756.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:18441750-18442874 FORWARD   Aliases: None	3.3	3.3	0.0	0.1	100.0%	-5.3
19156	AT3G42580.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr3:14701807-14706913 FORWARD   Aliases: T12K4.30	2.5	2.5	0.0	0.1	100.0%	-6.0
19157	AT5G61970.1   signal recognition particle-related / SRP-related, low similarity to Signal recognition particle 68 kDa protein (SRP68) from Homo sapiens SP:Q9UHB9, Canis familiaris SP:Q00004   chr5:24905843-24910554 FORWARD   Aliases: K22G18.11, K22G18_11	6.8	6.8	-0.0	-0.1	100.0%	-4.8
19158	AT1G63010.2   similar to SPX (SYG1/Pho81/XPR1) domain-containing protein [Arabidopsis thaliana] (TAIR:At4g22990.1); similar to SPX (SYG1/Pho81/XPR1) domain-containing protein [Arabidopsis thaliana] (TAIR:At4g11810.1); similar to OSJNBa0019K04.6 [Oryza sativa (japonica cultivar-group)] (GB:XP_473572.1); similar to SPX (SYG1/Pho81/XPR1) domain-containing protein-like [Oryza sativa (japonica cultivar-group)] (GB:BAD29367.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD46701.1); contains InterPro domain SPX, N-terminal (InterPro:IPR004331)   chr1:23351382-23356310 REVERSE   Aliases: F16P17.18, F16P17_18	7.5	7.5	0.0	0.1	100.0%	-5.2
19159	AT1G73820.1   Ssu72-like family protein, contains Pfam profile PF04722: Ssu72-like protein; similar to SSU72 protein (Swiss-Prot:P53538) (Saccharomyces cerevisiae)   chr1:27759173-27760872 REVERSE   Aliases: F25P22.24, F25P22_24	5.1	5.1	0.0	0.1	100.0%	-4.6
19160	AT1G27950.1   lipid transfer protein-related, low similarity to lipid transfer protein Picea abies GI:2627141; contains Pfam profile: PF00234: Protease inhibitor/seed storage/LTP family   chr1:9740691-9742146 FORWARD   Aliases: F13K9.6, F13K9_6	2.6	2.6	0.0	0.1	100.0%	-5.4
19161	AT4G33660.1   expressed protein   chr4:16167292-16167954 REVERSE   Aliases: T16L1.2	5.6	5.7	-0.0	-0.1	100.0%	-5.1
19162	AT3G04560.1   expressed protein   chr3:1226624-1229414 REVERSE   Aliases: F7O18.3, F7O18_3	9.1	9.0	0.0	0.1	100.0%	-5.0
19163	AT5G53240.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr5:21618707-21619962 FORWARD   Aliases: K19E1.4, K19E1_4	2.4	2.4	-0.0	-0.1	100.0%	-5.6
19164	AT1G36920.1   expressed protein   chr1:13984724-13986502 FORWARD   Aliases: F1O3.6, F1O3_6	2.5	2.5	0.0	0.1	100.0%	-5.8
19165	AT5G14600.1   expressed protein   chr5:4706948-4709146 FORWARD   Aliases: T15N1.90, T15N1_90	5.7	5.6	0.0	0.1	100.0%	-4.5
19166	AT1G20940.1   F-box family protein, contains Pfam:PF00646 F-box domain	3.2	3.2	0.0	0.1	100.0%	-4.9
19167	AT2G17430.1   seven transmembrane MLO family protein / MLO-like protein 7 (MLO7), identical to membrane protein Mlo7 (Arabidopsis thaliana) gi:14091584:gb:AAK53800; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr2:7575100-7577906 FORWARD   Aliases: F5J6.19, F5J6_19	2.7	2.7	0.0	0.1	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19168	AT1G15310.1   Symbol: ATHSRP54A   signal recognition particle 54 kDa protein 1 / SRP54 (SRP-54) (SRP-54A), identical to Swiss-Prot:P37106 signal recognition particle 54 kDa protein 1 (SRP54) (Arabidopsis thaliana)	7.1	7.0	0.0	0.1	100.0%	-4.7
19169	AT5G66150.1   glycosyl hydrolase family 38 protein, similar to lysosomal alpha-mannosidase SP:O09159 from (Mus musculus)   chr5:26456239-26461660 REVERSE   Aliases: K2A18.23, K2A18_23	2.4	2.5	-0.0	-0.1	100.0%	-5.8
19170	AT2G30500.1   kinase interacting family protein, similar to kinase interacting protein 1 (GI:13936326) (Petunia integrifolia)   chr2:13005236-13007149 REVERSE   Aliases: T6B20.15, T6B20_15	8.7	8.7	0.0	0.1	100.0%	-4.9
19171	AT5G45570.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At4g08430, At5g28235   chr5:18489528-18492801 FORWARD   Aliases: K2N11.2, K2N11_2	2.4	2.4	-0.0	-0.1	100.0%	-6.1
19172	AT4G17585.1   hypothetical protein   chr4:9792536-9793272 REVERSE   Aliases: FCAALL.48	2.4	2.4	0.0	0.1	100.0%	-5.7
19173	AT1G06050.1   expressed protein   chr1:1830604-1832552 REVERSE   Aliases: T21E18.10, T21E18_10	5.9	5.9	0.0	0.1	100.0%	-4.7
19174	AT4G08530.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:5421859-5422352 FORWARD   Aliases: T15F16.16, T15F16_16	2.4	2.4	0.0	0.1	100.0%	-5.7
19175	AT2G28960.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:12444991-12449424 REVERSE   Aliases: T9I4.4, T9I4_4	2.2	2.2	-0.0	-0.1	100.0%	-4.7
19176	AT5G60540.1   Symbol: EMB2407   SNO glutamine amidotransferase family protein, similar to pyridoxine synthesis protein PDX2 (Cercospora nicotianae) GI:9954418; contains Pfam profile PF01174: SNO glutamine amidotransferase family   chr5:24353849-24356028 REVERSE   Aliases: EMB2407, EMBRYO DEFECTIVE 2407, MUF9.1, MUF9_1	10.4	10.3	0.1	0.1	100.0%	-4.8
19177	AT3G22250.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:7867813-7870060 FORWARD   Aliases: MMP21.3	3.7	3.6	0.0	0.1	100.0%	-5.1
19178	AT2G28100.1   glycosyl hydrolase family 29 / alpha-L-fucosidase, putative, similar to alpha-L-fucosidase SP:P10901 from (Dictyostelium discoideum)   chr2:11981740-11983677 FORWARD   Aliases: F24D13.11, F24D13_11	2.6	2.6	0.0	0.1	100.0%	-5.6
19179	AT5G11260.1   Symbol: HY5   bZIP protein HY5 (HY5), identical to HY5 protein GI:2251085 from (Arabidopsis thaliana)   chr5:3593415-3594993 REVERSE   Aliases: BZIP TRANSCRIPTION FACTOR HY5, ELONGATED HYPOCOTYL 5, F2I11.150, F2I11_150, HY5, TED 5	5.1	5.1	-0.0	-0.1	100.0%	-4.7
19180	AT4G14390.1   ankyrin repeat family protein, contains Pfam profile: PF00023 ankyrin repeat   chr4:8289640-8292079 FORWARD   Aliases: DL3235W, FCAALL.188	3.3	3.4	-0.0	-0.1	100.0%	-5.0
19181	AT5G26080.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:9108000-9108425 FORWARD   Aliases: T1N24.105, T1N24_105	2.3	2.3	-0.0	-0.1	100.0%	-5.3
19182	AT3G23720.1   expressed protein   chr3:8537372-8537617 FORWARD   Aliases: MYM9.7	2.9	2.9	-0.0	-0.1	100.0%	-6.3
19183	AT1G51190.1   Symbol: PLT2   ovule development protein, putative, similar to ovule development protein AINTEGUMENTA (GI:1209099) (Arabidopsis thaliana)   chr1:18980954-18984286 FORWARD   Aliases: F11M15.6, F11M15_6, PLETHORA 2	2.5	2.5	0.0	0.1	100.0%	-5.6
19184	AT4G37930.1   Symbol: SHM1   glycine hydroxymethyltransferase / serine hydroxymethyltransferase / serine/threonine aldolase (SHM1), identical to serine hydroxymethyl transferase (Arabidopsis thaliana) GI:6899945   chr4:17831740-17834859 REVERSE   Aliases: F20D10.50, F20D10_50, SERINE HYDROXYMETHYLTRANSFERASE 1, SERINE TRANSHYDROXYMETHYLASE, SERINE TRANSHYDROXYMETHYLTRANSFERASE, STM	11.5	11.5	0.0	0.1	100.0%	-4.9
19185	AT3G62330.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr3:23074304-23076394 REVERSE   Aliases: T12C14.30	4.5	4.5	0.0	0.1	100.0%	-4.9
19186	AT2G47430.1   Symbol: CKI1   cytokinin-responsive histidine kinase (CKI1), identical to GB:D87545   chr2:19466115-19470612 REVERSE   Aliases: CYTOKININ INDEPENDENT 1, HISTIDINE KINASE, T30B22.27	2.9	2.9	0.0	0.1	100.0%	-5.4
19187	AT5G43220.1   hypothetical protein, similar to unknown protein (gb:AAF03435.1)	2.7	2.7	0.0	0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19188	AT3G24460.1   TMS membrane family protein / tumour differentially expressed (TDE) family protein, contains Pfam domain, PF03348: TMS membrane protein/tumour differentially expressed protein (TDE)   chr3:8885825-8889933 REVERSE   Aliases: MXP5.3	3.1	3.2	-0.0	-0.1	100.0%	-5.1
19189	AT5G64840.1   Symbol: ATGCN5	8.1	8.2	-0.1	-0.1	100.0%	-4.9
19190	AT1G76880.1   trihelix DNA-binding protein, putative, similar to DNA-binding protein DF1 (Pisum sativum) GI:13646986   chr1:28870488-28873119 FORWARD   Aliases: F7O12.5, F7O12_5	4.3	4.2	0.0	0.1	100.0%	-4.8
19191	AT3G14460.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr3:4851997-4856271 REVERSE   Aliases: MOA2.7	2.8	2.9	-0.0	-0.1	100.0%	-4.8
19192	AT5G27100.1   Symbol: ATGLR2.1   glutamate receptor family protein (GLR2.1) (GLR3), plant glutamate receptor family, PMID:11379626   chr5:9535108-9538336 REVERSE   Aliases: GLR2.1, T21B4.10, T21B4_10	3.4	3.4	-0.0	-0.1	100.0%	-4.5
19193	AT3G30640.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain   chr3:12198514-12201377 REVERSE   Aliases: MQP15.16	2.5	2.5	-0.0	-0.1	100.0%	-5.5
19194	AT4G25550.1   expressed protein   chr4:13048386-13051178 FORWARD   Aliases: M7J2.80, M7J2_80	7.3	7.4	-0.1	-0.1	100.0%	-4.6
19195	AT5G59580.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:24023305-24024915 REVERSE   Aliases: F2O15.16, F2O15_16	2.7	2.7	0.0	0.1	100.0%	-5.7
19196	AT3G63110.1   Symbol: ATIPT3	6.1	6.1	0.1	0.1	100.0%	-4.8
19197	AT2G38890.1   expressed protein, and genefinder   chr2:16248312-16249995 FORWARD   Aliases: T7F6.6, T7F6_6	2.0	2.0	0.0	0.1	100.0%	-6.1
19198	AT1G79030.1   DNAJ heat shock N-terminal domain-containing protein / S-locus protein, putative, similar to S-locus protein 5 (GI:6069485) (Brassica rapa); contains Pfam profile PF00226 DnaJ domain   chr1:29735807-29738463 REVERSE   Aliases: YUP8H12R.35, YUP8H12R_35	4.7	4.6	0.0	0.1	100.0%	-4.5
19199	AT5G65210.5   similar to bZIP family transcription factor (OBF4) [Arabidopsis thaliana] (TAIR:At5g10030.1); similar to TGACG-motif-binding protein (GB:AAA75414.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)   chr5:26075057-26078330 FORWARD   Aliases: MQN23.15, MQN23_15	3.9	3.8	0.0	0.1	100.0%	-4.7
19200	AT1G35290.1   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein   chr1:12947522-12948819 REVERSE   Aliases: T9I1.6, T9I1_6	2.5	2.5	0.0	0.1	100.0%	-4.6
19201	AT5G56970.1   Symbol: CKX3   FAD-binding domain-containing protein / cytokinin oxidase family protein, similar to cytokinin oxidase from Zea mays (gi:3882018) (gi:3341978)   chr5:23062170-23065494 REVERSE   Aliases: CYTOKININ OXIDASE, CYTOKININ OXIDASE 3, MHM17.8, MHM17_8	3.9	3.9	-0.0	-0.1	100.0%	-5.2
19202	AT5G64770.1   expressed protein   chr5:25914593-25915350 REVERSE   Aliases: MVP7.10, MVP7_10	3.5	3.5	-0.0	-0.1	100.0%	-5.2
19203	AT5G40030.1   protein kinase, putative, similar to stpk1 protein kinase (Solanum tuberosum) gi:1200256:emb:CAA62476   chr5:16043455-16045511 FORWARD   Aliases: MUD12.10, MUD12_10	2.2	2.2	-0.0	-0.1	100.0%	-5.7
19204	AT1G51290.1   F-box family protein (FBX10), contains Pfam F-box domain PF:00646; similar to F-box protein family, AtFBX9 (GP:20197985) {Arabidopsis thaliana}   chr1:19015841-19016974 FORWARD   Aliases: F11M15.14, F11M15_14	2.4	2.4	-0.0	-0.1	100.0%	-5.7
19205	AT1G29270.1   expressed protein   chr1:10230305-10231128 FORWARD   Aliases: F28N24.5, F28N24_5	2.4	2.5	-0.1	-0.1	100.0%	-4.3
19206	AT3G56490.1   zinc-binding protein, putative / protein kinase C inhibitor, putative, similar to 14 kDa zinc-binding protein (Protein kinase C inhibitor, PKCI) (Zea mays) Swiss-Prot:P42856   chr3:20952481-20954381 FORWARD   Aliases: T5P19.140	8.0	7.9	0.1	0.1	100.0%	-4.6
19207	AT1G04110.1   Symbol: SDD1   subtilase family protein, contains similarity to subtilisin-like protease GI:3687307 from (Lycopersicon esculentum)   chr1:1061456-1063783 REVERSE   Aliases: F20D22.12, F20D22_12, STOMATAL DENSITY AND DISTRIBUTION	2.5	2.5	-0.0	-0.1	100.0%	-5.5
19208	AT2G36840.1   ACT domain-containing protein, contains Pfam profile ACT domain PF01842   chr2:15458652-15460793 REVERSE   Aliases: T1J8.2, T1J8_2	2.9	2.9	0.0	0.1	100.0%	-5.4
19209	AT3G21440.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr3:7551188-7553585 REVERSE   Aliases: MHC9.12	3.7	3.7	0.0	0.1	100.0%	-5.3
19210	AT1G37000.1   expressed protein   chr1:14038479-14039586 FORWARD   Aliases: T32E20.25, T32E20_25	2.5	2.5	-0.0	-0.1	100.0%	-5.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19211	AT1G30795.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR000694   chr1:10935735-10936330 FORWARD   Aliases: None	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19212	AT3G30280.1   transferase family protein, similar to deacetylindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034), alcohol acyltransferase (Fragaria x ananassa)(GI:10121328)(PMID:10810141)   chr3:11916845-11918176 FORWARD   Aliases: T6J22.12	3.4	3.4	0.0	0.1	100.0%	-4.4
19213	AT5G35330.2   Symbol: MBD02   methyl-CpG-binding domain-containing protein, similar to methyl-CpG binding protein MBD4 (Mus musculus) GI:3800807; contains Pfam profile PF01429: Methyl-CpG binding domain   chr5:13540710-13542990 REVERSE   Aliases: MBD2, T26D22.18, T26D22_18	8.8	8.7	0.0	0.1	100.0%	-4.9
19214	AT1G24030.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; similar to protein kinase APK1A, SWISS-PROT:Q06548 (Arabidopsis thaliana)   chr1:8503242-8505449 FORWARD   Aliases: T23E23.18, T23E23_18	3.6	3.6	-0.0	-0.1	100.0%	-4.7
19215	AT4G39350.1   Symbol: CESA2   cellulose synthase, catalytic subunit (Ath-A), identical to gi:2827141   chr4:18296903-18302186 FORWARD   Aliases: ATH A, CELLULASE SYNTHASE 2, CELLULOSE SYNTHASE, T22F8.250, T22F8_250	6.5	6.5	-0.0	-0.1	100.0%	-4.8
19216	AT1G02370.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to DNA-binding protein (Triticum aestivum) GI:6958202; contains Pfam profile PF01535: PPR repeat   chr1:474500-476511 FORWARD   Aliases: T6A9.6, T6A9_6	5.5	5.6	-0.0	-0.1	100.0%	-4.8
19217	AT5G10450.2   Symbol: GRF6   similar to 14-3-3 protein GF14 kappa (GRF8) [Arabidopsis thaliana] (TAIR:At5g65430.2); similar to 14-3-3 g-1 protein [Nicotiana tabacum] (GB:BAD12179.1); similar to 14-3-3 protein [Solanum tuberosum] (GB:CAA72384.1); similar to GF14 lambda [Brassica napus] (GB:AAK26636.1); contains InterPro domain 14-3-3 protein (InterPro:IPR000308)   chr5:3283868-3286348 REVERSE   Aliases: 14 3 3 LIKE PROTEIN 1, AFT1, F12B17.200, F12B17_200, GF14 LAMBDA	10.3	10.2	0.0	0.1	100.0%	-5.3
19218	AT1G69100.1   aspartyl protease family protein, contains Pfam profile: PF00026 eukaryotic aspartyl protease   chr1:25983662-25985099 FORWARD   Aliases: F4N2.8, F4N2_8	2.7	2.7	-0.0	-0.1	100.0%	-5.7
19219	AT2G28970.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:12450996-12455240 FORWARD   Aliases: T9I4.5, T9I4_5	2.6	2.5	0.0	0.1	100.0%	-4.5
19220	AT5G49050.1   hypothetical protein   chr5:19901155-19901607 FORWARD   Aliases: K19E20.20, K19E20_20	3.2	3.2	0.0	0.1	100.0%	-5.3
19221	AT5G63830.1   zinc finger (HIT type) family protein, contains Pfam profile: PF04438 HIT zinc finger   chr5:25560776-25562017 REVERSE   Aliases: MGI19.3, MGI19_3	5.8	5.9	-0.0	-0.1	100.0%	-4.7
19222	AT5G42320.1   zinc carboxypeptidase family protein, contains Pfam domain, PF00246: Zinc carboxypeptidase   chr5:16935879-16938685 REVERSE   Aliases: K5J14.5, K5J14_5	6.3	6.2	0.0	0.1	100.0%	-5.1
19223	AT3G46760.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:17233012-17234025 FORWARD   Aliases: T6H20.210	2.7	2.7	0.0	0.1	100.0%	-4.7
19224	AT5G54270.1   Symbol: LHCB3   chlorophyll A-B binding protein / LHCB type III (LHCB3), identical to Lhcb3 protein (Arabidopsis thaliana) GI:4741952; contains Pfam profile PF00504: Chlorophyll A-B binding protein   chr5:22055555-22056794 FORWARD   Aliases: LHCB3*1, LIGHT HARVESTING CHLOROPHYLL BINDING PROTEIN 3, MDK4.9, MDK4_9	11.3	11.3	-0.0	-0.1	100.0%	-4.7
19225	AT3G59490.1   expressed protein   chr3:21995608-21997244 REVERSE   Aliases: T16L24.40	3.4	3.4	-0.0	-0.1	100.0%	-5.3
19226	AT3G04020.1   expressed protein   chr3:1041078-1042525 FORWARD   Aliases: T11I18.13, T11I18_13	3.4	3.4	-0.0	-0.1	100.0%	-5.5
19227	AT5G61030.1   RNA-binding protein, putative, similar to RNA-binding protein from (Solanum tuberosum) GI:15822705, (Nicotiana tabacum) GI:15822703, (Nicotiana sylvestris) GI:624925; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	10.2	10.2	0.0	0.1	100.0%	-4.8
19228	AT1G74340.1   dolichol phosphate-mannose biosynthesis regulatory protein-related, similar to dolichol phosphate-mannose biosynthesis regulatory protein SP:Q9Z324 from (Mus musculus)   chr1:27951784-27952329 REVERSE   Aliases: F1M20.2, F1M20_2	7.9	7.8	0.1	0.1	100.0%	-4.6
19229	AT1G33800.1   expressed protein, contains Pfam profile PF04669: Protein of unknown function (DUF579)   chr1:12261399-12262697 FORWARD   Aliases: F14M2.8, F14M2_8	2.8	2.7	0.1	0.1	100.0%	-4.1
19230	AT2G02050.1   NADH-ubiquinone oxidoreductase B18 subunit, putative, contains Pfam PF05676: NADH-ubiquinone oxidoreductase B18 subunit (NDUFB7); similar to NADH-ubiquinone oxidoreductase B18 subunit (EC 1.6.5.3) (EC 1.6.99.3) (Complex I-B18) (CI-B18) (Cell adhesion protein SQM1) (Swiss-Prot:P17568) (Homo sapiens); similar to NADH:ubiquinone oxidoreductase NDUFB7 subunit (GI:9651635) (Homo sapiens)	10.4	10.3	0.1	0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19231	AT5G59520.1   Symbol: ZIP2   zinc transporter (ZIP2), identical to zinc transporter ZIP2 (Arabidopsis thaliana) gi:3252868:gb:AAC24198; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563   chr5:24008479-24010024 REVERSE   Aliases: F2O15.25, F2O15_25, ZIP2	5.1	5.1	-0.0	-0.1	100.0%	-4.6
19232	AT2G39940.1   Symbol: COI1   coronatine-insensitive 1 / COI1 (FBL2), E3 ubiquitin ligase SCF complex F-box subunit; identical to LRR-containing F-box protein GI:3158394 from (Arabidopsis thaliana)   chr2:16679040-16682826 REVERSE   Aliases: CORONATINE INSENSITIVE 1, T28M21.10, T28M21_10	5.2	5.2	0.0	0.1	100.0%	-5.4
19233	AT3G53790.1   Symbol: TRFL4   telomere-binding protein, putative, similar to telomere binding protein TBP1 (Nicotiana glutinosa) gi:23664357:gb:AAN39330   chr3:19939456-19941245 FORWARD   Aliases: F5K20.90, TRF LIKE 4	3.2	3.2	-0.0	-0.1	100.0%	-5.1
19234	AT2G45520.1   expressed protein   chr2:18761830-18763362 REVERSE   Aliases: F17K2.5	8.6	8.6	-0.0	-0.1	100.0%	-4.8
19235	AT5G06839.1   bZIP family transcription factor, contains Pfam profile: PF00170 bZIP transcription factor   chr5:2120528-2126455 FORWARD   Aliases: None	3.0	2.9	0.1	0.1	100.0%	-4.3
19236	AT3G57490.1   40S ribosomal protein S2 (RPS2D), 40S ribosomal protein S2 - Arabidopsis thaliana, SWISSPROT:RS2_ARATH   chr3:21290643-21291925 REVERSE   Aliases: T8H10.90	7.9	8.0	-0.0	-0.1	100.0%	-4.5
19237	AT3G42920.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr3:14997907-14998416 REVERSE   Aliases: F18P9.80	3.4	3.4	-0.0	-0.1	100.0%	-5.3
19238	AT3G22870.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.0	3.0	-0.0	-0.1	100.0%	-5.0
19239	AT3G43280.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:15240766-15241239 REVERSE   Aliases: F7K15.130	2.4	2.4	0.0	0.1	100.0%	-5.5
19240	AT2G05920.1   subtilase family protein, contains similarity to cucumisin-like serine protease GI:3176874 from (Arabidopsis thaliana)   chr2:2269513-2272226 REVERSE   Aliases: T6P5.12, T6P5_12	8.4	8.5	-0.1	-0.1	100.0%	-4.5
19241	AT1G47200.1   MFP1 attachment factor, putative, contains similarity to MFP1 attachment factor 1 GI:7546725 from (Lycopersicon esculentum) similar to MFP1 attachment factor 1 (Glycine max) gi:7546729:gb:AAF63659   chr1:17300471-17301257 REVERSE   Aliases: F2G19.18, F2G19_18	5.0	5.1	-0.0	-0.1	100.0%	-4.8
19242	AT1G41870.1   hypothetical protein   chr1:15649932-15651492 FORWARD   Aliases: F5A13.13, F5A13_13	2.3	2.3	0.0	0.1	100.0%	-5.9
19243	AT4G00370.1   Symbol: ANTR2   sugar transporter family protein, contains Pfam profile PF00083: major facilitator superfamily protein   chr4:161539-166357 REVERSE   Aliases: A_IG005I10.NN, A_IG005I10_NN, F5I10.7, F5I10_7	7.6	7.6	0.1	0.1	100.0%	-4.3
19244	AT1G13230.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to gb:U42445 Cf-2.2 from Lycopersicon pimpinellifolium   chr1:4520628-4522541 FORWARD   Aliases: F3F19.26, F3F19_26	3.1	3.1	-0.0	-0.1	100.0%	-5.5
19245	AT3G26990.1   expressed protein, contains Pfam domain, PF04818: Protein of unknown function, DUF618   chr3:9949502-9953278 REVERSE   Aliases: MOJ10.6	2.4	2.4	0.0	0.1	100.0%	-5.5
19246	AT5G40680.1   kelch repeat-containing F-box family protein, contains Pfam:PF01344 Kelch motif   chr5:16305982-16307229 FORWARD   Aliases: MNF13.24, MNF13_24	3.8	3.8	-0.0	-0.1	100.0%	-5.0
19247	AT3G58180.1   PBS lyase HEAT-like repeat-containing protein, contains Pfam profile: PF03130: PBS lyase HEAT-like repeat; contains alternative donor splice site TT at exon 2, hypothetical protein C14A4.1 - Caenorhabditis elegans, PIR:T19243	7.6	7.7	-0.0	-0.1	100.0%	-4.8
19248	AT1G52380.1   Ran-binding protein 1 domain-containing protein / RanBP1 domain-containing protein, weak similarity to SP:Q09717 Ran-specific GTPase-activating protein 1 (Ran binding protein 1) (RANBP1) (Spi1-binding protein) {Schizosaccharomyces pombe}; contains Pfam profile PF00638: RanBP1 domain   chr1:19512654-19515207 FORWARD   Aliases: F19K6.4, F19K6_4	8.9	8.9	0.0	0.1	100.0%	-5.0
19249	AT1G49390.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to flavonol synthase GI:311658 from (Petunia hybrida), leucoanthocyanidin dioxygenase (Malus domestica)(SP:P51091); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr1:18283268-18284646 FORWARD   Aliases: F13F21.18, F13F21_18	3.3	3.4	-0.0	-0.1	100.0%	-4.3
19250	AT1G79230.1   Symbol: ST1   mercaptopyruvate sulfurtransferase (MST1) (RDH1), identical to mercaptopyruvate sulfurtransferase GI:6009981 and thiosulfate sulfurtransferase GI:5834508 from (Arabidopsis thaliana)   chr1:29805586-29808832 FORWARD   Aliases: ARABIDOPSIS THALIANA RHODANESE HOMOLOGUE 1, ATMST1, ATRDH1, MERCAPTOPYRUVATE SULFURTRANSFERASE, MERCAPTOPYRUVATE SULFURTRANSFERASE 1, MST1, YUP8H12R.17, YUP8H12R_17	10.2	10.1	0.1	0.1	100.0%	-4.7
19251	AT5G42630.1   myb family transcription factor (KAN4), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to	2.2	2.2	-0.0	-0.1	100.0%	-5.5
19252	AT1G21790.1   expressed protein   chr1:7654173-7655872 FORWARD   Aliases: F8K7.23, F8K7_23	3.9	3.9	0.0	0.1	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19253	AT3G48850.1   mitochondrial phosphate transporter, putative, similar to mitochondrial phosphate transporter GI:3318617 from (Arabidopsis thaliana)   chr3:18125511-18127475 REVERSE   Aliases: T21J18.120	3.5	3.4	0.0	0.1	100.0%	-4.9
19254	AT4G38040.1   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr4:17867432-17869296 FORWARD   Aliases: F20D10.160, F20D10_160	6.3	6.3	-0.0	-0.1	100.0%	-4.6
19255	AT2G25910.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g25920.1); similar to P0002B05.11 [Oryza sativa (japonica cultivar-group)] (GB:NP_918466.1); contains InterPro domain KH domain (InterPro:IPR004087); contains InterPro domain 3'-5' exonuclease (InterPro:IPR002562)   chr2:11056133-11059144 REVERSE   Aliases: F17H15.6, F17H15_6	7.6	7.7	-0.1	-0.1	100.0%	-4.8
19256	AT1G32430.1   F-box family protein, contains F-box domain Pfam:PF00646	4.6	4.5	0.0	0.1	100.0%	-5.1
19257	AT1G74960.2   Symbol: FAB1   3-ketoacyl-ACP synthase, putative, similar to 3-ketoacyl-ACP synthase (Cuphea pulcherrima) gi:3800747:gb:AAC68860; identical to cDNA beta-ketoacyl-ACP synthetase 2 nuclear gene for plastid product GI:14582700	7.7	7.7	-0.0	-0.1	100.0%	-5.0
19258	AT1G07650.1   leucine-rich repeat transmembrane protein kinase, putative, similar to GB:AAC50043 from (Arabidopsis thaliana) (Plant Mol. Biol. 37 (4), 587-596 (1998))	4.7	4.7	-0.0	-0.1	100.0%	-5.0
19259	AT3G19490.1   Symbol: ATNHD1	9.1	9.1	-0.0	-0.1	100.0%	-4.9
19260	AT5G20450.2   similar to myosin, putative [Arabidopsis thaliana] (TAIR:At5g20490.1); similar to unconventional myosin heavy chain [Zea mays] (GB:AAD17931.2)   chr5:6910601-6913212 REVERSE   Aliases: F7C8.40, F7C8_40	2.7	2.8	-0.0	-0.1	100.0%	-5.8
19261	AT3G55910.1   expressed protein, PA26, p53 regulated PA26-T3 nuclear protein, Homo sapiens, EMBL:AF033121   chr3:20753878-20754458 FORWARD   Aliases: F27K19.90	3.8	3.8	-0.0	-0.1	100.0%	-4.5
19262	AT5G41480.1   Symbol: GLA1   dihydrofolate synthetase/folylpolyglutamate synthetase (DHFS/FPGS1), nearly identical to GI:17976703; identical to cDNA dihydrofolate synthetase/folylpolyglutamate synthetase (dhfs/fpgs1 gene) GI:17976702   chr5:16613155-16615864 FORWARD   Aliases: A. THALIANA DHFS FPGS HOMOLOG A, ATDFA, GLOBULAR ARREST1, MYC6.18, MYC6_18	5.0	5.0	-0.0	-0.1	100.0%	-5.4
19263	AT2G31260.1   Symbol: APG9   autophagy 9 (APG9), identical to autophagy 9 protein GI:19912149 from (Arabidopsis thaliana)   chr2:13329098-13334477 REVERSE   Aliases: ATAPG9, AUTOPHAGY 9, F16D14.10, F16D14_10	3.8	3.8	-0.0	-0.1	100.0%	-4.8
19264	AT5G36090.1   hypothetical protein, contains Pfam profile PF03778: Protein of unknown function (DUF321)   chr5:14206288-14207186 FORWARD   Aliases: MAB16.3, MAB16_3	2.9	2.9	-0.0	-0.1	100.0%	-5.1
19265	AT1G62570.1   flavin-containing monooxygenase family protein / FMO family protein, low similarity to flavin-containing monooxygenase FMO3 (Rattus norvegicus) GI:12006730; contains Pfam profile PF00743: Flavin-binding monooxygenase-like   chr1:23172801-23175770 FORWARD   Aliases: T3P18.13, T3P18_13	4.4	4.4	0.1	0.1	100.0%	-4.7
19266	AT1G57750.1   cytochrome P450, putative, similar to cytochrome P450 GI:4688670 from (Catharanthus roseus)   chr1:21387646-21389374 REVERSE   Aliases: T8L23.21, T8L23_21	2.3	2.3	0.0	0.1	100.0%	-5.9
19267	AT2G25650.1   DNA-binding storekeeper protein-related, contains similarity to storekeeper protein (Solanum tuberosum) gi:14268476:emb:CAC39398; contains PF04504: Protein of unknown function, DUF573   chr2:10921664-10923294 FORWARD   Aliases: F3N11.10, F3N11_10	4.5	4.4	0.0	0.1	100.0%	-5.2
19268	AT1G60985.1   Symbol: SCRL6   Encodes a member of a family of small, secreted, cysteine rich proteins with sequence similarity to SCR (S locus cysteine-rich protein).   chr1:22460414-22460949 FORWARD   Aliases: SCR Like 6, SCRL6	3.0	3.0	-0.0	-0.1	100.0%	-5.4
19269	AT1G73710.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587, post-transcriptional control of chloroplast gene expression CRP1 (Zea mays) GI:3289002; contains Pfam profile PF01535: PPR repeat   chr1:27724851-27727826 FORWARD   Aliases: F25P22.13, F25P22_13	3.3	3.3	0.0	0.1	100.0%	-5.2
19270	AT1G78970.2   Symbol: LUP1   lupeol synthase (LUP1) / 2,3-oxidosqualene-triterpenoid cyclase, identical to lupeol synthase GI:1762150 from (Arabidopsis thaliana), 2,3-oxidosqualene-triterpenoid cyclase (Arabidopsis thaliana) GI:2738027; contains Pfam profile PF00432: Prenyltransferase and squalene oxidase repeat; contains TIGRfam profile TIGR01787: squalene/oxidosqualene cyclases; identical to cDNA 2,3-oxidosqualene-triterpenoid cyclase GI:2738026   chr1:29708233-29712737 FORWARD   Aliases: ATLUP1, LUPEOL SYNTHASE 1	3.0	3.0	0.0	0.1	100.0%	-5.2
19271	AT3G11110.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 Zinc finger, C3HC4 type (RING finger)   chr3:3479985-3480461 FORWARD   Aliases: F11B9.7	4.3	4.3	0.0	0.1	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19272	AT4G17483.1   palmitoyl protein thioesterase family protein   chr4:9747356-9748904 REVERSE   Aliases: FCAALL.16	4.5	4.5	-0.0	-0.1	100.0%	-5.1
19273	AT1G27570.1   phosphatidylinositol 3- and 4-kinase family protein, contains Pfam profile PF00454: Phosphatidylinositol 3- and 4-kinase	2.6	2.6	0.0	0.1	100.0%	-5.5
19274	AT3G43750.1   zinc finger (C3HC4-type RING finger) family protein, contains a zinc finger, C3HC4 type (RING finger), signature, PROSITE:PS00518   chr3:15657447-15658553 FORWARD   Aliases: T28A8.40	2.6	2.7	-0.0	-0.1	100.0%	-5.4
19275	AT5G38960.1   germin-like protein, putative, similar to germin-like protein subfamily 1 member 8 (SP:Q9LEA7); contains PS00725 germin family signature	2.2	2.2	-0.0	-0.1	100.0%	-5.8
19276	AT1G48420.1   desulfhydrase family, similar to similar to D-cysteine desulfhydrase (EC 4.4.1.15). (Swiss-Prot:P59329) (Escherichia coli O6); contains TIGRFAM TIGR01275: pyridoxal phosphate-dependent enzymes, D-cysteine desulfhydrase family profile   chr1:17900267-17902472 REVERSE   Aliases: T1N15.3, T1N15_3	11.6	11.5	0.0	0.1	100.0%	-5.4
19277	AT3G60920.1   beige/BEACH domain-containing protein, contains Pfam PF02138: Beige/BEACH domain; similar to LBA isoform gamma (GI:10257405) (Mus musculus); similar to beige-like protein (CDC4L) - Homo sapiens; similar to Neurobeachin: kinase A-anchoring, beige/Chediak-higashi protein homolog implicated in neuronal membrane traffic (AKAP550) (GI:11863541) (Drosophila melanogaster).	2.6	2.6	0.0	0.1	100.0%	-5.3
19278	AT2G34920.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g30860.1); similar to Hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:NP_912538.1)   chr2:14735106-14738235 REVERSE   Aliases: F19I3.15, F19I3_15	3.1	3.1	-0.0	-0.1	100.0%	-4.7
19279	AT5G23770.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr5:8014516-8016274 REVERSE   Aliases: MRO11.19, MRO11_19	3.2	3.3	-0.0	-0.1	100.0%	-5.6
19280	AT5G03540.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit   chr5:889565-894155 FORWARD   Aliases: F12E4.330, F12E4_330	6.7	6.6	0.0	0.1	100.0%	-4.5
19281	AT2G17160.1   protein kinase-related, identical to hypothetical protein GB:AAB81676; supported by tandem duplication of protein kinase family (GI:4584350) (TIGR_Ath1:At2g17170) (Arabidopsis thaliana)   chr2:7479836-7481094 FORWARD   Aliases: T23A1.2, T23A1_2	2.4	2.4	-0.0	-0.1	100.0%	-5.9
19282	AT1G13830.1   beta-1,3-glucanase-related, similar to beta-1,3-glucanase-like protein (GI:14279169) (Olea europaea) similar to Glucan endo-1,3-beta-glucosidase precursor (EC 3.2.1.39) ((1-3)-beta- glucan endohydrolase) ((1-3)-beta-glucanase) (Beta-1,3- endoglucanase) (Swiss-Prot:P52409) (Triticum aestivum)   chr1:4739877-4741029 REVERSE   Aliases: F16A14.5, F16A14_5	2.5	2.6	-0.1	-0.1	100.0%	-4.3
19283	AT2G06500.1   hAT dimerisation domain-containing protein / transposase-related, low similarity to transposase (Ipomoea purpurea) AB004906 GI:4063770   chr2:2580715-2583220 REVERSE   Aliases: T12H3.5, T12H3_5	3.0	2.9	0.0	0.1	100.0%	-5.4
19284	AT2G18490.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:8027750-8028505 FORWARD   Aliases: F24H14.16, F24H14_16	2.2	2.2	0.0	0.1	100.0%	-6.1
19285	AT3G28280.1   expressed protein   chr3:10541883-10542808 REVERSE   Aliases: MZF16.6	2.5	2.5	0.0	0.1	100.0%	-5.7
19286	AT3G42770.1   F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.5	0.0	0.1	100.0%	-5.2
19287	AT5G47900.1   expressed protein   chr5:19409209-19411387 FORWARD   Aliases: MCA23.24, MCA23_24	3.8	3.8	-0.0	-0.1	100.0%	-5.1
19288	AT1G63560.1   similar to protein kinase-related [Arabidopsis thaliana] (TAIR:At1g63600.1); similar to serine/threonine kinase -related protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_478602.1); contains InterPro domain Protein of unknown function DUF26 (InterPro:IPR002902)	2.3	2.3	-0.0	-0.1	100.0%	-5.5
19289	AT3G23770.1   glycosyl hydrolase family 17 protein, similar to A6 anther-specific protein SP:Q06915 (Arabidopsis thaliana)   chr3:8565501-8567500 FORWARD   Aliases: MYM9.12	2.2	2.2	-0.0	-0.1	100.0%	-6.0
19290	AT1G14440.2   zinc finger homeobox family protein / ZF-HD homeobox family protein   chr1:4938873-4940690 REVERSE   Aliases: F14L17.21, F14L17_21	2.2	2.2	-0.0	-0.1	100.0%	-5.9
19291	AT4G35310.1   Symbol: CPK5   calcium-dependent protein kinase, putative / CDPK, putative, similar to calmodulin-domain protein kinase CDPK isoform 6 (Arabidopsis thaliana) gi:1399275:gb:AAB03246; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048	6.1	6.0	0.0	0.1	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19292	AT1G17500.1   haloacid dehalogenase-like hydrolase family protein, similar to Potential phospholipid-transporting ATPase (EC 3.6.3.1) from Homo sapiens (SP:O43520), Mus musculus (SP:P70704); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr1:6018750-6023496 FORWARD   Aliases: F1L3.21, F1L3_21	3.9	4.0	-0.1	-0.1	100.0%	-4.8
19293	AT2G02680.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.1	2.1	0.1	0.1	100.0%	-4.6
19294	AT5G36140.1   Symbol: CYP716A2   cytochrome P450-related, similar to taxane 13-alpha-hydroxylase (Taxus cuspidata) GI:17148242   chr5:14229442-14230489 REVERSE   Aliases: MAB16.9, MAB16_9	2.7	2.6	0.0	0.1	100.0%	-5.5
19295	AT1G42700.1   hypothetical protein   chr1:16069371-16070032 FORWARD   Aliases: F8D11.10	3.2	3.2	0.0	0.1	100.0%	-5.5
19296	AT4G32000.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr4:15474089-15476661 REVERSE   Aliases: F10N7.190, F10N7_190	4.1	4.1	0.0	0.1	100.0%	-4.8
19297	AT5G50030.1   invertase/pectin methylesterase inhibitor family protein, contains similarity to pollen-specific protein Bnm1 Brassica napus GI:1857671; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr5:20371815-20372853 FORWARD   Aliases: MPF21.4, MPF21_4	3.1	3.1	-0.0	-0.1	100.0%	-5.1
19298	AT1G65420.1   expressed protein, contains Pfam profile PF04483: Protein of unknown function (DUF565)   chr1:24301148-24302233 REVERSE   Aliases: T8F5.20, T8F5_20	5.3	5.3	-0.0	-0.1	100.0%	-5.1
19299	AT3G55680.1   invertase/pectin methylesterase inhibitor family protein, contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor	3.2	3.2	-0.0	-0.1	100.0%	-5.0
19300	AT3G51360.1   aspartyl protease family protein, contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141   chr3:19075273-19077539 REVERSE   Aliases: F26O13.1	2.3	2.3	0.0	0.1	100.0%	-4.5
19301	AT1G62980.1   Symbol: ATEXPA18   expansin, putative (EXP18), identical to SWISS-PROT:Q9LQ07 alpha-expansin 18 precursor (At-EXP18)(Arabidopsis thaliana); alpha-expansin gene family, PMID:11641069   chr1:23335341-23336773 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A18, ATEXP18, ATHEXP ALPHA 1.25, EXP18, F16P17.14, F16P17_14	3.1	3.0	0.1	0.1	100.0%	-4.2
19302	AT1G06230.2   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr1:1907247-1910847 FORWARD   Aliases: F9P14.9, F9P14_9	5.2	5.3	-0.1	-0.1	100.0%	-4.7
19303	AT5G59540.2   similar to 2-oxoglutarate-dependent dioxygenase, putative [Arabidopsis thaliana] (TAIR:At5g59530.1); similar to CmE8 [Cucumis melo] (GB:BAB68392.1); contains InterPro domain H+-transporting two-sector ATPase, alpha/beta subunit, central region (InterPro:IPR000194); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)	7.4	7.3	0.1	0.1	100.0%	-4.7
19304	AT1G65240.1   aspartyl protease family protein, contains Pfam PF00026: Eukaryotic aspartyl protease profile; similar to CND41, chloroplast nucleoid DNA binding protein (GI:2541876) (Nicotiana tabacum)   chr1:24234530-24237012 REVERSE   Aliases: T23K8.15, T23K8_15	4.1	4.1	-0.0	-0.1	100.0%	-5.0
19305	AT4G29180.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr4:14385599-14389695 FORWARD   Aliases: F19B15.210, F19B15_210	2.9	2.8	0.0	0.1	100.0%	-4.7
19306	AT3G09590.1   pathogenesis-related protein, putative, similar to SP:Q05968 Pathogenesis-related protein 1 precursor {Hordeum vulgare}; contains Pfam profile PF00188: SCP-like extracellular protein   chr3:2944958-2945518 FORWARD   Aliases: F11F8.17	3.3	3.2	0.0	0.1	100.0%	-4.9
19307	ATMG00120.1   Symbol: ORF143	2.0	2.1	-0.1	-0.1	100.0%	-4.7
19308	AT5G07000.1   sulfotransferase family protein, similar to steroid sulfotransferase 3 (Brassica napus) GI:3420008, steroid sulfotransferase 1 (Brassica napus) GI:3420004; contains Pfam profile PF00685: Sulfotransferase domain   chr5:2171404-2172940 REVERSE   Aliases: MOJ9.17, MOJ9_17	2.8	2.8	0.0	0.1	100.0%	-5.4
19309	AT3G26220.1   Symbol: CYP71B3   cytochrome P450 family protein, identical to cytochrome P450 monooxygenase (CYP71B3) GB:D78602 (Arabidopsis thaliana) (Plant Mol. Biol. 37 (1), 39-52 (1998))	2.9	2.9	-0.0	-0.1	100.0%	-5.6
19310	AT5G45500.1   expressed protein, weak similarity to resistance complex protein I2C-2 (Lycopersicon esculentum) GI:2258317   chr5:18449685-18451475 REVERSE   Aliases: MFC19.17, MFC19_17	6.2	6.2	0.0	0.1	100.0%	-4.8
19311	AT1G54790.2   GDSL-motif lipase/hydrolase family protein, similar to early nodulin ENOD8 (Medicago sativa) GI:304037, elicitor-induced glycoprotein iEP4 (Daucus carota) GI:1911765, lanatoside 15'-O-acetyesterase (Digitalis lanata) GI:3688284; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family	3.1	3.1	-0.0	-0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19312	AT1G24400.1   Symbol: AATL2   lysine and histidine specific transporter, putative, similar to lysine and histidine specific transporter GI:2576361 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:8651396-8653817 REVERSE   Aliases: AATL2, AMINO ACID TRANSPORTER LIKE PROTEIN 2, F21J9.6	2.5	2.5	0.0	0.1	100.0%	-5.6
19313	AT4G21550.1   transcriptional factor B3 family protein, low similarity to SP:Q01593 Abscisic acid-insensitive protein 3 {Arabidopsis thaliana}, SP:P37398 Viviparous protein homolog {Oryza sativa}; contains Pfam profile PF02362: B3 DNA binding domain   chr4:11463999-11468691 FORWARD   Aliases: F18E5.170, F18E5_170	4.6	4.6	0.0	0.1	100.0%	-4.7
19314	AT5G20370.1   serine-rich protein-related, contains some similarity to serine-rich proteins   chr5:6886933-6887460 REVERSE   Aliases: F5O24.260, F5O24_260	3.7	3.8	-0.0	-0.1	100.0%	-5.3
19315	AT1G17545.1   protein phosphatase 2C-related / PP2C-related, similar to protein phosphatase 2C GI:3242077 from (Arabidopsis thaliana)   chr1:6033102-6033901 FORWARD   Aliases: F1L3.26, F1L3_26	3.2	3.2	-0.0	-0.1	100.0%	-5.4
19316	AT2G39140.1   pseudouridine synthase family protein   chr2:16337261-16340438 FORWARD   Aliases: AT2G39150, T16B24.22, T16B24_22	5.9	5.8	0.0	0.1	100.0%	-4.7
19317	AT1G10630.1   Gene encoding ADP-ribosylation factor and similar to other ARFs and ARF-like proteins. Members of this family are known to be essential for vesicle coating and uncoating and functions in GTP-binding. The gene is shown to play a role in cell division, cell expansion and cellulose production using antisense construct.   chr1:3512796-3514724 REVERSE   Aliases: F20B24.7, F20B24_7	8.6	8.6	0.0	0.1	100.0%	-5.0
19318	AT3G51850.1   Symbol: CPK13   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Arabidopsis thaliana) gi:836942:gb:AAA67655; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr3:19243444-19246862 FORWARD   Aliases: ATEM1.10	5.6	5.6	0.0	0.1	100.0%	-5.1
19319	AT4G30010.1   expressed protein   chr4:14672877-14673225 FORWARD   Aliases: F6G3.40, F6G3_40	10.7	10.6	0.0	0.1	100.0%	-5.4
19320	AT5G17870.1   plastid-specific ribosomal protein-related, contains similarity to plastid-specific ribosomal protein 6 precursor GI:7578927 from (Spinacia oleracea)   chr5:5907777-5908337 FORWARD   Aliases: MPI7.3, MPI7_3	8.1	8.0	0.1	0.1	100.0%	-4.4
19321	AT1G54070.1   dormancy/auxin associated protein-related   chr1:20186307-20186910 FORWARD   Aliases: F15I1.15, F15I1_15	3.1	3.0	0.0	0.1	100.0%	-5.7
19322	AT4G21105.1   expressed protein   chr4:11265662-11266982 FORWARD   Aliases: None	9.4	9.4	0.0	0.1	100.0%	-5.2
19323	AT5G42340.1   similar to armadillo/beta-catenin repeat family protein / U-box domain-containing family protein [Arabidopsis thaliana] (TAIR:At3g46510.1); similar to putative cell death-related protein SPL11 [Oryza sativa (japonica cultivar-group)] (GB:BAD61809.1); contains InterPro domain Zn-finger, modified RING (InterPro:IPR003613); contains InterPro domain Armadillo repeat (InterPro:IPR000225)   chr5:16945138-16947700 REVERSE   Aliases: MDH9.3, MDH9_3	2.8	2.8	0.0	0.1	100.0%	-5.5
19324	AT1G12100.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr1:4095496-4095843 FORWARD   Aliases: F12F1.2, F12F1_2	2.4	2.3	0.0	0.1	100.0%	-6.0
19325	AT1G07040.1   expressed protein   chr1:2160944-2163302 REVERSE   Aliases: F10K1.25, F10K1_25	9.4	9.4	0.1	0.1	100.0%	-4.9
19326	AT3G42690.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At2g11345, At4g04130   chr3:14777975-14781749 FORWARD   Aliases: T12K4.140	2.8	2.8	-0.0	-0.1	100.0%	-5.6
19327	AT3G49590.2   expressed protein   chr3:18388545-18391269 FORWARD   Aliases: T9C5.180	5.3	5.4	-0.0	-0.1	100.0%	-4.8
19328	AT5G50140.1   ankyrin repeat family protein, contains ankyrin repeat domains, Pfam:PF00023   chr5:20413082-20415423 FORWARD   Aliases: MPF21.16, MPF21_16	3.1	3.0	0.0	0.1	100.0%	-4.7
19329	AT4G18500.1   expressed protein   chr4:10209159-10209422 REVERSE   Aliases: F28J12.160, F28J12_160	3.3	3.3	-0.0	-0.1	100.0%	-5.3
19330	AT3G62430.1   F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.5	0.0	0.1	100.0%	-5.5
19331	AT3G28190.1   expressed protein   chr3:10513472-10514294 FORWARD   Aliases: MIG10.9	2.6	2.7	-0.0	-0.1	100.0%	-5.7
19332	AT5G62190.1   Symbol: PRH75   DEAD box RNA helicase (PRH75), nearly identical to RNA helicase (Arabidopsis thaliana) GI:1488521; contains Pfam profiles PF00270: DEAD/DEAH box helicase, PF00271: Helicase conserved C-terminal domain   chr5:24997494-25001199 REVERSE   Aliases: MMI9.2, MMI9_2, RNA HELICASE	6.9	7.0	-0.1	-0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19333	AT3G26510.5   similar to octicosapeptide/Phox/Bem1p (PB1) domain-containing protein [Arabidopsis thaliana] (TAIR:At1g70640.1); similar to PB1 domain, putative [Oryza sativa (japonica cultivar-group)] (GB:AAX96261.1); contains InterPro domain Octicosapeptide/Phox/Bem1p (InterPro:IPR000270)   chr3:9711574-9713897 REVERSE   Aliases: MFE16.2	4.4	4.4	0.1	0.1	100.0%	-4.7
19334	AT1G26970.1   protein kinase, putative, similar to protein kinase (Arabidopsis thaliana) gi:2852449:dbj:BAA24695; contains protein kinase domain, Pfam:PF00069	3.3	3.3	-0.0	-0.1	100.0%	-4.9
19335	AT5G04940.2   Symbol: SUVH1   SET domain-containing protein (SUVH1), contains Pfam profiles PF00856: SET domain, PF05033: Pre-SET motif, PF02182: YDG/SRA domain; identical to cDNA SUVH1 (SUVH1) GI:13517742   chr5:1454168-1456991 REVERSE   Aliases: MUG13.20, MUG13_20, SU(VAR)3 9 HOMOLOG 1	6.1	6.1	0.0	0.1	100.0%	-5.1
19336	AT5G60880.2   expressed protein   chr5:24505515-24507004 REVERSE   Aliases: MAE1.13, MAE1_13	3.9	3.8	0.0	0.1	100.0%	-4.9
19337	AT2G42990.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr2:17886121-17887631 FORWARD   Aliases: F23E6.2, F23E6_2	3.1	3.0	0.0	0.1	100.0%	-5.0
19338	AT3G02190.1   60S ribosomal protein L39 (RPL39B), similar to ribosomal protein L39 GB:P51424 (Arabidopsis thaliana)   chr3:405823-406408 REVERSE   Aliases: F1C9.36	8.8	8.9	-0.0	-0.1	100.0%	-5.1
19339	AT1G11040.1   DNAJ chaperone C-terminal domain-containing protein, contains Pfam profile PF01556: DnaJ C terminal region   chr1:3679225-3680924 REVERSE   Aliases: T19D16.7, T19D16_7	2.8	2.9	-0.0	-0.1	100.0%	-5.4
19340	NA	2.7	2.7	0.0	0.1	100.0%	-5.9
19341	AT3G19030.1   expressed protein, contains similarity to phosphoserine aminotransferase GB:P19689 from (Yersinia enterocolitica)   chr3:6563985-6564430 REVERSE   Aliases: K13E13.14	3.5	3.5	-0.1	-0.1	100.0%	-4.4
19342	AT1G58450.1   peptidyl-prolyl cis-trans isomerase FKBP-type family protein, similar to rof1 from (Arabidopsis thaliana) GI:1373396, GI:1354207; contains Pfam profile PF00515 TPR Domain   chr1:21721679-21722581 FORWARD   Aliases: F9K23.2, F9K23_2	3.0	3.0	0.0	0.1	100.0%	-5.4
19343	AT1G21640.1   Symbol: NADK2   ATP-NAD kinase family protein, contains similarity to NAD kinase (Homo sapiens) gi:20070086:gb:AAM01195; contains Pfam domain, PF01513: ATP-NAD kinase   chr1:7588600-7592875 FORWARD   Aliases: F8K7.5, F8K7_5	6.8	6.9	-0.0	-0.1	100.0%	-4.8
19344	AT1G31230.1   bifunctional aspartate kinase/homoserine dehydrogenase / AK-HSDH, nearly identical to gb:X71364 (PIR:S46497) aspartate kinase / homoserine dehydrogenase from Arabidopsis thaliana; contains ACT domain	10.1	10.2	-0.0	-0.1	100.0%	-4.8
19345	AT3G63040.1   expressed protein, predicted protein, C.elegans   chr3:23307621-23308184 REVERSE   Aliases: T20O10.140	2.2	2.2	-0.0	-0.1	100.0%	-5.9
19346	AT1G69280.1   expressed protein   chr1:26048823-26050333 REVERSE   Aliases: F4N2.23, F4N2_23	3.6	3.6	-0.0	-0.1	100.0%	-5.2
19347	AT1G79620.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana)   chr1:29962455-29967198 REVERSE   Aliases: F20B17.5, F20B17_5	3.5	3.4	0.0	0.1	100.0%	-4.5
19348	AT5G52975.1   expressed protein   chr5:21498683-21499261 FORWARD   Aliases: None	3.1	3.1	-0.0	-0.1	100.0%	-5.2
19349	AT1G18580.1   glycosyltransferase family protein 8, contains Pfam profile PF01501: Glycosyl transferase family 8; protein sequence is truncated due to a frameshift. This could be a pseudogene or a sequencing error may exist.   chr1:6395857-6398229 FORWARD   Aliases: F25I16.8, F25I16_8	2.4	2.4	0.0	0.1	100.0%	-5.4
19350	AT2G47850.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr2:19602743-19605651 FORWARD   Aliases: F17A22.24	5.9	5.9	0.0	0.1	100.0%	-4.8
19351	AT1G34650.1   homeobox-leucine zipper family protein / lipid-binding START domain-containing protein, similar to homeobox 1 (GP:12002853) {Picea abies}; contains Pfam PF00046: Homeobox domain and Pfam PF01852: START domain   chr1:12692989-12697756 FORWARD   Aliases: F21H2.11, F21H2_11	2.3	2.3	0.0	0.1	100.0%	-5.6
19352	AT4G08250.1   scarecrow transcription factor family protein, SCARECROW - Arabidopsis thaliana, PID:g1497987   chr4:5196784-5198235 FORWARD   Aliases: T12G13.90, T12G13_90	3.1	3.1	0.0	0.1	100.0%	-5.6
19353	AT4G23650.1   Symbol: CDPK6   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Marchantia polymorpha) gi:5162877:dbj:BAA81748; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr4:12324779-12327469 REVERSE   Aliases: CALCIUM DEPENDENT PROTEIN KINASE 6, CPK3, F9D16.120, F9D16_120	10.0	10.0	0.0	0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19354	AT2G24090.1   ribosomal protein L35 family protein, contains Pfam profile PF01632: ribosomal protein L35   chr2:10249056-10250693 FORWARD   Aliases: T29E15.29, T29E15_29	4.7	4.7	0.1	0.1	100.0%	-4.5
19355	AT1G22910.3   RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM); similar to GB:AAC33496   chr1:8105578-8108153 FORWARD   Aliases: F19G10.13, F19G10_13	4.2	4.2	-0.0	-0.1	100.0%	-4.9
19356	AT3G55660.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr3:20659921-20662367 REVERSE   Aliases: F1I16.70, KINASE PARTNER PROTEIN LIKE, KPP LIKE	3.4	3.4	0.0	0.1	100.0%	-5.3
19357	AT1G51490.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; similar to Cyanogenic Beta-Glucosidase (GI:1311386) (pdb:1CBG) (Trifolium repens) (J. Mol. Biol. 229 (3), 791-793 (1993))   chr1:19098556-19101120 FORWARD   Aliases: F5D21.16, F5D21_16	2.6	2.5	0.0	0.1	100.0%	-5.5
19358	AT4G19850.1   Symbol: ATPP2 A2   lectin-related, low similarity to PP2 lectin polypeptide (Cucurbita maxima) GI:410437   chr4:10776935-10777519 FORWARD   Aliases: T16H5.210, T16H5_210	2.9	2.9	0.0	0.1	100.0%	-5.4
19359	AT5G02240.1   expressed protein   chr5:451421-453155 FORWARD   Aliases: T1E22.5	12.3	12.3	-0.0	-0.1	100.0%	-4.9
19360	AT2G31830.1   endonuclease/exonuclease/phosphatase family protein, belongs to Pfam:PF03372: Endonuclease/Exonuclease/phosphatase family; contains 4 WD-40 repeats (PF00400);similar to SP:Q01968 Inositol polyphosphate 5-phosphatase OCRL-1 (EC 3.1.3.-)(Lowe's oculocerebrorenal syndrome protein) (SP:Q01968) (Homo sapiens)   chr2:13539982-13544742 REVERSE   Aliases: F20M17.13, F20M17_13	3.2	3.2	0.0	0.1	100.0%	-5.7
19361	AT3G62640.1   expressed protein   chr3:23177265-23177876 REVERSE   Aliases: F26K9.70	2.3	2.3	0.0	0.1	100.0%	-5.7
19362	AT1G17590.3   CCAAT-binding transcription factor (CBF-B/NF-YA) family protein, contains Pfam profile: PF02045 CCAAT-binding transcription factor (CBF-B/NF-YA) subunit B   chr1:6050215-6052561 REVERSE   Aliases: F1L3.29, F1L3_29	3.7	3.8	-0.1	-0.1	100.0%	-4.8
19363	AT5G17360.1   expressed protein   chr5:5720378-5721661 FORWARD   Aliases: MKP11.17, MKP11_17	2.9	2.9	0.0	0.1	100.0%	-5.7
19364	AT1G21360.1   expressed protein   chr1:7481353-7483425 FORWARD   Aliases: F24J8.2, F24J8_2	2.6	2.7	-0.1	-0.1	100.0%	-3.9
19365	AT3G03440.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr3:815651-818841 FORWARD   Aliases: T21P5.14, T21P5_14	3.2	3.2	-0.0	-0.1	100.0%	-5.2
19366	AT4G27600.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr4:13782521-13785118 REVERSE   Aliases: T29A15.90, T29A15_90	5.3	5.4	-0.0	-0.1	100.0%	-5.0
19367	AT5G18600.1   glutaredoxin family protein, contains glutaredoxin domain, INTERPRO:IPR002109   chr5:6183265-6183956 REVERSE   Aliases: T28N17.80, T28N17_80	4.0	4.1	-0.0	-0.1	100.0%	-5.3
19368	AT4G34020.2   similar to 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative [Arabidopsis thaliana] (TAIR:At3g14990.1); similar to 4-methyl-5(b-hydroxyethyl)-thiazole monophosphate biosynthesis protein, putative [Arabidopsis thaliana] (TAIR:At3g14990.2); similar to putative 4-methyl-5(b-hydroxyethyl)-thiazol monophosphate biosynthesis enzyme [Oryza sativa (japonica cultivar-group)] (GB:BAD54224.1); contains InterPro domain Protein of unknown function Thij/Pfpl (InterPro:IPR002818); contains InterPro domain DJ-1 protein (InterPro:IPR006287)	2.6	2.6	-0.0	-0.1	100.0%	-5.3
19369	AT1G72220.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger); similar to GI:4928397 from (Arabidopsis thaliana) (Plant Mol. Biol. 40 (4), 579-590 (1999))   chr1:27187943-27189492 REVERSE   Aliases: T9N14.22, T9N14_22	4.9	4.9	0.0	0.1	100.0%	-4.4
19370	AT4G26560.1   Symbol: CBL7   calcineurin B-like protein, putative, similar to calcineurin B-like protein 3 (Arabidopsis thaliana) GI:3309086, calcineurin B-like protein 2 (Arabidopsis thaliana) GI:3309084; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:13406739-13407979 REVERSE   Aliases: CALCINEURIN B LIKE 7, T15N24.10	3.1	3.1	-0.0	-0.1	100.0%	-5.7
19371	AT2G26570.1   expressed protein, contains Pfam profile PF05701: Plant protein of unknown function (DUF827); weak similarity to merozoite surface protein 3 alpha (GI:27596802) (Plasmodium vivax)   chr2:11306222-11309269 FORWARD   Aliases: T9J22.24, T9J22_24	6.5	6.6	-0.0	-0.1	100.0%	-4.9
19372	AT1G05540.1   expressed protein, contains Pfam profile PF03478: Protein of unknown function (DUF295)   chr1:1639285-1640810 FORWARD   Aliases: T25N20.19	4.3	4.3	0.0	0.1	100.0%	-4.9
19373	AT5G44750.1   Symbol: REV1   similar to UMUC-like DNA repair family protein [Arabidopsis thaliana] (TAIR:At1g49980.1); similar to PREDICTED: similar to deoxycytidyl transferase [Rattus norvegicus] (GB:XP_237071.3); contains InterPro domain UMUC-like DNA-repair protein (InterPro:IPR001126); contains InterPro domain BRCT (InterPro:IPR001357)	3.6	3.6	0.0	0.1	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19374	AT4G17900.1   zinc-binding family protein, similar to zinc-binding protein (Pisum sativum) GI:16117799; contains Pfam profile PF04640 : Protein of unknown function, DUF597   chr4:9945974-9948091 FORWARD   Aliases: T6K21.80, T6K21_80	4.8	4.8	-0.1	-0.1	100.0%	-4.2
19375	AT3G06460.1   GNS1/SUR4 membrane family protein, similar to SP:P25358 Elongation of fatty acids protein 2 (GNS1 protein) (V-SNARE bypass mutant gene 2 protein) {Saccharomyces cerevisiae}; contains Pfam profile PF01151: GNS1/SUR4 family   chr3:1982665-1983720 FORWARD   Aliases: F24P17.4, F24P17_4	3.7	3.7	0.0	0.1	100.0%	-5.1
19376	AT2G32710.2   Symbol: KRP4   kip-related protein 4 (KRP4) / cyclin-dependent kinase inhibitor 4 (ICK4), nearly identical to cyclin-dependent kinase inhibitor 4 (krp4) (Arabidopsis thaliana) GI:14422291   chr2:13880550-13882908 FORWARD   Aliases: ACK2, CYCLIN DEPENDENT KINASE INHIBITOR 2, F24L7.15, F24L7_15, ICK7, KIP RELATED PROTEIN 4	3.7	3.7	0.0	0.1	100.0%	-5.2
19377	AT5G10810.1   Symbol: ATER   enhancer of rudimentary protein, putative, identical to enhancer of rudimentary homolog SP:Q96319 from (Arabidopsis thaliana); contains Pfam profile: PF01133 enhancer of rudimentary   chr5:3418667-3420636 REVERSE   Aliases: ENHANCER OF RUDIMENTARY HOMOLOG ATER, T30N20.80, T30N20_80	8.6	8.6	0.1	0.1	100.0%	-4.7
19378	AT5G52770.1   heavy-metal-associated protein-related, contains low similarity to Pfam profile PF00403: Heavy-metal-associated domain   chr5:21406992-21407415 FORWARD   Aliases: F6N7.26, F6N7_26	2.8	2.7	0.0	0.1	100.0%	-5.7
19379	AT3G06500.1   beta-fructofuranosidase, putative / invertase, putative / saccharase, putative / beta-fructosidase, putative, similar to neutral invertase (Daucus carota) GI:4200165; contains Pfam profile PF04853: Plant neutral invertase   chr3:2012085-2015711 FORWARD   Aliases: F5E6.17, F5E6_17	6.2	6.2	0.0	0.1	100.0%	-4.9
19380	AT4G12360.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr4:7327989-7329101 REVERSE   Aliases: T4C9.200, T4C9_200	2.8	2.8	0.0	0.1	100.0%	-5.3
19381	AT1G31490.1   transferase family protein, contains similarity to anthranilate N-hydroxycinnamoyl benzoyltransferase GI:3288180, GI:2239091 from (Dianthus caryophyllus); contains Pfam profile PF02458 transferase family   chr1:11271209-11273275 REVERSE   Aliases: F27M3.28, F27M3_28	3.4	3.4	-0.0	-0.1	100.0%	-5.5
19382	AT4G24980.1   nodulin MtN21 family protein, similar to MtN21 (Medicago truncatula) GI:2598575   chr4:12847528-12848386 REVERSE   Aliases: F13M23.120, F13M23_120	3.0	3.0	0.0	0.1	100.0%	-5.5
19383	AT3G45940.1   alpha-xylosidase, putative, strong similarity to alpha-xylosidase precursor GI:4163997 from (Arabidopsis thaliana)   chr3:16897211-16900156 REVERSE   Aliases: F16L2.150	2.9	2.9	0.0	0.1	100.0%	-5.3
19384	AT1G06790.2   RNA polymerase Rpb7 N-terminal domain-containing protein, similar to SP:P35718 DNA-directed RNA polymerase III 25 kDa polypeptide (EC 2.7.7.6) {Saccharomyces cerevisiae}; contains Pfam profile PF03876: RNA polymerase Rpb7, N-terminal domain	5.7	5.6	0.0	0.1	100.0%	-4.6
19385	AT4G17010.1   expressed protein   chr4:9575831-9577922 FORWARD   Aliases: DL4535W, FCAALL.229	6.6	6.7	-0.1	-0.1	100.0%	-4.7
19386	AT2G39200.1   Symbol: MLO12   seven transmembrane MLO family protein / MLO-like protein 12 (MLO12), identical to SP:O80961 MLO-like protein 12 (AtMlo12) {Arabidopsis thaliana}, membrane protein Mlo12 (Arabidopsis thaliana) gi:14091594:gb:AAK53805; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr2:16363237-16366891 REVERSE   Aliases: T16B24.16, T16B24_16	2.8	2.8	0.0	0.1	100.0%	-4.5
19387	AT2G25360.1   zinc finger protein-related, contains weak similarity to zinc finger proteins and Pfam PF01485: IBR domain   chr2:10811328-10812840 FORWARD   Aliases: F13B15.2, F13B15_2	2.8	2.8	0.0	0.1	100.0%	-5.7
19388	AT1G12040.1   Symbol: LRX1   leucine-rich repeat family protein / extensin family protein (LRX1), similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965   chr1:4070122-4072565 FORWARD   Aliases: F12F1.9, F12F1_9, LEUCINE RICH REPEAT/EXTENSIN 1	3.1	3.0	0.1	0.1	100.0%	-4.6
19389	AT2G14880.1   SWIB complex BAF60b domain-containing protein, contains Pfam profile PF02201: BAF60b domain of the SWIB complex   chr2:6400414-6402020 REVERSE   Aliases: T26I20.4, T26I20_4	6.7	6.7	-0.0	-0.1	100.0%	-4.4
19390	AT1G48140.1   dolichol-phosphate mannosyltransferase-related, contains weak similarity to Swiss-Prot:Q9P2X0 dolichol-phosphate mannosyltransferase subunit 3 (Dolichol-phosphate mannose synthase subunit 3, Dolichyl-phosphate beta-D- mannosyltransferase subunit 3, Mannose-P-dolichol synthase subunit 3, MPD synthase subunit 3, DPM synthase complex subunit 3, Prostin 1 (Homo sapiens)	8.7	8.7	0.0	0.1	100.0%	-4.9
19391	AT4G28380.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979   chr4:14039762-14040937 REVERSE   Aliases: F20O9.70, F20O9_70	2.6	2.6	0.0	0.1	100.0%	-5.3
19392	AT5G63180.1   pectate lyase family protein, similar to pectate lyase GP:14289169 from (Salix gilgiana)	2.4	2.4	0.0	0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19393	AT4G16265.1   DNA-directed RNA polymerase II, putative, similar to SP:P36958 DNA-directed RNA polymerase II 15.1 kDa polypeptide (EC 2.7.7.6) {Drosophila melanogaster}; contains Pfam profile PF02150: RNA polymerases M/15 Kd subunit   chr4:9202371-9204086 REVERSE   Aliases: None	5.9	5.9	-0.0	-0.1	100.0%	-4.6
19394	AT3G28770.1   expressed protein   chr3:10797953-10804474 FORWARD   Aliases: T19N8.6	3.2	3.2	0.0	0.1	100.0%	-5.6
19395	ATCG00210.1   Symbol: YCF6   hypothetical protein   chrC:28089-28178 FORWARD   Aliases: YCF6	6.0	5.9	0.1	0.1	100.0%	-4.9
19396	AT4G35660.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function; expression supported by MPSS   chr4:16912797-16913663 FORWARD   Aliases: F8D20.170, F8D20_170	3.2	3.2	0.0	0.1	100.0%	-5.6
19397	AT5G56130.1   transducin family protein / WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to beta transducin-like protein HET-E2C*4 (GI:17225206) (Podospira anserina)   chr5:22739778-22742311 REVERSE   Aliases: MDA7.19, MDA7_19	6.2	6.2	0.1	0.1	100.0%	-4.7
19398	AT1G33770.1   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain   chr1:12242106-12244442 FORWARD   Aliases: F14M2.11, F14M2_11	2.5	2.5	0.0	0.1	100.0%	-5.5
19399	AT5G58390.1   peroxidase, putative, similar to peroxidase (Nicotiana tabacum) gi:5381253:dbj:BAA82306   chr5:23616793-23618551 REVERSE   Aliases: MCK7.26, MCK7_26	2.2	2.2	-0.0	-0.1	100.0%	-5.8
19400	AT2G39530.1   integral membrane protein, putative, contains 3 transmembrane domains; contains Pfam PF04535 : Domain of unknown function (DUF588); similar to putative ethylene responsive element binding protein (GI:22135858) (Arabidopsis thaliana)   chr2:16505564-16506549 REVERSE   Aliases: F12L6.19, F12L6_19	3.6	3.6	0.0	0.1	100.0%	-4.6
19401	AT2G31930.1   expressed protein   chr2:13584632-13585325 FORWARD   Aliases: F20M17.3, F20M17_3	2.5	2.5	0.0	0.1	100.0%	-5.2
19402	AT2G44580.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:18405072-18410488 REVERSE   Aliases: F16B22.7	2.9	2.9	0.0	0.1	100.0%	-5.4
19403	AT3G07530.1   expressed protein, ; expression supported by MPSS   chr3:2400799-2404286 FORWARD   Aliases: F21O3.24	4.6	4.5	0.0	0.1	100.0%	-5.0
19404	AT4G31730.1   Symbol: GDU1   expressed protein   chr4:15361097-15361801 FORWARD   Aliases: F28M20.80, F28M20_80, GLUTAMINE DUMPER 1	6.9	6.9	-0.0	-0.1	100.0%	-4.7
19405	AT4G13700.1   similar to serine/threonine protein phosphatase family protein [Arabidopsis thaliana] (TAIR:At3g07130.1); similar to phytase [Glycine max] (GB:AAK49438.1); contains InterPro domain Metallo-phosphoesterase (InterPro:IPR004843)   chr4:7957068-7958915 REVERSE   Aliases: F18A5.90, F18A5_90	2.8	2.8	-0.0	-0.1	100.0%	-5.5
19406	AT1G61660.2   basic helix-loop-helix (bHLH) family protein, contains Pfam domain, PF00010: Helix-loop-helix DNA-binding domain	5.0	5.1	-0.0	-0.1	100.0%	-4.9
19407	AT2G22330.1   Symbol: CYP79B3   cytochrome P450, putative, similar to cytochrome P450 79B2 (SP:O81346) (Arabidopsis thaliana)	3.7	3.6	0.0	0.1	100.0%	-4.9
19408	AT2G47470.3   Symbol: ATPDIL2 1   similar to thioredoxin family protein [Arabidopsis thaliana] (TAIR:At2g32920.1); similar to thioredoxin family protein [Arabidopsis thaliana] (TAIR:At1g04980.1); similar to protein disulfide-isomerase precursor [Nicotiana tabacum] (GB:CAA72092.1); contains InterPro domain Disulphide isomerase (InterPro:IPR005788); contains InterPro domain Thioredoxin type domain (InterPro:IPR006662); contains InterPro domain Thioredoxin domain 2 (InterPro:IPR006663)   chr2:19488492-19491085 FORWARD   Aliases: ATPDIL2 1, PDI LIKE 2 1, T30B22.23	9.9	9.9	-0.0	-0.1	100.0%	-4.7
19409	AT1G68230.1   reticulon family protein (RTNLB14), contains Pfam profile PF02453: Reticulon   chr1:25575848-25576584 FORWARD   Aliases: T22E19.14, T22E19_14	3.2	3.2	0.0	0.1	100.0%	-4.8
19410	AT3G62090.1   Symbol: PIL2   basic helix-loop-helix (bHLH) protein, putative, very strong similarity to PIF3 like basic Helix Loop Helix protein 2 (PIL2) (Arabidopsis thaliana) GI:22535494   chr3:22999522-23001684 REVERSE   Aliases: PHYTOCHROME INTERACTING FACTOR 3 LIKE 2, PHYTOCHROME INTERACTING FACTOR 6, PIF6, T17J13.50	4.1	4.1	0.0	0.1	100.0%	-4.8
19411	AT1G60030.1   xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family   chr1:22117531-22120510 REVERSE   Aliases: T2K10.8, T2K10_8	3.6	3.6	-0.0	-0.1	100.0%	-5.1
19412	AT5G07910.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560   chr5:2521570-2524202 REVERSE   Aliases: F13G24.110	3.8	3.8	0.0	0.1	100.0%	-5.0
19413	AT3G22200.1   Symbol: POP2   4-aminobutyrate aminotransferase / gamma-amino-N-butyrate transaminase / GABA transaminase / beta-alanine--oxoglutarate aminotransferase, identical to gamma-aminobutyrate transaminase subunit precursor (Arabidopsis thaliana) (EC 2.6.1.19) GI:14030435; contains Pfam profile PF00202: aminotransferase, class III; identical to cDNA gamma-aminobutyrate transaminase subunit precursor, nuclear gene for mitochondrial product GI:14030434	11.5	11.4	0.0	0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19414	AT1G12580.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains similarity to calcium-dependent protein kinase GI:5162877 from (Marchantia polymorpha)   chr1:4282897-4285827 FORWARD   Aliases: F5O11.32, F5O11_32	4.7	4.7	0.0	0.1	100.0%	-5.1
19415	AT1G04470.1   expressed protein, EST gb:ATTS5672 comes from this gene   chr1:1211072-1214590 REVERSE   Aliases: F19P19.7, F19P19_7	2.2	2.2	0.0	0.1	100.0%	-5.6
19416	AT4G15475.1   F-box family protein (FBL4), 99.7% identical to F-box protein family, AtFBL4 (GP:21536497) (Arabidopsis thaliana); similar to grr1 GI:2407790 from (Glycine max)	5.8	5.9	-0.0	-0.1	100.0%	-4.7
19417	AT4G03830.1   myosin heavy chain-related   chr4:1790438-1792456 FORWARD   Aliases: T7M24.5, T7M24_5	2.5	2.5	-0.0	-0.1	100.0%	-5.7
19418	AT1G79220.1   mitochondrial transcription termination factor family protein / mTERF family protein, weak similarity to mtDBP protein (Paracentrotus lividus) GI:4584695; contains Pfam profile PF02536: mTERF   chr1:29803828-29805418 FORWARD   Aliases: YUP8H12R.18, YUP8H12R_18	3.9	3.9	-0.0	-0.1	100.0%	-5.0
19419	AT1G14390.1   leucine-rich repeat transmembrane protein kinase, putative, similar to putative receptor-like protein kinase GI:2947063 from (Arabidopsis thaliana)   chr1:4924272-4926789 FORWARD   Aliases: F14L17.16, F14L17_16	3.2	3.2	0.0	0.1	100.0%	-5.7
19420	AT3G03040.1   F-box family protein, contains F-box domain Pfam:PF00646	4.2	4.2	-0.0	-0.1	100.0%	-5.0
19421	AT3G51990.1   protein kinase family protein, contains protein kinase domain, PF00069   chr3:19298856-19300308 FORWARD   Aliases: F4F15.100	6.3	6.3	-0.0	-0.1	100.0%	-5.0
19422	AT3G22070.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:7775336-7776116 REVERSE   Aliases: MZN24.27	2.9	2.9	-0.0	-0.1	100.0%	-5.3
19423	AT1G75880.2   family II extracellular lipase 1 (EXL1), EXL1 (PMID:11431566); similar to anter-specific proline-rich protein (APG) SP:P40602 (Arabidopsis thaliana)   chr1:28494111-28496116 FORWARD   Aliases: T4O12.12, T4O12_12	2.2	2.2	0.0	0.1	100.0%	-5.7
19424	AT1G54550.1   F-box family protein, contains Pfam:PF00646 F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain   chr1:20373318-20374653 FORWARD   Aliases: F20D21.36, F20D21_36	2.5	2.5	-0.0	-0.1	100.0%	-5.8
19425	AT2G13720.1   hypothetical protein, weak similarity to SP:P30182 DNA topoisomerase II (EC 5.99.1.3) {Arabidopsis thaliana}   chr2:5731089-5732330 FORWARD   Aliases: F13J11.7, F13J11_7	2.5	2.5	-0.0	-0.1	100.0%	-5.7
19426	AT5G53840.1   F-box family protein (FBL13), contains F-box domain PF:00646   chr5:21876374-21877898 REVERSE   Aliases: K6O8.1, K6O8_1	2.9	2.9	0.0	0.1	100.0%	-5.5
19427	ATCG00080.1   Symbol: PSBI   PSII I protein   chrC:7583-7693 FORWARD   Aliases: PSBI	10.1	10.0	0.1	0.1	100.0%	-5.1
19428	AT1G71710.1   inositol polyphosphate 5-phosphatase, putative, similar to inositol polyphosphate 5-phosphatase I (Arabidopsis thaliana) GI:10444261   chr1:26977229-26980493 REVERSE   Aliases: F14O23.9, F14O23_9	3.8	3.7	0.0	0.1	100.0%	-4.8
19429	AT4G12930.1   expressed protein   chr4:7573278-7573703 REVERSE   Aliases: F25G13.20, F25G13_20	2.3	2.3	0.0	0.1	100.0%	-5.5
19430	AT2G20670.1   expressed protein, contains Pfam profile PF04720: Protein of unknown function (DUF506)   chr2:8918941-8920615 REVERSE   Aliases: F23N11.1	3.3	3.3	0.0	0.1	100.0%	-4.9
19431	AT5G13290.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:4252846-4254435 REVERSE   Aliases: T31B5.110, T31B5_110	5.9	5.9	-0.0	-0.1	100.0%	-4.8
19432	AT2G03190.1   Symbol: ASK16   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At16), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1a GI:3068807 from (Arabidopsis thaliana)   chr2:964211-964898 FORWARD   Aliases: ARABIDOPSIS SKP1 LIKE 16, T18E12.14, T18E12_14	2.6	2.6	0.0	0.1	100.0%	-5.7
19433	AT1G67340.1   zinc finger (MYND type) family protein / F-box family protein   chr1:25233928-25235503 FORWARD   Aliases: F1N21.16	4.1	4.1	0.0	0.1	100.0%	-4.8
19434	AT1G61480.1   S-locus protein kinase, putative, similar to receptor protein kinase (IRK1) GI:836953 from (Ipomoea trifida); contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:22684981-22688140 REVERSE   Aliases: T1F9.2, T1F9_2	3.0	3.0	0.0	0.1	100.0%	-5.5
19435	AT3G04230.1   40S ribosomal protein S16 (RPS16B), similar to 40S ribosomal protein S16 GB:AAD22696 (Arabidopsis thaliana)   chr3:1112997-1113616 REVERSE   Aliases: T6K12.15, T6K12_15	6.2	6.2	-0.0	-0.1	100.0%	-4.6
19436	AT5G46450.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18852845-18856773 FORWARD   Aliases: K11I1.4, K11I1_4	2.7	2.7	-0.0	-0.1	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19437	AT1G49250.1   ATP dependent DNA ligase family protein, contains Pfam profile: PF01068 ATP dependent DNA ligase domain   chr1:18224201-18227924 FORWARD   Aliases: F13F21.31, F13F21_31	2.5	2.5	-0.0	-0.1	100.0%	-5.6
19438	AT3G01080.1   Symbol: WRKY58	3.8	3.9	-0.0	-0.1	100.0%	-5.0
19439	AT3G52780.2   purple acid phosphatase (PAP20), identical to purple acid phosphatase Gl:20257491 from (Arabidopsis thaliana)   chr3:19572305-19575173 REVERSE   Aliases: F3C22.180	2.6	2.6	0.0	0.1	100.0%	-5.5
19440	AT2G27250.2   Symbol: CLV3   CLAVATA3, CLAVATA3/ESR-Related (CLE) family of proteins; ligand for CLV1; responsible for negative regulation of meristem cell differentiation and replacement   chr2:11672064-11672846 REVERSE   Aliases: CLAVATA 3, CLAVATA3, F12K2.17, F12K2_17	2.6	2.6	-0.0	-0.1	100.0%	-5.4
19441	AT3G01910.2   Symbol: SOX   similar to nitrate reductase 1 (NR1) [Arabidopsis thaliana] (TAIR:At1g77760.1); similar to B Chain B, Sulfite Oxidase From Chicken Liver (GB:1SOX); contains InterPro domain Eukaryotic molybdopterin oxidoreductase (InterPro:IPR008335); contains InterPro domain Mo-co oxidoreductase dimerisation domain (InterPro:IPR005066); contains InterPro domain Oxidoreductase, molybdopterin binding (InterPro:IPR000572)   chr3:314703-316719 REVERSE   Aliases: F28J7.38, F28J7_38, SULFITE OXIDASE	11.4	11.5	-0.0	-0.1	100.0%	-5.3
19442	AT5G62420.1   aldo/keto reductase family protein, similar to chalcone reductase (Sesbania rostrata)(Gl:2792155); contains Pfam profile PF00248: oxidoreductase, aldo/keto reductase family   chr5:25082061-25083337 FORWARD   Aliases: K19B1.2, K19B1_2	3.2	3.1	0.1	0.1	100.0%	-4.6
19443	AT2G35990.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g37210.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54293.1); contains InterPro domain Conserved hypothetical protein 730 (InterPro:IPR005269)	2.6	2.6	-0.0	-0.1	100.0%	-5.1
19444	AT2G14810.1   expressed protein   chr2:6364547-6365552 REVERSE   Aliases: F26C24.5, F26C24_5	2.6	2.6	0.0	0.1	100.0%	-5.7
19445	AT5G56080.1   nicotianamine synthase, putative, similar to nicotianamine synthase (Lycopersicon esculentum)(Gl:4753801), nicotianamine synthase 2 (Hordeum vulgare)(Gl:4894912)   chr5:22728628-22729590 REVERSE   Aliases: MDA7.14, MDA7_14	2.6	2.6	-0.1	-0.1	100.0%	-4.1
19446	AT3G58330.1   expressed protein   chr3:21598339-21598979 REVERSE   Aliases: F9D24.240	3.3	3.3	0.0	0.1	100.0%	-5.4
19447	AT3G57410.1   Symbol: VLN3   villin 3 (VLN3), nearly identical to villin 3 (VLN3) (Arabidopsis thaliana) Gl:3415117   chr3:21254113-21262077 REVERSE   Aliases: F28O9.1, VILLIN 3	4.0	4.0	-0.0	-0.1	100.0%	-4.5
19448	AT5G11350.1   endonuclease/exonuclease/phosphatase family protein, contains Pfam profile PF03372: Endonuclease/Exonuclease/phosphatase family   chr5:3621570-3625646 FORWARD   Aliases: F2I11.240, F2I11_240	5.6	5.6	-0.0	-0.1	100.0%	-5.3
19449	AT2G23440.1   expressed protein   chr2:9986485-9986899 FORWARD   Aliases: F26B6.9, F26B6_9	2.8	2.8	0.0	0.1	100.0%	-5.7
19450	AT5G13230.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:4222517-4224985 FORWARD   Aliases: T31B5.50, T31B5_50	3.5	3.5	-0.0	-0.1	100.0%	-5.2
19451	AT2G33500.2   zinc finger (B-box type) family protein   chr2:14195063-14197330 REVERSE   Aliases: F4P9.27, F4P9_27	4.3	4.4	-0.0	-0.1	100.0%	-5.0
19452	AT5G38130.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase, Dianthus caryophyllus (gi:2239091); contains Pfam transferase family domain PF002458   chr5:15235179-15236602 REVERSE   Aliases: MXA21.5, MXA21_5	3.5	3.5	0.0	0.1	100.0%	-5.3
19453	AT5G13350.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) Gl:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr5:4279887-4282290 FORWARD   Aliases: T22N19.4	2.8	2.8	0.0	0.1	100.0%	-5.5
19454	AT1G35490.1   bZIP family transcription factor	2.2	2.2	0.0	0.1	100.0%	-5.9
19455	AT1G31510.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain; ; similar to F-box protein family, AtFBX9 (Gl:20197985) (Arabidopsis thaliana)	2.8	2.8	-0.0	-0.1	100.0%	-6.0
19456	AT5G61520.1   hexose transporter, putative, similar to	4.8	4.8	-0.0	-0.1	100.0%	-4.9
19457	AT5G61940.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr5:24885381-24889943 FORWARD   Aliases: K22G18.7, K22G18_7	2.7	2.7	-0.0	-0.1	100.0%	-5.3
19458	AT4G32560.3   similar to MGC89046 protein [Xenopus tropicalis] (GB:AAH82492.1)	4.9	4.9	-0.0	-0.1	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19459	AT1G03390.1   transferase family protein, similar to anthranilate N-hydroxycinnamoyl/benzoyltransferase from <i>Dianthus caryophyllus</i> (gi:2239091); contains Pfam transferase family domain PF002458   chr1:841032-842417 REVERSE   Aliases: F21B7.2, F21B7_2	3.0	3.0	0.0	0.1	100.0%	-5.6
19460	AT3G23295.1   expressed protein   chr3:8327674-8327898 FORWARD   Aliases: MLM24.1	2.5	2.5	-0.0	-0.1	100.0%	-5.6
19461	AT3G01410.1   RNase H domain-containing protein, low similarity to GAG-POL precursor ( <i>Oryza sativa</i> (japonica cultivar-group)) GI:5902445; contains Pfam profile: PF00075 RNase H   chr3:153446-155606 REVERSE   Aliases: T13O15.5, T13O15_5	5.5	5.5	-0.0	-0.1	100.0%	-4.6
19462	AT4G12020.1   Symbol: WRKY19	3.4	3.4	-0.1	-0.1	100.0%	-4.1
19463	AT5G15800.1   Symbol: SEP1   developmental protein SEPALLATA1 / floral homeotic protein (AGL2) (SEP1), identical to developmental protein SEPALLATA1 / floral homeotic protein (AGL2 / SEP1) SP:P29382 from ( <i>Arabidopsis thaliana</i> )   chr5:5151080-5154156 REVERSE   Aliases: AGL2, F14F8.180, F14F8_180, SEPALLATA1	2.8	2.8	-0.0	-0.1	100.0%	-5.4
19464	AT5G52580.1   expressed protein   chr5:21355278-21357204 FORWARD   Aliases: F6N7.6, F6N7_6	2.9	2.9	-0.0	-0.1	100.0%	-5.2
19465	AT3G55710.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:20684826-20686925 FORWARD   Aliases: F1I16.120	2.8	2.8	0.0	0.1	100.0%	-5.3
19466	AT5G19270.1   hypothetical protein   chr5:6485619-6487011 REVERSE   Aliases: T24G5.2	4.2	4.2	-0.0	-0.1	100.0%	-5.0
19467	AT2G33170.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase ( <i>Pinus sylvestris</i> ) gi:12054894:emb:CAC20842; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:14063327-14067718 REVERSE   Aliases: F25I18.9, F25I18_9	3.9	3.9	-0.0	-0.1	100.0%	-5.3
19468	AT2G02610.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain   chr2:710711-712818 FORWARD   Aliases: T8K22.9, T8K22_9	2.8	2.8	-0.0	-0.1	100.0%	-4.5
19469	AT3G15050.1   calmodulin-binding family protein, similar to SF16 protein ( <i>Helianthus annuus</i> ) GI:560150; contains Pfam profile PF00612: IQ calmodulin-binding motif   chr3:5066886-5067967 REVERSE   Aliases: K15M2.19	2.9	2.9	-0.0	-0.1	100.0%	-5.0
19470	AT2G43820.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr2:18159304-18160985 FORWARD   Aliases: F18O19.7	4.4	4.4	0.1	0.1	100.0%	-4.5
19471	AT1G22210.1   trehalose-6-phosphate phosphatase, putative, similar to trehalose-6-phosphate phosphatase (AtTPPB) GI:2944180 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF02358: Trehalose-phosphatase   chr1:7841507-7844045 FORWARD   Aliases: F16L1.6, F16L1_6	2.5	2.5	0.0	0.1	100.0%	-5.4
19472	AT3G17490.1   F-box family protein, similar to F-box protein family, AtFBX9 (GI:20197985) ( <i>Arabidopsis thaliana</i> ); contains Pfam PF00646: F-box domain and TIGRFAM TIGR01640: F-box protein interaction domain   chr3:5984833-5985999 FORWARD   Aliases: MKP6.4	3.5	3.5	-0.0	-0.1	100.0%	-5.6
19473	AT1G76240.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr1:28607707-28608822 REVERSE   Aliases: T23E18.17, T23E18_17	2.9	2.9	-0.0	-0.1	100.0%	-5.1
19474	AT3G12440.1   extensin family protein, contains similarity to Swiss-Prot:Q38913 extensin 1 precursor (AtExt1) (AtExt4) ( <i>Arabidopsis thaliana</i> )   chr3:3951206-3952267 REVERSE   Aliases: T2E22.24	2.8	2.8	0.0	0.1	100.0%	-5.7
19475	AT1G49015.1   eukaryotic translation initiation factor-related, contains similarity to eukaryotic translation initiation factor 3 subunit 9 SP:Q9C5Z1   chr1:18138196-18138980 FORWARD   Aliases: None	3.3	3.3	0.0	0.1	100.0%	-5.7
19476	AT3G08760.1   Symbol: ATSIK   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:2657924-2660833 REVERSE   Aliases: F17O14.23	4.5	4.5	-0.0	-0.1	100.0%	-4.8
19477	AT1G62310.1   transcription factor jumonji (jmc) domain-containing protein, similar to nuclear protein 5qNCA ( <i>Homo sapiens</i> ) GI:13161188; contains Pfam profile PF02373: jmc domain   chr1:23039704-23042966 REVERSE   Aliases: F24O1.3, F24O1_3	4.5	4.5	-0.0	-0.1	100.0%	-4.8
19478	AT2G41250.1   haloacid dehalogenase-like hydrolase family protein, low similarity to SP:Q94915 Rhythmically expressed gene 2 protein (DREG-2) ( <i>Drosophila melanogaster</i> ); contains InterPro accession IPR005834: Haloacid dehalogenase-like hydrolase   chr2:17207737-17209696 REVERSE   Aliases: F13H10.20, F13H10_20	4.7	4.7	0.0	0.1	100.0%	-4.9
19479	AT3G51030.1   Symbol: ATTRX1	10.7	10.8	-0.1	-0.1	100.0%	-4.4
19480	AT1G19540.1   isoflavone reductase, putative, similar to SP:P52577; contains isoflavone reductase domain PF02716   chr1:6765662-6767332 FORWARD   Aliases: F18O14.30, F18O14_30	3.4	3.4	-0.0	-0.1	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19481	AT5G42620.1   expressed protein   chr5:17083586-17088569 FORWARD   Aliases: MFO20.3, MFO20_3	3.1	3.1	0.0	0.1	100.0%	-5.6
19482	AT5G46560.1   expressed protein   chr5:18905288-18907689 FORWARD   Aliases: F10E10.3, F10E10_3	3.6	3.7	-0.0	-0.1	100.0%	-4.9
19483	AT4G01950.1   Symbol: ATGPAT3/GPAT3   Encodes a member of a family of proteins with glycerol-3-phosphate acyltransferase activity.   chr4:844409-846787 REVERSE   Aliases: ATGPAT3, GPAT3, T7B11.21, T7B11_21	3.2	3.2	-0.0	-0.1	100.0%	-4.9
19484	AT3G14080.2   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to U6 snRNA-associated Sm-like protein LSm1 (Small nuclear ribonuclear CaSm, Cancer-associated Sm-like) (Homo sapiens) SWISS-PROT:O15116; contains Pfam profile: PF01423 Sm protein   chr3:4667381-4669188 FORWARD   Aliases: MAG2.4	6.5	6.5	-0.0	-0.1	100.0%	-5.0
19485	AT1G54310.2   expressed protein   chr1:20277234-20279116 FORWARD   Aliases: F20D21.13, F20D21_13	3.7	3.7	0.0	0.1	100.0%	-4.8
19486	AT3G45220.1   serpin, putative / serine protease inhibitor, putative, similar to phloem serpin-1 (Cucurbita maxima) GI:9937311; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr3:16575866-16577315 REVERSE   Aliases: T14D3.160	2.8	2.8	-0.0	-0.1	100.0%	-5.7
19487	AT3G09750.1   expressed protein   chr3:2992187-2992574 REVERSE   Aliases: F11F8.34	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19488	AT3G19670.1   FF domain-containing protein / WW domain-containing protein, weak similarity to huntingtin-interacting protein HYPA/FBP11 (Homo sapiens) GI:3341980; contains Pfam profiles PF01846: FF domain, PF00397: WW domain   chr3:6828068-6836588 REVERSE   Aliases: MMB12.16	4.8	4.7	0.1	0.1	100.0%	-4.9
19489	AT1G48200.1   expressed protein   chr1:17800524-17802006 REVERSE   Aliases: F21D18.7, F21D18_7	5.5	5.5	0.0	0.1	100.0%	-4.5
19490	AT1G29140.1   pollen Ole e 1 allergen and extensin family protein, contains Pfam domain, PF01190: Pollen proteins Ole e I family   chr1:10179015-10180005 FORWARD   Aliases: F28N24.16, F28N24_16	2.3	2.3	-0.0	-0.1	100.0%	-5.8
19491	AT3G01830.2   calmodulin-related protein, putative, similar to regulator of gene silencing calmodulin-related protein GI:12963415 from (Nicotiana tabacum); Pfam HMM hit: EF hand   chr3:296061-299270 FORWARD   Aliases: F28J7.16, F28J7_16	2.5	2.5	0.0	0.1	100.0%	-5.1
19492	AT5G35090.1   expressed protein   chr5:13375644-13376318 FORWARD   Aliases: F7N22.40, F7N22_40	2.1	2.2	-0.0	-0.1	100.0%	-6.1
19493	AT1G51990.2   O-methyltransferase family 2 protein, similar to caffeic acid O-methyltransferase GI:5031492 from (Ocimum basilicum), (SP:Q00763) (Populus tremuloides)   chr1:19334618-19336336 FORWARD   Aliases: F5F19.5, F5F19_5	2.3	2.3	0.0	0.1	100.0%	-6.0
19494	AT2G22040.1   transducin family protein / WD-40 repeat family protein, similar to Pop3 (GI:3434986) (Schizosaccharomyces pombe); contains Pfam PF00400: WD domain, G-beta repeat (6 copies, 2 weak);   chr2:9381518-9383340 REVERSE   Aliases: T16B14.11, T16B14_11	4.2	4.1	0.1	0.1	100.0%	-4.7
19495	AT3G18140.2   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At2g22040.1); similar to hypothetical protein DDB0184464 [Dictyostelium discoideum] (GB:EAL61099.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr3:6212645-6214791 REVERSE   Aliases: MRC8.12	4.2	4.1	0.1	0.1	100.0%	-4.7
19496	AT4G20450.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr4:11024065-11029019 REVERSE   Aliases: F9F13.100, F9F13_100	2.5	2.6	-0.0	-0.1	100.0%	-4.4
19497	AT4G11230.1   respiratory burst oxidase, putative / NADPH oxidase, putative, similar to respiratory burst oxidase homolog F (gi:3242456), RbohAp108 (gi:2654868) from Arabidopsis thaliana, respiratory burst oxidase homolog (GI:16549087) from Solanum tuberosum; contains Pfam profile PF01794 Ferric reductase like transmembrane component   chr4:6840487-6845587 REVERSE   Aliases: F8L21.20, F8L21_20	2.3	2.3	-0.0	-0.1	100.0%	-5.0
19498	AT2G33620.3   DNA-binding family protein / AT-hook protein 1 (AHP1), identical to AT-hook protein 1 (Arabidopsis thaliana) gi:2598227:emb:CAA10857   chr2:14241325-14244634 FORWARD   Aliases: F4P9.39, F4P9_39	6.9	6.9	-0.0	-0.1	100.0%	-4.3
19499	AT5G17820.1   peroxidase 57 (PER57) (P57) (PRXR10), identical to SP:Q43729 Peroxidase 57 precursor (EC 1.11.1.7) (Atperox P57) (PRXR10) (ATP13a) {Arabidopsis thaliana}   chr5:5887908-5890164 REVERSE   Aliases: MVA3.170, MVA3_170	2.9	2.8	0.1	0.1	100.0%	-4.3
19500	AT3G49070.1   expressed protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	3.4	3.4	-0.0	-0.1	100.0%	-5.1
19501	AT5G55950.1   transporter-related, low similarity to UDP-sugar transporter (Drosophila melanogaster) GI:14971008, UDP-glucuronic acid transporter (Homo sapiens) GI:11463949   chr5:22675341-22677659 REVERSE   Aliases: MYN21.6, MYN21_6	2.6	2.7	-0.0	-0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19502	AT1G74070.1   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, contains Pfam domain, PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type   chr1:27855149-27856637 REVERSE   Aliases: F2P9.6, F2P9_6	4.4	4.4	-0.0	-0.1	100.0%	-4.6
19503	AT4G02980.1   Symbol: ABP1   auxin-binding protein 1 (ABP1), identical to Auxin-binding protein 1 precursor (ABP) (Swiss-Prot:P33487) (Arabidopsis thaliana)   chr4:1319656-1321477 REVERSE   Aliases: ABP, AT ERABP1, ENDOPLASMIC RETICULUM AUXIN BINDING PROTEIN 1, T4I9.14, T4I9_14	6.4	6.4	-0.0	-0.1	100.0%	-4.8
19504	AT4G00730.1   Symbol: ANL2   anthocyaninless2 (ANL2), nearly identical to Anthocyaninless2 (Arabidopsis thaliana) GI:5702094   chr4:299359-304486 REVERSE   Aliases: ANTHOCYANINLESS 2, F6N23.10, F6N23_10, HOMEODOMAIN PROTEIN AHDP	3.4	3.4	-0.0	-0.1	100.0%	-5.3
19505	AT1G43160.1   Symbol: RAP2.6	2.2	2.3	-0.0	-0.1	100.0%	-4.9
19506	AT3G60250.1   Symbol: CKB3   casein kinase II beta chain, putative (CKB3), similar to casein kinase II beta-3 chain (CK II) (Arabidopsis thaliana SWISS-PROT:O81275   chr3:22281317-22283088 REVERSE   Aliases: F27H5.40	7.0	7.0	0.0	0.1	100.0%	-5.0
19507	AT5G59100.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo)   chr5:23876120-23879355 REVERSE   Aliases: K18B18.7, K18B18_7	2.9	2.9	-0.0	-0.1	100.0%	-5.8
19508	AT1G16640.1   transcriptional factor B3 family protein, low similarity to reproductive meristem protein 1 (Arabidopsis thaliana) GI:13604227; contains Pfam profile PF02362: B3 DNA binding domain   chr1:5686596-5687693 FORWARD   Aliases: F19K19.7, F19K19_7	4.0	4.1	-0.0	-0.1	100.0%	-4.7
19509	AT3G49700.1   Symbol: ETO3   1-aminocyclopropane-1-carboxylate synthase, putative / ACC synthase, putative, similar to ACC synthases from Arabidopsis thaliana (GI:940370), Lycopersicon esculentum (GI:508609), Cucumis sativus (GI:3641649)	3.5	3.5	0.0	0.1	100.0%	-5.0
19510	AT4G00460.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr4:211085-213697 REVERSE   Aliases: A_IG005I10.1, A_IG005I10_1, F6N23.18, KINASE PARTNER PROTEIN LIKE, KPP LIKE	3.2	3.2	-0.0	-0.1	100.0%	-5.2
19511	AT1G29450.1   auxin-responsive protein, putative, similar to auxin-induced protein 6B (SP:P33083) (Glycine max)   chr1:10305937-10306485 REVERSE   Aliases: F15D2.4, F15D2_4	2.2	2.2	-0.0	-0.1	100.0%	-6.1
19512	AT2G25850.3   similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g32850.5); similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g32850.1); similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g32850.3); similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g32850.2); similar to nucleotidyltransferase family protein [Arabidopsis thaliana] (TAIR:At4g32850.6); similar to putative polynucleotide adenylyltransferase [Oryza sativa (indica cultivar-group)] (GB:AAW68018.1); similar to putative polynucleotide adenylyltransferase [Oryza sativa (indica cultivar-group)] (GB:AAW68015.1); similar to putative poly(A) polymerase [Oryza sativa (japonica cultivar-group)] (GB:XP_464757.1); contains InterPro domain Poly(A) polymerase, predicted RNA-binding domain (InterPro:IPR007010); contains InterPro domain Poly(A) polymerase, central region (InterPro:IPR007012); contains InterPro domain PAP/25A core domain (InterPro:IPR001201); contains InterPro domain DNA polymerase, beta-like region (InterPro:IPR002934)   chr2:11032588-11037705 REVERSE   Aliases: F17H15.12, F17H15_12	5.3	5.4	-0.1	-0.1	100.0%	-4.6
19513	AT4G25130.1   peptide methionine sulfoxide reductase, putative, strong similarity to SP:P54151 Peptide methionine sulfoxide reductase (EC 1.8.4.6) {Brassica napus}; contains Pfam profile PF01625: Peptide methionine sulfoxide reductase   chr4:12898603-12900074 REVERSE   Aliases: F24A6.2	9.9	9.9	-0.1	-0.1	100.0%	-4.6
19514	AT3G26420.1   Symbol: ARRZ 1A   Zinc finger-containing glycine-rich RNA-binding protein. Cold-inducible. Contributes to the enhancement of freezing tolerance.   chr3:9672754-9677242 FORWARD   Aliases: ARRZ 1A, F20C19.15	7.1	7.1	0.0	0.1	100.0%	-5.2
19515	AT3G26430.1   GDSL-motif lipase/hydrolase family protein, similar to early nodulin ENOD8 (Medicago sativa) GI:304037; contains InterPro Entry IPR001087 Lipolytic enzyme, G-D-S-L family   chr3:9672754-9677164 FORWARD   Aliases: F20C19.19	7.1	7.1	0.0	0.1	100.0%	-5.2
19516	AT2G18800.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endotransglycosylase TCH4 GI:886116 from (Arabidopsis thaliana)	2.9	2.8	0.0	0.1	100.0%	-4.7
19517	AT5G15700.1   DNA-directed RNA polymerase (RPOT2), identical to phage-type RNA polymerase rpoT2 (Arabidopsis thaliana) GI:11340683   chr5:5115303-5121843 REVERSE   Aliases: F14F8.80, F14F8_80	3.5	3.5	0.0	0.1	100.0%	-5.0
19518	AT2G02510.1   expressed protein   chr2:673304-674738 FORWARD   Aliases: T8K22.19, T8K22_19	9.7	9.7	0.0	0.1	100.0%	-5.3
19519	AT1G03150.1   GCN5-related N-acetyltransferase (GNAT) family protein, similar to SP:P07347 N-terminal acetyltransferase complex ARD1 subunit (Arrest-defective protein 1) {Saccharomyces cerevisiae}; contains Pfam profile PF00583: acetyltransferase, GNAT family   chr1:756414-758612 FORWARD   Aliases: F10O3.2, F10O3_2	5.2	5.3	-0.0	-0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19520	AT2G19340.2   membrane protein, putative, contains 3 transmembrane domains;   chr2:8382199-8383021 REVERSE   Aliases: F27F23.14, F27F23_14	4.2	4.1	0.0	0.1	100.0%	-5.4
19521	AT3G13770.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:4519654-4521540 FORWARD   Aliases: MMM17.3	2.9	2.9	0.0	0.1	100.0%	-5.4
19522	AT4G15290.1   Symbol: ATCSLB05   cellulose synthase family protein, similar to Zea mays cellulose synthase-5 (gi:9622882), -4 (gi:9622880)   chr4:8721490-8726669 REVERSE   Aliases: ATCSLB5, CSLB05, DL3690C, FCAALL.256	4.4	4.5	-0.0	-0.1	100.0%	-4.4
19523	AT1G75770.1   expressed protein   chr1:28453651-28454769 FORWARD   Aliases: F10A5.4, F10A5_4	2.8	2.9	-0.0	-0.1	100.0%	-5.5
19524	AT4G13570.1   histone H2A, putative, similar to histone H2A.F/Z from Arabidopsis thaliana GI:2407800, histone H2A.F/Z Strongylocentrotus purpuratus SP:P08991, histone H2A variant Drosophila melanogaster SP:P08985; contains Pfam profile PF00125 Core histone H2A/H2B/H3/H4	2.8	2.8	-0.0	-0.1	100.0%	-5.2
19525	AT3G18660.2   similar to glycogenin glucosyltransferase (glycogenin)-related [Arabidopsis thaliana] (TAIR:At1g77130.1); similar to P0018C10.26 [Oryza sativa (japonica cultivar-group)] (GB:NP_915047.1); similar to glycogenin-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81673.1); similar to secondary cell wall-related glycosyltransferase family 8 [Populus tremula x Populus tremuloides] (GB:AAX33316.1); similar to putative glycogenin [Oryza sativa (japonica cultivar-group)] (GB:XP_475247.1); contains InterPro domain Glycosyl transferase, family 8 (InterPro:IPR002495)   chr3:6419037-6421965 REVERSE   Aliases: MVE11.2	2.3	2.3	-0.0	-0.1	100.0%	-4.9
19526	AT5G02310.1   Symbol: CER3   eceriferum3 protein, putative, similar to eceriferum3 GI:1669655 from (Arabidopsis thaliana)   chr5:474277-482781 FORWARD   Aliases: AT5G02300, ECERIFERUM 3, T1E22.70, T1E22_70	5.1	5.1	-0.0	-0.1	100.0%	-5.4
19527	AT3G25010.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains (23 copies) Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596   chr3:9110110-9112755 REVERSE   Aliases: K3G3.4	3.1	3.1	-0.0	-0.1	100.0%	-5.2
19528	AT4G38020.1   tRNA/rRNA methyltransferase (SpoU) family protein, similar to SP:P18644 rRNA (adenosine-2'-O-)-methyltransferase (EC 2.1.1.66) {Streptomyces cyaneus}; contains Pfam profile PF00588: SpoU rRNA Methylase (RNA methyltransferase, TrmH) family   chr4:17861520-17863054 FORWARD   Aliases: F20D10.140, F20D10_140	6.5	6.6	-0.0	-0.1	100.0%	-4.4
19529	AT5G44230.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:17831563-17833536 FORWARD   Aliases: MLN1.16, MLN1_16	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19530	AT1G71170.1   6-phosphogluconate dehydrogenase NAD-binding domain-containing protein, contains Pfam profile: PF03446 NAD binding domain of 6-phosphogluconate   chr1:26834331-26835761 FORWARD   Aliases: F23N20.16, F23N20_16	7.8	7.7	0.0	0.1	100.0%	-5.3
19531	AT5G56860.1   zinc finger (GATA type) family protein, similar to unknown protein (pir :T04270)	2.8	2.8	-0.0	-0.1	100.0%	-5.4
19532	AT2G33270.1   thioredoxin family protein, contains Pfam profile: PF00085 Thioredoxin   chr2:14110758-14112281 FORWARD   Aliases: F4P9.4, F4P9_4	2.9	2.9	0.0	0.1	100.0%	-5.1
19533	AT4G14950.3   expressed protein   chr4:8545168-8548050 FORWARD   Aliases: DL3515W, FCAALL.221	4.3	4.4	-0.0	-0.1	100.0%	-4.8
19534	AT4G25890.1   60S acidic ribosomal protein P3 (RPP3A), acidic ribosomal protein P3a - maize, PIR2:T02037   chr4:13159500-13160457 REVERSE   Aliases: F14M19.170, F14M19_170	8.2	8.2	-0.0	-0.1	100.0%	-4.7
19535	AT4G38100.1   expressed protein   chr4:17886864-17888198 REVERSE   Aliases: F20D10.220, F20D10_220	6.8	6.8	-0.0	-0.1	100.0%	-4.6
19536	AT1G01200.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GB:D12541 GI:303736 from (Pisum sativum)   chr1:86516-88213 REVERSE   Aliases: F6F3.1, F6F3_1	3.3	3.2	0.0	0.1	100.0%	-5.3
19537	AT4G32660.3   Symbol: AME3   similar to protein kinase (AFC1) (AME2) [Arabidopsis thaliana] (TAIR:At3g53570.3); similar to protein kinase (AFC1) (AME2) [Arabidopsis thaliana] (TAIR:At3g53570.2); similar to protein kinase (AFC1) (AME2) [Arabidopsis thaliana] (TAIR:At3g53570.1); similar to putative protein kinase PK12 [Oryza sativa (japonica cultivar-group)] (GB:BAD52695.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr4:15756170-15759319 FORWARD   Aliases: F4D11.140, F4D11_140	5.9	6.0	-0.0	-0.1	100.0%	-4.9
19538	AT3G62630.1   expressed protein   chr3:23174723-23176171 REVERSE   Aliases: F26K9.60	3.5	3.4	0.0	0.1	100.0%	-5.1
19539	AT3G42440.1   hypothetical protein, several hypothetical proteins - Arabidopsis thaliana   chr3:14588317-14588810 FORWARD   Aliases: T32A11.10	2.6	2.6	-0.0	-0.1	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19540	AT3G18200.2   similar to nodulin MtN21 family protein [Arabidopsis thaliana] (TAIR:At1g75500.1); similar to putative nodulin MtN21 [Oryza sativa (japonica cultivar-group)] (GB:XP_463858.1); contains InterPro domain Protein of unknown function DUF6 (InterPro:IPR000620)   chr3:6234312-6236097 REVERSE   Aliases: MRC8.19	3.8	3.8	0.0	0.1	100.0%	-4.6
19541	AT3G60350.1   armadillo/beta-catenin repeat family protein / F-box family protein, contains Pfam profiles PF00514: Armadillo/beta-catenin-like repeat, PF00646: F-box domain; similar to F-box protein FBL2 (GI:6010699) (Rattus norvegicus)   chr3:22317084-22322161 REVERSE   Aliases: T8B10.10	3.4	3.5	-0.0	-0.1	100.0%	-5.4
19542	AT2G45040.1   matrix metalloproteinase, nearly identical to metalloproteinase (Arabidopsis thaliana) GI:3128477; contains InterPro accession IPR001818: Matrixin   chr2:18584725-18585989 FORWARD   Aliases: T14P1.15, T14P1.33, T14P1_33	3.8	3.8	-0.0	-0.1	100.0%	-4.7
19543	AT1G29200.1   expressed protein, contains Pfam PF03138: Plant protein family. The function of this family of plant proteins is unknown;   chr1:10206217-10210474 FORWARD   Aliases: F28N24.11, F28N24_11	2.8	2.8	-0.0	-0.1	100.0%	-5.2
19544	AT3G42910.1   expressed protein, ; expression supported by MPSS   chr3:14985091-14988749 REVERSE   Aliases: F18P9.70	2.5	2.5	-0.0	-0.1	100.0%	-5.6
19545	AT4G24830.1   arginosuccinate synthase family, contains Pfam profile: PF00764 arginosuccinate synthase	12.0	12.1	-0.1	-0.1	100.0%	-4.6
19546	AT5G66030.2   Golgi-localized GRIP domain-containing protein, contains Pfam profile PF01465: GRIP domain; supporting cDNA gi:20303028:gb:AF499634.1:   chr5:26422147-26427114 REVERSE   Aliases: K2A18.10, K2A18_10	8.5	8.5	0.0	0.1	100.0%	-5.2
19547	AT2G44250.1   expressed protein, contains Pfam profile PF03080: Arabidopsis proteins of unknown function   chr2:18300533-18302612 FORWARD   Aliases: F4I1.6	2.1	2.1	0.0	0.1	100.0%	-6.0
19548	AT1G10540.1   xanthine/uracil permease family protein, contains Pfam profile: PF00860 permease family   chr1:3474941-3477775 REVERSE   Aliases: T10O24.16, T10O24_16	3.1	3.1	0.0	0.1	100.0%	-5.2
19549	AT2G26300.1   Symbol: GPA1   guanine nucleotide binding protein (G-protein) alpha-1 subunit / GP-alpha-1 (GPA1), identical to SP:P18064 Guanine nucleotide-binding protein alpha-1 subunit (GP-alpha-1) {Arabidopsis thaliana}   chr2:11204373-11208070 FORWARD   Aliases: G PROTEIN ALPHA SUBUNIT, G PROTEIN ALPHA SUBUNIT 1, GP ALPHA 1, T1D16.6, T1D16_6	8.8	8.8	0.0	0.1	100.0%	-4.7
19550	AT1G29490.1   auxin-responsive family protein, similar to auxin-induced protein X10A (SP:P33080) (Glycine max)	2.4	2.4	-0.0	-0.1	100.0%	-6.0
19551	AT3G60020.1   Symbol: ASK5   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At5), putative, E3 ubiquitin ligase; similar to Skp1 GI:4959710 from (Medicago sativa)   chr3:22175821-22176282 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 5, ASK5, T2O9.2	2.5	2.4	0.0	0.1	100.0%	-6.0
19552	AT3G56060.1   glucose-methanol-choline (GMC) oxidoreductase family protein, similar to mandelonitrile lyase from Prunus serotina (SP:P52706, SP:P52707); contains Pfam profile PF00732 GMC oxidoreductase   chr3:20814112-20816992 REVERSE   Aliases: F18O21.20	2.4	2.4	0.0	0.1	100.0%	-5.8
19553	AT5G11380.1   1-deoxy-D-xylulose 5-phosphate synthase, putative / 1-deoxyxylulose-5-phosphate synthase, putative / DXP-synthase, putative, similar to 1-deoxy-D-xylulose 5-phosphate synthase 1 (Medicago truncatula) GI:21322713; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain   chr5:3629999-3633442 FORWARD   Aliases: F2I11.270, F2I11_270	4.2	4.2	0.0	0.1	100.0%	-4.9
19554	AT4G09940.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to AIG1 protein SP:P54120 (Arabidopsis thaliana); contains Pfam PF04548: AIG1 family;   chr4:6231783-6233394 FORWARD   Aliases: T5L19.70, T5L19_70	2.7	2.7	0.0	0.1	100.0%	-5.7
19555	AT1G12200.1   flavin-containing monooxygenase family protein / FMO family protein, low similarity to FMO2 from Homo sapiens (SP:Q99518); contains Pfam profile: PF00743 Flavin-binding monooxygenase-like   chr1:4137531-4140026 FORWARD   Aliases: T28K15.7, T28K15_7	9.9	9.8	0.0	0.1	100.0%	-5.0
19556	AT3G43860.1   glycosyl hydrolase family 9 protein, similar to cellulase GI:575404 from (Sambucus nigra).   chr3:15717981-15720776 FORWARD   Aliases: T28A8.150	2.1	2.1	-0.0	-0.1	100.0%	-5.6
19557	AT4G22850.1   expressed protein   chr4:11994054-11996240 FORWARD   Aliases: F7H19.30	4.2	4.2	0.0	0.1	100.0%	-5.3
19558	AT3G26670.3   expressed protein   chr3:9799223-9802280 REVERSE   Aliases: MLJ15.6	5.1	5.1	-0.0	-0.1	100.0%	-4.8
19559	AT5G46000.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	2.7	2.7	-0.0	-0.1	100.0%	-5.6
19560	AT5G66660.1   hypothetical protein   chr5:26626534-26627730 REVERSE   Aliases: MSN2.4, MSN2_4	2.8	2.8	0.0	0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19561	AT4G00590.1   asparaginase 2 family protein, very low similarity to glycosylasparaginase (SP:P20933) from Homo sapiens; contains Pfam profile PF01112: Asparaginase 2   chr4:252811-255042 FORWARD   Aliases: F6N23.5, F6N23_5	5.4	5.4	-0.0	-0.1	100.0%	-5.3
19562	AT5G48110.1   terpene synthase/cyclase family protein   chr5:19518383-19521583 REVERSE   Aliases: MDN11.20, MDN11_20	2.8	2.8	-0.0	-0.1	100.0%	-4.8
19563	AT3G56410.2   expressed protein   chr3:20927151-20932185 REVERSE   Aliases: T5P19.60	3.5	3.5	-0.0	-0.1	100.0%	-4.8
19564	AT1G74770.1   expressed protein   chr1:28094772-28098495 REVERSE   Aliases: F25A4.26, F25A4_26	3.0	3.0	-0.1	-0.1	100.0%	-4.6
19565	AT4G03580.1   expressed protein   chr4:1596983-1599089 FORWARD   Aliases: T5L23.7, T5L23_7	2.5	2.5	-0.0	-0.1	100.0%	-6.0
19566	AT1G78560.1   bile acid:sodium symporter family protein, low similarity to SP:Q12908 Ileal sodium/bile acid cotransporter {Homo sapiens}; contains Pfam profile PF01758: Sodium Bile acid symporter family   chr1:29551498-29553717 REVERSE   Aliases: T30F21.11, T30F21_11	6.1	6.1	0.0	0.1	100.0%	-4.8
19567	AT1G37080.1   expressed protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr1:14113899-14114696 REVERSE   Aliases: F28L22.13, F28L22_13	2.8	2.8	-0.0	-0.1	100.0%	-5.7
19568	AT2G17170.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; weak similarity to Protein kinase APK1A (EC 2.7.1.-) (Swiss-Prot:Q06548) (Arabidopsis thaliana)   chr2:7481818-7483520 FORWARD   Aliases: T23A1.3, T23A1_3	2.5	2.5	0.0	0.1	100.0%	-5.7
19569	AT4G27680.1   MSP1 protein, putative / intramitochondrial sorting protein, putative, similar to Swiss-Prot:P28737 MSP1 protein (TAT-binding homolog 4) (Saccharomyces cerevisiae); contains Pfam domain, PF00004: ATPase, AAA family   chr4:13821112-13823345 FORWARD   Aliases: T29A15.170, T29A15_170	7.7	7.8	-0.0	-0.1	100.0%	-4.7
19570	AT1G17490.1   expressed protein   chr1:6008582-6009409 FORWARD   Aliases: F28G4.23	8.7	8.7	-0.0	-0.1	100.0%	-5.1
19571	AT3G06790.2   plastid developmental protein DAG, putative, similar to DAG protein, chloroplast precursor (Garden snapdragon) SWISS-PROT:Q38732	8.8	8.9	-0.0	-0.1	100.0%	-4.6
19572	AT1G69220.2   Symbol: SIK1   serine/threonine protein kinase, putative, identical to serine/threonine kinase (Arabidopsis thaliana) gi:2352084:gb:AAB68776   chr1:26023851-26029834 REVERSE   Aliases: F4N2.24, SERINE/THREONINE KINASE SIK1	6.3	6.3	-0.0	-0.1	100.0%	-4.9
19573	AT1G18220.1   Symbol: ATPUP9	2.7	2.7	0.0	0.1	100.0%	-5.4
19574	AT1G09940.1   Symbol: HEMA2   glutamyl-tRNA reductase 2 / GluTR (HEMA2), identical to glutamyl-tRNA reductase 2, chloroplast (SP:P49294)   chr1:3236997-3239556 REVERSE   Aliases: F21M12.33, F21M12_33	4.7	4.7	-0.0	-0.1	100.0%	-4.7
19575	AT1G77730.1   pleckstrin homology (PH) domain-containing protein, similar to SP:P16258 Oxysterol-binding protein 1 {Oryctolagus cuniculus}; contains Pfam profile PF00169: PH domain   chr1:29219339-29220458 FORWARD   Aliases: T32E8.6, T32E8_6	2.5	2.5	-0.0	-0.1	100.0%	-5.8
19576	AT5G25440.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:8854842-8856761 REVERSE   Aliases: F18G18.180, F18G18_180	3.3	3.3	-0.0	-0.1	100.0%	-5.0
19577	AT3G27800.1   expressed protein   chr3:10303165-10303438 REVERSE   Aliases: MGF10.20	2.7	2.7	0.0	0.1	100.0%	-5.6
19578	AT5G54250.2   Symbol: ATCNGC4   cyclic nucleotide-regulated ion channel / cyclic nucleotide-gated channel (CNGC4), identical to cyclic nucleotide and calmodulin-regulated ion channel (cngc4) GI:4581203 from (Arabidopsis thaliana)	2.1	2.0	0.0	0.1	100.0%	-5.8
19579	AT1G67870.1   glycine-rich protein, contains non-consensus GG donor splice site at exon2; modeled to est match.   chr1:25453030-25454675 REVERSE   Aliases: T23K23.28, T23K23_28	2.7	2.7	0.0	0.1	100.0%	-4.2
19580	AT1G61690.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g28770.1); similar to FYVE zinc finger containing protein [Oryza sativa (japonica cultivar-group)] (GB:AAT85295.1); contains InterPro domain TPR repeat (InterPro:IPR001440); contains InterPro domain Zn-finger, FYVE type (InterPro:IPR000306)   chr1:22786366-22790447 REVERSE   Aliases: T13M11.5, T13M11_5	5.2	5.2	-0.0	-0.1	100.0%	-5.0
19581	AT2G14520.1   CBS domain-containing protein, contains Pfam profiles PF00571: CBS domain, PF01595: Domain of unknown function   chr2:6189275-6191730 REVERSE   Aliases: T13P21.10, T13P21_10	5.2	5.2	-0.0	-0.1	100.0%	-4.8
19582	AT1G76670.1   transporter-related, low similarity to glucose-6-phosphate/phosphate-translocator precursor (Solanum tuberosum) GI:2997593, GDP-Mannose transporter (Arabidopsis thaliana) GI:15487237; contains Pfam profile PF00892: Integral membrane protein	7.3	7.4	-0.0	-0.1	100.0%	-4.9
19583	AT2G22710.1   myb family protein   chr2:9658799-9661612 FORWARD   Aliases: T9I22.15, T9I22_15	3.9	3.9	0.0	0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19584	AT2G26150.1   Symbol: ATHSFA2   heat shock transcription factor family protein, contains Pfam profile: PF00447 HSF-type DNA-binding domain   chr2:11142760-11144474 FORWARD   Aliases: HSFA2, T19L18.4, T19L18_4	3.9	3.9	0.0	0.1	100.0%	-5.2
19585	AT3G11380.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:3564085-3565785 FORWARD   Aliases: F11B9.24	2.2	2.2	0.0	0.1	100.0%	-6.2
19586	AT5G44200.1   Symbol: CBP20   nuclear cap-binding protein, putative, similar to SP:P52298 20 kDa nuclear cap binding protein (CBP20) (NCBP interacting protein 1) {Homo sapiens}; non-consensus AT donor splice site at exon 4, AC acceptor splice site at exon 5; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:17819166-17821154 REVERSE   Aliases: ATCBP20, CAP BINDING PROTEIN 20, MLN1.12, MLN1_12	9.3	9.2	0.0	0.1	100.0%	-4.8
19587	AT4G23400.1   Symbol: PIP1;5/PIP1D   major intrinsic family protein / MIP family protein, contains Pfam profile: MIP PF00230   chr4:12220753-12222380 FORWARD   Aliases: F16G20.100, F16G20_100, PCR55, PIP1;5, PIP1D	3.4	3.4	0.0	0.1	100.0%	-4.7
19588	AT1G02890.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family; similar to mitochondrial sorting protein 1 (MSP1) (TAT-binding homolog 4) (Swiss-Prot:P28737) (Saccharomyces cerevisiae)   chr1:645092-651906 REVERSE   Aliases: F22D16.11, F22D16_11	8.3	8.3	-0.0	-0.1	100.0%	-4.9
19589	AT1G09155.1   Symbol: ATPP2 B15   SKP1 interacting partner 3-related, low similarity to SKP1 interacting partner 3 (Arabidopsis thaliana) GI:10716951	2.7	2.7	-0.1	-0.1	100.0%	-4.3
19590	AT3G55450.1   protein kinase, putative, similar to protein kinase APK1B (Arabidopsis thaliana) SWISS-PROT:P46573   chr3:20568986-20571189 FORWARD   Aliases: T22E16.110	7.4	7.4	0.0	0.1	100.0%	-4.9
19591	AT3G44540.2   similar to acyl CoA reductase, putative / male-sterility protein, putative [Arabidopsis thaliana] (TAIR:At5g22500.1); similar to putative fatty acyl coA reductase [Oryza sativa (japonica cultivar-group)] (GB:XP_481392.1); similar to putative fatty acyl coA reductase [Oryza sativa (japonica cultivar-group)] (GB:BAD31294.1); contains InterPro domain Male sterility protein (InterPro:IPR004262)   chr3:16135008-16138869 FORWARD   Aliases: F14L2.90	2.8	2.8	0.0	0.1	100.0%	-4.7
19592	AT5G20420.1   Symbol: CHR42   SNF2 domain-containing protein / helicase domain-containing protein, low similarity to SP:Q9U7E0 Transcriptional regulator ATRX homolog {Caenorhabditis elegans}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr5:6899017-6903268 REVERSE   Aliases: CHR42, F7C8.10, F7C8_10	3.6	3.6	-0.0	-0.1	100.0%	-5.6
19593	AT1G04640.2   Symbol: LIP2   similar to lipoyltransferase (LIP2p) [Arabidopsis thaliana] (TAIR:At4g31050.1); similar to COG0321: Lipoate-protein ligase B [Rubrobacter xylanophilus DSM 9941] (GB:ZP_00199769.1); contains InterPro domain Biotin/lipoate A/B protein ligase domain (InterPro:IPR004143); contains InterPro domain Lipoate-protein ligase B (InterPro:IPR000544)   chr1:1292110-1293247 FORWARD   Aliases: LIPOYLTRANSFERASE 2	4.9	4.9	0.0	0.1	100.0%	-5.1
19594	AT1G76370.1   protein kinase, putative, similar to protein kinase APK1B (Arabidopsis thaliana) SWISS-PROT:P46573; contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr1:28653343-28655378 REVERSE   Aliases: F15M4.13, F15M4_13	2.8	2.8	-0.0	-0.1	100.0%	-5.3
19595	AT1G51920.1   expressed protein   chr1:19297898-19298248 FORWARD   Aliases: T14L22.80, T14L22_80	3.1	3.1	0.0	0.1	100.0%	-4.9
19596	AT3G02280.1   flavodoxin family protein, low similarity to SP:Q05001 NADPH-cytochrome P450 reductase (EC 1.6.2.4) {Catharanthus roseus}, similar to NADPH-dependent FMN and FAD containing oxidoreductase (Homo sapiens) GI:6694369; contains Pfam profiles PF00258: flavodoxin, PF00667: FAD binding domain, PF00175: Oxidoreductase NAD-binding domain   chr3:453430-457848 FORWARD   Aliases: F14P3.7, F14P3_7	4.2	4.2	-0.0	-0.1	100.0%	-5.1
19597	AT1G30740.1   FAD-binding domain-containing protein, similar to SP:P30986 reticuline oxidase precursor (Berberine-bridge-forming enzyme) (BBE) (Tetrahydroprotoberberine synthase) (Eschscholzia californica); contains PF01565 FAD binding domain   chr1:10903011-10904612 FORWARD   Aliases: T5I8.19, T5I8_19	3.0	3.0	-0.0	-0.1	100.0%	-5.4
19598	AT5G51880.1   expressed protein   chr5:21106659-21108167 FORWARD   Aliases: MJM18.3, MJM18_3	8.1	8.0	0.0	0.1	100.0%	-5.1
19599	AT1G73330.1   Symbol: ATDR4   protease inhibitor, putative (DR4), identical to Dr4 GI:469114 from (Arabidopsis thaliana); contains Pfam profile PF00197: Trypsin and protease inhibitor   chr1:27572379-27573378 REVERSE   Aliases: T9L24.45, T9L24_45	4.9	4.9	-0.0	-0.1	100.0%	-4.8
19600	AT2G38290.2   Symbol: ATAMT2	4.4	4.5	-0.0	-0.1	100.0%	-4.9
19601	AT4G24210.1   Symbol: SLY1   F-box family protein / SLEEPY1 protein, contains Pfam PF00646: F-box domain; similar to F-box protein Fbx8 (GI:6164735) (Homo sapiens); identified as SLEEPY1 in McGinnis, et al, Plant Cell (2003) 15: 1120-1130.   chr4:12563563-12564492 FORWARD   Aliases: SLEEPY1, T22A6.40, T22A6_40	5.0	5.0	0.0	0.1	100.0%	-4.6
19602	AT1G62210.1   expressed protein   chr1:22989667-22990526 FORWARD   Aliases: F19K23.14, F19K23_14	3.3	3.3	0.0	0.1	100.0%	-4.8
19603	AT4G28040.4   similar to nodulin MtN21 family protein [Arabidopsis thaliana] (TAIR:At4g30420.1); similar to putative MtN21 [Oryza sativa (japonica cultivar-group)] (GB:BAD33609.1); contains InterPro domain Protein of unknown function DUF6 (InterPro:IPR000620)   chr4:13940352-13942829 FORWARD   Aliases: T13J8.150, T13J8_150	3.5	3.5	-0.0	-0.1	100.0%	-4.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19604	AT5G66820.1   expressed protein   chr5:26706285-26708340 FORWARD   Aliases: MUD21.8, MUD21_8	6.5	6.5	0.0	0.1	100.0%	-4.5
19605	AT4G22700.1   LOB domain family protein / lateral organ boundaries domain family protein (LBD32), identical to SP:O49651 Putative LOB domain protein 32 {Arabidopsis thaliana}; similar to lateral organ boundaries (LOB) domain-containing proteins from Arabidopsis thaliana	2.6	2.6	-0.0	-0.1	100.0%	-5.3
19606	AT4G00520.1   acyl-CoA thioesterase family protein, contains Pfam profile: PF02551 acyl-CoA thioesterase   chr4:229163-231699 FORWARD   Aliases: F6N23.3, F6N23_3	3.1	3.1	0.0	0.1	100.0%	-5.2
19607	AT5G14990.1   expressed protein   chr5:4850767-4853006 FORWARD   Aliases: F2G14.110, F2G14_110	2.6	2.6	0.0	0.1	100.0%	-5.7
19608	AT1G02050.1   chalcone and stilbene synthase family protein, Similar to rice chalcone synthase homolog, gp:U90341:2507617 and anther specific protein, gp:Y14507:2326772   chr1:359117-360441 REVERSE   Aliases: T7I23.4, T7I23_4	5.2	5.2	-0.0	-0.1	100.0%	-4.6
19609	AT1G01690.1   expressed protein   chr1:249141-259171 FORWARD   Aliases: T1N6.6, T1N6_6	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19610	AT3G01820.1   adenylate kinase family protein, contains Pfam profile: PF00406 adenylate kinase	5.3	5.3	0.0	0.1	100.0%	-4.6
19611	AT3G16970.1   self-incompatibility protein-related, similar to S1 self-incompatibility protein GB:CAA52380 (Papaver rhoeas) (Proc. Natl. Acad. Sci. U.S.A. 91 (6), 2265-2269 (1994))   chr3:5793674-5794096 REVERSE   Aliases: K14A17.13	3.6	3.6	-0.0	-0.1	100.0%	-5.3
19612	AT5G28140.1   hypothetical protein   chr5:10115253-10116616 REVERSE   Aliases: T24G3.70, T24G3_70	2.7	2.7	-0.0	-0.1	100.0%	-5.4
19613	AT1G08960.1   Symbol: CAX11   similar to cation exchanger, putative (CAX7) [Arabidopsis thaliana] (TAIR:At5g17860.1); similar to Putative potassium-dependent sodium-calcium exchanger-like protein [Oryza sativa (japonica cultivar-group)] (GB:XP_470536.1); contains InterPro domain Sodium/calcium exchanger membrane region (InterPro:IPR004837)	4.6	4.6	0.0	0.1	100.0%	-4.9
19614	AT3G57250.1   emsy N terminus domain-containing protein / ENT domain-containing protein, contains Pfam profile PF03735: ENT domain   chr3:21197698-21198230 FORWARD   Aliases: F28O9.100	2.4	2.4	0.0	0.1	100.0%	-5.6
19615	AT1G67440.1   Symbol: EMB1688   expressed protein, contains Pfam domain PF03193: Protein of unknown function, DUF258   chr1:25267467-25269382 REVERSE   Aliases: EMB1688, EMBRYO DEFECTIVE 1688, T1F15.10, T1F15_10	6.5	6.5	0.0	0.1	100.0%	-4.6
19616	AT1G34510.1   peroxidase, putative, similar to peroxidase ATP13a GB:CAA67312 from (Arabidopsis thaliana)   chr1:12615711-12617010 REVERSE   Aliases: F12K21.18, F12K21_18	2.5	2.5	0.1	0.1	100.0%	-4.3
19617	AT4G00700.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr4:286051-289514 FORWARD   Aliases: F6N23.8, F6N23_8	3.3	3.3	0.0	0.1	100.0%	-4.5
19618	AT2G28580.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g44930.1); similar to OSJNBa0070011.12 [Oryza sativa (japonica cultivar-group)] (GB:XP_474109.1); contains InterPro domain Plant protein of unknown function (InterPro:IPR004158)   chr2:12251936-12255527 FORWARD   Aliases: T8O18.13, T8O18_13	3.2	3.2	-0.0	-0.1	100.0%	-5.2
19619	AT4G23040.1   UBX domain-containing protein, similar to Ara4-interacting protein (Arabidopsis thaliana) GI:13160609; contains Pfam profile PF00789: UBX domain	5.1	5.1	0.0	0.1	100.0%	-4.6
19620	AT1G62030.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr1:22927915-22930263 REVERSE   Aliases: F8K4.22, F8K4_22	3.3	3.3	-0.0	-0.1	100.0%	-5.3
19621	AT2G04070.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr2:1354015-1355787 REVERSE   Aliases: F3L12.10, F3L12_10	3.5	3.5	0.0	0.1	100.0%	-5.0
19622	AT5G26570.1   Symbol: PWD   similar to starch excess protein (SEX1) [Arabidopsis thaliana] (TAIR:At1g10760.1); similar to starch associated protein R1 [Solanum tuberosum] (GB:AAK11735.1); contains InterPro domain Glycoside hydrolase, starch-binding domain (InterPro:IPR002044)   chr5:9261583-9267732 FORWARD   Aliases: ATGWD3, F9D12.1, F9D12_1, OK1, PHOSPHOGLUCAN WATER DIKINASE	7.4	7.4	0.0	0.1	100.0%	-4.7
19623	AT3G55130.1   ABC transporter family protein, breast cancer resistance protein 1 BCRP1, Mus musculus, EMBL:NP_036050   chr3:20444855-20447367 REVERSE   Aliases: T26I12.10	3.8	3.8	-0.0	-0.1	100.0%	-5.3
19624	AT1G80680.1   Symbol: PRE   nucleoporin family protein, contains Pfam profile: PF04096 nucleoporin autopeptidase   chr1:30328900-30333650 FORWARD   Aliases: F23A5.3, F23A5_3, MOS3, PRECOCIOUS, PRECOZ	6.2	6.2	-0.0	-0.1	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19625	AT1G58110.2   similar to bZIP family transcription factor [Arabidopsis thaliana] (TAIR:At1g35490.1); similar to putative transcription activator RF2a [Oryza sativa (japonica cultivar-group)] (GB:BAD87301.1); contains InterPro domain Basic-leucine zipper (bZIP) transcription factor (InterPro:IPR004827)	3.4	3.5	-0.0	-0.1	100.0%	-4.8
19626	AT5G14580.1   polyribonucleotide nucleotidyltransferase, putative, similar to Swiss-Prot:P05055 polyribonucleotide nucleotidyltransferase (EC 2.7.7.8) (Polynucleotide phosphorylase) (PNPase) (Escherichia coli)   chr5:4697243-4703069 REVERSE   Aliases: T15N1.70, T15N1_70	3.0	2.9	0.0	0.1	100.0%	-5.5
19627	AT3G31915.1   expressed protein, contains similarity to hypothetical proteins   chr3:12912330-12914770 FORWARD   Aliases: T1O13.15	2.8	2.8	0.0	0.1	100.0%	-5.6
19628	AT3G01590.2   aldose 1-epimerase family protein, similar to apospory-associated protein C; APOC (Chlamydomonas reinhardtii) GI:6970044 Pfam profile PF01263: Aldose 1-epimerase   chr3:226073-228630 FORWARD   Aliases: F4P13.13, F4P13_13	5.7	5.7	-0.0	-0.1	100.0%	-5.2
19629	AT2G03410.1   Mo25 family protein, similar to MO25 protein (early mouse development protein family) (Mouse) SWISS-PROT:Q06138   chr2:1033904-1034950 FORWARD   Aliases: T4M8.16, T4M8_16	2.9	2.9	0.0	0.1	100.0%	-5.6
19630	AT5G49780.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:20245813-20250321 FORWARD   Aliases: K2I5.15, K2I5_15	3.5	3.5	-0.0	-0.1	100.0%	-4.9
19631	AT5G20060.3   similar to phospholipase/carboxylesterase family protein [Arabidopsis thaliana] (TAIR:At1g52700.1); similar to biostress-resistance-related protein [Triticum aestivum] (GB:AAM29178.1); contains InterPro domain Phospholipase/Carboxylesterase (InterPro:IPR003140)   chr5:6776277-6779616 FORWARD   Aliases: F28I16.210, F28I16_210	9.0	9.0	-0.0	-0.1	100.0%	-4.8
19632	AT5G09490.1   40S ribosomal protein S15 (RPS15B), ribosomal protein S15 - Arabidopsis thaliana, EMBL:Z23161   chr5:2952219-2953246 REVERSE   Aliases: T5E8.290, T5E8_290	2.9	2.9	0.0	0.1	100.0%	-5.3
19633	ATCG00530.1   Symbol: YCF10   hypothetical protein   chrC:60741-61430 FORWARD   Aliases: YCF10	5.4	5.3	0.1	0.1	100.0%	-4.7
19634	AT3G31910.1   expressed protein   chr3:12910356-12912093 REVERSE   Aliases: T1O13.14	3.0	3.0	-0.0	-0.1	100.0%	-5.5
19635	ATCG00180.1   Symbol: RPOC1   RNA polymerase beta' subunit-1   chrC:20251-23084 REVERSE   Aliases: RPOC1	7.5	7.6	-0.1	-0.1	100.0%	-4.6
19636	AT4G16515.1   expressed protein   chr4:9305278-9305786 REVERSE   Aliases: None	4.1	4.1	-0.0	-0.1	100.0%	-5.0
19637	AT3G05920.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain   chr3:1768796-1769592 REVERSE   Aliases: F2O10.12, F2O10_12	2.9	2.9	-0.1	-0.1	100.0%	-4.5
19638	AT4G33800.1   expressed protein   chr4:16210017-16211414 REVERSE   Aliases: T16L1.290, T16L1_290	2.6	2.6	-0.0	-0.1	100.0%	-5.7
19639	AT3G10550.1   expressed protein   chr3:3292904-3296874 REVERSE   Aliases: F13M14.17	5.6	5.6	0.0	0.1	100.0%	-5.1
19640	AT5G42580.1   Symbol: CYP705A12   cytochrome P450 family protein, similar to Cytochrome P450 93A1 (SP:Q42798)	3.0	3.0	-0.0	-0.1	100.0%	-4.9
19641	AT2G43130.1   Symbol: ARA4   Ras-related protein (ARA-4) / small GTP-binding protein, putative, identical to SP:P28187 Ras-related protein ARA-4 {Arabidopsis thaliana}   chr2:17936731-17937998 REVERSE   Aliases: ARA 4, F14B2.27, F14B2.7, F14B2_27	3.7	3.7	0.0	0.1	100.0%	-5.1
19642	AT5G59810.1   subtilase family protein, subtilisin-like protease AIR3, Arabidopsis thaliana, EMBL:AF098632   chr5:24114041-24117783 REVERSE   Aliases: MMN10.6, MMN10_6	2.8	2.8	-0.0	-0.1	100.0%	-5.4
19643	AT4G19420.2   pectinacetyltransferase family protein, contains Pfam profile: PF03283 pectinacetyltransferase	3.6	3.6	0.0	0.1	100.0%	-5.1
19644	AT1G18380.1   expressed protein   chr1:6325869-6326621 FORWARD   Aliases: F15H18.27, F15H18_27	3.1	3.1	0.0	0.1	100.0%	-5.1
19645	AT1G73080.1   leucine-rich repeat transmembrane protein kinase, putative, similar to receptor protein kinase GI:1389566 from (Arabidopsis thaliana)   chr1:27488174-27491862 FORWARD   Aliases: F3N23.28, F3N23_28	6.1	6.2	-0.0	-0.1	100.0%	-5.2
19646	AT3G19850.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr3:6898187-6901248 REVERSE   Aliases: MPN9.9	2.2	2.2	0.0	0.1	100.0%	-6.0
19647	AT1G27240.1   paired amphipathic helix repeat-containing protein, low similarity to transcription co-repressor Sin3 (Xenopus laevis) GI:4960210; contains Pfam profile PF02671: Paired amphipathic helix repeat   chr1:9466224-9467063 FORWARD   Aliases: F17L21.3	3.8	3.8	-0.0	-0.1	100.0%	-5.1
19648	AT5G55780.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.8	0.0	0.1	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19649	AT2G38550.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136)   chr2:16139092-16141493 FORWARD   Aliases: T6A23.25, T6A23_25	9.5	9.4	0.0	0.1	100.0%	-4.6
19650	AT1G70880.1   Bet v I allergen family protein, similar to Csf-2 (Cucumis sativus)(GI:5762258)(J Am Soc Hortic Sci 124, 136-139 (1999)) ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:26726543-26727440 REVERSE   Aliases: F15H11.28, F15H11_28	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19651	AT1G61940.1   F-box family protein / tubby family protein, similar to putative Tub family protein GI:4309738 from (Arabidopsis thaliana)   chr1:22901064-22902240 REVERSE   Aliases: F8K4.13, F8K4_13	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19652	AT3G43420.1   expressed protein   chr3:15356303-15356667 FORWARD   Aliases: T5C2.120	2.5	2.5	0.0	0.1	100.0%	-5.5
19653	AT5G14550.2   expressed protein, contains Pfam profile PF03267: Arabidopsis protein of unknown function, DUF266   chr5:4691381-4693735 REVERSE   Aliases: T15N1.40, T15N1_40	5.2	5.2	-0.0	-0.1	100.0%	-5.0
19654	AT5G15360.1   expressed protein   chr5:4987440-4989185 REVERSE   Aliases: F8M21.250, F8M21_250	2.5	2.5	-0.0	-0.1	100.0%	-5.5
19655	AT3G21760.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:7667034-7668731 FORWARD   Aliases: MSD21.9	3.9	3.9	0.0	0.1	100.0%	-5.1
19656	AT4G28770.1   expressed protein   chr4:14211328-14213677 REVERSE   Aliases: F16A16.120, F16A16_120	7.5	7.5	-0.0	-0.1	100.0%	-5.0
19657	AT1G63980.2   similar to aldose 1-epimerase family protein [Arabidopsis thaliana] (TAIR:At5g15140.1); similar to CG11180-PA [Drosophila melanogaster] (GB:NP_611495.1); contains InterPro domain D111/G-patch domain (InterPro:IPR000467)   chr1:23744225-23746965 FORWARD   Aliases: F22C12.25, F22C12_25	9.2	9.2	-0.0	-0.1	100.0%	-4.9
19658	AT3G29080.1   expressed protein   chr3:11070589-11072613 FORWARD   Aliases: MXE2.4	2.9	2.9	0.0	0.1	100.0%	-4.7
19659	AT5G54690.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr5:22236661-22239066 REVERSE   Aliases: K5F14.3, K5F14_3	3.2	3.1	0.1	0.1	100.0%	-4.8
19660	AT2G47670.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Lycopersicon esculentum SP:Q43143, Arabidopsis thaliana SP:Q42534; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr2:19551061-19551876 REVERSE   Aliases: F17A22.6	2.4	2.4	0.0	0.1	100.0%	-5.2
19661	AT3G58100.1   glycosyl hydrolase family protein 17, similar to elicitor inducible chitinase Nt-SubE76 GI:11071974 from (Nicotiana tabacum); C-terminal homology only   chr3:21526176-21527464 REVERSE   Aliases: F9D24.10	6.7	6.7	-0.0	-0.1	100.0%	-4.4
19662	AT1G32800.1   PHD finger protein-related, contains low similarity to PHD-finger domain proteins   chr1:11881790-11883073 FORWARD   Aliases: F9L11.28	4.5	4.4	0.0	0.1	100.0%	-4.9
19663	AT1G77390.1   Symbol: CYCA1;2   cyclin, putative, similar to mitotic cyclin a2-type (Glycine max) GI:857397; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:29086798-29089031 REVERSE   Aliases: CYCA1, CYCLIN A1;2, F2P24.10, F2P24_10	3.1	3.1	-0.0	-0.1	100.0%	-5.4
19664	AT1G04300.1   meprin and TRAF homology domain-containing protein / MATH domain-containing protein, weak similarity to ubiquitin-specific protease 12 (Arabidopsis thaliana) GI:11993471;contains Pfam PF00917: Meprin And TRAF-Homology (MATH) domain   chr1:1148586-1154597 REVERSE   Aliases: F19P19.26, F19P19_26	6.2	6.2	0.0	0.1	100.0%	-5.3
19665	AT5G13270.1   pentatricopeptide (PPR) repeat-containing protein, contains INTERPRO:IPR002885 PPR repeats   chr5:4246957-4249215 REVERSE   Aliases: T31B5.90, T31B5_90	3.0	3.0	-0.0	-0.1	100.0%	-5.4
19666	AT5G01070.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr5:25424-25798 REVERSE   Aliases: F7J8.50, F7J8_50	3.3	3.3	-0.0	-0.1	100.0%	-5.3
19667	AT1G33930.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to SP:P54120 AIG1 protein {Arabidopsis thaliana}; contains Pfam profile PF04548: AIG1 family   chr1:12323868-12327064 FORWARD   Aliases: T3M13.5, T3M13_5	2.5	2.5	0.0	0.1	100.0%	-5.6
19668	AT1G17745.2   Symbol: PGDH   similar to D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative [Arabidopsis thaliana] (TAIR:At3g19480.1); similar to D-3-phosphoglycerate dehydrogenase, putative / 3-PGDH, putative [Arabidopsis thaliana] (TAIR:At4g34200.1); similar to putative phosphoglycerate dehydrogenase [Oryza sativa (japonica cultivar-group)] (GB:XP_482675.1); similar to OSJNBb0059K02.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_474138.1); contains InterPro domain D-3-phosphoglycerate dehydrogenase (InterPro:IPR006236); contains InterPro domain Amino acid-binding ACT (InterPro:IPR002912); contains InterPro domain D-isomer specific 2-hydroxyacid dehydrogenase, catalytic domain (InterPro:IPR006139); contains InterPro domain D-isomer specific 2-hydroxyacid dehydrogenase, NAD binding domain (InterPro:IPR006140)   chr1:6100957-6105258 FORWARD   Aliases: 3 PHOSPHOGLYCERATE DEHYDROGENASE	6.9	7.0	-0.1	-0.1	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19669	AT5G17520.1   Symbol: RCP1   root cap 1 (RCP1), identical to Gl:6137138   chr5:5772586-5775347 REVERSE   Aliases: K3M16.90, K3M16_90, MALTOSE EXCESS 1, MEX1, ROOT CAP 1	7.2	7.1	0.0	0.1	100.0%	-4.3
19670	AT1G32840.1   Ulp1 protease family protein, similar to At4g04010, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210, At3g32900   chr1:11896526-11899675 REVERSE   Aliases: F9L11.4, F9L11_4	2.2	2.2	-0.0	-0.1	100.0%	-6.0
19671	AT4G18780.1   Symbol: CESA8   cellulose synthase, catalytic subunit (IRX1), nearly identical to gi:12836997   chr4:10312665-10316797 REVERSE   Aliases: ATCESA8, CELLULASE SYNTHASE 8, F2A21.190, F2A21_190, IRREGULAR XYLEM 1, IRX1, LEAF WILTING 2, LEW2	3.6	3.5	0.0	0.1	100.0%	-4.3
19672	AT4G37450.1   Symbol: AGP18   arabinogalactan-protein (AGP18), identical to gi_11935088_gb_AAG41964   chr4:17605752-17606749 REVERSE   Aliases: ARABINOGALACTAN PROTEIN AGP18, ATAGP18, F6G17.100, F6G17_100	5.7	5.8	-0.0	-0.1	100.0%	-4.7
19673	AT1G33700.2   similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g49900.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g10060.1); similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g24180.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:AAP54244.1); similar to At5g49900 [Oryza sativa (japonica cultivar-group)] (GB:AAX95400.1); contains InterPro domain Protein of unknown function DUF608 (InterPro:IPR006775)   chr1:12207208-12214162 REVERSE   Aliases: F14M2.16, F14M2_16	9.1	9.1	-0.0	-0.1	100.0%	-5.5
19674	AT2G21680.1   kelch repeat-containing F-box family protein, low similarity to SKP1 interacting partner 6 (Arabidopsis thaliana) Gl:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:9274810-9276099 FORWARD   Aliases: F2G1.5, F2G1_5	3.6	3.6	-0.0	-0.1	100.0%	-5.1
19675	AT1G15850.1   transducin family protein / WD-40 repeat family protein, contains 3 WD-40 repeats (PF00400); mRNA-associated protein mrnp 41 (SP:P78406) (Homo sapiens); similar to mitotic checkpoint protein Gl:9294423 from (Arabidopsis thaliana)   chr1:5453240-5454083 REVERSE   Aliases: F7H2.18, F7H2_18	2.9	2.9	-0.0	-0.1	100.0%	-6.0
19676	AT3G42970.1   hypothetical protein   chr3:15035795-15036132 FORWARD   Aliases: F18P9.130	3.0	2.9	0.0	0.1	100.0%	-5.4
19677	AT3G53820.1   zinc finger (C2H2 type) family protein, contains Pfam profile: PF00096 zinc finger, C2H2 type   chr3:19949684-19950112 FORWARD   Aliases: F5K20.120	2.4	2.4	0.0	0.1	100.0%	-5.9
19678	AT1G64355.2   expressed protein, similar to hypothetical protein Tery02003428 [Trichodesmium erythraeum IMS101] (GB:ZP_00326379.1)   chr1:23889765-23890875 FORWARD   Aliases: None	3.8	3.8	0.0	0.1	100.0%	-5.0
19679	AT1G50930.1   expressed protein   chr1:18880566-18881374 FORWARD   Aliases: F8A12.15, F8A12_15	2.4	2.4	-0.0	-0.1	100.0%	-4.8
19680	AT1G15200.1   protein-protein interaction regulator family protein, contains Pfam PF04696: pinin/SDK/memA/ protein conserved region   chr1:5228331-5231055 REVERSE   Aliases: F9L1.14, F9L1_14	6.9	7.0	-0.0	-0.1	100.0%	-4.9
19681	AT5G47330.1   palmitoyl protein thioesterase family protein   chr5:19224333-19226049 FORWARD   Aliases: MQL5.19, MQL5_19	3.3	3.3	-0.0	-0.1	100.0%	-5.4
19682	AT3G12820.1   myb family transcription factor (MYB10), similar to myb factor Gl:1945279 from (Oryza sativa)   chr3:4074165-4075621 REVERSE   Aliases: MBK21.18	4.2	4.3	-0.0	-0.1	100.0%	-5.2
19683	AT1G64290.1   F-box protein-related, contains TIGRFAM TIGR01640 : F-box protein interaction domain;   chr1:23860841-23862151 REVERSE   Aliases: F15H21.5, F15H21_5	4.0	4.0	-0.0	-0.1	100.0%	-4.8
19684	AT3G56230.1   speckle-type POZ protein-related, contains Pfam PF00651 : BTB/POZ domain; similar to Speckle-type POZ protein (SP:O43791) (Homo sapiens)	2.5	2.5	0.0	0.1	100.0%	-4.4
19685	AT1G76860.1   small nuclear ribonucleoprotein, putative / snRNP, putative / Sm protein, putative, similar to SWISS-PROT:Q9Y4Z1 U6 snRNA-associated Sm-like protein LSm3 (MDS017) (Mouse)   chr1:28859355-28860644 REVERSE   Aliases: F7O12.3, F7O12_3	9.0	9.0	-0.0	-0.1	100.0%	-5.2
19686	AT5G38790.1   expressed protein, predicted protein, Arabidopsis thaliana; expression supported by MPSS	3.0	3.1	-0.1	-0.1	100.0%	-4.6
19687	AT4G38200.1   guanine nucleotide exchange family protein, similar to Brefeldin A-inhibited guanine nucleotide-exchange protein 2 (Homo sapiens) SP:Q9Y6D5; contains Pfam profile PF01369: Sec7 domain   chr4:17915287-17922726 FORWARD   Aliases: F20D10.320, F20D10_320	3.5	3.6	-0.0	-0.1	100.0%	-5.1
19688	AT2G43090.1   aconitase C-terminal domain-containing protein, contains Pfam profile PF00694: Aconitase C-terminal domain   chr2:17926004-17927506 FORWARD   Aliases: MFL8.15	8.6	8.5	0.1	0.1	100.0%	-4.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19689	AT3G58610.1   ketol-acid reductoisomerase, identical to ketol-acid reductoisomerase, chloroplast precursor (EC 1.1.1.86) (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase) (Swiss-Prot:Q05758) (Arabidopsis thaliana)   chr3:21682429-21685818 FORWARD   Aliases: F14P22.200, F14P22_200	12.5	12.5	-0.0	-0.1	100.0%	-5.1
19690	AT4G36030.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr4:17044948-17047318 REVERSE   Aliases: T19K4.160, T19K4_160	2.8	2.8	-0.0	-0.1	100.0%	-4.6
19691	AT3G07440.1   expressed protein   chr3:2381376-2383146 FORWARD   Aliases: F21O3.15	5.2	5.2	0.0	0.1	100.0%	-4.5
19692	AT3G61700.1   expressed protein   chr3:22847618-22848930 FORWARD   Aliases: F15G16.90	2.4	2.4	-0.0	-0.1	100.0%	-5.7
19693	AT5G26820.1   ferroportin-related, low similarity to ferroportin1 (Danio rerio) GI:7109245   chr5:9433622-9437103 FORWARD   Aliases: F2P16.6, F2P16_6	7.9	7.8	0.0	0.1	100.0%	-5.2
19694	AT3G26860.1   self-incompatibility protein-related, similar to S3 self-incompatibility protein (Papaver rhoeas) GI:1107841   chr3:9902753-9903121 REVERSE   Aliases: MDJ14.20	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19695	AT5G66700.1   Symbol: HB53   homeobox-leucine zipper family protein, similar to Homeobox-leucine zipper protein HAT5 (HD-ZIP protein 5) (SP:Q02283) (Arabidopsis thaliana); contains Pfam PF00046: Homeobox domain   chr5:26651632-26652988 FORWARD   Aliases: ATHB53, HB 8, MSN2.9, MSN2_9	2.5	2.5	-0.0	-0.1	100.0%	-5.5
19696	AT2G04580.1   hypothetical protein   chr2:1599679-1600830 REVERSE   Aliases: T1O3.1, T1O3_1	2.6	2.6	0.0	0.1	100.0%	-5.7
19697	AT1G15270.1   expressed protein, ESTs gb:AA650895, gb:AA720043 and gb:R29777 come from this gene   chr1:5250653-5252097 REVERSE   Aliases: F9L1.21, F9L1_21	6.9	6.9	0.0	0.1	100.0%	-4.7
19698	AT3G23570.1   diene lactone hydrolase family protein, similar to SP:Q9ZT66 Endo-1,3;1,4-beta-D-glucanase precursor (EC 3.2.1.-) {Zea mays}; contains Pfam profile: PF01738 diene lactone hydrolase family   chr3:8457785-8459698 REVERSE   Aliases: MDB19.5	10.3	10.3	0.1	0.1	100.0%	-4.4
19699	AT2G01130.1   similar to helicase domain-containing protein [Arabidopsis thaliana] (TAIR:At1g48650.1); similar to helicase domain-containing protein [Arabidopsis thaliana] (TAIR:At2g35920.1); similar to helicase domain-containing protein [Arabidopsis thaliana] (TAIR:At5g04895.1); similar to putative helicase [Oryza sativa] (GB:XP_469747.1); similar to putative ATP-dependent RNA helicase A [Oryza sativa (japonica cultivar-group)] (GB:NP_909005.1); similar to putative ATP-dependent RNA helicase [Oryza sativa (japonica cultivar-group)] (GB:AAP54231.1); contains InterPro domain Helicase-associated region (InterPro:IPR007502); contains InterPro domain Helicase, C-terminal (InterPro:IPR001650); contains InterPro domain Double-stranded RNA binding (DsRBD) domain (InterPro:IPR001159); contains InterPro domain DEAD/DEAH box helicase (InterPro:IPR001410)   chr2:88846-94659 REVERSE   Aliases: F10A8.28	2.7	2.7	-0.0	-0.1	100.0%	-5.5
19700	AT1G10530.1   expressed protein   chr1:3471457-3472673 REVERSE   Aliases: T10O24.15, T10O24_15	3.3	3.3	0.0	0.1	100.0%	-5.1
19701	AT3G53090.2   Symbol: UPL7   similar to HECT-domain-containing protein / ubiquitin-transferase family protein [Arabidopsis thaliana] (TAIR:At3g17205.1); similar to putative ubiquitin protein ligase, 5'-partial [Oryza sativa (japonica cultivar-group)] (GB:AAP68382.1); contains InterPro domain IQ calmodulin-binding region (InterPro:IPR000048); contains InterPro domain HECT domain (Ubiquitin-protein ligase) (InterPro:IPR000569)   chr3:19690186-19696338 FORWARD   Aliases: T4D2.20	3.7	3.7	0.0	0.1	100.0%	-4.9
19702	AT2G18690.1   expressed protein   chr2:8104504-8105909 FORWARD   Aliases: MSF3.7, MSF3_7	4.9	5.0	-0.0	-0.1	100.0%	-4.7
19703	AT1G55510.1   Symbol: BCDH BETA1   2-oxoisovalerate dehydrogenase, putative / 3-methyl-2-oxobutanoate dehydrogenase, putative / branched-chain alpha-keto acid dehydrogenase E1 beta subunit, putative, strong similarity to branched chain alpha-keto acid dehydrogenase E1 beta subunit (Arabidopsis thaliana) GI:7021286; contains Pfam profiles PF02779: Transketolase, pyridine binding domain, PF02780: Transketolase, C-terminal domain   chr1:20727016-20729284 FORWARD   Aliases: BRANCHED CHAIN ALPHA KETO ACID DECARBOXYLASE E1 BETA SUBUNIT, T5A14.9, T5A14_9	7.0	6.9	0.0	0.1	100.0%	-4.9
19704	AT3G28460.1   expressed protein, contains Pfam PF03602: Conserved hypothetical protein 95   chr3:10673303-10675632 REVERSE   Aliases: MFJ20.15	4.1	4.1	-0.0	-0.1	100.0%	-5.1
19705	AT3G06950.1   tRNA pseudouridine synthase family protein, similar to SP:P07649 tRNA pseudouridine synthase A (EC 4.2.1.70) (Uracil hydrolyase) {Escherichia coli}; contains Pfam profile PF01416: tRNA pseudouridine synthase   chr3:2192805-2194278 FORWARD   Aliases: F17A9.10	5.9	5.9	-0.0	-0.1	100.0%	-4.9
19706	AT5G62470.2   Symbol: MYB96   myb family transcription factor (MYB96), contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:25096217-25098314 REVERSE   Aliases: K19B1.8, K19B1_8	2.9	2.9	-0.0	-0.1	100.0%	-5.2
19707	AT1G27850.1   expressed protein, similar to En/Spm-like transposon protein GB:AAB95292 GI:2088658 from (Arabidopsis thaliana)   chr1:9699252-9703928 FORWARD   Aliases: F28L5.11, F28L5_11	4.2	4.2	0.0	0.1	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19708	AT3G24800.1   Symbol: PRT1   PRT1 protein (PRT1), E3, N-end rule ubiquitin ligase, contains two RING finger domain; identical to PRT1 (Arabidopsis thaliana) GI:3319884   chr3:9055516-9058005 FORWARD   Aliases: K7P8.19, PROTEOLYSIS 1, PRT1	8.5	8.5	0.0	0.1	100.0%	-5.1
19709	AT4G21630.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr4:11492260-11495512 REVERSE   Aliases: F17L22.90, F17L22_90	2.9	2.9	0.0	0.1	100.0%	-5.6
19710	AT1G78890.1   expressed protein   chr1:29661470-29662958 FORWARD   Aliases: F9K20.6, F9K20_6	6.5	6.4	0.0	0.1	100.0%	-4.6
19711	AT4G16640.1   matrix metalloproteinase, putative, metalloproteinase (Arabidopsis thaliana) GI:3128477; contains InterPro accession IPR001818: Matrixin	2.9	2.8	0.0	0.1	100.0%	-5.1
19712	AT2G39380.1   exocyst subunit EXO70 family protein, contains Pfam domain PF03081: Exo70 exocyst complex subunit;   chr2:16454084-16456161 REVERSE   Aliases: F12L6.4, F12L6_4	3.2	3.3	-0.0	-0.1	100.0%	-4.5
19713	AT2G18260.1   Symbol: SYP112	3.4	3.4	0.0	0.1	100.0%	-5.5
19714	AT2G30870.1   Symbol: ATGSTF10   glutathione S-transferase, putative, supported by cDNA GI:443698 GB:D17673   chr2:13148527-13150296 FORWARD   Aliases: ATGSTF4, EARLY DEHYDRATION INDUCED 13, ERD13, F7F1.8, F7F1_8, GLUTATHIONE S TRANSFERASE	9.3	9.3	0.1	0.1	100.0%	-4.3
19715	AT1G11880.1   expressed protein, contains Pfam profile PF04188: Protein of unknown function (DUF409)   chr1:4007704-4010432 REVERSE   Aliases: F12F1.28, F12F1_28	2.9	3.0	-0.0	-0.1	100.0%	-5.1
19716	AT3G28200.1   peroxidase, putative, similar to peroxidase ATP26a GB:CAA72487 GI:1890317 (Arabidopsis thaliana)	5.7	5.7	0.0	0.1	100.0%	-4.9
19717	AT2G31470.1   F-box family protein, contains F-box domain Pfam:PF00646	3.2	3.2	0.0	0.1	100.0%	-5.5
19718	AT1G23610.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8362904-8363215 REVERSE   Aliases: F28C11.24	3.1	3.1	-0.0	-0.1	100.0%	-5.1
19719	AT5G56510.1   pumilio/Puf RNA-binding domain-containing protein, contains similarity to RNA-binding protein   chr5:22898947-22901068 FORWARD   Aliases: MKN22.2, MKN22_2	3.3	3.3	0.0	0.1	100.0%	-5.2
19720	AT1G62970.1   DNAJ heat shock N-terminal domain-containing protein, low similarity to AHM1 (Triticum aestivum) GI:6691467; contains Pfam profile PF00226: DnaJ domain   chr1:23326982-23329718 FORWARD   Aliases: F16P17.12, F16P17_12	4.3	4.3	-0.0	-0.1	100.0%	-4.9
19721	AT1G11580.1   pectin methylesterase, putative, similar to pectin methylesterase GI:1617583 from (Lycopersicon esculentum)   chr1:3888690-3890811 FORWARD   Aliases: ATPMEPCRA, T23J18.24, T23J18_24	10.6	10.6	0.1	0.1	100.0%	-4.6
19722	AT3G60390.1   Symbol: HAT3   homeobox-leucine zipper protein 3 (HAT3) / HD-ZIP protein 3, identical to Homeobox-leucine zipper protein HAT3 (SP:P46602) (Arabidopsis thaliana)   chr3:22331570-22333561 REVERSE   Aliases: HOMEBOX PROTEIN, T8B10.50	3.6	3.7	-0.0	-0.1	100.0%	-5.0
19723	AT4G20410.1   Symbol: GSNAP   gamma-soluble NSF attachment protein / gamma-SNAP, identical to gamma-soluble NSF attachment protein; gamma-SNAP (Arabidopsis thaliana) GI:6013206   chr4:11013961-11016571 REVERSE   Aliases: F9F13.60, F9F13_60, GAMMA SNAP, GAMMA SOLUBLE NSF ATTACHMENT PROTEIN	8.4	8.4	0.0	0.1	100.0%	-5.0
19724	AT3G13228.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:4266971-4268258 FORWARD   Aliases: None	2.7	2.7	0.0	0.1	100.0%	-5.7
19725	AT3G26650.1   Symbol: GAPA   glyceraldehyde 3-phosphate dehydrogenase A, chloroplast (GAPA) / NADP-dependent glyceraldehydephosphate dehydrogenase subunit A, identical to SP:P25856 Glyceraldehyde 3-phosphate dehydrogenase A, chloroplast precursor (EC 1.2.1.13) (NADP-dependent glyceraldehydephosphate dehydrogenase subunit A) {Arabidopsis thaliana}   chr3:9796330-9798282 FORWARD   Aliases: GAPA 1, GLYCERALDEHYDE 3 PHOSPHATE DEHYDROGENASE A SUBUNIT, GLYCERALDEHYDE 3 PHOSPHATE DEHYDROGENASE A SUBUNIT, MLJ15.3	10.3	10.4	-0.0	-0.1	100.0%	-4.6
19726	AT3G61130.1   glycosyl transferase family 8 protein, contains Pfam profile: PF01501 glycosyl transferase family 8   chr3:22632967-22636691 FORWARD   Aliases: T20K12.30	5.1	5.0	0.0	0.1	100.0%	-5.1
19727	AT3G53290.1   Symbol: CYP71B30P   cytochrome P450, putative, Similar to Cytochrome P450 71B31 (SP:Q9SCN2)(Arabidopsis thaliana); conatins Pfam profile: PF00067 cytochrome P450   chr3:19769135-19770581 FORWARD   Aliases: T4D2.210	2.9	3.0	-0.0	-0.1	100.0%	-5.2
19728	AT1G18640.2   Symbol: PSP   3-phosphoserine phosphatase (PSP), nearly identical to 3-phosphoserine phosphatase GI:3759177 from (Arabidopsis thaliana)	9.7	9.7	-0.0	-0.1	100.0%	-5.0
19729	AT1G27980.1   pyridoxal-dependent decarboxylase family protein, similar to sphingosine-1-phosphate lyase (Homo sapiens) GI:10129683; contains Pfam profile PF00282: Pyridoxal-dependent decarboxylase conserved domain	7.8	7.7	0.0	0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19730	AT5G63420.1   Symbol: EMB2746   metallo-beta-lactamase family protein	4.5	4.5	0.0	0.1	100.0%	-4.9
19731	AT3G28420.1   expressed protein   chr3:10655707-10656561 REVERSE   Aliases: MFJ20.12	2.8	2.8	0.0	0.1	100.0%	-5.7
19732	AT5G15450.1   heat shock protein 100, putative / HSP100, putative / heat shock protein clpB, putative / HSP100/ClpB, putative, similar to HSP100/ClpB GI:9651530 (Phaseolus lunatus)   chr5:5014402-5018350 REVERSE   Aliases: T20K14.60, T20K14_60	9.0	9.0	-0.1	-0.1	100.0%	-4.8
19733	AT1G26780.1   Symbol: MYB117	2.6	2.6	-0.0	-0.1	100.0%	-5.4
19734	AT4G11770.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:7082273-7083463 REVERSE   Aliases: T5C23.200, T5C23_200	3.6	3.6	-0.0	-0.1	100.0%	-5.4
19735	AT5G59340.1   Symbol: WOX2   similar to homeobox-leucine zipper transcription factor family protein [Arabidopsis thaliana] (TAIR:At3g18010.1); similar to putative homeodomain transcription factor [Oryza sativa (indica cultivar-group)] (GB:CAC09359.1); similar to narrow sheath 2 [Zea mays] (GB:AAR31212.1); contains InterPro domain Homeobox (InterPro:IPR001356)   chr5:23950630-23951916 REVERSE   Aliases: MNC17.25, MNC17_25	3.2	3.2	-0.0	-0.1	100.0%	-5.2
19736	AT2G03470.2   myb family transcription factor / ELM2 domain-containing protein, contains Pfam profile: PF00249 Myb-like DNA-binding domain; contains Pfam profile: PF01448 ELM2 domain	5.2	5.2	0.0	0.1	100.0%	-4.5
19737	AT3G49760.1   bZIP transcription factor family protein, similar to bZIP transcription factor GI:1769891 from (Arabidopsis thaliana)   chr3:18466333-18467109 REVERSE   Aliases: T16K5.110	2.6	2.6	0.0	0.1	100.0%	-4.3
19738	AT1G76380.3   DNA-binding bromodomain-containing protein, contains bromodomain, INTERPRO:IPR001487   chr1:28656048-28659474 REVERSE   Aliases: F15M4.12, F15M4_12	5.1	5.1	-0.0	-0.1	100.0%	-4.9
19739	AT3G19085.1   expressed protein   chr3:6599595-6600590 FORWARD   Aliases: K13E13.22	2.3	2.3	-0.0	-0.1	100.0%	-6.0
19740	AT5G53740.1   expressed protein   chr5:21828859-21832134 FORWARD   Aliases: MGN6.10, MGN6_10	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19741	AT3G21870.1   cyclin family protein, similar to cyclin 2 (Trypanosoma brucei) GI:7339572, cyclin 6 (Trypanosoma cruzi) GI:12005317; contains Pfam profile PF00134: Cyclin, N-terminal domain   chr3:7703878-7704836 REVERSE   Aliases: MEK6.1	3.9	3.9	0.0	0.1	100.0%	-5.0
19742	AT5G66120.2   3-dehydroquinate synthase, putative, similar to aroB (Neisseria gonorrhoeae)(GI:2661441); contains 3-dehydroquinate synthase domain PF01761   chr5:26448602-26451004 REVERSE   Aliases: K2A18.20, K2A18_20	10.8	10.8	-0.0	-0.1	100.0%	-4.9
19743	AT3G22320.1   Symbol: ATRPABC24.3   DNA-directed RNA polymerase, putative, similar to SP:P19388 DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) {Homo sapiens}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain   chr3:7890893-7892330 REVERSE   Aliases: MCB17.20	10.0	10.0	-0.0	-0.1	100.0%	-4.8
19744	AT1G35330.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr1:12965024-12966091 FORWARD   Aliases: T9I1.10, T9I1_10	2.6	2.6	-0.0	-0.1	100.0%	-5.0
19745	AT2G15670.1   hypothetical protein   chr2:6835215-6836703 FORWARD   Aliases: F9O13.22	2.5	2.5	0.0	0.1	100.0%	-5.7
19746	AT2G37360.1   ABC transporter family protein   chr2:15680634-15682999 REVERSE   Aliases: F3G5.15, F3G5_15	2.4	2.4	0.0	0.1	100.0%	-4.9
19747	AT5G59660.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:24052913-24057205 FORWARD   Aliases: MTH12.10, MTH12_10	3.1	3.1	0.0	0.1	100.0%	-5.6
19748	AT3G29635.1   transferase family protein, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234; contains Pfam profile PF02458 transferase family   chr3:11468330-11469706 REVERSE   Aliases: T13J10.13	3.0	3.0	0.0	0.1	100.0%	-5.2
19749	AT5G58784.1   dehydrololichyl diphosphate synthase, putative / DEDOL-PP synthase, putative, similar to GI:796076   chr5:23757176-23758220 REVERSE   Aliases: None	2.4	2.3	0.0	0.1	100.0%	-5.6
19750	AT5G49870.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.1	3.1	-0.0	-0.1	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19751	AT2G20620.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr2:8899010-8900325 REVERSE   Aliases: F23N11.6, F23N11_6	2.9	3.0	-0.0	-0.1	100.0%	-5.6
19752	AT2G36730.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:15412147-15413652 REVERSE   Aliases: F13K3.13, F13K3_13	5.7	5.7	-0.0	-0.1	100.0%	-5.2
19753	AT3G20930.1   RNA recognition motif (RRM)-containing protein, contains Pfam profile: PF00076 RNA recognition motif   chr3:7331731-7334034 FORWARD   Aliases: MFD22.4	6.6	6.6	-0.0	-0.1	100.0%	-4.5
19754	AT1G47350.1   F-box family protein-related, contains TIGR01640: F-box protein interaction domain   chr1:17360887-17363162 REVERSE   Aliases: T3F24.4, T3F24_4	3.6	3.6	0.0	0.1	100.0%	-5.5
19755	AT5G42490.1   kinesin motor family protein, contains Pfam domain, PF00225: Kinesin motor domain   chr5:17005837-17009850 REVERSE   Aliases: MDH9.19, MDH9_19	2.7	2.7	0.0	0.1	100.0%	-5.7
19756	AT5G66620.1   LIM domain-containing protein, contains Pfam profile PF00412: LIM domain	4.0	4.0	-0.0	-0.1	100.0%	-5.4
19757	AT5G60160.1   aspartyl aminopeptidase, putative, similar to SP:Q9ULA0 Aspartyl aminopeptidase (EC 3.4.11.21) {Homo sapiens}; contains Pfam profile PF02127: Aminopeptidase I zinc metalloprotease (M18)   chr5:24240942-24244094 REVERSE   Aliases: F15L12.1, F15L12_1	9.8	9.7	0.0	0.1	100.0%	-4.8
19758	AT4G13100.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:7636435-7639034 REVERSE   Aliases: F25G13.190, F25G13_190	3.7	3.7	-0.0	-0.1	100.0%	-5.0
19759	AT4G36620.1   zinc finger (GATA type) family protein   chr4:17268912-17269668 REVERSE   Aliases: AP22.1, AP22_1	2.9	2.9	-0.0	-0.1	100.0%	-5.4
19760	AT2G25950.1   expressed protein   chr2:11075729-11077738 FORWARD   Aliases: F17H15.2	9.3	9.4	-0.0	-0.1	100.0%	-4.6
19761	AT2G47700.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type(RING finger)	4.6	4.6	-0.0	-0.1	100.0%	-4.9
19762	AT3G63400.2   peptidyl-prolyl cis-trans isomerase cyclophilin-type family protein, similar to cyclophilin (Digitalis lanata) GI:1563719; contains Pfam profile PF00160: peptidyl-prolyl cis-trans isomerase, cyclophilin-type; contains AT-donor splice site at intron 9   chr3:23422999-23426604 FORWARD   Aliases: MAA21.30	3.7	3.7	-0.0	-0.1	100.0%	-5.3
19763	AT1G30410.1   Symbol: ATMRP13   ATP-binding cassette transport protein, putative, similar to MgATP-energized glutathione S-conjugate pump (Arabidopsis thaliana) GI:2909781; contains Pfam profiles PF00005: ABC transporter, PF00664: ABC transporter transmembrane region   chr1:10739339-10747305 FORWARD   Aliases: T4K22.13, T4K22_13	4.8	4.8	0.0	0.1	100.0%	-4.3
19764	AT1G30420.1   Symbol: ATMRP12   ATP-binding cassette transport protein, putative, contains Pfam profiles PF00005: ABC transporter, PF00664: ABC transporter transmembrane region   chr1:10748798-10756298 FORWARD   Aliases: T4K22.1, T4K22_1	4.8	4.8	0.0	0.1	100.0%	-4.3
19765	AT1G65890.1   acyl-activating enzyme 12 (AAE12), similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501; identical to cDNA acyl-activating enzyme 12 (At1g65890) mRNA GI:29893228, acyl-activating enzyme 12 (Arabidopsis thaliana) GI:29893229   chr1:24516120-24518322 REVERSE   Aliases: F12P19.6, F12P19_6	2.7	2.7	0.0	0.1	100.0%	-5.6
19766	AT4G33865.1   40S ribosomal protein S29 (RPS29C)   chr4:16233214-16234201 REVERSE   Aliases: None	12.4	12.4	-0.0	-0.1	100.0%	-5.5
19767	AT3G28540.2   similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At3g28510.1); similar to AAA-type ATPase family protein [Arabidopsis thaliana] (TAIR:At3g28520.1); similar to hypothetical protein [Solanum tuberosum] (GB:AAU89729.1); contains InterPro domain AAA ATPase (InterPro:IPR003593); contains InterPro domain AAA ATPase, central region (InterPro:IPR003959)   chr3:10695681-10697360 FORWARD   Aliases: T20D4.4	3.3	3.2	0.0	0.1	100.0%	-5.3
19768	AT5G07380.2   similar to P0436E04.8 [Oryza sativa (japonica cultivar-group)] (GB:NP_908349.1)   chr5:2332477-2336049 FORWARD   Aliases: T2I1.90, T2I1_90	2.9	2.9	-0.0	-0.1	100.0%	-5.3
19769	AT2G04500.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.5	0.0	0.1	100.0%	-5.3
19770	AT1G35820.1   hypothetical protein   chr1:13309331-13310469 REVERSE   Aliases: F10O5.1, F10O5_1	2.3	2.3	-0.0	-0.1	100.0%	-5.4
19771	AT1G63240.1   expressed protein   chr1:23459686-23462301 REVERSE   Aliases: F9N12.14, F9N12_14	3.0	3.0	-0.0	-0.1	100.0%	-5.2
19772	AT3G06490.1   Symbol: MYB108	4.0	4.0	0.0	0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19773	AT5G45110.1   ankyrin repeat family protein / BTB/POZ domain-containing protein, contains Pfam domain, PF00023: Ankyrin repeat and Pfam domain, PF00651: BTB/POZ domain   chr5:18246137-18248749 FORWARD   Aliases: K17O22.11, K17O22_11	6.1	6.1	-0.0	-0.1	100.0%	-5.0
19774	AT5G56200.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:22764994-22766475 FORWARD   Aliases: K24C1.1, K24C1_1	3.9	3.9	-0.0	-0.1	100.0%	-4.7
19775	AT2G38500.1   expressed protein   chr2:16124505-16126177 REVERSE   Aliases: T6A23.30	4.2	4.1	0.0	0.1	100.0%	-5.4
19776	AT2G14670.1   sucrose transporter, putative / sucrose-proton symporter, putative, similar to sucrose-proton symporter SUC1 (Arabidopsis thaliana) GI:407094, SUC2 (Arabidopsis thaliana) GI:407092, sucrose transporter (Arabidopsis thaliana) GI:12057172; contains Pfam profile PF00083: major facilitator superfamily protein   chr2:6281688-6283399 REVERSE   Aliases: T6B13.9, T6B13_9	3.2	3.2	0.0	0.1	100.0%	-5.4
19777	AT4G13740.1   Symbol: EMB2597   expressed protein   chr4:7975184-7977362 FORWARD   Aliases: EMB2597, EMBRYO DEFECTIVE 2597, F18A5.130, F18A5_130	3.2	3.2	-0.0	-0.1	100.0%	-5.2
19778	AT1G01250.1   encodes a member of the DREB subfamily A-4 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 17 members in this subfamily including TINY.   chr1:104491-105324 REVERSE   Aliases: F6F3.6, F6F3_6	3.2	3.2	0.0	0.1	100.0%	-5.3
19779	AT1G20860.1   phosphate transporter family protein, similar to phosphate transporter (Catharanthus roseus) GI:2208908, inorganic phosphate transporter 1 (Solanum tuberosum) GI:1420871; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:7253996-7258666 REVERSE   Aliases: F9H16.16, F9H16_16	3.3	3.3	0.0	0.1	100.0%	-5.1
19780	AT2G14160.1   RNA recognition motif (RRM)-containing protein   chr2:5983547-5983883 REVERSE   Aliases: T22C12.9, T22C12_9	2.6	2.6	0.0	0.1	100.0%	-5.5
19781	AT1G19290.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:6666717-6668954 FORWARD   Aliases: T29M8.15	3.0	3.0	-0.0	-0.1	100.0%	-5.7
19782	AT2G23340.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 16 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr2:9945079-9945953 FORWARD   Aliases: T20D16.3, T20D16_3	9.5	9.6	-0.0	-0.1	100.0%	-5.3
19783	AT1G63580.1   protein kinase-related   chr1:23580996-23581917 FORWARD   Aliases: F2K11.6, F2K11_6	2.6	2.6	0.0	0.1	100.0%	-5.2
19784	AT3G14470.1   disease resistance protein (NBS-LRR class), putative, domain signature NBS-LRR exists, suggestive of a disease resistance protein.   chr3:4857947-4861254 FORWARD   Aliases: MOA2.9	2.8	2.9	-0.0	-0.1	100.0%	-4.6
19785	AT4G34970.1   actin-depolymerizing factor, putative, similar to SP:Q9ZNT3 Actin-depolymerizing factor 5 (ADF-5) (AtADF5) {Arabidopsis thaliana}; contains Pfam profile PF00241: Cofilin/tropomyosin-type actin-binding protein	2.8	2.8	-0.0	-0.1	100.0%	-5.1
19786	AT1G63910.1   Symbol: ATMYB103   myb family transcription factor (MYB103), contains Pfam profile: PF00249 myb-like DNA-binding domain	2.3	2.3	-0.0	-0.1	100.0%	-5.5
19787	AT1G59950.1   aldo/keto reductase, putative, similar to NADPH-dependent codeinone reductase GI:6478210 (Papaver somniferum), NAD(P)H dependent 6'-deoxychalcone synthase (Glycine max)(GI:18728)   chr1:22071698-22074253 REVERSE   Aliases: F23H11.26, F23H11_26	2.7	2.7	0.0	0.1	100.0%	-5.6
19788	AT4G03570.1   expressed protein   chr4:1590411-1594103 REVERSE   Aliases: T5L23.6, T5L23_6	3.4	3.4	0.0	0.1	100.0%	-5.4
19789	AT4G30300.1   Symbol: ATNAP15   ABC transporter family protein, ribonuclease L inhibitor - Mus musculus,PIR2:JC6555   chr4:14831011-14831556 REVERSE   Aliases: F17I23.360, F17I23_360	2.4	2.4	0.0	0.1	100.0%	-5.7
19790	AT2G19200.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr2:8340300-8341703 FORWARD   Aliases: T20K24.25, T20K24_25	2.5	2.5	-0.0	-0.1	100.0%	-5.4
19791	AT2G24250.2   similar to F-box family protein [Arabidopsis thaliana] (TAIR:At1g64840.1); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810)   chr2:10320366-10322000 REVERSE   Aliases: F27D4.23	4.5	4.5	0.0	0.1	100.0%	-5.3
19792	AT1G79090.2   expressed protein, 11408 (cDNA not full-length)	3.7	3.7	0.0	0.1	100.0%	-5.2
19793	AT4G39920.1   Symbol: POR   tubulin folding cofactor C / Porcino (POR), identical to tubulin-folding cofactor C (Porcino; POR) GI:20514261 from (Arabidopsis thaliana); identical to cDNA tubulin folding cofactor C GI:20514260   chr4:18515743-18517268 FORWARD   Aliases: PORCINO, T5J17.90, T5J17_90, TFC C, TUBULIN FOLDING COFACTOR C	5.7	5.7	-0.0	-0.1	100.0%	-4.8
19794	AT1G14290.1   acid phosphatase, putative, similar to acid phosphatase (Lupinus albus) GI:5360721; contains Pfam profile PF01598 sterol desaturase   chr1:4880046-4881947 REVERSE   Aliases: F14L17.5, F14L17_5	4.5	4.4	0.0	0.1	100.0%	-4.7



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19795	AT3G43590.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr3:15520609-15523562 FORWARD   Aliases: F22J12.30	6.7	6.7	-0.0	-0.1	100.0%	-4.5
19796	AT3G05470.1   formin homology 2 domain-containing protein / FH2 domain-containing protein, contains formin homology 2 domain, Pfam:PF02181   chr3:1579673-1582553 REVERSE   Aliases: F22F7.8, F22F7_8	3.2	3.2	-0.0	-0.1	100.0%	-5.3
19797	AT3G13950.1   expressed protein   chr3:4604156-4605432 FORWARD   Aliases: MDC16.7	3.0	3.0	-0.0	-0.1	100.0%	-5.2
19798	AT5G05480.1   expressed protein   chr5:1622071-1624270 REVERSE   Aliases: MOP10.2, MOP10_2	6.6	6.6	0.0	0.1	100.0%	-4.8
19799	AT2G07070.1   AT hook motif-containing protein, contains Pfam profile PF02178: AT hook motif   chr2:2932225-2934311 REVERSE   Aliases: T4E14.17, T4E14_17	3.2	3.2	-0.0	-0.1	100.0%	-5.3
19800	AT1G73470.2   expressed protein   chr1:27628983-27631359 FORWARD   Aliases: T9L24.34, T9L24_34	8.0	8.0	0.0	0.1	100.0%	-4.7
19801	AT3G51210.1   flavonol 3-sulfotransferase-related, contains weak similarity to Swiss-Prot:P52836 flavonol 3-sulfotransferase (F3-ST) (Flaveria chloraefolia)   chr3:19031865-19032180 FORWARD   Aliases: F24M12.250	2.7	2.8	-0.0	-0.1	100.0%	-5.6
19802	AT2G45950.1   Symbol: ASK20   SKP1 family protein, similar to glycoprotein FP21 SP:P52285 from (Dictyostelium discoideum); contains Pfam profile PF01466: Skp1 family, dimerisation domain   chr2:18911397-18914871 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 20, ASK20, F4I18.7	9.5	9.6	-0.1	-0.1	100.0%	-4.9
19803	AT3G61415.1   Symbol: ASK21   SKP1 family protein, low similarity to SP:P52285 Glycoprotein FP21 precursor {Dictyostelium discoideum}; contains Pfam profile PF01466: Skp1 family, dimerisation domain   chr3:22733685-22737383 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 21, ASK21	9.5	9.6	-0.1	-0.1	100.0%	-4.9
19804	AT2G47930.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr2:19624045-19624751 REVERSE   Aliases: T9J23.8, T9J23_8	3.1	3.0	0.0	0.1	100.0%	-4.7
19805	AT2G02640.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain   chr2:732387-734270 FORWARD   Aliases: T8K22.6, T8K22_6	2.7	2.7	-0.0	-0.1	100.0%	-5.6
19806	AT1G74730.1   expressed protein   chr1:28082592-28084009 FORWARD   Aliases: F25A4.30, F25A4_30	8.0	8.0	-0.0	-0.1	100.0%	-4.5
19807	AT2G46300.1   expressed protein   chr2:19015364-19016631 FORWARD   Aliases: T3F17.5	3.8	3.7	0.0	0.1	100.0%	-5.1
19808	AT1G21210.1   Symbol: WAK4   wall-associated kinase 4	2.8	2.8	-0.0	-0.1	100.0%	-5.3
19809	AT1G63310.1   expressed protein, similar to unknown protein GB:AAC69930 from (Arabidopsis thaliana)   chr1:23489982-23490750 REVERSE   Aliases: F9N12.7, F9N12_7	2.5	2.6	-0.0	-0.1	100.0%	-4.1
19810	AT1G30870.1   cationic peroxidase, putative, similar to cationic peroxidase (gi:1232069); similar to EST gb:AI100412   chr1:10991466-10993004 FORWARD   Aliases: T17H7.19	3.2	3.1	0.0	0.1	100.0%	-4.7
19811	AT1G55600.1   Symbol: WRKY10	2.9	2.9	-0.0	-0.1	100.0%	-5.4
19812	ATCG00600.1   Symbol: PETG   Cytochrome b6-f complex, subunit V. Disruption of homologous gene in Chlamydomonas results in disruption of cytochrome b6-f complex.   chrC:65998-66111 FORWARD   Aliases: PETG	4.8	4.8	-0.0	-0.1	100.0%	-4.9
19813	AT5G24880.1   expressed protein, ; expression supported by MPSS   chr5:8552746-8554077 FORWARD   Aliases: F6A4.90, F6A4_90	3.5	3.5	-0.1	-0.1	100.0%	-4.4
19814	AT4G15250.1   zinc finger (B-box type) family protein   chr4:8709942-8711106 REVERSE   Aliases: DL3670C, FCAALL.247	2.7	2.7	0.0	0.1	100.0%	-5.5
19815	AT1G23570.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8355070-8356353 REVERSE   Aliases: F28C11.33	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19816	AT2G25520.1   phosphate translocator-related, low similarity to SP:P52178 Triose phosphate/phosphate translocator, non-green plastid, chloroplast precursor (CTPT) {Brassica oleracea}, phosphoenolpyruvate/phosphate translocator precursor (Mesembryanthemum crystallinum) GI:9295275   chr2:10867906-10869435 FORWARD   Aliases: F13B15.18, F13B15_18	7.0	6.9	0.0	0.1	100.0%	-4.8
19817	AT1G26550.1   peptidyl-prolyl cis-trans isomerase PPIC-type family protein, similar to SP:Q9Y237 Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4 (EC 5.2.1.8) (Rotamase Pin4) (PPIase Pin4) (Parvulin 14) {Homo sapiens}; contains Pfam profile PF00639: PPIC-type PPIASE domain   chr1:9171119-9172926 FORWARD   Aliases: T1K7.8, T1K7_8	11.4	11.4	-0.0	-0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19818	AT2G05260.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr2:1918332-1920039 FORWARD   Aliases: F5G3.16, F5G3_16	6.4	6.4	0.0	0.1	100.0%	-4.8
19819	AT3G17340.1   importin-related, contains Pfam profile PF03810: Importin-beta N-terminal domain	2.8	2.8	-0.0	-0.1	100.0%	-5.0
19820	AT1G25270.1   nodulin MtN21 family protein, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr1:8857713-8859896 FORWARD   Aliases: F4F7.34, F4F7_34	2.6	2.6	-0.0	-0.1	100.0%	-5.6
19821	AT5G06520.1   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein, contains Pfam profile: PF01805 surp module   chr5:1987251-1989373 REVERSE   Aliases: F15M7.5, F15M7_5	3.0	2.9	0.0	0.1	100.0%	-5.3
19822	AT4G05530.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to peroxisomal short-chain alcohol dehydrogenase GI:4105190 from (Homo sapiens)   chr4:2816392-2818362 FORWARD   Aliases: T1J24.9, T1J24_9	9.0	9.0	-0.0	-0.1	100.0%	-4.6
19823	AT2G40800.1   expressed protein   chr2:17031469-17034051 REVERSE   Aliases: T7D17.2, T7D17_2	4.2	4.2	-0.0	-0.1	100.0%	-5.2
19824	AT5G50870.1   ubiquitin-conjugating enzyme, putative, strong similarity to ubiquitin conjugating enzyme (Lycopersicon esculentum) GI:886679; contains Pfam profile PF00179: Ubiquitin-conjugating enzyme   chr5:20716709-20718302 REVERSE   Aliases: K3K7.1, K3K7_1	10.2	10.2	-0.0	-0.1	100.0%	-4.9
19825	AT5G18650.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	7.5	7.5	0.0	0.1	100.0%	-4.9
19826	AT5G28220.1   expressed protein, predicted proteins, Arabidopsis thaliana, D.melanogaster, C.elegans and S.pombe   chr5:10190365-10193123 REVERSE   Aliases: F26C17.8, F26C17_8	6.4	6.4	0.0	0.1	100.0%	-4.7
19827	AT2G35620.1   leucine-rich repeat transmembrane protein kinase, putative, similar to somatic embryogenesis receptor-like kinase 1 (SERK1) (Zea mays) gi:13897318:emb:CAC37640; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr2:14968026-14971719 REVERSE   Aliases: T20F21.18, T20F21_18	4.5	4.5	-0.0	-0.1	100.0%	-4.9
19828	AT5G03280.1   Symbol: EIN2   ethylene-insensitive 2 (EIN2), identical to EIN2 (Arabidopsis thaliana) gi:5231113:gb:AAD41076; member of the natural resistance-associated macrophage protein (NRAMP) metal transporter family, PMID:11500563; metal transport capacity has not been shown, PMID:11500563, PMID:1038174	4.3	4.4	-0.0	-0.1	100.0%	-4.9
19829	AT1G28260.2   expressed protein   chr1:9875587-9879254 REVERSE   Aliases: F3H9.9, F3H9_9	4.4	4.4	-0.0	-0.1	100.0%	-4.9
19830	AT4G02075.1   Symbol: PIT1   zinc finger (C3HC4-type RING finger) family protein, contains InterPro Entry IPR001841 Zn-finger, RING   chr4:913419-916476 REVERSE   Aliases: PITCHOUN 1	2.8	2.8	0.0	0.1	100.0%	-4.6
19831	AT3G29010.1   expressed protein, ; expression supported by MPSS   chr3:11008477-11009214 FORWARD   Aliases: K5K13.4	4.1	4.2	-0.0	-0.1	100.0%	-4.9
19832	AT3G27810.1   Symbol: ATMYB21   myb family transcription factor (MYB3) (MYB21), contains Pfam profile: PF00249 myb-like DNA-binding domain ;identical to ATMYB3 GI:2280528 from (Arabidopsis thaliana); identical to cDNA putative transcription factor (MYB21) mRNA, partial cds GI:3941431   chr3:10308658-10311545 FORWARD   Aliases: AT3G27812, ATMYB3, MGF10.23	2.5	2.5	0.0	0.1	100.0%	-6.2
19833	AT1G22300.3   Symbol: GRF10   14-3-3 protein GF14 epsilon (GRF10), identical to 14-3-3 protein GF14 epsilon GI:5802798, SP:P48347 from (Arabidopsis thaliana)	10.2	10.2	0.0	0.1	100.0%	-5.2
19834	AT5G17770.1   Symbol: ATCBR   NADH-cytochrome b5 reductase, identical to NADH-cytochrome b5 reductase (Arabidopsis thaliana) GI:4240116   chr5:5864253-5866650 REVERSE   Aliases: MVA3.120, MVA3_120	9.0	9.0	-0.0	-0.1	100.0%	-5.2
19835	AT5G04820.1   ovate family protein, 62% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.7	4.6	0.0	0.1	100.0%	-5.0
19836	AT1G18940.1   nodulin family protein, similar to nodulin-like protein (Arabidopsis thaliana) GI:3329368, nodule-specific protein Nlj70 (Lotus japonicus) GI:3329366   chr1:6543843-6545583 FORWARD   Aliases: F14D16.8, F14D16_8	3.7	3.7	0.0	0.1	100.0%	-4.6
19837	AT3G44230.1   hypothetical protein   chr3:15943121-15943735 FORWARD   Aliases: T10D17.20	2.7	2.7	0.0	0.1	100.0%	-5.5
19838	AT5G07540.2   Symbol: GRP16   similar to glycine-rich protein (GRP17) [Arabidopsis thaliana] (TAIR:At5g07530.1); similar to pollen coat oleosin-glycine rich protein [Capsella rubella] (GB:AAR15461.1); contains InterPro domain Oleosin (InterPro:IPR000136)   chr5:2386014-2387248 REVERSE   Aliases: ATGRP 6, ATGRP16, T2I1.250, T2I1_250	3.4	3.4	0.0	0.1	100.0%	-5.3
19839	AT4G08820.1   hypothetical protein   chr4:5621761-5623206 FORWARD   Aliases: T32A17.130, T32A17_130	3.7	3.8	-0.0	-0.1	100.0%	-5.2
19840	AT1G19500.1   expressed protein   chr1:6754943-6755527 REVERSE   Aliases: F18O14.44	3.4	3.4	-0.0	-0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19841	AT3G04390.1   xanthine dehydrogenase family protein, similar to xanthine dehydrogenase from Bos taurus, GI:1620375   chr3:1165381-1165771 REVERSE   Aliases: T27C4.3, T27C4_3	2.9	2.9	0.0	0.1	100.0%	-4.8
19842	AT3G51100.2   expressed protein   chr3:18991762-18993241 REVERSE   Aliases: F24M12.140	9.1	9.1	0.0	0.1	100.0%	-5.0
19843	AT5G24280.1   expressed protein, ; expression supported by MPSS   chr5:8251381-8261431 REVERSE   Aliases: MOP9.10, MOP9_10	4.8	4.8	-0.0	-0.1	100.0%	-4.8
19844	AT3G42880.1   leucine-rich repeat transmembrane protein kinase, putative, receptor-like protein kinase PRK1, Lycopersicon esculentum, PIR:T07865   chr3:14965575-14967565 FORWARD   Aliases: F18P9.40	3.5	3.5	-0.0	-0.1	100.0%	-5.3
19845	AT5G07680.2   Symbol: ANAC079/ANAC080   no apical meristem (NAM) family protein, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (GI:1944132) (Arabidopsis thaliana)   chr5:2435984-2437500 FORWARD   Aliases: ANAC079, ANAC080, MBK20.13, MBK20_13	2.8	2.9	-0.0	-0.1	100.0%	-5.0
19846	AT3G57270.1   Symbol: BG1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase GI:16903144 from (Prunus persica)   chr3:21202216-21204168 REVERSE   Aliases: BETA 1,3 GLUCANASE 1, F28O9.120	2.7	2.6	0.0	0.1	100.0%	-5.3
19847	AT4G25450.2   Symbol: ATNAP8	6.1	6.1	-0.0	-0.1	100.0%	-5.0
19848	AT1G31720.1   expressed protein   chr1:11356083-11357062 FORWARD   Aliases: F27M3.8, F27M3_8	2.9	2.8	0.0	0.1	100.0%	-4.0
19849	AT3G51350.1   aspartyl protease family protein, contains Eukaryotic and viral aspartyl proteases active site, PROSITE:PS00141   chr3:19071301-19074489 REVERSE   Aliases: F26O13.3	2.8	2.9	-0.0	-0.1	100.0%	-4.3
19850	AT5G61380.1   Symbol: TOC1   ABI3-interacting protein 1 (AIP1), identical to pseudo-response regulator 1 GI:7576354 from (Arabidopsis thaliana); timing of CAB expression 1 protein (TOC1) GI:9247019; contains Pfam profile PF00072: Response regulator receiver domain; identical to cDNA ABI3-interacting protein 1 (aip1 gene) GI:6996312   chr5:24692313-24695776 FORWARD   Aliases: APRR1, MFB13.13, MFB13_13, PRR1, PSEUDO RESPONSE REGULATOR 1, TIMING OF CAB EXPRESSION 1, TIMING OF CAB1 1	5.3	5.4	-0.0	-0.1	100.0%	-5.0
19851	AT1G53360.1   F-box family protein-related, similar to hypothetical protein GI:4589954 from (Arabidopsis thaliana); contains TIGRFAM TIGR01640: F-box protein interaction domain   chr1:19911185-19912216 FORWARD   Aliases: F12M16.25, F12M16_25	2.5	2.5	-0.0	-0.1	100.0%	-5.6
19852	AT5G44260.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr5:17846853-17848452 REVERSE   Aliases: K9L2.1, K9L2_1	2.5	2.5	0.0	0.1	100.0%	-5.5
19853	AT3G28550.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:10701944-10705166 REVERSE   Aliases: MZN14.2	2.7	2.7	-0.1	-0.1	100.0%	-4.9
19854	AT2G15880.1   leucine-rich repeat family protein / extensin family protein, similar to extensin-like protein (Lycopersicon esculentum) gi:5917664:gb:AAD55979; contains leucine-rich repeats, Pfam:PF00560; contains proline rich extensin domains, INTERPRO:IPR002965	2.6	2.5	0.1	0.1	100.0%	-4.8
19855	AT3G45440.1   lectin protein kinase family protein, contains Legume lectins beta-chain signature, PROSITE:PS00307 and PS00108: Serine/Threonine protein kinases active-site signature, PROSITE:PS00108	2.7	2.7	-0.0	-0.1	100.0%	-5.5
19856	AT1G78310.1   VQ motif-containing protein, contains PF05678: VQ motif   chr1:29468549-29469946 REVERSE   Aliases: F3F9.15, F3F9_15	3.3	3.3	0.0	0.1	100.0%	-4.8
19857	AT3G22170.1   Symbol: FHY3   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr3:7822025-7825891 REVERSE   Aliases: MKA23.12	5.3	5.3	-0.0	-0.1	100.0%	-4.4
19858	AT5G65205.1   short-chain dehydrogenase/reductase (SDR) family protein, contains INTERPRO family IPR002198 short chain dehydrogenase/reductase SDR family   chr5:26068036-26069250 REVERSE   Aliases: None	5.6	5.6	0.0	0.1	100.0%	-4.9
19859	AT3G43160.1   expressed protein, merozoite surface protein 2 (MSP-2), EMBL:PFU72951, Plasmodium falciparum   chr3:15177549-15179213 FORWARD   Aliases: F7K15.10	5.3	5.4	-0.0	-0.1	100.0%	-4.2
19860	AT5G01860.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:335627-336274 FORWARD   Aliases: T20L15.130, T20L15_130	3.1	3.1	0.0	0.1	100.0%	-5.1
19861	AT5G27080.1   WD-40 repeat family protein, contains 5 WD-40 repeats (PF00400); similar to fizzy1 (GI:3298595) {Xenopus laevis};   chr5:9529606-9531084 REVERSE   Aliases: F15P11.5, F15P11_5	3.1	3.1	0.0	0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19862	AT5G04550.1   expressed protein, contains Pfam domain PF05003: protein of unknown function (DUF668)   chr5:1303181-1306117 REVERSE   Aliases: T32M21.140, T32M21_140	3.4	3.4	0.0	0.1	100.0%	-5.4
19863	AT5G44760.1   C2 domain-containing protein, contains INTERPRO:IPR000008 C2 domain   chr5:18077813-18079991 FORWARD   Aliases: K23L20.10, K23L20_10	3.5	3.5	-0.0	-0.1	100.0%	-5.2
19864	AT4G39300.2   expressed protein   chr4:18286787-18288332 FORWARD   Aliases: T22F8.210, T22F8_210	4.7	4.7	-0.0	-0.1	100.0%	-4.6
19865	AT2G20650.2   zinc finger (C3HC4-type RING finger) family protein   chr2:8910718-8914363 REVERSE   Aliases: F23N11.3	4.3	4.4	-0.0	-0.1	100.0%	-4.7
19866	AT4G12330.1   Symbol: CYP706A7   cytochrome P450 family protein, contains Pfam profile:PF00067 cytochrome p450   chr4:7317558-7319737 REVERSE   Aliases: T4C9.170, T4C9_170	2.5	2.5	-0.1	-0.1	100.0%	-4.3
19867	AT1G74700.1   Symbol: NUZ   RNase Z, identical to RNase Z (GI:20975609) (Arabidopsis thaliana)   chr1:28068927-28070878 FORWARD   Aliases: F25A4.32, F25A4_32, RNASE Z	5.0	5.0	-0.0	-0.1	100.0%	-5.1
19868	AT2G26290.1   protein kinase, putative, similar to auxin-regulated dual specificity cytosolic kinase (Lycopersicon esculentum) gi:14484938:gb:AAK62821	3.2	3.2	0.0	0.1	100.0%	-4.5
19869	AT4G38070.1   bHLH family protein, contains Pfam profile: PF00010 helix-loop-helix DNA-binding domain; PMID: 12679534; putative bHLH131 transcription factor   chr4:17876529-17882563 FORWARD   Aliases: F20D10.190, F20D10_190	3.0	3.0	0.0	0.1	100.0%	-5.5
19870	AT2G18245.1   expressed protein   chr2:7944369-7946680 FORWARD   Aliases: None	3.3	3.3	-0.0	-0.1	100.0%	-5.2
19871	AT4G25220.1   transporter, putative, similar to glycerol-3-phosphate transporter (glycerol 3-phosphate permease) (Homo sapiens) GI:7543982   chr4:12920937-12922895 FORWARD   Aliases: F24A6.60, F24A6_60	2.7	2.6	0.0	0.1	100.0%	-4.6
19872	AT3G51540.1   expressed protein, mucin 5AC, Homo sapiens, PIR:S53363   chr3:19126321-19128189 FORWARD   Aliases: F26O13.180	3.1	3.0	0.0	0.1	100.0%	-4.5
19873	AT1G03890.1   cupin family protein, similar to Arabidopsis thaliana 12S seed storage proteins SP:P15455 (gi:808937) and SP:P15456, Brassica napus cruciferin storage protein, gi:762919, and others; contains Pfam profile PF00190 Cupin; Location of ESTs YAY049-3' end, gb:Z26364 and YAY049-5' end, gb:Z26363   chr1:989212-991019 FORWARD   Aliases: F21M11.18, F21M11_18	2.4	2.4	-0.0	-0.1	100.0%	-5.9
19874	AT3G59270.1   syntaxin-related family protein, contains a novel domain similar to F-box that is shared among other proteins in Arabidopsis; similar to proteins At1g56610, At3g54160, At1g47920 (syntaxin SYP81), At5g41830, At3g44180, At1g48390, At3g59270 (Arabidopsis thaliana)   chr3:21917570-21918849 REVERSE   Aliases: F25L23.130	2.5	2.5	-0.0	-0.1	100.0%	-5.7
19875	AT2G24200.1   cytosol aminopeptidase, identical to cytosol aminopeptidase SP:P30184 from (Arabidopsis thaliana); contains Pfam profiles: PF00883 cytosol aminopeptidase family catalytic domain, PF02789: cytosol aminopeptidase family N-terminal domain   chr2:10293889-10296635 REVERSE   Aliases: F27D4.11, F27D4_11	10.8	10.8	0.0	0.1	100.0%	-5.0
19876	AT2G46150.1   expressed protein, and genefinder   chr2:18968476-18969449 FORWARD   Aliases: T3F17.20	3.1	3.1	0.0	0.1	100.0%	-5.6
19877	AT2G29820.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:12735439-12736605 REVERSE   Aliases: T27A16.8, T27A16_8	3.0	3.0	-0.0	-0.1	100.0%	-5.0
19878	AT2G37720.1   expressed protein   chr2:15825160-15828373 FORWARD   Aliases: F13M22.22, F13M22_22	2.1	2.1	-0.0	-0.1	100.0%	-5.7
19879	AT1G78130.1   transporter-related, low similarity to spinster type III (Drosophila melanogaster) GI:12003974; contains Pfam profile: PF00083 major facilitator superfamily protein   chr1:29405033-29406961 FORWARD   Aliases: T11I11.7, T11I11_7	3.6	3.5	0.0	0.1	100.0%	-4.8
19880	AT5G10280.1   Symbol: MYB92   myb family transcription factor (MYB92), contains PFAM profile myb DNA binding domain PF00249; identical to cDNA putative transcription factor (MYB92) GI:3941523   chr5:3232570-3234211 FORWARD   Aliases: F18D22.50, F18D22_50	2.6	2.5	0.0	0.1	100.0%	-4.4
19881	AT3G18520.2   similar to histone deacetylase family protein [Arabidopsis thaliana] (TAIR:At5g61060.1); similar to histone deacetylase HDA110 isoform 3 [Zea mays] (GB:AAM93214.1); similar to histone deacetylase HDA110 isoform 1 [Zea mays] (GB:AAM93212.1); contains InterPro domain Histone deacetylase family (InterPro:IPR000286); contains InterPro domain Zn-finger, Ran-binding (InterPro:IPR001876)   chr3:6361185-6365621 FORWARD   Aliases: MYF24.24	6.1	6.1	0.0	0.1	100.0%	-4.8
19882	AT5G19900.1   PRLI-interacting factor, putative, strong similarity to PRLI-interacting factor A (Arabidopsis thaliana) GI:11139262   chr5:6728162-6730047 REVERSE   Aliases: F28I16.50, F28I16_50	7.2	7.1	0.0	0.1	100.0%	-5.0



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19883	AT5G45300.2   similar to glycosyl hydrolase family 14 protein [Arabidopsis thaliana] (TAIR:At2g45880.1); similar to beta-amylase [Castanea crenata] (GB:AAK30294.1); contains InterPro domain Glycoside hydrolase, family 14 (InterPro:IPR001554); contains InterPro domain Plant protein of unknown function DUF822 (InterPro:IPR008540)   chr5:18370835-18374102 FORWARD   Aliases: K9E15.8, K9E15_8	5.0	5.0	-0.0	-0.1	100.0%	-4.7
19884	AT1G73240.1   expressed protein   chr1:27545848-27548581 REVERSE   Aliases: T18K17.9, T18K17_9	3.9	3.9	-0.0	-0.1	100.0%	-5.0
19885	AT4G33730.1   pathogenesis-related protein, putative, similar to SP:P33154 Pathogenesis-related protein 1 precursor (PR-1) {Arabidopsis thaliana}; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:16185101-16185619 FORWARD   Aliases: T16L1.220, T16L1_220	3.0	3.0	0.0	0.1	100.0%	-4.2
19886	AT5G48080.1   expressed protein, ; expression supported by MPSS   chr5:19501391-19502198 FORWARD   Aliases: MDN11.16, MDN11_16	4.4	4.4	0.0	0.1	100.0%	-5.0
19887	AT3G26980.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr3:9947403-9949277 REVERSE   Aliases: MOJ10.7	8.6	8.6	-0.0	-0.1	100.0%	-4.9
19888	AT1G14960.1   major latex protein-related / MLP-related, low similarity to major latex protein {Papaver somniferum}(GI:20810) contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family   chr1:5159194-5160076 REVERSE   Aliases: F10B6.39, F10B6_39	3.2	3.3	-0.1	-0.1	100.0%	-4.5
19889	AT1G64830.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr1:24094934-24096229 REVERSE   Aliases: F13O11.13, F13O11_13	2.7	2.7	-0.0	-0.1	100.0%	-5.4
19890	AT5G48900.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from (Fragaria x ananassa); non-consensus AG donor splice site at exon 2   chr5:19842363-19846318 FORWARD   Aliases: K19E20.1, K19E20_1	4.0	3.9	0.0	0.1	100.0%	-5.0
19891	AT3G31310.1   hypothetical protein   chr3:12679707-12681196 FORWARD   Aliases: T22B15.2	2.0	2.1	-0.0	-0.1	100.0%	-5.8
19892	AT2G02410.1   expressed protein   chr2:632639-634831 FORWARD   Aliases: AT2G02420, T16F16.20, T16F16_20	3.7	3.7	-0.0	-0.1	100.0%	-5.1
19893	AT1G67990.1   caffeoyl-CoA 3-O-methyltransferase, putative, similar to GI:2960356 (Populus balsamifera subsp. trichocarpa), GI:684942 (Medicago sativa subsp. sativa)   chr1:25493118-25494530 FORWARD   Aliases: T23K23.16, T23K23_16	2.4	2.3	0.0	0.1	100.0%	-5.8
19894	AT2G13270.1   expressed protein   chr2:5499735-5500937 FORWARD   Aliases: F15O11.9, F15O11_9	2.1	2.1	0.0	0.1	100.0%	-6.0
19895	AT4G15270.1   glucosyltransferase-related, contains some similarity to glucosyltransferase GI:14349251 from (Nicotiana tabacum)   chr4:8716601-8717796 REVERSE   Aliases: DL3680C, FCAALL.253	5.1	5.1	0.0	0.1	100.0%	-4.7
19896	AT5G19610.1   sec7 domain-containing protein, similar to SP:Q42510 Pattern formation protein EMB30 (GNOM) {Arabidopsis thaliana}; contains Pfam profile PF01369: Sec7 domain   chr5:6617748-6622047 REVERSE   Aliases: T29J13.30, T29J13_30	2.3	2.3	-0.0	-0.1	100.0%	-5.8
19897	AT3G26470.1   expressed protein   chr3:9687335-9688879 FORWARD   Aliases: F20C19.20	3.1	3.2	-0.0	-0.1	100.0%	-4.1
19898	AT2G46590.2   Symbol: DAG2   similar to Dof zinc finger protein DAG1 / Dof affecting germination 1 (DAG1) / transcription factor BBFa (BBFA) [Arabidopsis thaliana] (TAIR:At3g61850.1); similar to Dof zinc finger protein [Oryza sativa] (GB:BAA78572.1); contains InterPro domain Zn-finger, Dof type (InterPro:IPR003851)   chr2:19140112-19141976 FORWARD   Aliases: DOF AFFECTING GERMINATION 2, F13A10.12	2.6	2.6	0.0	0.1	100.0%	-5.7
19899	AT2G18070.1   expressed protein   chr2:7859611-7860748 FORWARD   Aliases: T27K22.6, T27K22_6	2.4	2.4	0.0	0.1	100.0%	-5.6
19900	AT2G06700.1   expressed protein   chr2:2671715-2672368 REVERSE   Aliases: T14A4.14, T14A4_14	4.7	4.7	-0.0	-0.1	100.0%	-4.7
19901	AT5G59410.1   expressed protein   chr5:23976815-23978032 REVERSE   Aliases: F2O15.9, F2O15_9	8.3	8.3	-0.0	-0.1	100.0%	-4.8
19902	AT3G07520.1   Symbol: ATGLR1.4   glutamate receptor family protein (GLR1.4), plant glutamate receptor family, PMID:11379626   chr3:2394897-2398297 REVERSE   Aliases: F21O3.23, GLR1.4	3.4	3.4	-0.0	-0.1	100.0%	-5.3
19903	AT3G12910.1   expressed protein   chr3:4110046-4110655 FORWARD   Aliases: MGH6.1, MGH6.22, MGH6_1, MJM20.5	2.2	2.2	-0.0	-0.1	100.0%	-6.2
19904	AT3G11340.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:3556713-3558275 FORWARD   Aliases: F11B9.23	3.0	3.0	-0.0	-0.1	100.0%	-4.6
19905	AT2G15520.1   zinc finger protein, putative, strong similarity to zinc finger protein (Arabidopsis thaliana) GI:976277	3.8	3.8	-0.0	-0.1	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19906	AT4G03280.2   Symbol: PETC   cytochrome B6-F complex iron-sulfur subunit, chloroplast / Rieske iron-sulfur protein / plastoquinol-plastocyanin reductase (petC), identical to gi:9843639; identical to cDNA rieske iron-sulfur protein precursor (petC) GI:5725449   chr4:1440177-1441861 FORWARD   Aliases: F4C21.21, F4C21_21, PGR1, PHOTOSYNTHETIC ELECTRON TRANSFER C, PROTON GRADIENT REGULATION 1, RIESKE IRON SULFUR PROTEIN PRECURSOR	11.2	11.1	0.0	0.1	100.0%	-4.6
19907	AT3G61120.1   Symbol: AGL13   MADS-box protein (AGL13)   chr3:22629234-22631466 REVERSE   Aliases: AGAMOUS LIKE 13, MADS BOX PROTEIN AGL13, T20K12.20	2.1	2.0	0.0	0.1	100.0%	-6.1
19908	AT5G37610.1   expressed protein   chr5:14955351-14955842 FORWARD   Aliases: K12B20.7, K12B20_7	2.8	2.8	0.0	0.1	100.0%	-5.4
19909	AT2G37840.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:15858968-15863379 FORWARD   Aliases: AT2G37850, T8P21.25, T8P21_25	4.7	4.6	0.0	0.1	100.0%	-5.0
19910	AT4G20220.1   expressed protein   chr4:10918686-10922406 FORWARD   Aliases: F1C12.140, F1C12_140	2.6	2.6	0.0	0.1	100.0%	-5.9
19911	AT4G09930.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to AIG1 protein SP:P54120 (Arabidopsis thaliana); contains Pfam PF04548: AIG1 family;   chr4:6228553-6230045 FORWARD   Aliases: T5L19.60, T5L19_60	2.7	2.7	0.0	0.1	100.0%	-5.6
19912	AT1G17980.2   nucleotidyltransferase family protein, contains Pfam profiles: PF01909 nucleotidyltransferase domain, PF04926 poly(A) polymerase predicted RNA binding domain   chr1:6187509-6191681 REVERSE   Aliases: F2H15.20, F2H15_20	5.4	5.4	-0.0	-0.1	100.0%	-4.8
19913	AT4G30490.1   AFG1-like ATPase family protein, contains Pfam profile: PF03969 AFG1-like ATPase	7.9	7.9	0.0	0.1	100.0%	-4.8
19914	AT3G28580.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr3:10716860-10718566 FORWARD   Aliases: MZN14.6	2.9	2.9	-0.0	-0.1	100.0%	-5.4
19915	AT2G43310.1   expressed protein   chr2:18003158-18003599 FORWARD   Aliases: F14B2.31	2.6	2.6	0.0	0.1	100.0%	-5.7
19916	AT3G10260.3   reticulon family protein, weak similarity to Nogo-C protein (Rattus norvegicus) GI:6822251; contains Pfam profile PF02453: Reticulon; identical to cDNA GI:32331854   chr3:3171231-3172964 REVERSE   Aliases: F14P13.14	6.8	6.8	0.0	0.1	100.0%	-5.1
19917	AT5G10790.1   Symbol: UBP22   ubiquitin-specific protease 22 (UBP22), almost identical to ubiquitin-specific protease 22 GI:11993484 (Arabidopsis thaliana), one amino acid difference   chr5:3410540-3412634 FORWARD   Aliases: T30N20.60, T30N20_60, UBIQUITIN SPECIFIC PROTEASE 22	5.2	5.2	0.0	0.1	100.0%	-5.2
19918	AT4G17080.1   MORN (Membrane Occupation and Recognition Nexus) repeat-containing protein /phosphatidylinositol-4-phosphate 5-kinase-related, low similarity to phosphatidylinositol-4-phosphate 5-kinase AtPIP5K1 (Arabidopsis thaliana) GI:3702691; contains Pfam profile PF02493: MORN repeat   chr4:9601587-9603831 FORWARD   Aliases: DL4570W, FCAALL.347	5.4	5.4	-0.0	-0.1	100.0%	-4.8
19919	AT4G05340.1   hypothetical protein   chr4:2725687-2726062 FORWARD   Aliases: C6L9.20, C6L9_20	2.5	2.5	-0.0	-0.1	100.0%	-5.6
19920	AT5G37590.1   kinesin light chain-related, low similarity to kinesin light chain (Plectonema boryanum) GI:2645229; contains Pfam profile PF00515: TPR Domain   chr5:14947728-14949473 REVERSE   Aliases: K12B20.5, K12B20_5	3.8	3.8	0.0	0.1	100.0%	-5.3
19921	AT4G10540.1   subtilase family protein, contains similarity to subtilase; SP1 GI:9957714 from (Oryza sativa)   chr4:6512511-6515739 REVERSE   Aliases: F7L13.120, F7L13_120	2.3	2.3	0.0	0.1	100.0%	-6.1
19922	AT4G04970.1   Symbol: ATGSL1	3.5	3.5	0.0	0.1	100.0%	-5.1
19923	AT5G37370.2   pre-mRNA splicing factor PRP38 family protein (SRL1), contains Pfam profile PF03371: PRP38 family   chr5:14829915-14833750 REVERSE   Aliases: MNJ8.19, MNJ8_19	6.4	6.4	0.0	0.1	100.0%	-5.0
19924	AT5G22380.1   Symbol: ANAC090   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr5:7408783-7410099 REVERSE   Aliases: ANAC090, MWD9.18, MWD9_18	2.2	2.2	0.0	0.1	100.0%	-6.0
19925	AT5G04530.1   beta-ketoacyl-CoA synthase family protein, KCS1 fatty acid elongase 3-ketoacyl-CoA synthase 1, Arabidopsis thaliana, EMBL:AF053345   chr5:1291823-1293689 REVERSE   Aliases: T32M21.130, T32M21_130	2.4	2.4	0.0	0.1	100.0%	-5.9
19926	AT5G14690.1   expressed protein, predicted protein, Arabidopsis thaliana   chr5:4733802-4734550 REVERSE   Aliases: T9L3.3	3.2	3.2	-0.0	-0.1	100.0%	-4.6
19927	AT3G04670.2   Symbol: WRKY39	6.1	6.1	0.0	0.1	100.0%	-5.1
19928	AT2G43150.1   proline-rich extensin-like family protein, similar to CRANTZ hydroxyproline-rich glycoprotein (Manihot esculenta) gi:7211797:gb:AAF40442; similar to extensin gi:1165322:gb:AAB53156; contains proline-rich extensin domains, INTERPRO:IPR002965	2.7	2.7	-0.0	-0.1	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19929	AT3G44780.1   expressed protein   chr3:16332611-16333591 REVERSE   Aliases: T32N15.5	2.7	2.7	-0.0	-0.1	100.0%	-5.5
19930	AT5G41685.1   mitochondrial import receptor subunit TOM7 / translocase of outer membrane 7 kDa subunit (TOM7.1), identical to SP:Q9ASY8 Mitochondrial import receptor subunit TOM7 (Translocase of outer membrane 7 kDa subunit) {Arabidopsis thaliana}   chr5:16686314-16686950 REVERSE   Aliases: None	7.4	7.4	-0.0	-0.1	100.0%	-4.6
19931	AT5G37530.1   thiF family protein, similar to SP:P30138 Adenylyltransferase thiF (EC 2.7.7.-) {Escherichia coli}; contains Pfam profile PF00899: ThiF family   chr5:14923719-14926407 FORWARD   Aliases: MPA22.7, MPA22_7	3.7	3.6	0.0	0.1	100.0%	-5.0
19932	AT2G27330.1   RNA recognition motif (RRM)-containing protein   chr2:11702112-11703693 REVERSE   Aliases: F12K2.9	6.3	6.3	0.0	0.1	100.0%	-4.9
19933	AT1G43890.1   Symbol: ATRAB18   Ras-related GTP-binding protein, putative, similar to GTP-binding protein(RAB1Y) GI:1370173 from (Lotus japonicus)   chr1:16649176-16651079 FORWARD   Aliases: ATRAB18, F28H19.15, F28H19_15	6.6	6.6	0.0	0.1	100.0%	-4.8
19934	AT5G18140.1   DNAJ heat shock N-terminal domain-containing protein, similar to DnaJ protein Tid-1 (Homo sapiens) GI:17066575; contains Pfam profile PF00226 DnaJ domain   chr5:5998201-5999890 FORWARD   Aliases: MRG7.10, MRG7_10	7.6	7.6	0.0	0.1	100.0%	-4.8
19935	AT4G29570.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase homolog DesA (Arabidopsis thaliana) GI:4836443, cytidine deaminase 8 (CDA8) (Arabidopsis thaliana) GI:5080714; similar to cytidine deaminase (CDD) (Arabidopsis thaliana) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14507404-14508488 FORWARD   Aliases: T16L4.80, T16L4_80	2.4	2.4	-0.0	-0.1	100.0%	-5.6
19936	AT4G08840.1   pumilio/Puf RNA-binding domain-containing protein, contains similarity to RNA binding protein PufA (Dictyostelium discoideum) gi:5106561:gb:AAD39751   chr4:5631295-5633609 FORWARD   Aliases: T32A17.150, T32A17_150	3.3	3.3	-0.0	-0.1	100.0%	-5.2
19937	AT3G20980.1   expressed protein   chr3:7355969-7357972 FORWARD   Aliases: MSA6.3	2.9	2.9	0.0	0.1	100.0%	-5.4
19938	AT4G36370.1   expressed protein   chr4:17187253-17187945 FORWARD   Aliases: F23E13.210, F23E13_210	3.2	3.2	-0.0	-0.1	100.0%	-5.4
19939	NA	8.9	8.9	-0.0	-0.1	100.0%	-4.9
19940	AT3G44190.1   pyridine nucleotide-disulphide oxidoreductase family protein, low similarity to dihydrolipoamide dehydrogenase from Clostridium magnum (GI:472330); contains Pfam profile PF00070 Pyridine nucleotide-disulphide oxidoreductase domain   chr3:15912784-15914595 REVERSE   Aliases: F26G5.140	7.4	7.4	-0.0	-0.1	100.0%	-4.9
19941	AT5G37420.1   hypothetical protein, contains Pfam PF04510 : Family of unknown function (DUF577); common family comprised of At5g37410, At5g37400, At5g37920, At5g37460, At5g37650, At5g37470, At5g37420, At5g37430   chr5:14857373-14859300 FORWARD   Aliases: T25O11.7, T25O11_7	3.3	3.3	0.0	0.1	100.0%	-5.5
19942	AT2G43050.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:17909563-17911520 FORWARD   Aliases: ATPMEPCRD, MFL8.9	3.1	3.1	0.0	0.1	100.0%	-4.8
19943	AT3G20840.1   Symbol: PLT1   similar to ovule development protein, putative [Arabidopsis thaliana] (TAIR:At1g51190.1); similar to OSJNBa0014K14.15 [Oryza sativa (japonica cultivar-group)] (GB:XP_473084.1); contains InterPro domain Pathogenesis-related transcriptional factor and ERF (InterPro:IPR001471)   chr3:7300681-7303699 FORWARD   Aliases: MOE17.15, PLETHORA 1	3.1	3.1	0.0	0.1	100.0%	-5.5
19944	AT3G16700.1   fumarylacetoacetate hydrolase family protein, contains Pfam domain, PF01557: fumarylacetoacetate hydrolase family protein   chr3:5687790-5689722 FORWARD   Aliases: MGL6.17	3.9	3.9	-0.0	-0.1	100.0%	-5.1
19945	AT5G04370.2   similar to S-adenosyl-L-methionine:carboxyl methyltransferase family protein [Arabidopsis thaliana] (TAIR:At3g11480.1); similar to SAM:benzoic acid carboxyl methyltransferase [Antirrhinum majus] (GB:AAF98284.1); contains InterPro domain SAM dependent carboxyl methyltransferase (InterPro:IPR005299)   chr5:1231713-1234148 FORWARD   Aliases: T19N18.100, T19N18_100	2.6	2.6	0.0	0.1	100.0%	-5.5
19946	AT2G27990.1   homeodomain-containing protein   chr2:11928510-11931775 REVERSE   Aliases: T1E2.9, T1E2_9	2.7	2.8	-0.0	-0.1	100.0%	-5.2
19947	AT1G58200.2   mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein, contains Pfam profile PF00924: Mechanosensitive ion channel   chr1:21551852-21556763 REVERSE   Aliases: F16M22.2, F16M22_2	8.5	8.6	-0.0	-0.1	100.0%	-4.9
19948	AT2G36470.1   expressed protein   chr2:15306441-15308069 REVERSE   Aliases: F1O11.10, F1O11_10	2.9	2.9	0.0	0.1	100.0%	-5.0
19949	AT1G09150.1   pseudouridine synthase and archaeosine transglycosylase (PUA) domain-containing protein, similar to MCT-1 (putative oncogene) (Homo sapiens) GI:6177738; contains Pfam profile PF01472: PUA domain   chr1:2946264-2949161 FORWARD   Aliases: T12M4.18, T12M4_18	7.6	7.7	-0.0	-0.1	100.0%	-4.8
19950	AT2G36940.1   expressed protein   chr2:15518865-15519066 REVERSE   Aliases: T1J8.12, T1J8_12	3.0	3.0	-0.0	-0.1	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19951	AT2G35080.1   expressed protein, ; expression supported by MPSS   chr2:14796324-14798527 REVERSE   Aliases: T4C15.25, T4C15_25	3.9	3.8	0.0	0.1	100.0%	-5.1
19952	AT4G26980.1   expressed protein   chr4:13548552-13550721 REVERSE   Aliases: F10M23.320, F10M23_320	3.8	3.9	-0.0	-0.1	100.0%	-5.1
19953	AT2G12610.1   expressed protein, ; expression supported by MPSS   chr2:5148919-5150611 FORWARD   Aliases: T4E5.7, T4E5_7	2.1	2.2	-0.0	-0.1	100.0%	-6.0
19954	AT5G44370.1   transporter-related, similar to vesicular glutamate transporter 2 (Mus musculus) GI:15811369, Na-dependent inorganic phosphate cotransporter (Homo sapiens) GI:7328923; contains Pfam profile PF00083: major facilitator superfamily protein   chr5:17892112-17894791 REVERSE   Aliases: K9L2.16, K9L2_16	5.0	5.0	-0.0	-0.1	100.0%	-5.0
19955	AT1G47330.1   expressed protein, contains Pfam profile PF01595: Domain of unknown function   chr1:17353490-17356733 FORWARD   Aliases: T3F24.6, T3F24_6	7.6	7.5	0.0	0.1	100.0%	-4.9
19956	AT1G26610.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr1:9193337-9195267 FORWARD   Aliases: T1K7.2, T1K7_2	4.0	4.0	-0.0	-0.1	100.0%	-5.2
19957	AT5G62400.1   expressed protein   chr5:25071840-25072832 REVERSE   Aliases: MMI9.23, MMI9_23	2.5	2.5	-0.0	-0.1	100.0%	-5.7
19958	AT2G22290.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein GI:550072 from (Homo sapiens)   chr2:9473524-9474768 FORWARD   Aliases: T26C19.5, T26C19_5	2.2	2.2	-0.0	-0.1	100.0%	-5.6
19959	AT1G34010.1   expressed protein   chr1:12359529-12361169 REVERSE   Aliases: F12G12.17, F12G12_17	5.5	5.5	-0.0	-0.1	100.0%	-4.6
19960	AT2G32740.1   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr2:13893903-13895309 FORWARD   Aliases: F24L7.12, F24L7_12	2.9	2.9	-0.0	-0.1	100.0%	-5.8
19961	AT2G26020.1   Symbol: PDF1.2b   plant defensin-fusion protein, putative (PDF1.2b), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to antifungal protein 1 preprotein (Raphanus sativus) gi:609322:gb:AAA69541   chr2:11096328-11096675 FORWARD   Aliases: PDF1.2b, T19L18.17, T19L18_17	3.1	3.1	-0.0	-0.1	100.0%	-4.9
19962	AT1G01760.1   adenosine-deaminase family / editase family, similar to double-stranded RNA-specific editase GB:AAF69673 GI:7770275 from (Danio rerio)   chr1:276866-278448 REVERSE   Aliases: T1N6.17, T1N6_17	2.5	2.5	0.0	0.1	100.0%	-5.7
19963	AT5G13890.3   expressed protein, contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)   chr5:4478845-4480923 REVERSE   Aliases: MAC12.15, MAC12_15	5.5	5.5	-0.0	-0.1	100.0%	-4.6
19964	AT2G20515.1   expressed protein   chr2:8845935-8846768 REVERSE   Aliases: None	2.3	2.3	-0.0	-0.1	100.0%	-5.5
19965	AT4G15730.1   expressed protein   chr4:8951111-8957630 REVERSE   Aliases: DL3905C, FCAALL.370	3.3	3.3	0.0	0.1	100.0%	-5.4
19966	AT3G21290.1   dentin sialophosphoprotein-related, contains weak similarity to Dentin sialophosphoprotein precursor (Swiss-Prot:Q9NZW4) (Homo sapiens)   chr3:7482137-7488941 FORWARD   Aliases: MXL8.16	4.5	4.5	0.0	0.1	100.0%	-4.9
19967	AT4G12250.1   Symbol: GAE5   NAD-dependent epimerase/dehydratase family protein, similar to nucleotide sugar epimerase from Vibrio vulnificus GI:3093975 (PID:g3093975), WbnF (Escherichia coli) GI:5739472, CAPI protein {Staphylococcus aureus} SP:P39858; contains Pfam profile PF01370 NAD dependent epimerase/dehydratase family	4.6	4.6	0.0	0.1	100.0%	-5.1
19968	AT3G59050.1   amine oxidase family protein, similar to polyamine oxidase (EC 1.5.3.11) precursor - Zea mays (SP:O64411); contains Pfam profile PF01593 amine oxidase, flavin-containing   chr3:21835673-21838486 REVERSE   Aliases: F17J16.100	6.2	6.2	0.0	0.1	100.0%	-4.8
19969	AT1G03600.1   photosystem II family protein, similar to SP:P74367 {Synechocystis sp.}; similar to ESTs emb:Z27038, gb:AA451546, emb:Z29876, gb:T45359 and gb:R90316   chr1:898875-899654 FORWARD   Aliases: F21B7.21, F21B7.37, F21B7_37	8.4	8.4	-0.0	-0.1	100.0%	-4.2
19970	AT3G12490.2   similar to cysteine protease inhibitor, putative / cystatin, putative [Arabidopsis thaliana] (TAIR:At5g05110.1); similar to cysteine protease inhibitor CPI-1 [Brassica oleracea] (GB:AAL59842.1); contains InterPro domain Cystatin C/M (InterPro:IPR003243); contains InterPro domain Cysteine protease inhibitor (InterPro:IPR000010)	12.8	12.7	0.0	0.1	100.0%	-5.1
19971	AT3G30660.1   hypothetical protein   chr3:12209587-12209820 FORWARD   Aliases: MED16.2	2.1	2.1	0.0	0.1	100.0%	-5.2
19972	AT5G60240.1   expressed protein   chr5:24268608-24268854 FORWARD   Aliases: F15L12.5, F15L12_5	3.2	3.2	0.0	0.1	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19973	AT1G02570.1   expressed protein   chr1:541380-543983 FORWARD   Aliases: T14P4.23, T14P4_23	3.9	3.9	-0.0	-0.1	100.0%	-5.1
19974	AT5G60120.1   Symbol: TOE2   AP2 domain-containing transcription factor, putative, Similar to Floral homeotic protein APETALA2 protein (SP:P47927) (Arabidopsis thaliana); homolog HAP2, Hyacinthus orientalis, EMBL:AF134116	3.2	3.2	0.0	0.1	100.0%	-4.3
19975	AT2G01390.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr2:172255-174136 FORWARD   Aliases: F10A8.29	2.6	2.6	-0.0	-0.1	100.0%	-5.5
19976	AT2G30120.1   expressed protein   chr2:12867618-12868987 REVERSE   Aliases: T27E13.14, T27E13_14	2.8	2.8	0.0	0.1	100.0%	-5.8
19977	AT1G10910.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:3639908-3643974 FORWARD   Aliases: T19D16.17, T19D16_17	4.5	4.5	-0.0	-0.1	100.0%	-4.8
19978	AT3G05240.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:1493690-1495387 REVERSE   Aliases: T12H1.21, T12H1_21	3.9	3.9	-0.0	-0.1	100.0%	-5.0
19979	AT2G46880.2   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	2.8	2.8	0.0	0.1	100.0%	-5.4
19980	AT1G22630.1   expressed protein, contains Pfam PF00684 : DnaJ central domain (4 repeats)   chr1:8003304-8004286 FORWARD   Aliases: F12K8.2	2.9	2.8	0.0	0.1	100.0%	-5.4
19981	AT5G57240.2   similar to oxysterol-binding family protein [Arabidopsis thaliana] (TAIR:At4g25850.1); similar to oxysterol-binding protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_483346.1); contains InterPro domain Oxysterol-binding protein (InterPro:IPR000648)   chr5:23210395-23212702 FORWARD   Aliases: MJB24.5, MJB24_5	3.3	3.3	0.0	0.1	100.0%	-5.5
19982	AT3G45540.1   zinc finger (C3HC4-type RING finger) family protein, contains a Prosite:PS00518 Zinc finger, C3HC4 type (RING finger), signature	2.8	2.8	-0.0	-0.1	100.0%	-5.3
19983	AT3G45900.1   expressed protein   chr3:16885387-16887007 REVERSE   Aliases: F16L2.110	5.6	5.6	-0.0	-0.1	100.0%	-5.0
19984	AT4G28420.2   similar to aminotransferase, putative [Arabidopsis thaliana] (TAIR:At2g20610.1); similar to putative nicotianamine aminotransferase A [Oryza sativa (japonica cultivar-group)] (GB:XP_465161.1); contains InterPro domain Aminotransferase, class I and II (InterPro:IPR004839); contains InterPro domain Tyrosine/nicotianamine aminotransferases (InterPro:IPR005958); contains InterPro domain 1-aminocyclopropane-1-carboxylate synthase (InterPro:IPR001176)   chr4:14055667-14057584 FORWARD   Aliases: F2009.100, F2009_100	3.0	3.0	0.0	0.1	100.0%	-5.4
19985	AT2G45050.1   zinc finger (GATA type) family protein, identical to cDNA GATA transcription factor 2 GI:2959731	2.6	2.6	-0.0	-0.1	100.0%	-5.4
19986	AT5G56630.1   phosphofructokinase family protein, similar to phosphofructokinase (Amycolatopsis methanolica) GI:17432243; contains Pfam profile PF00365: Phosphofructokinase   chr5:22941148-22944189 FORWARD   Aliases: MIK19.8, MIK19_8	10.0	10.0	0.0	0.1	100.0%	-5.0
19987	AT4G25560.1   myb family transcription factor (MYB18), contains PFAM profile: Myb DNA binding domain PF00249   chr4:13052564-13053627 FORWARD   Aliases: M7J2.70, M7J2_70	3.1	3.1	0.0	0.1	100.0%	-4.9
19988	AT2G35480.1   expressed protein   chr2:14917489-14919127 FORWARD   Aliases: T32F12.14, T32F12_14	4.3	4.3	0.0	0.1	100.0%	-4.8
19989	AT1G13970.1   expressed protein   chr1:4779520-4782531 REVERSE   Aliases: F16A14.19	3.5	3.5	0.0	0.1	100.0%	-4.3
19990	AT2G29330.1   tropinone reductase, putative / tropine dehydrogenase, putative, similar to tropinone reductase SP:P50165 from (Datura stramonium)   chr2:12601667-12603407 FORWARD   Aliases: F16P2.29, F16P2_29	2.1	2.1	0.0	0.1	100.0%	-4.9
19991	AT5G20680.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr5:6998105-7001912 FORWARD   Aliases: T1M15.80, T1M15_80	5.0	5.0	-0.0	-0.1	100.0%	-5.4
19992	AT3G16660.1   expressed protein   chr3:5676835-5677921 FORWARD   Aliases: MGL6.12	5.7	5.6	0.0	0.1	100.0%	-4.8
19993	AT5G06640.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:2039860-2041929 REVERSE   Aliases: F15M7.17, F15M7_17	3.2	3.2	-0.1	-0.1	100.0%	-4.3
19994	AT1G09890.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g09910.1); similar to PREDICTED OSJNBb0011H15.45 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_507326.1)   chr1:3215093-3217540 REVERSE   Aliases: F21M12.28, F21M12_28	3.4	3.4	0.0	0.1	100.0%	-5.4
19995	AT5G40820.1   FAT domain-containing protein / phosphatidylinositol 3- and 4-kinase family protein, similar to Atr protein (Xenopus laevis) GI:11385422; contains Pfam profiles PF00454 Phosphatidylinositol 3- and 4-kinase, PF02259 FAT domain, PF02260 FAT C domain   chr5:16359973-16371126 REVERSE   Aliases: MHK7.5, MHK7_5	4.2	4.2	0.0	0.1	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
19996	AT1G54380.1   spliceosome protein-related, contains Pfam domain, PF04938: Survival motor neuron (SMN) interacting protein 1 (SIP1)   chr1:20301632-20304575 REVERSE   Aliases: F20D21.20, F20D21_20	4.6	4.6	-0.0	-0.1	100.0%	-5.3
19997	AT4G10020.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to sterol-binding dehydrogenase steroleosin GI:15824408 from (Sesamum indicum)	2.6	2.6	-0.0	-0.1	100.0%	-5.4
19998	AT1G48640.1   lysine and histidine specific transporter, putative, similar to lysine and histidine specific transporter GI:2576361 from (Arabidopsis thaliana); contains Pfam profile PF01490: Transmembrane amino acid transporter protein   chr1:17990026-17992659 FORWARD   Aliases: F11I4.17, F11I4_17	3.8	3.7	0.0	0.1	100.0%	-4.8
19999	AT5G14000.1   Symbol: ANAC084   no apical meristem (NAM) family protein, contains Pfam PF02365: No apical meristem (NAM) domain;   chr5:4518010-4519302 FORWARD   Aliases: ANAC084, MAC12.3, MAC12_3	3.3	3.4	-0.0	-0.1	100.0%	-4.7
20000	AT3G32100.1   hypothetical protein   chr3:13100684-13101017 FORWARD   Aliases: F1M23.29	2.4	2.4	-0.0	-0.1	100.0%	-6.1
20001	AT4G03640.1   hypothetical protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250   chr4:1614812-1618126 FORWARD   Aliases: T5L23.14, T5L23_14	2.7	2.7	0.0	0.1	100.0%	-5.6
20002	AT5G40860.1   hypothetical protein   chr5:16388659-16389213 FORWARD   Aliases: MHK7.9, MHK7_9	2.9	2.9	0.0	0.1	100.0%	-4.4
20003	AT1G02270.1   endonuclease/exonuclease/phosphatase family protein / calcium-binding EF hand family protein, contains Pfam profiles: PF03372 endonuclease/exonuclease/phosphatase family, PF00036 EF hand   chr1:443157-446227 REVERSE   Aliases: T6A9.35	6.1	6.0	0.0	0.1	100.0%	-5.0
20004	AT5G41050.1   expressed protein   chr5:16450545-16451546 REVERSE   Aliases: MEE6.12, MEE6_12	2.9	2.9	0.0	0.1	100.0%	-5.1
20005	AT3G45390.1   lectin protein kinase family protein, contains Protein kinases ATP-binding region signature, Prosite:PS00107 and Legume lectins beta-chain signature, Prosite:PS00307   chr3:16658906-16660959 REVERSE   Aliases: F18N11.150	2.7	2.7	0.0	0.1	100.0%	-5.0
20006	AT5G39630.1   vesicle transport v-SNARE family protein, similar to v-SNARE AtVTI1a (GI:10177700) Arabidopsis thaliana; contains Pfam profile PF05008: Vesicle transport v-SNARE protein   chr5:15885490-15886942 FORWARD   Aliases: MIJ24.100, MIJ24_100	2.6	2.6	-0.0	-0.1	100.0%	-5.4
20007	AT4G08880.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At3g24380, At5g36840, At5g35010, At3g42740, At4g05290, At2g14770, At3g43390, At2g05560, At1g34730, At1g27790, At1g34740, At1g27780, At5g36850, At3g42730, At1g52020, At3g24390, At4g05280, At1g25886, At4g03300   chr4:5685008-5691310 FORWARD   Aliases: T3H13.8, T3H13_8	2.3	2.3	-0.0	-0.1	100.0%	-6.2
20008	AT2G17960.1   hypothetical protein   chr2:7819462-7820211 REVERSE   Aliases: T27K22.17, T27K22_17	3.0	3.0	0.0	0.1	100.0%	-5.3
20009	AT2G22000.1   expressed protein   chr2:9369406-9370082 FORWARD   Aliases: F7D8.32, F7D8_32	2.9	2.8	0.0	0.1	100.0%	-4.9
20010	AT3G57560.1   aspartate/glutamate/uridylate kinase family protein, similar to acetylglutamate kinase from Porphyra purpurea (SP:P31595), Campylobacter jejuni (GI:6650364) contains Pfam profile PF00696: Amino acid kinase family   chr3:21321802-21323289 REVERSE   Aliases: T8H10.160	6.7	6.7	0.0	0.1	100.0%	-4.6
20011	AT5G48550.1   F-box family protein-related, similar to unknown protein (gb AAF19735.1); contains TIGRFAM TIGR01640 : F-box protein interaction domain   chr5:19696143-19697786 FORWARD   Aliases: K15N18.1, K15N18_1	3.7	3.7	-0.0	-0.1	100.0%	-5.4
20012	AT2G17480.1   Symbol: MLO8   seven transmembrane MLO family protein / MLO-like protein 8 (MLO8), identical to membrane protein Mlo8 (Arabidopsis thaliana) gi:14091586:gb:AAK53801; similar to MLO protein SWISS-PROT:P93766, NCBI_gi:1877221 (Hordeum vulgare)(Barley)   chr2:7597377-7601172 REVERSE   Aliases: F5J6.21	3.9	3.8	0.0	0.1	100.0%	-4.9
20013	AT2G19890.1   expressed protein, contains Pfam profile PF04396: Protein of unknown function, DUF537; expression supported by MPSS   chr2:8594326-8596719 FORWARD   Aliases: F6F22.8, F6F22_8	2.9	2.9	0.0	0.1	100.0%	-5.7
20014	AT2G14730.1   expressed protein   chr2:6312631-6314391 FORWARD   Aliases: T6B13.5	3.0	3.0	-0.0	-0.1	100.0%	-5.3
20015	AT5G60920.1   Symbol: COB   phytochelatin synthetase, putative / COBRA cell expansion protein COB, putative, similar to phytochelatin synthetase GI:29570314; similar to GB:AAK56072; identified in Roudier, et al, Plant Phys. (2002) 130:538-548 (PMID:12376623); identical to cDNA putative phytochelatin synthetase GI:3559804; contains Pfam profile PF04833: Phytochelatin synthetase-like conserved region   chr5:24528422-24531354 REVERSE   Aliases: COBRA, MSL3.40, MSL3_40	5.5	5.5	-0.0	-0.1	100.0%	-4.7
20016	AT2G27660.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.8	3.8	-0.0	-0.1	100.0%	-4.5
20017	AT3G52900.1   expressed protein, contains Pfam profile PF04949: Family of unknown function (DUF662)   chr3:19624098-19625005 FORWARD   Aliases: F8J2.70	3.6	3.6	-0.0	-0.1	100.0%	-4.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20018	AT4G19185.1   integral membrane family protein, contains Pfam profile:PF00892 integral membrane protein DUF6   chr4:10489096-10491668 REVERSE   Aliases: None	7.0	7.0	-0.0	-0.1	100.0%	-5.1
20019	AT1G62540.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenase GB:AAA21178 GI:349534 from <i>Oryctolagus cuniculus</i> (SP:P32417), SP:P97501 from <i>Mus musculus</i> ; contains Pfam profile PF00743 Flavin-binding monooxygenase-like   chr1:23155459-23159382 FORWARD   Aliases: T3P18.10, T3P18_10	2.8	2.8	-0.0	-0.1	100.0%	-5.3
20020	AT5G37510.2   Symbol: EMB1467   NADH-ubiquinone dehydrogenase, mitochondrial, putative, similar to NADH-ubiquinone oxidoreductase 75 kDa subunit, mitochondrial from <i>Solanum tuberosum</i> (SP:Q43644)   chr5:14914640-14917877 FORWARD   Aliases: EMB1467, EMBRYO DEFECTIVE 1467, MPA22.5, MPA22_5	11.1	11.1	0.0	0.1	100.0%	-4.8
20021	AT1G35183.1   expressed protein, ; expression supported by MPSS   chr1:12884416-12884568 FORWARD   Aliases: T32G9.50, T32G9_50	2.6	2.6	-0.0	-0.1	100.0%	-5.9
20022	AT2G15640.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.0	3.0	-0.0	-0.1	100.0%	-5.5
20023	AT3G05140.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:1435704-1438347 REVERSE   Aliases: T12H1.10, T12H1_10	2.4	2.4	0.0	0.1	100.0%	-5.6
20024	AT1G19670.1   Symbol: ATCLH1	2.5	2.5	-0.0	-0.1	100.0%	-5.5
20025	AT4G27290.1   S-locus protein kinase, putative, similar to S-receptor kinase gi:392557:gb:AAA62232; contains Pfam domains PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain and PF01453: Lectin (probable mannose binding)   chr4:13666287-13669208 FORWARD   Aliases: M4I22.100, M4I22_100	2.3	2.3	-0.0	-0.1	100.0%	-5.1
20026	AT3G21380.1   similar to jacalin lectin family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g52040.1); similar to myrosinase binding protein [ <i>Brassica napus</i> ] (GB:CAA70587.1); contains InterPro domain Jacalin-related lectin (InterPro:IPR001229)	2.9	2.9	-0.0	-0.1	100.0%	-5.5
20027	AT1G69470.1   expressed protein   chr1:26117238-26117660 FORWARD   Aliases: F10D13.12, F10D13_12	3.0	3.0	-0.0	-0.1	100.0%	-5.2
20028	AT1G29090.1   peptidase C1A papain family protein, contains similarity to cysteine protease SPCP1 GI:13491750 from ( <i>Ipomoea batatas</i> ); contains Pfam profile PF00112: Papain family cysteine protease   chr1:10162969-10164438 REVERSE   Aliases: F28N24.20, F28N24_20	3.3	3.3	0.0	0.1	100.0%	-5.2
20029	AT3G61810.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase precursor GI:4097948 from ( <i>Oryza sativa</i> ); contains Pfam profile PF00332: Glycosyl hydrolases family 17   chr3:22888143-22889444 FORWARD   Aliases: F21F14.9	3.2	3.2	-0.0	-0.1	100.0%	-4.8
20030	AT4G39120.1   inositol monophosphatase family protein, low similarity to Mono-phosphatase ( <i>Streptomyces anulatus</i> ) GI:1045231; contains Pfam profile PF00459: Inositol monophosphatase family   chr4:18225572-18227901 REVERSE   Aliases: T22F8.20, T22F8_20	3.8	3.8	-0.0	-0.1	100.0%	-4.9
20031	AT4G00650.1   Symbol: FRI   FRIGIDA protein, identical to Swiss-Prot:Q9FDW0 FRIGIDA protein ( <i>Arabidopsis thaliana</i> )   chr4:269026-271503 FORWARD   Aliases: F6N23.25, F6N23_25, FLA, FLOWERING LOCUS A, FRIGIDA	4.0	4.0	-0.0	-0.1	100.0%	-5.2
20032	AT1G23120.1   major latex protein-related / MLP-related, low similarity to major latex protein { <i>Papaver somniferum</i> } (GI:294060); Location of EST gb:T88564 ; contains Pfam profile PF00407: Pathogenesis-related protein Bet v I family	5.4	5.4	0.0	0.1	100.0%	-4.7
20033	AT3G48860.2   expressed protein   chr3:18128471-18133015 FORWARD   Aliases: T21J18.130	6.8	6.8	0.0	0.1	100.0%	-4.8
20034	AT1G19610.1   Symbol: LCR78/PDF1.4   plant defensin-fusion protein, putative (PDF1.4), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to SWISS-PROT:P30224, Cysteine-rich antifungal protein 1 precursor (AFP1)( <i>Arabidopsis thaliana</i> )   chr1:6781474-6782030 REVERSE   Aliases: F14P1.6, F14P1_6, LCR78, Low molecular weight cysteine rich 78, PDF1.4	3.2	3.2	-0.0	-0.1	100.0%	-5.2
20035	AT3G53810.1   lectin protein kinase, putative, similar to receptor lectin kinase 3 ( <i>Arabidopsis thaliana</i> ) gi:4100060:gb:AAD00733; contains protein kinase domain, Pfam:PF00069; contains legume lectins alpha and beta domains, Pfam:PF00138 and Pfam:PF00139   chr3:19943970-19946212 REVERSE   Aliases: F5K20.110	4.2	4.2	-0.0	-0.1	100.0%	-5.0
20036	AT5G06120.1   Ran-binding protein, putative, similar to SP:Q9UIA9 Ran-binding protein 16 { <i>Homo sapiens</i> }; contains Pfam profile PF03810: Importin-beta N-terminal domain   chr5:1844079-1852602 FORWARD   Aliases: K16F4.8, K16F4_8	7.7	7.7	-0.0	-0.1	100.0%	-4.8
20037	AT3G63020.1   expressed protein, predicted protein, <i>Arabidopsis thaliana</i>   chr3:23305400-23306014 FORWARD   Aliases: T20O10.120	2.5	2.5	0.0	0.1	100.0%	-5.6
20038	AT5G24210.1   lipase class 3 family protein, contains Pfam profile PF01764: Lipase   chr5:8217341-8219622 FORWARD   Aliases: MOP9.2, MOP9_2	3.3	3.3	-0.0	-0.1	100.0%	-5.4
20039	AT3G13150.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:4227747-4229658 REVERSE   Aliases: MJG19.10	2.5	2.5	-0.0	-0.1	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20040	AT1G50360.1   Symbol: VIIIA   myosin family protein, contains Pfam profiles: PF00063 myosin head (motor domain), PF00612 IQ calmodulin-binding motif   chr1:18654356-18660774 FORWARD   Aliases: ATVIIIA, F14I3.6, F14I3_6	2.9	2.9	0.0	0.1	100.0%	-5.0
20041	AT4G09700.1   expressed protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr4:6126772-6127887 FORWARD   Aliases: F17A8.50, F17A8_50	1.9	1.9	0.0	0.1	100.0%	-6.1
20042	AT4G19020.1   chromomethylase 2 (CMT2), nearly identical to chromomethylase CMT2 (Arabidopsis thaliana) GI:14583094   chr4:10414537-10421211 FORWARD   Aliases: F13C5.190, F13C5_190	3.8	3.8	-0.0	-0.1	100.0%	-5.1
20043	AT5G35510.1   expressed protein   chr5:13717060-13717266 FORWARD   Aliases: MOK9.11, MOK9_11	2.4	2.5	-0.0	-0.1	100.0%	-6.0
20044	AT2G39010.1   Symbol: PIP2;6/PIP2E   aquaporin, putative, similar to plasma membrane aquaporin 2b GI:7209560 from (Raphanus sativus)   chr2:16298555-16301112 FORWARD   Aliases: PIP2;6, PIP2E, T7F6.18, T7F6_18	2.6	2.6	0.0	0.1	100.0%	-4.3
20045	AT2G35380.2   similar to peroxidase, putative [Arabidopsis thaliana] (TAIR:At1g44970.1); similar to peroxidase prx15 precursor [Spinacia oleracea] (GB:AAF63027.1); contains InterPro domain Haem peroxidase (InterPro:IPR002016); contains InterPro domain Plant peroxidase (InterPro:IPR000823)   chr2:14899728-14901072 FORWARD   Aliases: T32F12.24, T32F12_24	2.7	2.7	0.0	0.1	100.0%	-4.3
20046	AT5G06200.1   integral membrane family protein, similar to unknown protein (gb:AAF00668.1); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr5:1877334-1878117 FORWARD   Aliases: MBL20.8, MBL20_8	2.5	2.6	-0.0	-0.1	100.0%	-4.4
20047	AT1G32030.1   expressed protein, contains Pfam profile PF03754: Domain of unknown function (DUF313); expression supported by MPSS   chr1:11514574-11515575 FORWARD   Aliases: T12O21.7, T12O21_7	3.0	3.0	0.0	0.1	100.0%	-5.4
20048	AT3G57380.1   expressed protein, contains Pfam domain, PF04577: Protein of unknown function (DUF563)   chr3:21240779-21242706 FORWARD   Aliases: F28O9.230	4.1	4.1	-0.0	-0.1	100.0%	-4.7
20049	AT3G06050.1   Symbol: ATPRXIIF/PRXIIF   Encodes a mitochondrial matrix localized peroxiredoxin involved in redox homeostasis. Knockout mutants have reduced root growth under certain oxidative stress conditions.   chr3:1826160-1827867 REVERSE   Aliases: ATPRXIIF, F24F17.3, F24F17_3, PRXIIF	10.1	10.1	0.1	0.1	100.0%	-4.5
20050	AT3G30290.1   Symbol: CYP702A8   cytochrome P450 family protein, similar to Cytochrome P450 85 (SP:Q43147) {Lycopersicon esculentum}; similar to GB:C71417 from (Arabidopsis thaliana) (Nature 391 (6666), 485-488 (1998))   chr3:11919709-11922025 REVERSE   Aliases: T6J22.4	2.9	2.8	0.0	0.1	100.0%	-5.1
20051	AT5G25370.1   Symbol: PLDALPHA3   phospholipase D, putative (PLDZETA), identical to phospholipase D zeta SP:P58766 from (Arabidopsis thaliana); similar to phospholipase D (Lycopersicon esculentum) GI:12060550; contains Pfam profile PF00614: Phospholipase D. Active site motif   chr5:8804243-8807550 REVERSE   Aliases: F18G18.110, F18G18_110, PLD ZETA 1, PLDZETA	3.1	3.1	-0.0	-0.1	100.0%	-4.9
20052	AT2G45680.1   TCP family transcription factor, putative, similar to PCF2 (GI:2580440) (Oryza sativa)   chr2:18827320-18828963 REVERSE   Aliases: F17K2.21	3.3	3.3	0.0	0.1	100.0%	-5.1
20053	AT1G24060.1   expressed protein   chr1:8509365-8510051 REVERSE   Aliases: T23E23.21, T23E23_21	2.6	2.6	-0.0	-0.1	100.0%	-5.7
20054	AT3G24680.1   zinc finger protein, putative, identical to zinc-finger protein GI:976277 from (Arabidopsis thaliana)   chr3:9015507-9016970 REVERSE   Aliases: MSD24.2	3.1	3.1	-0.0	-0.1	100.0%	-5.5
20055	AT3G05640.2   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase-2C GB:AAC36699 from (Mesembryanthemum crystallinum)   chr3:1640407-1643127 REVERSE   Aliases: F18C1.9, F18C1_9	5.0	5.0	0.0	0.1	100.0%	-4.9
20056	AT1G03170.1   expressed protein   chr1:769632-770684 FORWARD   Aliases: F15K9.22, F15K9_22	3.8	3.8	-0.0	-0.1	100.0%	-4.9
20057	AT3G26690.2   MutT/nudix family protein, similar to SP:Q09790 Diadenosine 5',5'''-P1,P6-hexaphosphate hydrolase (EC 3.6.1.-) (Ap6A hydrolase) {Schizosaccharomyces pombe}; contains Pfam profile PF00293: NUDIX domain	8.4	8.4	0.0	0.1	100.0%	-5.1
20058	AT2G28085.1   auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana)   chr2:11975197-11975697 REVERSE   Aliases: None	2.7	2.7	0.0	0.1	100.0%	-5.7
20059	AT5G59120.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo); non-consensus AA acceptor site at exon 6   chr5:23881956-23885275 REVERSE   Aliases: MNC17.1	3.0	3.0	-0.0	-0.1	100.0%	-5.4



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20060	AT1G69190.1   dihydropterin pyrophosphokinase, putative / dihydropteroate synthase, putative / DHPS, putative, similar to dihydropterin pyrophosphokinase /dihydropteroate synthase (Pisum sativum) gi:1934972:emb:CAA69903   chr1:26016794-26018173 REVERSE   Aliases: F4N2.15	4.2	4.2	-0.0	-0.1	100.0%	-5.1
20061	AT5G45650.1   subtilase family protein, contains Pfam domain, PF00082: Subtilase family; contains Pfam domain, PF02225: protease associated (PA) domain   chr5:18530658-18536095 REVERSE   Aliases: MRA19.5, MRA19_5	2.6	2.6	-0.0	-0.1	100.0%	-5.0
20062	AT1G65950.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr1:24550367-24554807 REVERSE   Aliases: F12P19.11, F12P19_11	4.8	4.8	0.0	0.1	100.0%	-4.8
20063	AT4G34500.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	4.9	4.9	-0.0	-0.1	100.0%	-4.7
20064	AT5G55550.3   RNA recognition motif (RRM)-containing protein, similar to DAZ associated protein 1 (Homo sapiens) GI:8671754; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)	6.9	6.9	0.0	0.1	100.0%	-4.8
20065	AT1G80370.1   Symbol: CYCA2;4   cyclin, putative, similar to cyclin A2 (Lycopersicon esculentum) GI:5420276; contains Pfam profiles PF00134: Cyclin, N-terminal domain, PF02984: Cyclin, C-terminal domain   chr1:30218597-30221753 FORWARD   Aliases: CYCA2;4, Cyclin A2;4, F5I6.12, F5I6_12	2.9	2.9	-0.0	-0.1	100.0%	-5.5
20066	AT1G45150.1   expressed protein   chr1:17079888-17084886 REVERSE   Aliases: F27F5.22, F27F5_22	6.8	6.8	-0.0	-0.1	100.0%	-4.9
20067	AT5G44700.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:18050091-18054121 REVERSE   Aliases: K23L20.3, K23L20_3	2.1	2.1	-0.0	-0.1	100.0%	-5.4
20068	AT4G37360.1   Symbol: CYP81D2   cytochrome P450 family protein, cytochrome P450 monooxygenase, Arabidopsis thaliana, PID:d1029478   chr4:17567118-17568852 REVERSE   Aliases: F6G17.10, F6G17_10	2.6	2.6	-0.0	-0.1	100.0%	-5.5
20069	AT1G54150.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:20219101-20221365 FORWARD   Aliases: F15I1.25, F15I1_25	6.6	6.6	-0.0	-0.1	100.0%	-5.2
20070	AT2G45200.1   Symbol: GOS12   Golgi SNARE 12 protein / Golgi SNAP receptor complex member 1, identical to Probable 28 kDa Golgi SNARE protein (Golgi SNAP receptor complex member 1) (SP:O22151) {Arabidopsis thaliana}   chr2:18644582-18646858 REVERSE   Aliases: ATGOS12, F4L23.29, GOLGI SNARE 12	9.3	9.3	0.0	0.1	100.0%	-4.7
20071	AT4G38760.1   expressed protein, KIAA0169 gene, Homo sapiens, D79991   chr4:18091796-18095595 REVERSE   Aliases: T9A14.40, T9A14_40	2.6	2.6	-0.0	-0.1	100.0%	-5.6
20072	AT4G31610.1   Symbol: REM1   transcriptional factor B3 family protein / reproductive meristem protein 1 (REM1), similar to reproductive meristem gene 1 from (Brassica oleracea var. botrytis) GI:3170424; contains Pfam profile PF02362: B3 DNA binding domain; identical to cDNA reproductive meristem protein 1 (REM1) GI:13604226	2.3	2.3	0.0	0.1	100.0%	-5.8
20073	AT2G14130.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g32840, At4g04010, At2g06430, At2g15140, At2g04980, At3g44500, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210, At3g32900   chr2:5967882-5972527 FORWARD   Aliases: T22C12.6, T22C12_6	2.4	2.4	0.0	0.1	100.0%	-5.7
20074	AT1G71120.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr1:26824734-26826082 REVERSE   Aliases: F23N20.11, F23N20_11	2.6	2.6	-0.0	-0.1	100.0%	-5.7
20075	AT1G76290.1   AMP-dependent synthetase and ligase family protein, similar to AMP-binding protein GI:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501   chr1:28628337-28630302 REVERSE   Aliases: F15M4.21, F15M4_21	3.3	3.3	-0.0	-0.1	100.0%	-5.4
20076	AT5G49430.1   transducin family protein / WD-40 repeat family protein, similar to WD-repeat protein 9 (SP:Q9NSI6) {Homo sapiens}; contains Pfam PF00400: WD domain, G-beta repeat (4 copies)   chr5:20054564-20062680 REVERSE   Aliases: K7J8.10, K7J8_10	3.0	3.0	0.0	0.1	100.0%	-5.3
20077	AT3G19770.2   similar to vacuolar sorting protein 9 domain-containing protein / VPS9 domain-containing protein [Arabidopsis thaliana] (TAIR:At5g09320.1); similar to putative Vacuolar sorting protein (with alternative splicing) [Oryza sativa (japonica cultivar-group)] (GB:AAT77027.1); similar to putative vacuolar sorting protein , 5'-partial [Oryza sativa (japonica cultivar-group)] (GB:AAS07379.1); contains InterPro domain Vacuolar sorting protein 9 (InterPro:IPR003123)   chr3:6866836-6869485 FORWARD   Aliases: MMB12.26	3.4	3.4	0.0	0.1	100.0%	-5.2
20078	AT1G06750.1   expressed protein   chr1:2074029-2076349 FORWARD   Aliases: F4H5.16, F4H5_16	2.6	2.6	0.0	0.1	100.0%	-5.8
20079	AT1G68000.1   Symbol: ATPIS1	5.2	5.2	0.0	0.1	100.0%	-4.5
20080	AT1G63590.1   receptor-like protein kinase-related, contains Pfam PF01657: Domain of unknown function; similar to receptor-like protein kinase 4 (GI:13506745) {Arabidopsis thaliana}   chr1:23583559-23584365 FORWARD   Aliases: F2K11.5, F2K11_5	2.4	2.4	0.0	0.1	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20081	AT2G36690.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to IDS3 (Hordeum vulgare)(GI:4514655), leucoanthocyanidin dioxygenase (SP:P51091)(Malus domestica); contains PF03171 2OG-Fe(II) oxygenase superfamily domain   chr2:15387009-15389066 FORWARD   Aliases: F13K3.9, F13K3_9	2.8	2.8	-0.0	-0.1	100.0%	-4.7
20082	AT1G47810.1   F-box family protein, contains F-box domain Pfam:PF00646	2.4	2.4	0.0	0.1	100.0%	-5.8
20083	AT2G46990.1   Symbol: IAA20   auxin-responsive protein / indoleacetic acid-induced protein 20 (IAA20), identical to SP:O24410 Auxin-responsive protein IAA20 (Indoleacetic acid-induced protein 20) {Arabidopsis thaliana}   chr2:19314924-19316056 FORWARD   Aliases: F14M4.18	4.0	4.0	-0.0	-0.1	100.0%	-5.3
20084	AT5G55020.1   Symbol: MYB120	2.2	2.2	0.0	0.1	100.0%	-5.6
20085	AT4G11700.1   expressed protein, contains Pfam profile PF04776: Protein of unknown function (DUF626)   chr4:7058080-7058631 REVERSE   Aliases: T5C23.130, T5C23_130	2.4	2.4	0.0	0.1	100.0%	-5.7
20086	AT5G18525.1   WD-40 repeat family protein, contains Pfam profile PF00400: WD domain, G-beta repeat   chr5:6146760-6149757 REVERSE   Aliases: None	4.3	4.3	-0.0	-0.1	100.0%	-5.3
20087	AT3G30200.1   fructose-6-phosphate 2-kinase-related / fructose-2,6-bisphosphatase-related, similar to fructose-6-phosphate 2-kinase/fructose-2,6-bisphosphatase (Arabidopsis thaliana) GI:13096098   chr3:11830231-11836741 REVERSE   Aliases: MIL15.2	3.4	3.4	0.0	0.1	100.0%	-4.8
20088	AT1G48610.2   AT hook motif-containing protein, contains Pfam profile PF02178: AT hook motif   chr1:17974348-17976971 REVERSE   Aliases: T1N15.24, T1N15_24	3.8	3.8	-0.0	-0.1	100.0%	-5.1
20089	AT2G42850.1   Symbol: CYP718	3.3	3.3	-0.0	-0.1	100.0%	-4.2
20090	AT1G53110.1   expressed protein   chr1:19793857-19796157 FORWARD   Aliases: F8L10.22	3.6	3.6	-0.0	-0.1	100.0%	-4.9
20091	AT1G52990.1   thioredoxin family protein, similar to SP:P48384 Thioredoxin M-type, chloroplast precursor (TRX-M) {Pisum sativum}; contains Pfam profile PF00085: Thioredoxin   chr1:19744171-19747117 REVERSE   Aliases: F8L10.14, F8L10_14	2.6	2.6	-0.0	-0.1	100.0%	-5.4
20092	AT1G71290.1   F-box family protein-related, contains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domaincontains weak hit to TIGRFAM TIGR01640 : F-box protein interaction domain;   chr1:26876305-26876904 FORWARD   Aliases: F3I17.6, F3I17_6	2.5	2.5	-0.0	-0.1	100.0%	-6.0
20093	AT1G52520.1   far-red impaired responsive protein, putative, similar to far-red impaired response protein FAR1 (Arabidopsis thaliana) gi:5764395:gb:AAD51282; contains Pfam:PF03101 domain: FAR1 family   chr1:19569438-19572053 FORWARD   Aliases: F6D8.26, F6D8_26	3.7	3.7	0.0	0.1	100.0%	-5.4
20094	AT5G60530.1   late embryogenesis abundant protein-related / LEA protein-related, similar to late embryogenesis abundant protein (Picea glauca) GI:1350543   chr5:24351133-24353005 REVERSE   Aliases: MUF9.16, MUF9_16	2.8	2.8	-0.0	-0.1	100.0%	-5.3
20095	AT1G10060.2   branched-chain amino acid aminotransferase 1 / branched-chain amino acid transaminase 1 (BCAT1), nearly identical to SP:Q93Y32 Branched-chain amino acid aminotransferase 1, mitochondrial precursor (EC 2.6.1.42) (Atbcat-1) {Arabidopsis thaliana}; contains Pfam profile: PF01063 aminotransferase class IV   chr1:3284241-3287109 FORWARD   Aliases: T27I1.8, T27I1_8	2.6	2.6	0.0	0.1	100.0%	-5.5
20096	AT4G10070.1   KH domain-containing protein, DNA-directed RNA polymerase (EC 2.7.7.6) II largestchain - mouse, PIR2:A28490   chr4:6295604-6299755 REVERSE   Aliases: F28M11.1	3.3	3.3	-0.0	-0.1	100.0%	-5.5
20097	AT4G31805.1   WRKY family transcription factor, identical to WRKY DNA-binding protein 18 (WRKY18) GI:13506730 from (Arabidopsis thaliana)   chr4:15385460-15386781 FORWARD   Aliases: None	2.4	2.4	-0.0	-0.1	100.0%	-5.7
20098	AT5G20760.1   hypothetical protein   chr5:7032529-7033191 FORWARD   Aliases: T1M15.160, T1M15_160	3.2	3.2	0.0	0.1	100.0%	-5.3
20099	AT2G02700.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.0	3.0	-0.0	-0.1	100.0%	-5.3
20100	AT3G58550.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, contains Pfam protease inhibitor/seed storage/LTP family domain   chr3:21660341-21661264 REVERSE   Aliases: F14P22.140	4.0	4.0	0.0	0.1	100.0%	-5.0
20101	AT5G61350.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:24685199-24687727 FORWARD   Aliases: MFB13.1, MFB13_1	2.6	2.6	-0.0	-0.1	100.0%	-4.6
20102	AT2G46500.2   phosphatidylinositol 3- and 4-kinase family protein / ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr2:19093633-19096005 REVERSE   Aliases: F11C10.19, F11C10_19	8.0	8.0	0.0	0.1	100.0%	-4.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20103	AT3G23090.1   expressed protein   chr3:8214318-8217087 REVERSE   Aliases: MXC7.13	4.9	4.8	0.0	0.1	100.0%	-4.8
20104	AT3G47100.1   expressed protein   chr3:17356555-17357091 FORWARD   Aliases: F13I12.150	2.7	2.7	-0.0	-0.1	100.0%	-5.4
20105	AT2G44190.1   expressed protein, contains Pfam profile: PF04484 family of unknown function (DUF566)   chr2:18279267-18281573 FORWARD   Aliases: F6E13.32	7.2	7.2	-0.0	-0.1	100.0%	-4.6
20106	AT2G36190.1   beta-fructosidase, putative / beta-fructofuranosidase, putative, similar to beta-fructofuranosidase GI:18324 from (Daucus carota)   chr2:15181809-15184949 REVERSE   Aliases: F9C22.8	3.4	3.4	0.0	0.1	100.0%	-5.4
20107	AT5G47730.1   SEC14 cytosolic factor, putative / polyphosphoinositide-binding protein, putative, similar to polyphosphoinositide binding protein SEC14 homolog Ssh1p (GI:2739044) {Glycine max}   chr5:19351523-19354327 REVERSE   Aliases: MCA23.5, MCA23_5	4.5	4.5	-0.0	-0.1	100.0%	-4.6
20108	AT2G19960.1   hAT dimerisation domain-containing protein / transposase-related, very low similarity to transposase (Ipomoea purpurea) AB004906 GI:4063770; contains Pfam profile PF05699: hAT family dimerisation domain   chr2:8629296-8629817 FORWARD   Aliases: T2G17.24, T2G17_24	2.3	2.3	-0.0	-0.1	100.0%	-5.7
20109	AT3G47470.1   Symbol: CAB4   chlorophyll A-B binding protein 4, chloroplast / LHCl type III CAB-4 (CAB4), identical to SP:P27521 Chlorophyll A-B binding protein 4, chloroplast precursor (LHCl type III CAB-4) (LHCP) {Arabidopsis thaliana}	10.1	10.0	0.0	0.1	100.0%	-4.4
20110	AT5G19560.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr5:6603293-6606132 FORWARD   Aliases: KINASE PARTNER PROTEIN LIKE, KPP LIKE, T20D1.80, T20D1_80	2.9	2.9	0.0	0.1	100.0%	-4.6
20111	AT5G58000.1   phosphatase-related, weak similarity to CTD phosphatase-like 3 (Arabidopsis thaliana) GI:22212705; contains Pfam profiles PF02453: Reticulon, PF00533: BRCA1 C Terminus (BRCT) domain, PF03031: NLI interacting factor   chr5:23494121-23499150 FORWARD   Aliases: MTI20.26, MTI20_26	5.2	5.2	-0.0	-0.1	100.0%	-5.1
20112	AT4G09110.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:5812485-5813393 FORWARD   Aliases: T8A17.5	2.7	2.7	0.0	0.1	100.0%	-5.0
20113	AT4G15545.1   expressed protein   chr4:8875918-8877755 FORWARD   Aliases: None	8.6	8.6	0.0	0.1	100.0%	-4.7
20114	AT1G59930.1   expressed protein   chr1:22064748-22065146 REVERSE   Aliases: F23H11.24, F23H11_24	2.4	2.4	0.0	0.1	100.0%	-5.1
20115	AT2G46200.2   expressed protein, low similarity to ES18 (Mus musculus) GI:4416181   chr2:18981737-18983923 REVERSE   Aliases: T3F17.15	3.9	3.9	0.0	0.1	100.0%	-5.0
20116	AT4G26340.1   F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	-0.0	-0.1	100.0%	-5.7
20117	AT4G03050.2   Symbol: AOP3   similar to 2-oxoglutarate-dependent dioxygenase, putative (AOP2) [Arabidopsis thaliana] (TAIR:At4g03060.1); similar to putative 2-oxoglutarate-dependent dioxygenase [Oryza sativa (japonica cultivar-group)] (GB:XP_482416.1); contains InterPro domain Isopenicillin N synthase (InterPro:IPR002283); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)   chr4:1344212-1346391 FORWARD   Aliases: T4I9.7, T4I9_7	3.7	3.7	-0.0	-0.1	100.0%	-5.2
20118	AT1G48800.1   terpene synthase/cyclase family protein, similar to terpene cyclase GI:9293912 from (Arabidopsis thaliana)   chr1:18053512-18056643 FORWARD   Aliases: F11I4.3, F11I4_3	2.3	2.3	0.0	0.1	100.0%	-6.0
20119	AT3G57230.1   Symbol: AGL16   MADS-box protein (AGL16), MADS-box transcription factor DEFH125 - Antirrhinum majus, PIR:T17029; contains Pfam domain PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain); contains Pfam domain PF01486: K-box region   chr3:21188689-21191911 FORWARD   Aliases: F28O9.80	8.6	8.6	-0.0	-0.1	100.0%	-5.2
20120	AT5G02890.1   transferase family protein, contains Pfam profile PF02458: Transferase family   chr5:670063-671467 REVERSE   Aliases: F9G14.200, F9G14_200	3.0	3.0	-0.0	-0.1	100.0%	-4.9
20121	AT5G06600.2   Symbol: UBP12   ubiquitin-specific protease 12 (UBP12), almost identical to ubiquitin-specific protease 12 GI:11993471 (Arabidopsis thaliana), one amino acid difference   chr5:2019108-2027946 REVERSE   Aliases: F15M7.13, F15M7_13, UBIQUITIN SPECIFIC PROTEASE 12	5.2	5.3	-0.0	-0.1	100.0%	-4.9
20122	AT1G08065.1   carbonic anhydrase family protein, similar to storage protein (dioscorin) (Dioscorea cayenensis) GI:433463; contains Pfam profile PF00194: Eukaryotic-type carbonic anhydrase   chr1:2511785-2513149 REVERSE   Aliases: T6D22.30, T6D22_30	2.2	2.2	-0.0	-0.1	100.0%	-5.7
20123	AT5G35830.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr5:14017543-14018646 REVERSE   Aliases: MIK22.14, MIK22_14	2.4	2.4	0.0	0.1	100.0%	-5.6
20124	AT1G31600.3   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam profiles PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family, PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)   chr1:11312942-11316416 REVERSE   Aliases: AT1G31610, F27M3.19, F27M3_19	5.6	5.6	-0.0	-0.1	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20125	AT3G49150.1   F-box family protein, contains F-box domain Pfam:PF00646	2.5	2.5	0.0	0.1	100.0%	-5.5
20126	AT2G28710.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr2:12330051-12330521 FORWARD   Aliases: T11P11.2, T11P11_2	3.7	3.7	-0.0	-0.1	100.0%	-4.3
20127	AT5G14310.1   expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873   chr5:4615321-4617618 FORWARD   Aliases: F18O22.100, F18O22_100	4.5	4.5	-0.0	-0.1	100.0%	-5.1
20128	AT1G07180.1   Symbol: ATNDI1	3.3	3.3	-0.0	-0.1	100.0%	-5.0
20129	AT4G38170.1   far-red impaired responsive protein, putative / SWIM zinc finger family protein, similar to far-red impaired response protein (Arabidopsis thaliana) GI:5764395; contains Pfam profile PF04434: SWIM zinc finger	4.1	4.1	0.0	0.1	100.0%	-5.0
20130	AT3G13240.1   hypothetical protein   chr3:4275767-4276247 FORWARD   Aliases: MDC11.17	3.2	3.3	-0.0	-0.1	100.0%	-5.5
20131	AT3G15357.1   expressed protein   chr3:5187123-5187717 FORWARD   Aliases: None	3.1	3.1	0.0	0.1	100.0%	-5.5
20132	AT4G33020.1   Symbol: ZIP9   metal transporter, putative (ZIP9), identical to putative metal transporter ZIP9 (Arabidopsis thaliana) gi:17385790:gb:AAL38435; similar to Zn and Cd transporter ZNT1 (Thlaspi caerulescens) gi:7381054:gb:AAF61374; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563	2.9	2.8	0.0	0.1	100.0%	-4.3
20133	AT5G54830.1   DOMON domain-containing protein / dopamine beta-monooxygenase N-terminal domain-containing protein, contains Pfam PF03351: DOMON domain   chr5:22290302-22293527 FORWARD   Aliases: MBG8.9, MBG8_9	3.2	3.2	-0.0	-0.1	100.0%	-5.4
20134	AT5G15890.1   expressed protein   chr5:5187690-5189351 REVERSE   Aliases: F1N13.30, F1N13_30	2.7	2.6	0.0	0.1	100.0%	-4.9
20135	AT1G57570.1   jacalin lectin family protein, similar to myrosinase-binding protein homolog (Arabidopsis thaliana) GI:2997767; contains Pfam profile PF01419 jacalin-like lectin domain	3.9	4.0	-0.0	-0.1	100.0%	-5.2
20136	AT1G53510.1   Symbol: ATMPK18   similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK19) [Arabidopsis thaliana] (TAIR:At3g14720.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK16) [Arabidopsis thaliana] (TAIR:At5g19010.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK20) [Arabidopsis thaliana] (TAIR:At2g42880.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK9) [Arabidopsis thaliana] (TAIR:At3g18040.1); similar to mitogen-activated protein kinase, putative / MAPK, putative (MPK8) [Arabidopsis thaliana] (TAIR:At1g18150.2); similar to MAP kinase-like protein [Oryza sativa (japonica cultivar-group)] (GB:NP_917813.1); similar to putative mitogen-activated protein kinase [Oryza sativa (japonica cultivar-group)] (GB:NP_916793.1); similar to putative mitogen-activated protein kinase wjumk1 [Oryza sativa (japonica cultivar-group)] (GB:CAD54742.1); similar to MAPK6 [Oryza sativa (japonica cultivar-group)] (GB:AAR11478.1); similar to mitogen-activated protein kinase 7-like [Oryza sativa (japonica cultivar-group)] (GB:BAD61401.1); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr1:19974332-19978061 REVERSE   Aliases: F22G10.12	3.4	3.3	0.0	0.1	100.0%	-4.8
20137	AT5G67350.1   expressed protein   chr5:26885516-26886712 REVERSE   Aliases: K8K14.7, K8K14_7	3.8	3.7	0.0	0.1	100.0%	-5.0
20138	AT5G55470.1   Symbol: ATNHX3	4.2	4.2	-0.0	-0.1	100.0%	-5.2
20139	AT5G40320.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.2	3.2	0.0	0.1	100.0%	-5.1
20140	AT3G57720.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr3:21398699-21400703 FORWARD   Aliases: F15B8.90	3.0	2.9	0.0	0.1	100.0%	-5.5
20141	AT3G55720.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr3:20690799-20692426 FORWARD   Aliases: F1I16.130	2.7	2.7	-0.0	-0.1	100.0%	-4.4
20142	AT5G60770.1   Symbol: ATNRT2.4   high-affinity nitrate transporter, putative, strong similarity to trans-membrane nitrate transporter protein AtNRT2:1 (Arabidopsis thaliana) GI:3747058, high-affinity nitrate transporter ACH1 (Arabidopsis thaliana) GI:3608362   chr5:24461622-24464252 FORWARD   Aliases: MAE1.3, MAE1_3	3.0	3.0	0.0	0.1	100.0%	-5.3
20143	AT3G53910.1   malate dehydrogenase-related, similar to malate dehydrogenase precursor (Medicago sativa) GI:2827084   chr3:19970834-19971424 REVERSE   Aliases: F5K20.210	2.4	2.4	-0.0	-0.1	100.0%	-5.9
20144	AT3G02400.1   forkhead-associated domain-containing protein / FHA domain-containing protein / AT hook motif-containing protein, contains Pfam profiles PF00498: FHA domain, PF02178: AT hook motif   chr3:489837-491594 FORWARD   Aliases: F16B3.3, F16B3_3	6.5	6.5	-0.0	-0.1	100.0%	-4.9
20145	AT1G12310.1   calmodulin, putative, similar to calmodulin SP:P04465 from (Trypanosoma brucei gambiense)   chr1:4187163-4188054 REVERSE   Aliases: F5O11.35, F5O11_35	7.4	7.3	0.0	0.1	100.0%	-4.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20146	AT1G19800.3   Symbol: TGD1   expressed protein, contains Pfam PF02405: Domain of unknown function DUF140; similar to TOLUENE TOLERANCE PROTEIN TTG2B {Brucella melitensis 16M} (GI:17982923)   chr1:6846363-6848087 FORWARD   Aliases: F14P1.27, F14P1_27, TRIGALACTOSYLDIACYLGLYCEROL 1	6.5	6.5	0.0	0.1	100.0%	-5.0
20147	AT2G46310.1   encodes a member of the ERF (ethylene response factor) subfamily B-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 7 members in this subfamily.	3.4	3.4	-0.0	-0.1	100.0%	-5.3
20148	AT4G12980.1   auxin-responsive protein, putative, similar to auxin-induced protein AIR12 GI:11357190 (Arabidopsis thaliana)   chr4:7589392-7591099 REVERSE   Aliases: F25G13.70, F25G13_70	5.0	5.0	-0.0	-0.1	100.0%	-5.0
20149	AT2G14960.1   Symbol: GH3.1   encodes a protein similar to IAA-amido synthases. Lines carrying an insertion in this gene are hypersensitive to auxin.	2.3	2.3	-0.0	-0.1	100.0%	-5.4
20150	AT1G05900.2   endonuclease-related, similar to endonuclease III (Homo sapiens) GI:1753174; contains Pfam profile PF00633: Helix-hairpin-helix motif   chr1:1786871-1789673 FORWARD   Aliases: T20M3.18, T20M3_18	3.6	3.6	-0.0	-0.1	100.0%	-5.1
20151	AT3G60790.1   F-box protein-related, contains weak hit to Pfam PF00646: F-box domain   chr3:22475598-22477923 FORWARD   Aliases: T4C21.200	3.0	3.0	-0.0	-0.1	100.0%	-5.5
20152	AT1G32250.1   calmodulin, putative, similar to calmodulin GB:M59770 GI:160127 from (Plasmodium falciparum); contains INTERPRO:IPR002048 calcium-binding EF-hand domain	2.9	2.9	0.0	0.1	100.0%	-5.6
20153	AT4G25210.1   expressed protein, weak similarity to storekeeper protein (Solanum tuberosum) GI:14268476; contains Pfam profile PF04504: Protein of unknown function, DUF573   chr4:12918338-12919752 FORWARD   Aliases: F24A6.50, F24A6_50	7.6	7.6	0.0	0.1	100.0%	-5.0
20154	AT5G62640.2   Symbol: ELF5   similar to proline-rich family protein [Arabidopsis thaliana] (TAIR:At1g61080.1); similar to PREDICTED: similar to WW domain binding protein 11 [Gallus gallus] (GB:XP_425454.1); similar to putative diaphanous homologue [Oryza sativa (japonica cultivar-group)] (GB:XP_478998.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr5:25166659-25169767 REVERSE   Aliases: EARLY FLOWERING 5, MRG21.6, MRG21_6	6.7	6.7	-0.0	-0.1	100.0%	-5.1
20155	AT5G60290.1   expressed protein   chr5:24280090-24281069 FORWARD   Aliases: F15L12.16, F15L12_16	3.8	3.8	-0.0	-0.1	100.0%	-5.1
20156	AT3G61960.2   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At3g53930.1); similar to OSJNBa0070M12.8 [Oryza sativa (japonica cultivar-group)] (GB:XP_474430.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)	6.0	6.0	0.0	0.1	100.0%	-4.8
20157	AT5G18160.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain; similar to Probable disease resistance RPP8-like protein 2 (Swiss-Prot:Q9MAG6) (Arabidopsis thaliana)   chr5:6002772-6003911 FORWARD   Aliases: MRG7.12, MRG7_12	3.0	3.1	-0.0	-0.1	100.0%	-5.4
20158	AT1G68240.2   similar to phytochrome interacting factor 3 (PIF3) [Arabidopsis thaliana] (TAIR:At1g09530.1); similar to phytochrome interacting factor 3 (PIF3) [Arabidopsis thaliana] (TAIR:At1g09530.2); similar to putative BP-5 protein [Oryza sativa (japonica cultivar-group)] (GB:BAD81566.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr1:25578527-25579791 REVERSE   Aliases: T22E19.13, T22E19_13	2.8	2.8	0.0	0.1	100.0%	-5.5
20159	AT4G30320.1   allergen V5/Tpx-1-related family protein, similar to SP:Q40374 Pathogenesis-related protein PR-1 precursor {Medicago truncatula}; contains Pfam profile PF00188: SCP-like extracellular protein   chr4:14835839-14836324 FORWARD   Aliases: F17I23.340, F17I23_340	3.4	3.5	-0.0	-0.1	100.0%	-4.1
20160	AT4G17220.1   Symbol: ATMAP70 5   Encodes a microtubule associated protein (MAP70-5). Expressed in all tissues.   chr4:9656849-9659474 REVERSE   Aliases: ATMAP70 5, DL4645C, FCAALL.385	3.5	3.5	0.0	0.1	100.0%	-4.5
20161	AT2G40980.1   expressed protein   chr2:17109168-17111880 FORWARD   Aliases: T3K9.25, T3K9_25	3.2	3.2	0.0	0.1	100.0%	-5.5
20162	AT5G14620.1   Symbol: DRM2   cytosine methyltransferase (DRM2), identical to cytosine methyltransferase GI:7658293 from (Arabidopsis thaliana)   chr5:4715256-4718707 REVERSE   Aliases: AT5G14630, DMT7, DOMAINS REARRANGED METHYLTRANSFERASE 2, NA METHYLTRANSFERASE, T15N1.110, T15N1_110	4.4	4.4	-0.0	-0.1	100.0%	-5.4
20163	AT5G08520.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr5:2755176-2758335 REVERSE   Aliases: F8L15.2	5.6	5.6	0.0	0.0	100.0%	-4.6
20164	AT2G35050.1   protein kinase family protein, contains Pfam profile: PF00069 Eukaryotic protein kinase domain   chr2:14776787-14782114 FORWARD   Aliases: F19I3.28, F19I3_28	7.1	7.1	0.0	0.0	100.0%	-5.0
20165	AT1G30800.1   expressed protein, ; expression supported by MPSS   chr1:10936977-10937696 FORWARD   Aliases: T17H7.8, T17H7_8	2.4	2.4	0.0	0.0	100.0%	-5.8
20166	AT3G16690.1   nodulin MtN3 family protein, contains Pfam PF03083 MtN3/saliva family   chr3:5684386-5686496 REVERSE   Aliases: MGL6.16	3.3	3.3	0.0	0.0	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20167	AT3G18030.1   Symbol: ATHAL3A   halotolerance protein (HAL3A), identical to GB:AAD51616 from (Arabidopsis thaliana); similar to Halotolerance protein Hal3b (SP:P94063)(Arabidopsis thaliana); contains Pfam PF02441: Flavoprotein   chr3:6167690-6168954 REVERSE   Aliases: ATHAL3, HAL3, HAL3A, MBG14.4	5.7	5.7	0.0	0.0	100.0%	-4.5
20168	AT5G45060.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:18199265-18203722 FORWARD   Aliases: K17O22.2, K17O22_2	3.2	3.2	0.0	0.0	100.0%	-5.0
20169	AT1G23750.1   DNA-binding protein-related, contains weak similarity to G-quartet DNA binding protein 3 (Tetrahymena thermophila) gi:4583503:gb:AAD25098   chr1:8400145-8401476 FORWARD   Aliases: F5O8.30, F5O8_30	6.7	6.6	0.0	0.0	100.0%	-4.5
20170	AT5G56610.2   similar to dual specificity protein phosphatase family protein [Arabidopsis thaliana] (TAIR:At2g35680.1); similar to putative PTEN-like phosphatase [Oryza sativa (japonica cultivar-group)] (GB:BAD86944.1); contains InterPro domain Tyrosine specific protein phosphatase and dual specificity protein phosphatase (InterPro:IPR000387); contains InterPro domain Dual specificity protein phosphatase (InterPro:IPR000340)   chr5:22933957-22935564 FORWARD   Aliases: MIK19.6, MIK19_6	6.2	6.2	-0.0	-0.0	100.0%	-4.6
20171	AT1G06530.1   myosin heavy chain-related, similar to myosin heavy chain (GI:1408194) {Placopecten magellanicus}; similar to Myosin heavy chain, clone 203 (Fragment) (SP:P39922){Hydra attenuata}; contains one transmembrane domain   chr1:2001593-2002595 FORWARD   Aliases: F12K11.14, F12K11_14	11.3	11.3	-0.0	-0.0	100.0%	-5.5
20172	AT1G71691.2   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 from (Arabidopsis thaliana);	2.5	2.5	-0.0	-0.0	100.0%	-5.7
20173	AT5G26350.1   expressed protein   chr5:9253111-9253640 REVERSE   Aliases: F9D12.102, F9D12_102	3.4	3.4	-0.0	-0.0	100.0%	-5.0
20174	AT3G55110.1   ABC transporter family protein, ATP-binding cassette-sub-family G-member 2, Mus musculus, EMBL:AF140218   chr3:20435570-20438354 REVERSE   Aliases: T15C9.110	2.8	2.8	-0.0	-0.0	100.0%	-5.5
20175	AT2G26980.5   Symbol: CIPK3   similar to protein kinase family protein / NAF domain-containing protein [Arabidopsis thaliana] (TAIR:At5g21326.1); similar to serine/threonine kinase [Sorghum bicolor] (GB:CAA73067.1); similar to serine/threonine kinase [Sorghum bicolor] (GB:CAA73068.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain NAF domain (InterPro:IPR004041); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr2:11521781-11525401 REVERSE   Aliases: CBL INTERACTING PROTEIN KINASE 3, T20P8.3, T20P8_3	3.4	3.4	-0.0	-0.0	100.0%	-4.6
20176	NA	5.4	5.5	-0.1	-0.0	100.0%	-4.7
20177	AT2G15050.2   lipid transfer protein, putative, similar to SP:Q42641 nonspecific lipid-transfer protein A precursor (LTP A) (Wax-associated protein 9A) {Brassica oleracea}; contains Pfam Protease inhibitor/seed storage/LTP family domain PF00234   chr2:6525934-6527242 FORWARD   Aliases: T15J14.9, T15J14_9	3.3	3.3	-0.0	-0.0	100.0%	-5.2
20178	AT5G43920.1   transducin family protein / WD-40 repeat family protein, contains 7 WD-40 repeats (PF00400); similar to will die slowly protein (WDS) (SP:Q9V3J8) (Drosophila melanogaster)   chr5:17690624-17692857 FORWARD   Aliases: MRH10.1, MRH10_1	4.2	4.2	-0.0	-0.0	100.0%	-5.1
20179	AT1G77790.1   glycosyl hydrolase family 17 protein, similar to endo-1,3-beta-glucanase GB:BAA21110 (Gossypium hirsutum)   chr1:29255586-29256870 REVERSE   Aliases: T32E8.12, T32E8_12	2.1	2.1	-0.0	-0.0	100.0%	-5.7
20180	AT2G40110.2   yippee family protein, similar to mdgl-1 (Mus musculus) GI:10441648, Yippee protein (Drosophila melanogaster) GI:5713279; contains Pfam profile PF03226: Yippee putative zinc-binding protein   chr2:16755018-16756590 FORWARD   Aliases: F27I1.3, F27I1_3	6.8	6.8	-0.0	-0.0	100.0%	-4.7
20181	AT1G12560.1   Symbol: ATEXPA7   expansin, putative (EXP7), similar to expansin GI:2828241 from (Brassica napus); alpha-expansin gene family, PMID:11641069   chr1:4276555-4277691 FORWARD   Aliases: ARABIDOPSIS THALIANA EXPANSIN A7, ATEXP7, ATHEXP ALPHA 1.26, EXP7, F5O11.30, F5O11_30	3.1	3.1	0.0	0.0	100.0%	-4.6
20182	AT5G61010.2   similar to exocyst subunit EXO70 family protein [Arabidopsis thaliana] (TAIR:At3g29400.1); similar to putative leucine zipper-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_465879.1); contains InterPro domain Exo70 exocyst complex subunit (InterPro:IPR004140)   chr5:24571067-24573975 FORWARD   Aliases: MAF19.1, MAF19_1	3.0	3.0	0.0	0.0	100.0%	-5.1
20183	AT5G37160.1   tRNA-splicing endonuclease positive effector-related, contains similarity to SEN1, a positive effector of tRNA-splicing endonuclease (Saccharomyces cerevisiae) gi:172574:gb:AAB63976   chr5:14722656-14725606 FORWARD   Aliases: MJG14.23, MJG14_23	3.1	3.1	0.0	0.0	100.0%	-5.3
20184	AT5G64400.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g09570.1); similar to unknown protein [Oryza sativa] (GB:XP_469336.1); contains InterPro domain Protein of unknown function DUF657 (InterPro:IPR007017)   chr5:25766066-25767582 FORWARD   Aliases: MSJ1.24, MSJ1_24	12.3	12.3	0.0	0.0	100.0%	-5.5
20185	AT3G66656.1   MADS-box family protein, contains Pfam profile: PF00319 SRF-type transcription factor (DNA-binding and dimerisation domain)   chr3:2091268-2091804 REVERSE   Aliases: T8E24.5, T8E24_5	3.0	3.0	0.0	0.0	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20186	AT4G20330.1   transcription initiation factor-related, contains weak similarity to Transcription initiation factor IIE, beta subunit (TFIIE-beta) (Swiss-Prot:P29084) (Homo sapiens)   chr4:10982528-10984526 REVERSE   Aliases: F9F13.2, F9F13_2	8.0	8.0	0.0	0.0	100.0%	-4.8
20187	AT5G57000.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g72690.1)   chr5:23080941-23082506 REVERSE   Aliases: MHM17.12, MHM17_12	5.5	5.5	-0.0	-0.0	100.0%	-4.8
20188	AT2G47460.1   Symbol: MYB12   MYB12 belongs to subgroup 7 of the R2R3-MYB family. It strongly activates the promoters of chalcone synthase (CHS), flavanone 3-hydroxylase (F3H), flavonol synthase (FLS) and - to a lesser extent - chalcone flavanone isomerase (CHI), but cannot activate the promoters of flavonoid-3'hydroxylase (F3'H) and dihydroflavonol 4-reductase (DF). The activation requires a functional MYB recognition element (MRE). Results from the myb12-1f allele indicate that an activation domain might be present in the C-terminus. Overexpression or knock-out plants do not show any obvious phenotype under greenhouse conditions. Young myb12-ko seedlings contain reduced amounts of flavonoids (quercetin and kaempferol), while seedlings as well as leaves of MYB12-OX plants displayed an increased flavonoid content. They did not show any significant difference in anthocyanin content. Expression of CHS and FLS shows a clear correlation to MYB12 expression levels. CHI and F3H show increased transcript levels in the MYB12-OX lines, but no differences in the knock-out. Even in the absence of functional MYB12, flavonol biosynthesis is not completely absent, suggesting functional redundancy.   chr2:19483407-19486538 FORWARD   Aliases: MYB12, T30B22.24	3.2	3.2	0.0	0.0	100.0%	-4.3
20189	AT2G41610.1   expressed protein   chr2:17354235-17355317 FORWARD   Aliases: T32G6.13, T32G6_13	3.4	3.3	0.0	0.0	100.0%	-4.7
20190	AT5G40590.1   DC1 domain-containing protein, predicted protein, Arabidopsis thaliana   chr5:16268665-16269546 REVERSE   Aliases: MNF13.11, MNF13_11	2.6	2.7	-0.0	-0.0	100.0%	-4.3
20191	AT5G23180.1   hypothetical protein   chr5:7801477-7801893 FORWARD   Aliases: MKD15.4, MKD15_4	2.5	2.5	-0.0	-0.0	100.0%	-5.7
20192	AT4G12460.1   oxysterol-binding family protein, similar to SP:P22059 Oxysterol-binding protein 1 {Homo sapiens}; contains Pfam profiles PF00169: PH domain, PF01237: Oxysterol-binding protein	3.2	3.2	0.0	0.0	100.0%	-5.0
20193	AT1G09970.2   leucine-rich repeat transmembrane protein kinase, putative, Similar to A. thaliana receptor-like protein kinase (gb:RLK5_ARATH). ESTs gb:ATTS0475,gb:ATTS4362 come from this gene isoform contains a TG acceptor site at intron.	5.7	5.6	0.0	0.0	100.0%	-4.8
20194	AT2G35680.1   dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain   chr2:15003792-15006164 REVERSE   Aliases: T20F21.13, T20F21_13	7.0	7.0	0.0	0.0	100.0%	-4.8
20195	AT4G16890.1   Symbol: SNC1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr4:9500525-9505474 REVERSE   Aliases: BAL, BALL, DL4475C, FCAALL.51, SUPPRESSOR OF NPR1 1, CONSTITUTIVE 1	4.7	4.7	0.0	0.0	100.0%	-4.8
20196	AT4G23130.2   Symbol: CRK5   receptor-like protein kinase 6 (RLK6), identical to receptor-like protein kinase 6 (Arabidopsis thaliana) GI:13506749; contains Pfam domain PF00069: Protein kinase domain   chr4:12117668-12120145 REVERSE   Aliases: CYSTEINE RICH RLK5, F7H19.320, F7H19_320, RECEPTOR LIKE PROTEIN KINASE 6, RLK6	3.0	3.0	-0.0	-0.0	100.0%	-5.1
20197	AT4G37980.2   Symbol: ELI3 1	2.5	2.5	0.0	0.0	100.0%	-5.4
20198	AT3G46770.1   transcriptional factor B3 family protein, contains Pfam profile PF02362: B3 DNA binding domain   chr3:17235049-17236301 FORWARD   Aliases: T6H20.200	3.1	3.0	0.0	0.0	100.0%	-5.1
20199	AT3G53510.1   ABC transporter family protein, breast cancer resistance protein (BCRP), Homo sapiens, EMBL:AF098951   chr3:19848191-19850840 REVERSE   Aliases: F4P12.210	2.5	2.5	0.0	0.0	100.0%	-5.0
20200	AT3G28520.1   AAA-type ATPase family protein, contains Pfam profile: ATPase family PF00004   chr3:10689560-10690996 FORWARD   Aliases: T20D4.3	3.7	3.7	0.0	0.0	100.0%	-5.2
20201	AT1G76160.1   Symbol: SKS5   multi-copper oxidase type I family protein, similar to pollen-specific BP10 protein (SP:Q00624)(Brassica napus); contains Pfam profile: PF00394 Multicopper oxidase   chr1:28582836-28586006 REVERSE   Aliases: SKS5, T23E18.10, T23E18_10	8.3	8.3	0.0	0.0	100.0%	-4.8
20202	AT4G33240.1   phosphatidylinositol-4-phosphate 5-kinase family protein, similar to SP:Q9Z1T6 FYVE finger-containing phosphoinositide kinase (EC 2.7.1.68) (1-phosphatidylinositol-4-phosphate kinase) (PIP5K) (PtdIns(4)P-5-kinase) {Mus musculus}; contains Pfam profiles PF01504: Phosphatidylinositol-4-phosphate 5-Kinase, PF01363: FYVE zinc finger, PF00118: TCP-1/cpn60 chaperonin family   chr4:16029209-16037282 REVERSE   Aliases: F4I10.170, F4I10_170	4.4	4.4	-0.0	-0.0	100.0%	-4.9
20203	AT5G09340.1   ubiquitin, putative, similar to ubiquitin SP:P42740 from (Aglaothamnion neglectum)   chr5:2896676-2896915 REVERSE   Aliases: T5E8.140, T5E8_140	2.6	2.6	-0.0	-0.0	100.0%	-5.8
20204	AT5G38670.1   F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profile PF00646: F-box domain   chr5:15493016-15494101 FORWARD   Aliases: MBB18.22, MBB18_22	2.5	2.5	0.0	0.0	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20205	AT3G29020.1   Symbol: MYB110	3.1	3.1	0.0	0.0	100.0%	-5.3
20206	AT5G51470.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr5:20924513-20926566 FORWARD   Aliases: K17N15.2, K17N15_2	2.3	2.3	0.0	0.0	100.0%	-5.7
20207	AT5G25390.2   encodes a member of the ERF (ethylene response factor) subfamily B-6 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 12 members in this subfamily including RAP2.11.   chr5:8820479-8821995 FORWARD   Aliases: F18G18.130, F18G18_130	4.0	4.0	0.0	0.0	100.0%	-5.1
20208	AT4G39270.2   leucine-rich repeat transmembrane protein kinase, putative, receptor protein kinase erecta, Arabidopsis thaliana	4.5	4.6	-0.0	-0.0	100.0%	-4.5
20209	AT2G34210.1   KOW domain-containing transcription factor family protein   chr2:14453017-14457601 FORWARD   Aliases: F13P17.5, F13P17_5	2.7	2.7	0.0	0.0	100.0%	-5.6
20210	AT4G10180.1   Symbol: DET1   light-mediated development protein 1 / deetiolated1 (DET1), identical to Light-mediated development protein DET1 (Deetiolated1) (Swiss-Prot:P48732) (Arabidopsis thaliana)   chr4:6346459-6349272 FORWARD   Aliases: DE ETIOLATED 1, FUS2, FUSCA 2, T9A4.17	7.0	7.0	0.0	0.0	100.0%	-4.7
20211	AT4G36170.1   expressed protein   chr4:17113875-17119837 FORWARD   Aliases: F23E13.60, F23E13_60	2.3	2.3	0.0	0.0	100.0%	-6.0
20212	AT1G74910.3   ADP-glucose pyrophosphorylase family protein, contains Pfam profile PF00483: Nucleotidyl transferase; low similarity to mannose-1-phosphate guanylyltransferase (Hypocrea jecorina) GI:3323397   chr1:28139022-28142339 REVERSE   Aliases: F25A4.12, F25A4_12	6.3	6.3	0.0	0.0	100.0%	-5.0
20213	AT2G02780.1   leucine-rich repeat transmembrane protein kinase, putative   chr2:781846-784645 REVERSE   Aliases: T20F6.8, T20F6_8	2.9	2.9	-0.0	-0.0	100.0%	-4.9
20214	AT4G17560.1   ribosomal protein L19 family protein, similar to plastid ribosomal protein L19 precursor (Spinacia oleracea) gi:7582403:gb:AAF64312   chr4:9780292-9782194 FORWARD   Aliases: DL4815W, FCAALL.39	5.1	5.1	-0.0	-0.0	100.0%	-4.2
20215	AT3G02640.1   expressed protein   chr3:564891-565715 REVERSE   Aliases: F16B3.27, F16B3_27	3.7	3.7	0.0	0.0	100.0%	-5.1
20216	AT1G79060.1   expressed protein   chr1:29746641-29748493 FORWARD   Aliases: YUP8H12R.32, YUP8H12R_32	2.4	2.4	0.0	0.0	100.0%	-5.7
20217	AT2G02140.1   Symbol: LCR72/PDF2.6   plant defensin-fusion protein, putative (PDF2.6), plant defensin protein family member, personal communication, Bart Thomma (Bart.Thomma@agr.kuleuven.ac.be); similar to protease inhibitor II (Brassica rapa) gi:1209258:gb:AAA91049   chr2:544706-545424 FORWARD   Aliases: F5O4.9, F5O4_9, LCR72, Low molecular weight cysteine rich 72, PDF2.6	3.4	3.4	0.0	0.0	100.0%	-5.2
20218	AT1G18210.2   calcium-binding protein, putative, similar to SP:Q9M7R0 Calcium-binding allergen Ole e 8 (PCA18/PCA23) {Olea europaea}; contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:6266602-6268821 REVERSE   Aliases: T10F20.22	12.4	12.4	0.0	0.0	100.0%	-4.9
20219	AT3G04010.1   glycosyl hydrolase family 17 protein, similar to beta-1,3-glucanase GB:S12402 (Nicotiana sp), GB:CAA03908 (Citrus sinensis), GB:S44364 (Lycopersicon esculentum)	3.7	3.7	-0.0	-0.0	100.0%	-4.1
20220	AT1G18360.1   hydrolase, alpha/beta fold family protein, similar to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162,(Rattus norvegicus) GI:19697886; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr1:6316688-6319420 REVERSE   Aliases: F15H18.13, F15H18_13	5.3	5.2	0.0	0.0	100.0%	-4.8
20221	AT2G15800.1   expressed protein, and genefinder   chr2:6887907-6889823 FORWARD   Aliases: F19G14.20, F19G14_20	3.0	3.0	-0.0	-0.0	100.0%	-5.5
20222	AT1G14220.1   ribonuclease T2 family protein, contains similarity to S-like ribonuclease PD1 GI:9957752 from (Prunus dulcis); contains ribonuclease T2 family histidine protein motif   chr1:4858637-4859596 REVERSE   Aliases: F7A19.32, F7A19_32	2.4	2.4	0.0	0.0	100.0%	-5.5
20223	AT4G25980.1   cationic peroxidase, putative, similar to cationic peroxidase (Arachis hypogaea) gi:166475:gb:AAA32676   chr4:13189402-13191516 FORWARD   Aliases: F20B18.90, F20B18_90	2.8	2.8	-0.0	-0.0	100.0%	-5.6
20224	AT3G62810.1   complex 1 family protein / LVR family protein, contains Pfam PF05347: Complex 1 protein (LYR family)   chr3:23238683-23239341 FORWARD   Aliases: F26K9.240	10.5	10.5	0.0	0.0	100.0%	-4.9
20225	AT3G58300.1   hypothetical protein   chr3:21593741-21594367 REVERSE   Aliases: F9D24.210	3.0	3.0	0.0	0.0	100.0%	-5.3
20226	AT4G18425.1   expressed protein, contains Pfam profile PF05078: Protein of unknown function (DUF679)   chr4:10181345-10182151 REVERSE   Aliases: None	2.9	2.9	-0.0	-0.0	100.0%	-4.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20227	AT3G24220.1   Symbol: nced6   9-cis-epoxycarotenoid dioxygenase, putative / neoxanthin cleavage enzyme, putative / carotenoid cleavage dioxygenase, putative, similar to GB:CAB10168 from ( <i>Lycopersicon esculentum</i> ) (J. Exp. Bot. 47, 2111-2112 (1997)); similar to 9-cis-epoxycarotenoid dioxygenase ( <i>Phaseolus vulgaris</i> )(GI:6715257)   chr3:8761441-8763179 FORWARD   Aliases: ATNCED6, MUJ8.12	2.8	2.8	0.0	0.0	100.0%	-5.5
20228	AT1G75160.1   expressed protein, contains Pfam profile PF04788: Protein of unknown function (DUF620)   chr1:28213098-28215465 FORWARD   Aliases: F22H5.11, F22H5_11	2.1	2.1	-0.0	-0.0	100.0%	-5.5
20229	AT3G10920.2   Symbol: MSD1   similar to superoxide dismutase (Mn), putative / manganese superoxide dismutase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g56350.1); similar to superoxide dismutase [ <i>Raphanus sativus</i> ] (GB:AAL07333.1); contains InterPro domain Manganese and iron superoxide dismutase (InterPro:IPR001189)   chr3:3417982-3419858 FORWARD   Aliases: F9F8.26, MANGANESE SUPEROXIDE DISMUTASE 1	9.2	9.2	-0.0	-0.0	100.0%	-4.8
20230	AT1G15050.1   Symbol: IAA34   auxin-responsive AUX/IAA family protein, similar to auxin-responsive protein IAA12 (Indoleacetic acid-induced protein 12)( <i>Arabidopsis thaliana</i> ); contains Pfam profile: PF02309: AUX/IAA family	4.5	4.5	0.0	0.0	100.0%	-5.2
20231	AT3G26020.2   similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g21650.1); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g13460.1); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g13460.2); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'gamma) [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g15415.2); similar to serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B' (B'gamma) [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g15415.1); similar to putative protein phosphatase PP2A0 B' subunit gamma isoform [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_477422.1); similar to putative B' regulatory subunit of PP2A (AtB'gamma) [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_479842.1); similar to putative B' regulatory subunit of protein phosphatase [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_470388.1); contains InterPro domain Protein phosphatase 2A, regulatory B subunit (B56 family) (InterPro:IPR002554)   chr3:9514933-9518200 FORWARD   Aliases: MPE11.30	4.5	4.5	0.0	0.0	100.0%	-4.7
20232	ATCG00150.1   Symbol: ATP1   ATPase a subunit	2.8	2.8	-0.0	-0.0	100.0%	-5.1
20233	AT5G58040.1   fip1 motif-containing protein, contains Pfam profile PF05182: Fip1 motif	7.2	7.2	0.0	0.0	100.0%	-4.7
20234	AT1G19510.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain   chr1:6756284-6757368 REVERSE   Aliases: F18O14.26, F18O14_26	2.3	2.3	-0.0	-0.0	100.0%	-6.0
20235	AT4G01840.1   Symbol: KCO5   outward rectifying potassium channel, putative (KCO5), identical to KCO5 protein ( <i>Arabidopsis thaliana</i> ) gi:6522947:emb:CAB62162; similar to kco1 ( <i>Arabidopsis thaliana</i> ) gi:2230761:emb:CAA69158; member of the 2 pore, 4 transmembrane (2P/4TM) K+ channel family, PMID:11500563	4.7	4.7	-0.0	-0.0	100.0%	-5.0
20236	AT5G64300.1   Symbol: ATGCH   similar to riboflavin biosynthesis protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g22450.1); similar to GTP cyclohydrolase II / 3,4-dihydroxy-2-butanone-4-phosphate synthase [ <i>Lycopersicon esculentum</i> ] (GB:CAA05308.1); similar to putative riboflavin biosynthesis protein ribA [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_483002.1); contains InterPro domain GTP cyclohydrolase II (InterPro:IPR000926); contains InterPro domain 3,4-Dihydroxy-2-butanone 4-phosphate synthase (InterPro:IPR000422)   chr5:25735630-25738388 FORWARD   Aliases: GTP CYCLOHYDROLASE II, MSJ1.14, MSJ1_14	7.7	7.7	0.0	0.0	100.0%	-5.0
20237	AT4G39330.2   similar to mannitol dehydrogenase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g21730.1); similar to mannitol dehydrogenase, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g21890.1); similar to putative sinapyl alcohol dehydrogenase [ <i>Populus tremula</i> x <i>Populus tremuloides</i> ] (GB:AAM95578.1); contains InterPro domain Zinc-containing alcohol dehydrogenase superfamily (InterPro:IPR002085)	3.5	3.5	-0.0	-0.0	100.0%	-5.1
20238	AT1G63220.1   C2 domain-containing protein, similar to phloem protein RPP16 ( <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)) GI:21998839; contains Pfam profile PF00168: C2 domain   chr1:23452584-23454106 FORWARD   Aliases: F9N12.16, F9N12_16	7.5	7.4	0.0	0.0	100.0%	-4.7
20239	AT1G75730.1   expressed protein   chr1:28439367-28443328 REVERSE   Aliases: F10A5.7, F10A5_7	2.8	2.8	-0.0	-0.0	100.0%	-5.3
20240	AT3G62920.1   expressed protein   chr3:23271692-23272268 FORWARD   Aliases: T20O10.20	4.9	4.9	-0.0	-0.0	100.0%	-4.9
20241	AT3G61400.1   2-oxoglutarate-dependent dioxygenase, putative, similar to 2A6 (GI:599622) and tomato ethylene synthesis regulatory protein E8 (SP:P10967); 1-aminocyclopropane-1-carboxylate oxidase homolog - <i>Arabidopsis thaliana</i> , PIR:S59548	2.6	2.6	-0.0	-0.0	100.0%	-5.5
20242	AT5G07510.2   Symbol: GRP14   similar to glycine-rich protein (GRP18) [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g07520.1); similar to pollen coat oleosin-glycine rich protein [ <i>Sisymbrium irio</i> ] (GB:AAR15428.1); similar to pollen coat oleosin-glycine rich protein [ <i>Capsella rubella</i> ] (GB:AAR15467.1); contains InterPro domain Eggshell protein (InterPro:IPR002952); contains InterPro domain Oleosin (InterPro:IPR000136)	3.1	3.2	-0.0	-0.0	100.0%	-5.2
20243	AT1G73655.1   immunophilin / FKBP-type peptidyl-prolyl cis-trans isomerase family protein, similar to (Peptidyl-prolyl cis-trans isomerase) (PPIase) (Rotamase) (SP:Q26486) ( <i>Spodoptera frugiperda</i> ); contains Pfam PF00254: peptidyl-prolyl cis-trans isomerase, FKBP-type   chr1:27694020-27695475 REVERSE   Aliases: None	7.3	7.3	-0.0	-0.0	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20244	AT5G59650.1   leucine-rich repeat protein kinase, putative, contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr5:24048572-24052326 FORWARD   Aliases: MTH12.9, MTH12_9	2.8	2.8	-0.0	-0.0	100.0%	-5.5
20245	AT5G50270.1   F-box family protein, contains F-box domain Pfam:PF00646	3.1	3.1	-0.0	-0.0	100.0%	-5.1
20246	AT4G25250.1   invertase/pectin methylesterase inhibitor family protein, similar to pectinesterase from Arabidopsis thaliana SP:Q42534, Lycopersicon esculentum SP:Q43143; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr4:12934572-12935383 FORWARD   Aliases: F24A6.90, F24A6_90	2.3	2.3	-0.0	-0.0	100.0%	-5.8
20247	AT5G41320.1   expressed protein   chr5:16551670-16553217 FORWARD   Aliases: MYC6.3, MYC6_3	2.7	2.6	0.0	0.0	100.0%	-5.5
20248	AT1G15040.2   glutamine amidotransferase-related   chr1:5179617-5181369 REVERSE   Aliases: T15D22.12, T15D22_12	3.5	3.5	-0.0	-0.0	100.0%	-5.2
20249	AT1G14640.1   SWAP (Suppressor-of-White-APricot)/surp domain-containing protein, similar to human splicing factor GB:CAA59494 GI:899298 from (Homo sapiens); contains Pfam profile PF01805: Surp module   chr1:5023651-5025950 FORWARD   Aliases: T5E21.18, T5E21_18	2.3	2.3	-0.0	-0.0	100.0%	-5.7
20250	AT4G02860.1   similar to phenazine biosynthesis PhzC/PhzF family protein [Arabidopsis thaliana] (TAIR:At1g03210.1); similar to phenazine biosynthesis family protein [Oryza sativa (japonica cultivar-group)] (GB:AAU89223.1); contains InterPro domain Phenazine biosynthesis PhzC/PhzF protein (InterPro:IPR003719)   chr4:1268713-1270525 REVERSE   Aliases: T5J8.18, T5J8_18	9.4	9.3	0.0	0.0	100.0%	-4.7
20251	AT3G29780.1   Symbol: RALFL27   expressed protein   chr3:11674220-11674668 FORWARD   Aliases: RALF LIKE 27, T26G12.18	3.0	3.0	-0.0	-0.0	100.0%	-4.1
20252	AT3G31940.1   hypothetical protein   chr3:12943265-12944247 FORWARD   Aliases: F8N14.6	2.2	2.2	0.0	0.0	100.0%	-5.9
20253	AT5G03870.1   glutaredoxin family protein, contains Pfam profile PF00462: Glutaredoxin	4.0	4.0	0.0	0.0	100.0%	-5.0
20254	AT1G04670.1   expressed protein, ; expression supported by MPSS   chr1:1301984-1302531 FORWARD   Aliases: T1G11.23, T1G11_23	3.1	3.1	-0.0	-0.0	100.0%	-6.0
20255	AT3G26550.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.6	-0.0	-0.0	100.0%	-5.5
20256	AT4G09130.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097: Zinc finger, C3HC4 type (RING finger)   chr4:5815846-5816919 FORWARD   Aliases: T8A17.9	2.3	2.2	0.0	0.0	100.0%	-5.8
20257	AT3G19940.1   sugar transporter, putative, similar to sugar transport protein (Arabidopsis thaliana) GI:16524; contains Pfam profile PF00083: major facilitator superfamily protein   chr3:6938217-6939981 FORWARD   Aliases: MPN9.18	3.3	3.3	-0.0	-0.0	100.0%	-5.2
20258	AT3G49380.1   calmodulin-binding family protein   chr3:18322894-18324475 REVERSE   Aliases: F2K15.240	2.9	2.9	0.0	0.0	100.0%	-5.1
20259	AT3G20850.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:7304163-7304567 FORWARD   Aliases: MOE17.16	2.5	2.5	0.0	0.0	100.0%	-5.5
20260	AT5G16560.1   Symbol: KAN   myb family transcription factor (KAN1), contains Pfam profile: PF00249 myb-like DNA-binding domain; identical to cDNA GARP-like putative transcription factor KANADI1 (KAN1) GI:15723590   chr5:5406866-5411427 REVERSE   Aliases: KANADI, MQK4.31, MQK4_31	2.2	2.2	-0.0	-0.0	100.0%	-6.0
20261	AT1G61420.1   S-locus lectin protein kinase family protein, contains Pfam domains, PF00954: S-locus glycoprotein family, PF00069: Protein kinase domain, and PF01453: Lectin (probable mannose binding)   chr1:22664125-22667303 REVERSE   Aliases: T1F9.9, T1F9_9	3.0	3.0	0.0	0.0	100.0%	-5.4
20262	AT1G04350.1   2-oxoglutarate-dependent dioxygenase, putative, Similar to Arabidopsis 2A6 (gb:X83096) and to tomato ethylene synthesis regulatory protein E8 (SP:P10967); EST gb:T76913 comes from this gene   chr1:1165164-1166767 FORWARD   Aliases: F19P19.22, F19P19_22	4.9	4.9	0.0	0.0	100.0%	-5.1
20263	AT3G29690.1   transferase-related, similar to anthocyanin 5-aromatic acyltransferase from Gentiana triflora GI:4185599, malonyl CoA:anthocyanin 5-O-glucoside-6'''-O-malonyltransferase from Perilla frutescens GI:17980232, Salvia splendens GI:17980234   chr3:11543249-11544028 REVERSE   Aliases: MOD1.5	3.2	3.2	0.0	0.0	100.0%	-5.1
20264	AT3G55820.1   expressed protein   chr3:20725020-20725634 FORWARD   Aliases: F1116.230	3.2	3.2	-0.0	-0.0	100.0%	-5.3
20265	AT3G23190.1   lesion inducing protein-related, similar to ORF, able to induce HR-like lesions (Nicotiana tabacum)   chr3:8279339-8280919 FORWARD   Aliases: K14B15.15	3.7	3.7	-0.0	-0.0	100.0%	-4.6
20266	AT4G08730.1   expressed protein   chr4:5577387-5578776 REVERSE   Aliases: T32A17.40, T32A17_40	3.6	3.6	0.0	0.0	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20267	AT5G23800.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr5:8022219-8024692 REVERSE   Aliases: MRO11.16, MRO11_16	3.2	3.2	-0.0	-0.0	100.0%	-5.5
20268	AT2G44065.2   ribosomal protein L2 family protein, similar to ribosomal protein L2 (Gossypium arboreum) GI:17644114; contains Pfam profile PF03947: Ribosomal Proteins L2, C-terminal domain   chr2:18235586-18238483 FORWARD   Aliases: None	5.2	5.2	-0.0	-0.0	100.0%	-4.9
20269	AT5G08440.1   expressed protein   chr5:2720670-2727166 FORWARD   Aliases: F8L15.170, F8L15_170	3.0	3.0	0.0	0.0	100.0%	-5.7
20270	AT4G35280.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr4:16787434-16788288 REVERSE   Aliases: F23E12.160, F23E12_160	3.6	3.6	0.0	0.0	100.0%	-5.1
20271	AT3G29375.1   XH domain-containing protein, contains Pfam profile: PF03469: XH domain   chr3:11281388-11283196 FORWARD   Aliases: None	5.3	5.3	0.0	0.0	100.0%	-4.4
20272	AT3G23040.1   hypothetical protein   chr3:8186087-8186897 FORWARD   Aliases: MXC7.7	4.0	4.1	-0.0	-0.0	100.0%	-4.8
20273	AT2G24330.1   expressed protein   chr2:10354240-10356905 REVERSE   Aliases: T28I24.6, T28I24_6	4.8	4.8	-0.0	-0.0	100.0%	-4.8
20274	AT4G13770.1   Symbol: CYP83A1   cytochrome P450 family protein   chr4:7990481-7992305 REVERSE   Aliases: CYTOCHROME P450 83A1, CYTOCHROME P450 MONOOXYGENASE, F18A5.160, F18A5_160, REF2	3.2	3.3	-0.0	-0.0	100.0%	-4.5
20275	AT3G54490.1   eukaryotic rpb5 RNA polymerase subunit family protein, similar to SP:P19388 DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) {Homo sapiens}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain	2.4	2.4	0.0	0.0	100.0%	-5.6
20276	AT3G63490.2   ribosomal protein L1 family protein, ribosomal protein L1, S.oleracea, EMBL:SORPL1   chr3:23455190-23457820 FORWARD   Aliases: MAA21.120	5.9	5.9	0.0	0.0	100.0%	-4.8
20277	AT5G46160.2   ribosomal protein L14 family protein / huellenlos paralog (HLP), contains Pfam profile PF00238: Ribosomal protein L14p/L23e; identical to cDNA HUELLENLOS PARALOG (HLP) nuclear gene for mitochondrial product GU:18140859   chr5:18728582-18729734 REVERSE   Aliases: MCL19.22, MCL19_22	9.4	9.4	0.0	0.0	100.0%	-4.9
20278	AT3G04870.2   Symbol: ZDS   zeta-carotene desaturase (ZDS1) / carotene 7,8-desaturase, identical to SP:Q38893 Zeta-carotene desaturase, chloroplast precursor (EC 1.14.99.30) (Carotene 7,8-desaturase) {Arabidopsis thaliana}   chr3:1342614-1347430 FORWARD   Aliases: PDE181, PIGMENT DEFECTIVE EMBRYO, PRE ZETA CAROTENE DESATURASE PRECURSOR, T9J14.18, ZETA CAROTENE DESATURASE	7.5	7.6	-0.0	-0.0	100.0%	-4.9
20279	AT1G34360.1   translation initiation factor 3 (IF-3) family protein, low similarity to Translation initiation factor IF-3 from (subsp. Schizaphis graminum) {Buchnera aphidicola} SP:P46243, {Salmonella typhimurium} SP:P33321; contains Pfam profiles PF05198: Translation initiation factor IF-3 N-terminal domain, PF00707: Translation initiation factor IF-3 C-terminal domain   chr1:12542867-12546150 FORWARD   Aliases: F7P12.8, F7P12_8	4.1	4.1	-0.0	-0.0	100.0%	-5.3
20280	AT5G38630.1   Symbol: ACYB 1	8.5	8.5	0.0	0.0	100.0%	-5.0
20281	AT3G43240.1   ARID/BRIGHT DNA-binding domain-containing protein, contains Pfam profile PF01388: ARID/BRIGHT DNA binding domain	6.3	6.2	0.0	0.0	100.0%	-4.9
20282	AT3G19910.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:6926314-6929572 FORWARD   Aliases: MPN9.16	9.0	9.0	-0.0	-0.0	100.0%	-4.8
20283	AT5G45700.1   NLI interacting factor (NIF) family protein, contains Pfam profile PF03031: NLI interacting factor   chr5:18554576-18555423 FORWARD   Aliases: MRA19.9, MRA19_9	2.2	2.2	0.0	0.0	100.0%	-5.9
20284	AT5G61170.1   40S ribosomal protein S19 (RPS19C), 40S ribosomal protein S19, Oryza sativa, SWISSPROT:RS19_ORYSA	10.8	10.8	-0.0	-0.0	100.0%	-4.9
20285	AT4G30640.1   F-box family protein (FBL19), contains similarity to SKP1 interacting partner 1 GI:10716947 from (Arabidopsis thaliana)   chr4:14952676-14953688 FORWARD   Aliases: F17I23.20, F17I23_20	2.9	2.9	0.0	0.0	100.0%	-5.1
20286	AT3G20530.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:7166066-7167930 FORWARD   Aliases: K10D20.14	3.0	3.0	0.0	0.0	100.0%	-5.5
20287	AT3G58020.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam profile PF00226 DnaJ domain   chr3:21489288-21494286 FORWARD   Aliases: T10K17.230	3.8	3.8	-0.0	-0.0	100.0%	-5.4
20288	AT4G05000.2   vacuolar protein sorting-associated protein 28 family protein / VPS28 family protein, contains similarity to Swiss-Prot:Q02767 vacuolar protein sorting-associated protein VPS28 (Saccharomyces cerevisiae)   chr4:2563057-2564738 FORWARD   Aliases: C17L7.5	4.1	4.1	0.0	0.0	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20289	AT3G61710.3   expressed protein, similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:AAU90282.1); contains InterPro domain Autophagy protein Apg6 (InterPro:IPR007243)   chr3:22850290-22853407 REVERSE   Aliases: F21F14.6	6.6	6.6	0.0	0.0	100.0%	-4.9
20290	AT3G20865.1   arabinogalactan-protein, putative (AGP), similar to gi:10880503:gb:AAG24281   chr3:7308510-7308968 REVERSE   Aliases: None	2.9	2.9	0.0	0.0	100.0%	-5.0
20291	AT2G40260.1   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:16823896-16825551 REVERSE   Aliases: T7M7.13	3.1	3.1	-0.0	-0.0	100.0%	-5.2
20292	AT1G17370.1   oligouridylate-binding protein, putative, similar to oligouridylate binding protein (Nicotiana plumbaginifolia) GI:6996560; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:5951535-5955030 REVERSE   Aliases: F28G4.17	6.8	6.7	0.0	0.0	100.0%	-4.6
20293	AT2G23270.1   expressed protein, ; similar to GP:2464853:gnl:PID:e353149:Z99707   chr2:9910295-9910925 FORWARD   Aliases: T20D16.10, T20D16_10	3.8	3.8	-0.0	-0.0	100.0%	-5.0
20294	AT3G61170.1   pentatricopeptide (PPR) repeat-containing protein, strong similarity to PCMP-H2 (Arabidopsis thaliana) GI:5050911; contains Pfam profile PF01535: PPR repeat   chr3:22649666-22652212 REVERSE   Aliases: T20K12.70	3.9	3.9	0.0	0.0	100.0%	-4.9
20295	AT1G33265.1   expressed protein, contains Pfam profile PF03647: Uncharacterised protein family (UPF0136); supporting cDNA gi:23198247:gb:BT000332.1:   chr1:12066575-12068391 FORWARD   Aliases: None	7.9	7.9	-0.0	-0.0	100.0%	-4.5
20296	AT5G51650.1   hypothetical protein   chr5:20995429-20996475 REVERSE   Aliases: K17N15.20, K17N15_20	3.0	3.0	0.0	0.0	100.0%	-5.4
20297	AT2G38320.1   expressed protein   chr2:16062367-16065058 FORWARD   Aliases: T19C21.19, T19C21_19	3.1	3.1	-0.0	-0.0	100.0%	-4.3
20298	AT2G03130.1   ribosomal protein L12 family protein   chr2:940741-941073 FORWARD   Aliases: T18E12.20, T18E12_20	5.1	5.1	0.0	0.0	100.0%	-5.1
20299	AT5G48950.2   thioesterase family protein, contains Pfam profile PF03061: thioesterase family protein   chr5:19863379-19864661 FORWARD   Aliases: K19E20.6, K19E20_6	3.2	3.2	-0.0	-0.0	100.0%	-5.5
20300	AT5G61670.2   expressed protein   chr5:24800807-24803171 FORWARD   Aliases: K11J9.20, K11J9_20	8.5	8.5	-0.0	-0.0	100.0%	-5.0
20301	AT2G31450.1   endonuclease-related, similar to endonuclease III (Homo sapiens) GI:1753174; contains Pfam profile PF00633: Helix-hairpin-helix motif   chr2:13408209-13411254 REVERSE   Aliases: T28P16.6, T28P16_6	5.5	5.5	0.0	0.0	100.0%	-4.9
20302	AT1G06400.1   Symbol: ARA2   Ras-related GTP-binding protein (ARA-2), identical to Ras-related protein ARA-2 SP:P28185 from (Arabidopsis thaliana)   chr1:1950843-1952726 REVERSE   Aliases: ARA 2, SMALL GTP BINDING PROTEIN, T2D23.10, T2D23_10	9.0	9.1	-0.0	-0.0	100.0%	-4.7
20303	AT1G65490.1   expressed protein   chr1:24358434-24358975 FORWARD   Aliases: F5I14.26	2.3	2.3	0.0	0.0	100.0%	-5.5
20304	AT3G46670.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr3:17203574-17205382 REVERSE   Aliases: F12A12.190	3.3	3.3	0.0	0.0	100.0%	-5.4
20305	AT5G55600.1   agenet domain-containing protein / bromo-adjacent homology (BAH) domain-containing protein, contains Pfam profile PF01426: BAH domain and PF05641: Agenet domain	4.1	4.1	0.0	0.0	100.0%	-4.8
20306	AT3G01250.1   expressed protein   chr3:79312-80112 FORWARD   Aliases: T4P13.6, T4P13_6	2.6	2.6	0.0	0.0	100.0%	-5.8
20307	AT4G05250.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:2691458-2692414 FORWARD   Aliases: C17L7.170, C17L7_170	2.5	2.5	0.0	0.0	100.0%	-5.8
20308	AT1G06070.1   bZIP transcription factor, putative (bZIP69), similar to transcriptional activator RF2a GB:AF005492 GI:2253277 from (Oryza sativa); contains Pfam profile PF00170: bZIP transcription factor   chr1:1834828-1837647 REVERSE   Aliases: T21E18.12, T21E18_12	4.2	4.2	-0.0	-0.0	100.0%	-5.2
20309	AT2G47280.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:19423918-19425322 FORWARD   Aliases: T8I13.12	3.1	3.1	0.0	0.0	100.0%	-5.3
20310	AT2G46240.1   IQ domain-containing protein / BAG domain-containing protein, contains Pfam profiles PF00612: IQ calmodulin-binding motif, PF02179: BAG (Apoptosis regulator Bcl-2 protein) domain   chr2:18993234-18997020 FORWARD   Aliases: T3F17.11	4.8	4.8	0.0	0.0	100.0%	-5.2
20311	AT5G08240.1   expressed protein   chr5:2650838-2652387 REVERSE   Aliases: F8L15.11	3.1	3.1	0.0	0.0	100.0%	-4.2
20312	AT5G43720.1   expressed protein   chr5:17574393-17576581 REVERSE   Aliases: MQD19.5, MQD19_5	4.8	4.8	-0.0	-0.0	100.0%	-5.1



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20313	AT3G11220.1   Paxneb protein-related, contains Pfam profile PF05625: PAXNEB protein; similar to Paxneb protein (GI:10129788) (Mus musculus); similar to PAX neighbour protein (GI:15887001) (Takifugu rubripes)   chr3:3513537-3516414 REVERSE   Aliases: F11B9.14	2.2	2.2	-0.0	-0.0	100.0%	-5.7
20314	AT1G26690.1   emp24/gp25L/p24 family protein, similar to SP:P49755 Transmembrane protein Tmp21 precursor (21 kDa Transmembrane trafficking protein) {Homo sapiens}; contains Pfam profile PF01105: emp24/gp25L/p24 family   chr1:9224132-9225738 REVERSE   Aliases: T24P13.7, T24P13_7	6.0	6.0	0.0	0.0	100.0%	-4.9
20315	AT1G79440.1   Symbol: ALDH5F1   succinate-semialdehyde dehydrogenase (SSADH1), similar to succinate-semialdehyde dehydrogenase (NADP+) (SSDH) (Escherichia coli) SWISS-PROT:P25526; identical to succinic semialdehyde dehydrogenase mRNA, nuclear gene encoding mitochondrial protein GI:6684441; contains TIGRfam profile TIGR01780:succinic semialdehyde dehydrogenase; contains Pfam profile PF00171: aldehyde dehydrogenase (NAD) family protein	8.9	8.9	0.0	0.0	100.0%	-4.6
20316	AT5G48990.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr5:19879515-19880851 FORWARD   Aliases: K19E20.12, K19E20_12	5.3	5.3	-0.0	-0.0	100.0%	-5.0
20317	AT2G44820.2   expressed protein   chr2:18491426-18492885 FORWARD   Aliases: F16B22.34, F16B22_34	8.7	8.6	0.0	0.0	100.0%	-5.1
20318	AT4G10310.1   Symbol: HKT1   sodium transporter (HKT1), identical to sodium transporter AtHKT1 (Arabidopsis thaliana) gi:7716474:gb:AAF68393   chr4:6391980-6395803 FORWARD   Aliases: ATHKT1, HIGH AFFINITY K+ TRANSPORTER 1, HKT1, T9A4.5	2.2	2.2	-0.0	-0.0	100.0%	-5.2
20319	AT2G33250.1   expressed protein   chr2:14104509-14105788 FORWARD   Aliases: F25I18.1, F25I18_1	9.2	9.2	0.0	0.0	100.0%	-5.0
20320	AT5G41680.2   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; similar to receptor-like protein kinase (GI:4008006) (Arabidopsis thaliana); similar to receptor-like kinase RHG1 (GI:21239380) (GI:21239382) (Glycine max)	3.4	3.4	-0.0	-0.0	100.0%	-4.6
20321	AT4G26930.1   Symbol: MYB97   myb family transcription factor (MYB97), contains Pfam profile: PF00249 myb-like DNA-binding domain ;similar to anther-specific myb-related protein 2 GI:11066263 from (Nicotiana tabacum)   chr4:13527776-13529178 FORWARD   Aliases: F10M23.270, F10M23_270	2.4	2.4	0.0	0.0	100.0%	-5.7
20322	AT4G33600.1   expressed protein   chr4:16144453-16145867 REVERSE   Aliases: T16L1.90, T16L1_90	2.9	2.9	-0.0	-0.0	100.0%	-5.4
20323	AT3G49190.1   condensation domain-containing protein, contains Pfam profile PF00668: Condensation domain   chr3:18242861-18245370 REVERSE   Aliases: F2K15.50	3.2	3.2	0.0	0.0	100.0%	-5.5
20324	AT1G21390.1   Symbol: EMB2170   expressed protein   chr1:7489140-7490726 REVERSE   Aliases: EMB2170, EMBRYO DEFECTIVE 2170, F24J8.30, F24J8_30	4.0	4.0	-0.0	-0.0	100.0%	-4.6
20325	AT3G28690.2   similar to protein kinase, putative [Arabidopsis thaliana] (TAIR:At5g15080.1); similar to putative protein kinase [Oryza sativa (japonica cultivar-group)] (GB:NP_917446.1); similar to serine/threonine protein kinase [Aster tripolium] (GB:BAC57958.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr3:10756744-10759105 FORWARD   Aliases: MZN14.22	4.2	4.2	-0.0	-0.0	100.0%	-4.6
20326	NA	9.9	9.9	-0.0	-0.0	100.0%	-5.3
20327	AT2G40060.1   expressed protein   chr2:16733562-16735263 FORWARD   Aliases: T28M21.22, T28M21_22	9.6	9.6	-0.0	-0.0	100.0%	-5.2
20328	AT3G11960.2   cleavage and polyadenylation specificity factor (CPSF) A subunit C-terminal domain-containing protein, similar to Splicing factor 3B subunit 3 (Spliceosome associated protein 130) (SAP 130) (SF3b130) (Pre-mRNA splicing factor SF3b 130kDa subunit) (SP:Q15393) (Homo sapiens); contains Pfam PF03178 : CPSF A subunit region   chr3:3786437-3793663 FORWARD   Aliases: MEC18.7	4.4	4.4	0.0	0.0	100.0%	-5.1
20329	AT1G18510.1   expressed protein   chr1:6373288-6374083 FORWARD   Aliases: F15H18.2, F15H18_2	3.2	3.2	0.0	0.0	100.0%	-5.5
20330	AT5G16100.1   expressed protein   chr5:5258554-5259722 REVERSE   Aliases: T21H19.20, T21H19_20	2.1	2.1	-0.0	-0.0	100.0%	-6.0
20331	AT4G02230.1   60S ribosomal protein L19 (RPL19C), similar to L19 from several species   chr4:979229-980667 REVERSE   Aliases: T2H3.3, T2H3_3	10.6	10.6	-0.0	-0.0	100.0%	-4.6
20332	AT5G22060.1   Symbol: ATJ2   DNAJ heat shock protein, putative, strong similarity to SP:O60884 DnaJ homolog subfamily A member 2 (Dnj3) Homo sapiens, several plant DnaJ proteins from PGR; contains Pfam profiles PF00226 DnaJ domain, PF00684 DnaJ central domain (4 repeats), PF01556 DnaJ C terminal region   chr5:7303625-7305800 REVERSE   Aliases: None	9.1	9.1	0.0	0.0	100.0%	-4.7
20333	AT2G46680.2   Symbol: ATHB 7	6.7	6.7	0.0	0.0	100.0%	-4.6
20334	AT1G80080.1   Symbol: TMM   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; contains some similarity to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596   chr1:30132898-30134484 REVERSE   Aliases: F18B13.16, F18B13_16, TOO MANY MOUTHS	2.4	2.4	-0.0	-0.0	100.0%	-5.7

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20335	AT2G16090.1   zinc finger protein-related, contains similarity to zinc finger proteins and Pfam domain, PF01485: IBR domain   chr2:6993916-6997130 REVERSE   Aliases: F7H1.11, F7H1_11	3.6	3.6	0.0	0.0	100.0%	-5.2
20336	AT5G36870.1   Symbol: ATGSL09   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr5:14535546-14551160 FORWARD   Aliases: ATGSL9, F5H8.14, F5H8_14, GLUCAN SYNTHASE LIKE 9, GSL09	4.9	4.9	-0.0	-0.0	100.0%	-4.5
20337	AT5G52690.1   heavy-metal-associated domain-containing protein, contains Pfam profile PF00403: Heavy-metal-associated domain	2.6	2.6	0.0	0.0	100.0%	-5.6
20338	AT1G72580.1   hypothetical protein   chr1:27338068-27338364 REVERSE   Aliases: F28P22.23, F28P22_23	2.9	2.9	-0.0	-0.0	100.0%	-5.6
20339	AT3G14850.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g29050.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73054.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD73055.1); contains InterPro domain Protein of unknown function DUF231 (InterPro:IPR004253)   chr3:4995604-4997700 FORWARD   Aliases: T21E2.11	3.4	3.3	0.0	0.0	100.0%	-4.4
20340	AT5G59800.1   Symbol: MBD7   methyl-CpG-binding domain-containing protein, contains Pfam profile PF01429: Methyl-CpG binding domain   chr5:24111712-24113758 REVERSE   Aliases: MMN10.2, MMN10_2	4.3	4.4	-0.0	-0.0	100.0%	-4.9
20341	AT1G63650.2   Symbol: EGL3   basic helix-loop-helix (bHLH) family protein, similar to bHLH transcription factor (JAF13) GB:AAC39455 (Petunia x hybrida); contains Pfam profile: PF00010 Helix-loop-helix DNA-binding domain   chr1:23603168-23606518 FORWARD   Aliases: ATMYC 2, EGL1, ENHANCER OF GLABRA3, F24D7.16, F24D7_16	3.3	3.3	0.0	0.0	100.0%	-5.4
20342	AT2G43700.1   lectin protein kinase family protein, contains pfam domains PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr2:18123567-18125921 FORWARD   Aliases: F18O19.19	3.4	3.4	-0.0	-0.0	100.0%	-5.3
20343	AT1G50730.1   expressed protein   chr1:18798943-18806931 FORWARD   Aliases: F4M15.4, F4M15_4	4.6	4.6	-0.0	-0.0	100.0%	-4.7
20344	AT3G44570.1   hypothetical protein   chr3:16169891-16170822 FORWARD   Aliases: F14L2.120	2.1	2.1	-0.0	-0.0	100.0%	-6.0
20345	AT2G45610.1   expressed protein, low similarity to PrMC3 (Pinus radiata) GI:5487873   chr2:18798537-18799660 FORWARD   Aliases: F17K2.14	3.1	3.1	-0.0	-0.0	100.0%	-5.6
20346	AT1G21710.1   Symbol: OGG1   8-oxoguanine-DNA glycosylase (OGG1), similar to SP:O15527 N-glycosylase/DNA lyase (Includes: 8-oxoguanine DNA glycosylase (EC 3.2.2.-); DNA-(apurinic or apyrimidinic site) lyase (EC 4.2.99.18) {Homo sapiens}); contains Pfam profiles PF00633: Helix-hairpin-helix motif and PF00730: HhH-GPD superfamily base excision DNA repair protein; identical to cDNA 8-oxoguanine-DNA glycosylase (OGG1 gene) GI:16074116   chr1:7624385-7626105 FORWARD   Aliases: F8K7.14, F8K7_14	6.3	6.3	0.0	0.0	100.0%	-4.9
20347	AT3G23220.1   encodes a member of the ERF (ethylene response factor) subfamily B-3 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 18 members in this subfamily including ATERF-1, ATERF-2, AND ATERF-5.   chr3:8288009-8288395 FORWARD   Aliases: K14B15.13	3.5	3.5	0.0	0.0	100.0%	-5.4
20348	AT5G48290.2   similar to heavy-metal-associated domain-containing protein [Arabidopsis thaliana] (TAIR:At3g07600.1); similar to OSJNBa0016002.17 [Oryza sativa (japonica cultivar-group)] (GB:XP_472812.1); contains InterPro domain Proline-rich region (InterPro:IPR000694)   chr5:19586122-19587025 FORWARD   Aliases: K23F3.1, K23F3_1	2.3	2.3	-0.0	-0.0	100.0%	-4.6
20349	AT4G02540.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	6.7	6.8	-0.0	-0.0	100.0%	-4.6
20350	AT3G62170.1   Symbol: VGDH2   pectinesterase family protein, contains Pfam profiles: PF01095 pectinesterase, PF04043 plant invertase/pectin methylesterase inhibitor ;similar to pollen-specific pectin esterase GI:1620652 from (Brassica rapa subsp. pekinensis)   chr3:23027198-23029484 REVERSE   Aliases: T17J13.130, VGDH2	3.1	3.1	-0.0	-0.0	100.0%	-5.4
20351	AT5G20070.1   MutT/nudix family protein, low similarity to SP:Q19427 NADH pyrophosphatase (EC 3.6.1.-) {Caenorhabditis elegans}; contains Pfam profile PF00293: NUDIX domain   chr5:6779862-6782484 FORWARD   Aliases: F28I16.220, F28I16_220	9.7	9.7	0.0	0.0	100.0%	-5.1
20352	AT4G15330.1   Symbol: CYP705A1   cytochrome P450 family protein   chr4:8751391-8753134 REVERSE   Aliases: DL3710C, FCAALL.270	3.3	3.3	0.0	0.0	100.0%	-4.0
20353	AT5G08000.1   glycosyl hydrolase family protein 17, similar to beta-1,3-glucanase GI:15150341 from (Camellia sinensis); C-terminal homology only   chr5:2563610-2565492 FORWARD   Aliases: F13G24.200, F13G24_200	3.0	3.0	-0.0	-0.0	100.0%	-5.5
20354	AT1G19190.1   expressed protein, contains similarity to anther-specific and pathogenesis response protein (PrMC3) GI:5487873 from (Pinus radiata)   chr1:6623867-6624968 FORWARD   Aliases: T29M8.6, T29M8_6	4.4	4.4	-0.0	-0.0	100.0%	-5.1
20355	AT4G31760.1   peroxidase, putative, similar to peroxidase (Spinacia oleracea) gi:1781338:emb:CAA71496   chr4:15368266-15369730 REVERSE   Aliases: F28M20.50, F28M20_50	3.6	3.6	0.0	0.0	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20356	AT1G46840.1   F-box family protein, contains F-box domain Pfam:PF00646; contains 1 predicted transmembrane domain; similar to Probable disease resistance RPP8-like protein 2 (Swiss-Prot:Q9MAG6) (Arabidopsis thaliana)   chr1:17272625-17274146 FORWARD   Aliases: F2G19.29, F2G19_29	2.7	2.7	0.0	0.0	100.0%	-5.7
20357	AT5G42790.1   Symbol: PAF1   20S proteasome alpha subunit F1 (PAF1), (gb:AAC32062.1)   chr5:17176278-17178298 REVERSE   Aliases: 20S PROTEASOME SUBUNIT PAF1, MJB21.17, MJB21_17, PAF1	10.2	10.1	0.0	0.0	100.0%	-4.8
20358	AT1G70610.1   Symbol: ATTAP1	6.1	6.1	0.0	0.0	100.0%	-4.7
20359	AT2G05160.1   zinc finger (CCCH-type) family protein / RNA recognition motif (RRM)-containing protein, contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr2:1859008-1860928 REVERSE   Aliases: F5G3.6, F5G3_6	2.1	2.1	-0.0	-0.0	100.0%	-5.7
20360	AT2G41190.1   amino acid transporter family protein, low similarity to vesicular GABA transporter (Rattus norvegicus) GI:2587061; belongs to INTERPRO:IPR002422 amino acid/polyamine transporter, family II   chr2:17174357-17177485 REVERSE   Aliases: T3K9.4, T3K9_4	6.2	6.2	-0.0	-0.0	100.0%	-4.8
20361	AT2G18830.1   hypothetical protein   chr2:8163286-8163483 REVERSE   Aliases: MSF3.21, MSF3_21	2.8	2.8	0.0	0.0	100.0%	-5.6
20362	AT3G46040.1   40S ribosomal protein S15A (RPS15aD), cytoplasmic ribosomal protein S15a, Arabidopsis thaliana, EMBL:ATAF1412   chr3:16925554-16926744 FORWARD   Aliases: F12M12.10	10.4	10.4	-0.0	-0.0	100.0%	-5.3
20363	AT1G33230.1   expressed protein   chr1:12046621-12050026 FORWARD   Aliases: T9L6.9, T9L6_9	7.5	7.6	-0.0	-0.0	100.0%	-4.8
20364	AT5G19800.1   hydroxyproline-rich glycoprotein family protein, similar to extensin (Catharanthus roseus) gi:1486263:dbj:BAA13175; contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:6690650-6690940 FORWARD   Aliases: T29J13.220, T29J13_220	3.7	3.8	-0.0	-0.0	100.0%	-4.7
20365	AT3G03200.1   Symbol: ANAC045   no apical meristem (NAM) family protein, similar to NAC2 (GI:6456751) {Arabidopsis thaliana}   chr3:736148-738534 REVERSE   Aliases: ANAC045, T17B22.11, T17B22_11	2.2	2.2	-0.0	-0.0	100.0%	-5.8
20366	AT3G21420.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to SP:Q9ZWQ9 Flavonol synthase (EC 1.14.11.-) {Citrus unshiu}; contains Pfam profile PF03171: oxidoreductase, 2OG-Fe(II) oxygenase family   chr3:7541509-7543524 FORWARD   Aliases: MHC9.10	8.7	8.8	-0.0	-0.0	100.0%	-4.6
20367	AT1G19450.1   integral membrane protein, putative / sugar transporter family protein, similar to GB:U43629 GI:1209756 integral membrane protein from (Beta vulgaris); contains Pfam profile PF00083: major facilitator superfamily protein; contains TIGRFam TIGR00879: Sugar transporter   chr1:6731425-6734873 REVERSE   Aliases: F18O14.22, F18O14_22	7.9	7.9	-0.0	-0.0	100.0%	-5.0
20368	AT3G59700.1   Symbol: ATHLECRK   lectin protein kinase, putative, similar to receptor lectin kinase 3 (Arabidopsis thaliana) gi:4100060:gb:AAD00733   chr3:22063110-22065252 FORWARD   Aliases: ARABIDOPSIS THALIANA LECTIN RECEPTOR KINASE, LECRK1, T16L24.250	3.5	3.5	-0.0	-0.0	100.0%	-4.6
20369	AT2G23930.1   small nuclear ribonucleoprotein G, putative / snRNP-G, putative / Sm protein G, putative, similar to small nuclear ribonucleoprotein G (snRNP-G, Sm protein G, Sm-G, SmG) (Homo sapiens) SWISS-PROT:Q15357   chr2:10189345-10190320 FORWARD   Aliases: T29E15.13, T29E15_13	9.6	9.6	0.0	0.0	100.0%	-5.0
20370	AT2G18500.1   ovate family protein, 69% similar to ovate protein (GI:23429649) (Lycopersicon esculentum); contains TIGRFAM TIGR01568 : uncharacterized plant-specific domain TIGR01568	4.9	4.9	-0.0	-0.0	100.0%	-4.9
20371	AT5G39620.1   Ras-related GTP-binding protein, putative, similar to GTP-binding protein RAB7A GI:1370182 from (Lotus japonicus)   chr5:15881394-15883010 REVERSE   Aliases: MIJ24.90, MIJ24_90	2.7	2.7	-0.0	-0.0	100.0%	-5.3
20372	AT2G28490.1   cupin family protein, similar to preproMP27-MP32 (Cucurbita cv. Kurokawa Amakuri) GI:691752, allergen Gly m Bd 28K (Glycine max) GI:12697782, vicilin (Matteuccia struthiopteris) GI:1019792; contains Pfam profile PF00190: Cupin   chr2:12185674-12188089 REVERSE   Aliases: T17D12.5, T17D12_5	2.9	2.9	0.0	0.0	100.0%	-5.5
20373	AT1G06100.1   fatty acid desaturase family protein, similar to delta 9 acyl-lipid desaturase (ADS1) GI:2970034 from (Arabidopsis thaliana)   chr1:1851529-1853018 FORWARD   Aliases: T21E18.15, T21E18_15	2.7	2.7	0.0	0.0	100.0%	-5.3
20374	AT5G62120.1   Symbol: ARR23   hypothetical protein   chr5:24964181-24965451 REVERSE   Aliases: ARABIDOPSIS RESPONSE REGULATOR 23, MTG10.15, MTG10_15	2.4	2.4	0.0	0.0	100.0%	-5.7
20375	AT3G16560.1   protein phosphatase 2C-related / PP2C-related, contains protein phosphatase 2C domain   chr3:5635602-5638488 REVERSE   Aliases: MDC8.3	3.4	3.4	-0.0	-0.0	100.0%	-4.4
20376	AT2G39190.2   Symbol: ATATH8	2.9	2.8	0.0	0.0	100.0%	-5.4
20377	AT2G03710.3   Symbol: AGL3   MADS-box protein (AGL3)   chr2:1129286-1131778 FORWARD   Aliases: AGAMOUS LIKE 3, AGL3, F19B11.16, F19B11_16, MADS BOX PROTEIN	2.7	2.7	0.0	0.0	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20378	AT3G52480.1   expressed protein   chr3:19463232-19464140 REVERSE   Aliases: F22O6.140	3.2	3.3	-0.0	-0.0	100.0%	-4.6
20379	AT5G53640.1   F-box family protein, contains F-box domain Pfam:PF00646	3.1	3.1	-0.0	-0.0	100.0%	-5.1
20380	AT1G50450.1   expressed protein   chr1:18691453-18694039 REVERSE   Aliases: F11F12.19, F11F12_19	8.7	8.7	-0.0	-0.0	100.0%	-4.4
20381	AT5G54190.2   Symbol: PORA   similar to protochlorophyllide reductase B, chloroplast / PCR B / NADPH-protochlorophyllide oxidoreductase B (PORB) [Arabidopsis thaliana] (TAIR:At4g27440.1); similar to NADPH:protochlorophyllide oxidoreductase [Nicotiana tabacum] (GB:BA93003.1); similar to NADPH:protochlorophyllide oxidoreductase [Daucus carota] (GB:AAF20949.1); contains InterPro domain Light-dependent protochlorophyllide reductase (InterPro:IPR005979)	4.0	4.0	0.0	0.0	100.0%	-5.0
20382	AT5G57530.1   xyloglucan:xyloglucosyl transferase, putative / xyloglucan endotransglycosylase, putative / endo-xyloglucan transferase, putative, similar to xyloglucan endotransglycosylase XTR9 Gl:4218963 from (Arabidopsis thaliana)   chr5:23317547-23318831 REVERSE   Aliases: MUA2.10, MUA2_10	2.5	2.5	0.0	0.0	100.0%	-4.3
20383	AT3G54110.1   Symbol: ATPUMP1   plant uncoupling mitochondrial protein (PUMP), identical to plant uncoupling mitochondrial protein (Arabidopsis thaliana) Gl:3115108   chr3:20049670-20052179 FORWARD   Aliases: F24B22.70, PUMP, UCP, UCP2, UNCOUPLING PROTEIN, UNCOUPLING PROTEIN PUMP2	10.9	10.9	0.0	0.0	100.0%	-5.1
20384	AT1G01150.1   expressed protein, ; expression supported by MPSS   chr1:70115-71998 REVERSE   Aliases: F6F3.30	2.2	2.2	-0.0	-0.0	100.0%	-6.1
20385	AT3G60290.1   similar to oxidoreductase, 2OG-Fe(II) oxygenase family protein [Arabidopsis thaliana] (TAIR:At2g44800.1); similar to Fe2+ dioxygenase-like [Sisymbrium irio] (GB:AAR15425.1); contains InterPro domain 2OG-Fe(II) oxygenase superfamily (InterPro:IPR005123)   chr3:22293604-22295531 FORWARD   Aliases: F27H5.80	3.0	3.0	0.0	0.0	100.0%	-5.6
20386	AT3G26700.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr3:9811187-9813901 FORWARD   Aliases: MLJ15.17	3.1	3.1	-0.0	-0.0	100.0%	-5.1
20387	AT4G19600.1   cyclin family protein, similar to cyclin T2a (Homo sapiens) Gl:2981198; contains Pfam profile PF00134: Cyclin, N-terminal domain	7.5	7.5	-0.0	-0.0	100.0%	-4.9
20388	AT5G42180.1   peroxidase 64 (PER64) (P64) (PRXR4), identical to SP:Q43872 Peroxidase 64 precursor (EC 1.11.1.7) (Atperox P64) (PRXR4) (ATP17a) {Arabidopsis thaliana}   chr5:16869860-16871448 FORWARD   Aliases: MJC20.29, MJC20_29	3.1	3.1	0.0	0.0	100.0%	-4.3
20389	AT3G57260.1   Symbol: BGL2   glycosyl hydrolase family 17 protein, similar to glucan endo-1,3-beta-glucosidase, acidic isoform precursor SP:P33157 from (Arabidopsis thaliana)   chr3:21199496-21200838 REVERSE   Aliases: BETA 1,3 GLUCANASE, BETA 1,3 GLUCANASE 2, BG2, F28O9.110, PATHOGENESIS RELATED PROTEIN 2, PR2	2.8	2.8	0.0	0.0	100.0%	-5.4
20390	AT4G09420.1   disease resistance protein (TIR-NBS class), putative, domain signature TIR-NBS exists, suggestive of a disease resistance protein.   chr4:5962208-5963788 REVERSE   Aliases: T15G18.160, T15G18_160	3.7	3.8	-0.0	-0.0	100.0%	-4.8
20391	AT1G65180.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.5	0.0	0.0	100.0%	-5.2
20392	AT1G47530.1   ripening-responsive protein, putative, similar to ripening regulated protein DDTFR18 (Lycopersicon esculentum) Gl:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr1:17454120-17456861 FORWARD   Aliases: F16N3.20, F16N3_20	4.8	4.8	0.0	0.0	100.0%	-4.8
20393	AT2G20430.1   Symbol: RIC6   p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain	3.4	3.4	0.0	0.0	100.0%	-5.3
20394	AT3G26270.1   Symbol: CYP71B25   cytochrome P450 71B25, putative (CYP71B25), identical to Cytochrome P450 71B25 (SP:Q9LTL2) (Arabidopsis thaliana); contains Pfam profile: PF00067 cytochrome P450   chr3:9628799-9630437 REVERSE   Aliases: MTC11.5	3.0	3.0	0.0	0.0	100.0%	-5.5
20395	AT5G27340.1   hypothetical protein   chr5:9635888-9636887 FORWARD   Aliases: F21A20.50, F21A20_50	3.7	3.7	0.0	0.0	100.0%	-5.3
20396	AT2G35890.1   Symbol: CPK25   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase, isoform AK1 (CDPK). (Arabidopsis thaliana) SWISS-PROT:Q06850; contains protein kinase domain, Pfam:PF00069; contains EF hand domain (calcium-binding EF-hand), Pfam:PF00036, INTERPRO:IPR002048   chr2:15074254-15076215 REVERSE   Aliases: F11F19.20, F11F19_20	2.9	2.9	0.0	0.0	100.0%	-5.7
20397	AT3G18300.1   expressed protein, ; expression supported by MPSS   chr3:6283402-6284226 FORWARD   Aliases: MYF24.2	3.7	3.7	-0.0	-0.0	100.0%	-4.9
20398	AT2G25735.1   expressed protein   chr2:10982138-10982837 REVERSE   Aliases: None	2.8	2.8	-0.0	-0.0	100.0%	-4.8
20399	AT5G25930.1   leucine-rich repeat family protein / protein kinase family protein, contains similarity to Swiss-Prot:P47735 receptor-like protein kinase 5 precursor (Arabidopsis thaliana); contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr5:9050797-9053981 FORWARD   Aliases: F18A17.4	5.6	5.6	0.0	0.0	100.0%	-4.7
20400	AT3G03660.1   homeobox-leucine zipper transcription factor family protein, similar to to PRESSED FLOWER (GP:17907768) {Arabidopsis thaliana}   chr3:891261-892169 REVERSE   Aliases: T12J13.6, T12J13_6	2.5	2.5	-0.0	-0.0	100.0%	-5.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20401	AT2G47750.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr2:19567197-19570261 REVERSE   Aliases: F17A22.14	2.2	2.1	0.0	0.0	100.0%	-5.7
20402	AT2G30580.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:13033077-13037738 FORWARD   Aliases: T6B20.7, T6B20_7	6.0	6.0	-0.0	-0.0	100.0%	-5.1
20403	AT4G09040.1   RNA recognition motif (RRM)-containing protein, low similarity to enhancer binding protein-1; EBP1 (Entamoeba histolytica) GI:8163877, SP:P19682 28 kDa ribonucleoprotein, chloroplast precursor (28RNP) {Nicotiana sylvestris}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr4:5794529-5797331 REVERSE   Aliases: F23J3.70, F23J3_70	2.8	2.8	-0.0	-0.0	100.0%	-4.9
20404	AT2G40780.1   hypothetical protein   chr2:17028953-17029826 FORWARD   Aliases: T7D17.4, T7D17_4	4.4	4.4	0.0	0.0	100.0%	-4.9
20405	AT5G48430.1   expressed protein, low similarity to extracellular dermal glycoprotein EDGP precursor (Daucus carota) GI:285741, SP:P13917 Basic 7S globulin precursor {Glycine max}; expression supported by MPSS   chr5:19645118-19646338 REVERSE   Aliases: MJE7.6, MJE7_6	3.8	3.8	-0.0	-0.0	100.0%	-4.5
20406	AT3G60330.1   ATPase, plasma membrane-type, putative / proton pump, putative, similar to P-type H(+)-transporting ATPase from Nicotiana plumbaginifolia (SP:Q08435, SP:Q08436), Lycopersicon esculentum (GI:5901757, SP:P22180), Solanum tuberosum (GI:435003); contains InterPro accession IPR001757: ATPase, E1-E2 type   chr3:22309738-22314484 FORWARD   Aliases: T8B10.1	3.2	3.2	-0.0	-0.0	100.0%	-4.3
20407	AT1G07910.1   encodes a tRNA ligase that resembles the yeast RNA ligase in structure and function but very different in sequence.   chr1:2446709-2454554 FORWARD   Aliases: T6D22.1, T6D22_1	5.3	5.3	-0.0	-0.0	100.0%	-4.8
20408	AT2G33180.1   expressed protein   chr2:14073545-14074544 FORWARD   Aliases: F25I18.8, F25I18_8	3.8	3.8	-0.0	-0.0	100.0%	-4.8
20409	AT3G42860.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr3:14957176-14959155 REVERSE   Aliases: F18P9.20	3.7	3.7	0.0	0.0	100.0%	-5.6
20410	AT5G04430.2   KH domain-containing protein NOVA, putative, astrocytic NOVA-like RNA-binding protein, Homo sapiens, U70477   chr5:1250252-1253834 REVERSE   Aliases: T19N18.7	6.1	6.1	-0.0	-0.0	100.0%	-4.7
20411	AT3G47490.2   HNH endonuclease domain-containing protein, contains Pfam domain PF01844: HNH endonuclease   chr3:17509322-17510286 FORWARD   Aliases: F1P2.40	6.3	6.3	-0.0	-0.0	100.0%	-4.7
20412	AT1G33260.2   protein kinase family protein, contains Pfam profile: PF00069: Eukaryotic protein kinase domain   chr1:12064489-12066356 FORWARD   Aliases: T16O9.6, T16O9_6	3.9	3.9	0.0	0.0	100.0%	-5.1
20413	AT5G54590.2   protein kinase family protein, contains eukaryotic protein kinase domain, INTERPRO:IPR000719   chr5:22197706-22199924 FORWARD   Aliases: MRB17.9, MRB17_9	3.9	3.9	-0.0	-0.0	100.0%	-5.2
20414	AT5G26310.1   UDP-glucuronosyl/UDP-glucosyl transferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase   chr5:9234688-9236388 FORWARD   Aliases: F9D12.4, F9D12_4	3.4	3.4	0.0	0.0	100.0%	-4.5
20415	AT2G32290.1   beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative, similar to beta-amylase GI:13560977 from (Castanea crenata)   chr2:13721624-13724006 REVERSE   Aliases: T32F6.19, T32F6_19	2.9	2.9	0.0	0.0	100.0%	-5.5
20416	AT1G73840.1   hydroxyproline-rich glycoprotein family protein, similar to proline-rich protein precursor GB:AAC34889 (Glycine max)   chr1:27767346-27770025 REVERSE   Aliases: F25P22.26, F25P22_26	5.8	5.7	0.0	0.0	100.0%	-4.8
20417	AT3G09930.1   GDSL-motif lipase/hydrolase family protein, similar to SP:P40602 Anther-specific proline-rich protein APG precursor {Arabidopsis thaliana}; contains Pfam profile: PF00657 lipase acylhydrolase with GDSL-like motif   chr3:3053265-3055415 FORWARD   Aliases: F8A24.1	1.9	1.9	-0.0	-0.0	100.0%	-5.9
20418	AT2G41860.2   Symbol: CPK14   calcium-dependent protein kinase, putative / CDPK, putative, similar to calmodulin-domain protein kinase CDPK isoform 7 (Arabidopsis thaliana) gi:1399277;gb:AAB03247   chr2:17474724-17476864 REVERSE   Aliases: T11A7.4, T11A7_4	2.8	2.8	0.0	0.0	100.0%	-5.3
20419	AT4G25720.3   similar to putative glutamine cyclotransferase precursor [Oryza sativa (japonica cultivar-group)] (GB:BAD67954.1); contains InterPro domain Glutamine cyclotransferase (InterPro:IPR007788)   chr4:13099821-13102587 REVERSE   Aliases: L73G19.100, L73G19_100	8.3	8.4	-0.0	-0.0	100.0%	-4.6
20420	AT1G05480.1   SNF2 domain-containing protein / helicase domain-containing protein, low similarity to SP:Q9U7E0 Transcriptional regulator ATRX homolog {Caenorhabditis elegans}; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain   chr1:1618601-1620560 REVERSE   Aliases: T25N20.23	3.1	3.1	0.0	0.0	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20421	AT5G17670.1   expressed protein   chr5:5821062-5822738 FORWARD   Aliases: MVA3.2, MVA3_2	7.4	7.4	0.0	0.0	100.0%	-4.5
20422	AT2G22440.1   expressed protein   chr2:9535990-9536997 FORWARD   Aliases: F14M13.16, F14M13_16	2.8	2.8	0.0	0.0	100.0%	-5.6
20423	AT1G72050.2   zinc finger (C2H2 type) family protein, contains multiple zinc finger domains: PF00096: Zinc finger, C2H2 type   chr1:27118744-27121117 FORWARD   Aliases: F28P5.6, F28P5_6	6.3	6.3	-0.0	-0.0	100.0%	-5.1
20424	AT2G16630.1   proline-rich family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr2:7216321-7218104 FORWARD   Aliases: T24I21.4, T24I21_4	3.0	3.0	0.0	0.0	100.0%	-5.4
20425	AT1G13460.2   serine/threonine protein phosphatase 2A (PP2A) regulatory subunit B', putative, similar to SWISS-PROT:Q28653 serine/threonine protein phosphatase 2A, 56 kDa regulatory subunit, delta isoform (PP2A, B subunit, B' delta isoform, PP2A, B subunit, B56 delta isoform, PP2A, B subunit, PR61 delta isoform, PP2A, B subunit, R5 delta isoform, PP2A, B subunit, B'-gamma) (Oryctolagus cuniculus); contains Pfam domain, PF01603: Protein phosphatase 2A regulatory B subunit (B56 family)   chr1:4615810-4618326 FORWARD   Aliases: T6J4.19, T6J4_19	4.5	4.5	-0.0	-0.0	100.0%	-5.0
20426	AT2G15390.2   Symbol: FUT4   xyloglucan fucosyltransferase, putative (FUT4), identical to SP:Q9SJP2 Probable fucosyltransferase 4 (EC 2.4.1.-) (AtFUT4) {Arabidopsis thaliana}; similar to SP:Q9SWH5 Galactoside 2-alpha-L-fucosyltransferase (EC 2.4.1.69) (Xyloglucan alpha-(1,2)-fucosyltransferase) (AtFUT1) {Arabidopsis thaliana}   chr2:6716343-6718117 REVERSE   Aliases: ATFUT4, F26H6.9, F26H6_9	3.2	3.2	0.0	0.0	100.0%	-4.4
20427	AT2G28160.1   basic helix-loop-helix (bHLH) family protein   chr2:12011785-12013199 FORWARD   Aliases: F24D13.5, F24D13_5	2.8	2.7	0.0	0.0	100.0%	-4.7
20428	AT5G57830.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr5:23446517-23448222 REVERSE   Aliases: MTI20.7, MTI20_7	4.6	4.6	-0.0	-0.0	100.0%	-4.6
20429	AT3G21070.2   Symbol: NADK1   ATP-NAD kinase family protein, contains Pfam domain, PF01513: ATP-NAD kinase   chr3:7379805-7383980 REVERSE   Aliases: MSA6.11	3.6	3.6	0.0	0.0	100.0%	-4.5
20430	AT5G58970.2   Symbol: ATUCP2	8.1	8.1	-0.0	-0.0	100.0%	-4.8
20431	AT2G44570.1   glycosyl hydrolase family 9 protein   chr2:18401318-18403344 REVERSE   Aliases: F16B22.6	2.8	2.8	-0.0	-0.0	100.0%	-5.3
20432	AT1G76190.1   auxin-responsive family protein, similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) (Vigna radiata)   chr1:28597119-28597490 FORWARD   Aliases: T23E18.13, T23E18_13	2.5	2.5	0.0	0.0	100.0%	-5.6
20433	AT3G28260.1   hypothetical protein   chr3:10535777-10537381 FORWARD   Aliases: MZF16.21	2.5	2.5	0.0	0.0	100.0%	-5.9
20434	AT1G60430.1   Symbol: ARPC3   ARP2/3 complex 21 kDa subunit family, contains Pfam PF04062: P21-ARC (ARP2/3 complex 21 kDa subunit); similar to Arp2/3 complex subunit p21-Arc (GI:6983853) (Mus musculus); similar to ARP2/3 complex 21 kDa subunit (P21-ARC) (Actin-related protein 2/3 complex subunit 3) (Swiss-Prot:O15145) (Homo sapiens); similar to Chain E, Crystal Structure Of Arp23 COMPLEX Length(GI:17943203) (   chr1:22268056-22269667 REVERSE   Aliases: ARPC3, T13D8.30, T13D8_30	5.2	5.2	0.0	0.0	100.0%	-5.3
20435	AT2G04480.1   expressed protein   chr2:1554279-1555511 REVERSE   Aliases: T1O3.11, T1O3_11	3.0	3.0	-0.0	-0.0	100.0%	-5.4
20436	AT1G74180.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Hcr2-0B (Lycopersicon esculentum) gi:3894387:gb:AAC78593   chr1:27900858-27904569 REVERSE   Aliases: F9E11.6, F9E11_6	2.6	2.6	-0.0	-0.0	100.0%	-5.1
20437	AT3G27420.1   expressed protein   chr3:10149824-10151538 FORWARD   Aliases: K1G2.14	4.2	4.2	-0.0	-0.0	100.0%	-4.8
20438	AT1G62820.1   calmodulin, putative, similar to calmodulin SP:P04465 from (Trypanosoma brucei gambiense); contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr1:23267336-23268014 REVERSE   Aliases: F23N19.25, F23N19_25	6.9	6.9	0.0	0.0	100.0%	-4.8
20439	AT3G31320.1   hypothetical protein   chr3:12697106-12698481 FORWARD   Aliases: T22B15.7	3.1	3.1	0.0	0.0	100.0%	-5.4
20440	AT1G23580.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8357435-8358695 REVERSE   Aliases: F28C11.28	3.4	3.4	0.0	0.0	100.0%	-5.5
20441	AT3G45210.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr3:16568258-16568955 REVERSE   Aliases: T14D3.150	4.7	4.7	0.0	0.0	100.0%	-4.8
20442	AT4G27670.1   Symbol: HSP21   25.3 kDa small heat shock protein, chloroplast precursor (HSP25.3-P), identical to small heat shock protein, chloroplast precursor SP:P31170 from (Arabidopsis thaliana); identified in Scharf, K-D., et al, Cell Stress & Chaperones (2001) 6: 225-237.	3.5	3.5	-0.0	-0.0	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20443	AT3G03990.1   esterase/lipase/thioesterase family protein, low similarity to 3-oxoadipate enol-lactone hydrolase (Pseudomonas sp. B13) GI:17736948, esterase V (Pseudomonas sp.) GI:402521; contains Interpro entry IPR000379   chr3:1033775-1034913 FORWARD   Aliases: T11I18.10, T11I18_10	8.4	8.5	-0.0	-0.0	100.0%	-4.6
20444	AT1G14430.1   glyoxal oxidase-related, low similarity to glyoxal oxidase precursor (glx1) (Phanerochaete chrysosporium) GI:1050302   chr1:4934115-4937016 FORWARD   Aliases: F14L17.20, F14L17_20	2.8	2.8	0.0	0.0	100.0%	-5.4
20445	AT1G26740.1   expressed protein, similar to 50S ribosomal protein L32 (SP:P80339) {Thermus thermophilus}   chr1:9244974-9246588 REVERSE   Aliases: T24P13.27	7.3	7.3	-0.0	-0.0	100.0%	-4.4
20446	AT3G10950.1   60S ribosomal protein L37a (RPL37aB), similar to putative 60S ribosomal protein L37a GB:AAD28753 (Gossypium hirsutum)   chr3:3423898-3424571 FORWARD   Aliases: F9F8.23	3.1	3.1	0.0	0.0	100.0%	-5.3
20447	AT1G53790.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	4.2	4.1	0.0	0.0	100.0%	-4.9
20448	AT5G19990.1   Symbol: ATSUG1	10.4	10.3	0.0	0.0	100.0%	-4.1
20449	AT5G20000.1   Symbol: RPT6A   26S proteasome AAA-ATPase subunit, putative, almost identical to 26S proteasome AAA-ATPase subunit RPT6a GI:6652888 from (Arabidopsis thaliana); almost identical to a member of conserved Sug1 CAD family AtSUG1 GI:13537115 from (Arabidopsis thaliana)   chr5:6756635-6759751 FORWARD   Aliases: 26S PROTEASOME AAA ATPASE SUBUNIT, F28I16.150, F28I16_150	10.4	10.3	0.0	0.0	100.0%	-4.1
20450	AT2G18940.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile: PF01535 PPR repeat   chr2:8210812-8213477 REVERSE   Aliases: F19F24.14, F19F24_14	5.1	5.1	0.0	0.0	100.0%	-4.5
20451	AT1G20340.1   Symbol: DRT112	9.2	9.2	-0.0	-0.0	100.0%	-4.4
20452	AT3G45860.1   receptor-like protein kinase, putative, similar to receptor-like protein kinase 4 (gi:13506745), 5 (gi:13506747), and 6 (gi:13506749) from Arabidopsis thaliana; contains Pfam protein kinase domain PF00069   chr3:16874386-16877026 REVERSE   Aliases: F16L2.70	3.0	3.0	-0.0	-0.0	100.0%	-5.8
20453	AT4G04900.1   Symbol: RIC10   p21-rho-binding domain-containing protein, contains Pfam PF00786: P21-Rho-binding domain   chr4:2486216-2487777 REVERSE   Aliases: ROP INTERACTIVE CRIB MOTIF CONTAINING PROTEIN 10, T1J1.7, T1J1_7	3.6	3.6	-0.0	-0.0	100.0%	-4.7
20454	AT2G32620.1   Symbol: ATCSLB02   cellulose synthase family protein, similar to Zea mays cellulose synthase-5 (gi:9622882), -4 (gi:9622880), -9 (gi:9622890)   chr2:13847821-13851401 FORWARD   Aliases: ATCSLB2, CSLB02, T26B15.18, T26B15_18	3.1	3.1	-0.0	-0.0	100.0%	-5.2
20455	AT3G10580.1   myb family transcription factor, contains PFAM profile: PF00249 myb-like DNA binding domain; similar to transcription factor MYBS1 (GI:24850303) (Oryza sativa (japonica cultivar-group)); similar to I-box binding factor (GI:6688529) (Lycopersicon esculentum)   chr3:3307088-3308235 REVERSE   Aliases: F13M14.13	2.4	2.4	0.0	0.0	100.0%	-5.3
20456	AT1G08650.1   Symbol: PPCK1   phosphoenolpyruvate carboxylase kinase, identical to phosphoenolpyruvate carboxylase kinase (Arabidopsis thaliana) gi:6318613;gb:AAF06968; contains protein kinase domain, Pfam:PF00069	2.9	2.9	0.0	0.0	100.0%	-4.9
20457	AT2G24010.1   Symbol: SCPL23	2.5	2.5	-0.0	-0.0	100.0%	-5.9
20458	AT5G59150.1   Ras-related GTP-binding protein, putative, similar to Ras-related protein Rab11C SP:Q40193 from (Lotus japonicus)   chr5:23893835-23895655 FORWARD   Aliases: MNC17.6, MNC17_6	10.1	10.1	-0.0	-0.0	100.0%	-5.5
20459	AT2G34230.1   expressed protein, contains Pfam profiles PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr2:14461718-14464048 FORWARD   Aliases: F13P17.7, F13P17_7	3.0	3.0	0.0	0.0	100.0%	-5.3
20460	AT3G51200.1   auxin-responsive family protein, similar to auxin-induced protein TGSAUR12 (GI:10185816) (Tulipa gesneriana)   chr3:19029832-19030152 REVERSE   Aliases: F24M12.240	2.4	2.4	0.0	0.0	100.0%	-5.7
20461	AT4G27120.2   expressed protein   chr4:13602096-13604375 REVERSE   Aliases: T24A18.70, T24A18_70	8.3	8.3	0.0	0.0	100.0%	-4.9
20462	AT5G57910.1   expressed protein, similar to unknown protein (emb:CAB79781.1)   chr5:23468375-23469828 REVERSE   Aliases: MTI20.17, MTI20_17	5.5	5.5	-0.0	-0.0	100.0%	-4.7
20463	AT1G62130.1   AAA-type ATPase family protein, contains Pfam domain, PF00004: ATPase, AAA family   chr1:22966030-22972585 REVERSE   Aliases: F19K23.7, F19K23_7	3.5	3.4	0.0	0.0	100.0%	-5.3
20464	AT4G39220.1   Symbol: ATRER1A   RER1A protein, identical to SP:O48670 RER1A protein (AtRER1A) {Arabidopsis thaliana}   chr4:18263611-18265765 FORWARD   Aliases: T22F8.120, T22F8_120	7.3	7.3	0.0	0.0	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20465	AT4G32630.1   similar to human Rev interacting-like protein-related / hRIP protein-related [Arabidopsis thaliana] (TAIR:At4g13350.2); similar to human Rev interacting-like protein-related / hRIP protein-related [Arabidopsis thaliana] (TAIR:At4g13350.1); similar to human Rev interacting-like protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_464581.1); contains InterPro domain Human Rev interacting-like protein (hRIP) (InterPro:IPR001164)   chr4:15737974-15741639 FORWARD   Aliases: F4D11.170, F4D11_170	2.8	2.8	0.0	0.0	100.0%	-5.3
20466	AT4G30140.1   GDSL-motif lipase/hydrolase family protein, low similarity to family II lipases EXL3 GI:15054386, EXL1 GI:15054382 from (Arabidopsis thaliana); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase   chr4:14738393-14740682 REVERSE   Aliases: F6G3.170, F6G3_170	2.4	2.4	-0.0	-0.0	100.0%	-5.3
20467	AT3G53170.1   pentatricopeptide (PPR) repeat-containing protein, low similarity to fertility restorer (Petunia x hybrida) GI:22128587; contains Pfam profile PF01535: PPR repeat   chr3:19715707-19717136 REVERSE   Aliases: T4D2.100	3.8	3.8	-0.0	-0.0	100.0%	-5.3
20468	AT1G07620.1   GTP1/OBG family protein, similar to SP:P20964 Spo0B-associated GTP-binding protein {Bacillus subtilis}; contains Pfam profile PF01018: GTP1/OBG family   chr1:2342274-2346184 REVERSE   Aliases: F24B9.32, F24B9_32	4.5	4.5	0.0	0.0	100.0%	-4.9
20469	AT2G38080.1   Symbol: IRX12   Encodes a protein with similarity to laccase that may be involved in cell wall biosynthesis. Mutants have a mild irregular xylem phenotype.   chr2:15941540-15944694 FORWARD   Aliases: F16M14.1, F16M14_1, IRX12	2.8	2.8	0.0	0.0	100.0%	-4.7
20470	AT1G69560.1   Symbol: MYB105	2.4	2.4	-0.0	-0.0	100.0%	-5.6
20471	AT1G65540.1   calcium-binding EF hand family protein, similar to leucine zipper-EF-hand containing transmembrane protein 1 (Homo sapiens) GI:4235226; contains Pfam profile PF00036: EF hand   chr1:24366045-24369674 REVERSE   Aliases: F5I14.7, F5I14_7	4.9	4.9	-0.0	-0.0	100.0%	-5.3
20472	AT2G27550.1   Symbol: ATC   centroradialis protein, putative (CEN), strong similarity to SP:Q41261 CENTRORADIALIS protein {Antirrhinum majus}; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein   chr2:11780330-11781758 FORWARD   Aliases: ARABIDOPSIS THALIANA CENTRORADIALIS, ATC, F10A12.20	3.4	3.5	-0.0	-0.0	100.0%	-4.6
20473	AT4G02580.1   NADH-ubiquinone oxidoreductase 24 kDa subunit, putative, similar to NADH-ubiquinone oxidoreductase 24 kDa subunit, mitochondrial precursor (EC 1.6.5.3) (EC 1.6.99.3) (Polypeptide II) (Swiss-Prot:P04394) (Bos taurus)   chr4:1134494-1137156 FORWARD   Aliases: T10P11.14, T10P11_14	9.9	9.9	-0.0	-0.0	100.0%	-4.5
20474	AT4G35470.1   leucine-rich repeat family protein, similar to Leucine-rich repeat protein SHOC-2 (Ras-binding protein Sur-8) (SP:Q9UQ13) {Homo sapiens}, PIR:T12704; contains Pfam PF00560: Leucine Rich Repeat domains   chr4:16846306-16849151 FORWARD   Aliases: F15J1.40, F15J1_40	3.9	3.9	-0.0	-0.0	100.0%	-4.9
20475	AT1G71810.1   ABC1 family protein, contains Pfam domain, PF03109: ABC1 family   chr1:27006076-27011838 REVERSE   Aliases: F14O23.19, F14O23_19	4.6	4.6	0.0	0.0	100.0%	-5.1
20476	AT2G24310.1   expressed protein   chr2:10351438-10352590 FORWARD   Aliases: T28I24.4, T28I24_4	2.4	2.4	-0.0	-0.0	100.0%	-5.6
20477	AT5G28570.1   hypothetical protein   chr5:10574625-10575163 FORWARD   Aliases: T10I18.4, T10I18_4	4.0	4.0	-0.0	-0.0	100.0%	-5.6
20478	AT3G25090.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:9140046-9141101 REVERSE   Aliases: MJL12.3	3.2	3.2	0.0	0.0	100.0%	-5.0
20479	AT2G25640.1   similar to transcription elongation factor-related [Arabidopsis thaliana] (TAIR:At5g25520.2); similar to PREDICTED: PHD finger protein 3 [Mus musculus] (GB:XP_129836.3); similar to mKIAA0244 protein [Mus musculus] (GB:BAC65512.1); contains InterPro domain Transcription elongation factor S-II, central region (InterPro:IPR003618)   chr2:10917576-10921047 FORWARD   Aliases: F3N11.9, F3N11_9	3.7	3.7	0.0	0.0	100.0%	-4.5
20480	AT1G48670.1   auxin-responsive GH3 family protein, similar to auxin-responsive GH3 product (Glycine max) GI:18591; contains Pfam profile PF03321: GH3 auxin-responsive promoter   chr1:18002614-18004868 REVERSE   Aliases: F11I4.14, F11I4_14	2.6	2.6	0.0	0.0	100.0%	-4.7
20481	AT1G53950.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr1:20150116-20151656 REVERSE   Aliases: T18A20.25	2.3	2.3	0.0	0.0	100.0%	-5.8
20482	AT4G36500.1   expressed protein   chr4:17225915-17226613 REVERSE   Aliases: AP22.75, AP22_75	3.7	3.7	-0.0	-0.0	100.0%	-4.9
20483	AT5G19850.1   hydrolase, alpha/beta fold family protein, low similarity to hydrolase (Terrabacter sp. DBF63) GI:14196240; contains Pfam profile PF00561: hydrolase, alpha/beta fold family   chr5:6709361-6711675 REVERSE   Aliases: T29J13.270, T29J13_270	4.8	4.8	-0.0	-0.0	100.0%	-5.1
20484	AT5G55750.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr5:22582027-22583247 REVERSE   Aliases: MDF20.19, MDF20_19	2.0	2.0	0.0	0.0	100.0%	-6.1
20485	AT3G50140.1   expressed protein, contains Pfam profile PF03140: Plant protein of unknown function   chr3:18603455-18605547 REVERSE   Aliases: F3A4.220	2.4	2.4	-0.0	-0.0	100.0%	-5.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20486	AT4G17120.1   expressed protein   chr4:9615997-9624221 REVERSE   Aliases: DL4595C, FCAALL.360	3.5	3.5	-0.0	-0.0	100.0%	-5.5
20487	AT1G21510.1   expressed protein   chr1:7531523-7532494 REVERSE   Aliases: F24J8.12, F24J8_12	3.0	3.0	-0.0	-0.0	100.0%	-5.4
20488	AT5G57350.1   Symbol: AHA3   ATPase 3, plasma membrane-type / proton pump 3, nearly identical to SP:P20431 ATPase 3, plasma membrane-type (EC 3.6.3.6) (Proton pump 3) {Arabidopsis thaliana}; contains InterPro accession IPR001757: ATPase, E1-E2 type   chr5:23248105-23253798 REVERSE   Aliases: MJB24.16, MJB24_16, P TYPE H(+) ATPASE ISOFORM 3	7.0	7.0	-0.0	-0.0	100.0%	-5.1
20489	AT5G05140.1   transcription elongation factor-related, low similarity to transcription elongation factor TFIIIS.h (Mus musculus) GI:3288547, elongin A (Mus musculus) GI:6009624   chr5:1519914-1522668 FORWARD   Aliases: MUG13.28	4.0	4.1	-0.0	-0.0	100.0%	-4.6
20490	AT4G24820.2   26S proteasome regulatory subunit, putative (RPN7), contains similarity to ubiquitin activating enzyme GI:3647283 from (Lycopersicon esculentum)	8.8	8.9	-0.0	-0.0	100.0%	-4.5
20491	AT2G30710.1   RabGAP/TBC domain-containing protein, similar to SP:Q08484 GTPase-activating protein GYP1 {Saccharomyces cerevisiae}; contains Pfam profile PF00566: TBC domain   chr2:13092963-13096338 REVERSE   Aliases: T11J7.10, T11J7_10	4.9	5.0	-0.0	-0.0	100.0%	-5.0
20492	AT2G18380.1   zinc finger (GATA type) family protein   chr2:7989950-7991096 REVERSE   Aliases: T30D6.11, T30D6_11	3.1	3.1	-0.0	-0.0	100.0%	-5.5
20493	AT3G54950.1   patatin-related, low similarity to patatin (GI:169500)(Solanum tuberosum); contains Patatin domain PF01734   chr3:20369873-20372210 REVERSE   Aliases: T15C9.3	3.7	3.7	0.0	0.0	100.0%	-4.7
20494	AT5G27910.1   CCAAT-box binding transcription factor Hap5a, putative   chr5:9940740-9941303 REVERSE   Aliases: F15F15.1	2.4	2.4	0.0	0.0	100.0%	-5.4
20495	AT2G43670.1   glycosyl hydrolase family protein 17, similar to glucan endo-1,3-beta-glucosidase precursor SP:P52409 from (Triticum aestivum); C terminal homology only	5.1	5.1	-0.0	-0.0	100.0%	-5.0
20496	AT1G18520.1   senescence-associated family protein, similar to senescence-associated protein 5 (Hemerocallis hybrid cultivar) gi:3551954:gb:AAC34855   chr1:6374925-6376309 FORWARD   Aliases: F15H18.1, F15H18_1	4.0	4.0	0.0	0.0	100.0%	-5.3
20497	AT3G16170.1   acyl-activating enzyme 13 (AAE13), similar to malonyl CoA synthetase GB:AAF28840 from (Bradyrhizobium japonicum); contains Pfam AMP-binding enzyme domain PF00501; identical to cDNA acyl-activating enzyme 13 (At3g16170) GI:29893232, acyl-activating enzyme 13 (Arabidopsis thaliana) GI:29893233   chr3:5476080-5480308 FORWARD   Aliases: MSL1.21	7.5	7.5	-0.0	-0.0	100.0%	-4.6
20498	AT5G49790.1   hypothetical protein, low similarity to keratin-associated protein 16.1 (Mus musculus) GI:14030401   chr5:20250372-20250737 FORWARD   Aliases: K2I5.16, K2I5_16	2.5	2.5	-0.0	-0.0	100.0%	-5.6
20499	AT1G55180.1   Symbol: PLDEPSILON   phospholipase D, putative (PLDEPSILON), identical to SP:Q9C888 Phospholipase D epsilon (EC 3.1.4.4) (AtPLDepsilon) (PLD epsilon) (PLDalpha3) {Arabidopsis thaliana}; similar to GI:6573119 from (Lycopersicon esculentum) (Plant Physiol. 122 (1), 292 (2000))   chr1:20588724-20591296 REVERSE   Aliases: F7A10.25, F7A10_25, PHOSPHOLIPASE D ALPHA 4, PLDALPHA4	2.8	2.8	0.0	0.0	100.0%	-5.0
20500	AT5G62040.1   brother of FT and TFL1 protein (BFT), identical to SP:Q9FIT4 BROTHER of FT and TFL1 protein {Arabidopsis thaliana}; contains Pfam profile PF01161: Phosphatidylethanolamine-binding protein   chr5:24940036-24940935 FORWARD   Aliases: MTG10.11, MTG10_11	2.6	2.6	-0.0	-0.0	100.0%	-5.3
20501	AT2G03430.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr2:1036029-1037613 REVERSE   Aliases: T4M8.14, T4M8_14	7.6	7.6	0.0	0.0	100.0%	-5.0
20502	AT1G25240.1   epsin N-terminal homology (ENTH) domain-containing protein / clathrin assembly protein-related, contains Pfam PF01417: ENTH domain. ENTH (Epsin N-terminal homology) domain; similar to clathrin assembly protein AP180 (GI:6492344) (Xenopus laevis)   chr1:8845218-8846480 FORWARD   Aliases: F4F7.37, F4F7_37	2.5	2.5	-0.0	-0.0	100.0%	-5.2
20503	AT3G11370.1   DC1 domain-containing protein, contains Pfam protein PF03107 DC1 domain   chr3:3561105-3562886 FORWARD   Aliases: F11B9.29	2.1	2.1	-0.0	-0.0	100.0%	-4.5
20504	AT1G49240.1   Symbol: ACT8   actin 8 (ACT8), identical to SP:Q96293 Actin 8 {Arabidopsis thaliana}; nearly identical to SP:Q96292 Actin 2 (Arabidopsis thaliana) GI:1669387, and to At3g18780	7.3	7.4	-0.0	-0.0	100.0%	-4.6
20505	AT3G02420.1   expressed protein   chr3:495892-498841 REVERSE   Aliases: F16B3.5, F16B3_5	7.4	7.4	0.0	0.0	100.0%	-4.5
20506	AT2G30090.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr2:12850660-12852674 REVERSE   Aliases: T27E13.17, T27E13_17	3.5	3.5	-0.0	-0.0	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20507	AT2G42800.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; and grail   chr2:17815019-17816667 REVERSE   Aliases: F7D19.20, F7D19_20	4.4	4.4	0.0	0.0	100.0%	-5.1
20508	AT1G78690.1   phospholipid/glycerol acyltransferase family protein, similar to SP:Q16635 Tafazzin from Homo sapiens; contains Pfam profile: PF01553 Acyltransferase   chr1:29601548-29603522 FORWARD   Aliases: F9K20.27, F9K20_27	5.9	5.9	0.0	0.0	100.0%	-4.5
20509	AT5G08600.1   U3 ribonucleoprotein (Utp) family protein, contains Pfam profile: PF04615 Utp14 protein   chr5:2786299-2789737 FORWARD   Aliases: MAH20.16, MAH20_16	3.2	3.2	0.0	0.0	100.0%	-5.5
20510	AT4G09470.1   expressed protein   chr4:6010994-6012217 REVERSE   Aliases: T15G18.110, T15G18_110	3.0	3.0	-0.0	-0.0	100.0%	-4.8
20511	AT2G12880.1   zinc knuckle (CCHC-type) family protein, contains Pfam domain, PF00098: Zinc knuckle   chr2:5298605-5298964 FORWARD   Aliases: T18E17.4	2.6	2.6	0.0	0.0	100.0%	-5.9
20512	AT3G51950.2   similar to RNA recognition motif (RRM)-containing protein [Arabidopsis thaliana] (TAIR:At3g63450.1); similar to putative DAZ associated protein 1 [Oryza sativa (japonica cultivar-group)] (GB:XP_479561.1); contains InterPro domain Zn-finger, C-x8-C-x5-C-x3-H type (InterPro:IPR000571); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr3:19288756-19292304 REVERSE   Aliases: F4F15.60	7.4	7.4	-0.0	-0.0	100.0%	-5.3
20513	AT4G10370.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.8	-0.0	-0.0	100.0%	-5.5
20514	AT5G15100.1   auxin efflux carrier family protein, contains auxin efflux carrier domain, Pfam:PF03547   chr5:4892162-4893940 REVERSE   Aliases: F2G14.220, F2G14_220	2.5	2.5	0.0	0.0	100.0%	-5.8
20515	AT1G73350.1   expressed protein   chr1:27579344-27580787 REVERSE   Aliases: T9L24.52, T9L24_52	4.0	4.0	0.0	0.0	100.0%	-5.1
20516	AT1G43950.1   Symbol: ARF23   auxin-responsive factor, putative, similar to auxin response factor 9 (Arabidopsis thaliana) GI:4580575; contains Pfam profile PF02362: B3 DNA binding domain; non-consensus TT donor splice site at exon 5   chr1:16675022-16676392 REVERSE   Aliases: ARF23, AUXIN RESPONSE FACTOR 23, F9C16.11, F9C16_11	2.4	2.4	-0.0	-0.0	100.0%	-5.9
20517	AT4G04700.1   Symbol: CPK27   calcium-dependent protein kinase, putative / CDPK, putative, similar to calcium-dependent protein kinase (Nicotiana tabacum) gi:3283996:gb:AAC25423; contains protein kinase domain, Pfam:PF00069   chr4:2385274-2387984 REVERSE   Aliases: T4B21.21, T4B21_21	3.8	3.8	-0.0	-0.0	100.0%	-4.6
20518	AT5G24900.1   Symbol: CYP714A2   cytochrome P450 family protein, similar to Cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus); fatty acid omega-hydroxylase cytochrome P450 4A11 - Homo sapiens, PIR:I53015   chr5:8563812-8566815 REVERSE   Aliases: F6A4.110, F6A4_110	2.7	2.7	0.0	0.0	100.0%	-5.3
20519	AT5G65100.1   ethylene insensitive 3 family protein, contains Pfam profile: PF04873 ethylene insensitive 3   chr5:26024061-26025734 REVERSE   Aliases: MQN23.3, MQN23_3	3.3	3.3	0.0	0.0	100.0%	-5.5
20520	AT3G43120.1   auxin-responsive protein-related, similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) from (Phaseolus aureus)   chr3:15105071-15106498 FORWARD   Aliases: F7M19.130	2.4	2.4	-0.0	-0.0	100.0%	-5.8
20521	AT5G58010.1   basic helix-loop-helix (bHLH) family protein, bHLH transcription factor GBOF-1, Tulipa gesneriana, EMBL:AF185269; contains Pfam profile PF00010: Helix-loop-helix DNA-binding domain   chr5:23500771-23502115 REVERSE   Aliases: F2C19.2, F2C19_2	4.0	4.0	-0.0	-0.0	100.0%	-4.3
20522	AT4G08980.3   F-box family protein (FBW2), contains similarity to N7 protein GI:3273101 from (Medicago truncatula)   chr4:5758587-5760555 FORWARD   Aliases: T3H13.1, T3H13_1	6.0	6.0	0.0	0.0	100.0%	-4.9
20523	AT5G24655.1   expressed protein   chr5:8440698-8441221 REVERSE   Aliases: None	8.3	8.3	0.0	0.0	100.0%	-5.0
20524	AT5G57770.1   expressed protein   chr5:23417967-23420338 REVERSE   Aliases: MRI1.13, MRI1_13	3.1	3.1	-0.0	-0.0	100.0%	-5.3
20525	AT4G21190.1   Symbol: EMB1417   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr4:11291508-11294019 REVERSE   Aliases: EMB1417, EMBRYO DEFECTIVE 1417, F7J7.130, F7J7_130	3.9	3.9	-0.0	-0.0	100.0%	-5.0
20526	AT3G47740.1   Symbol: ATATH2	2.2	2.2	0.0	0.0	100.0%	-4.9
20527	AT3G03220.1   Symbol: ATEXPA13   expansin, putative (EXP13), similar to expansin precursor GB:AAD13631 from (Lycopersicon esculentum); alpha-expansin gene family, PMID:11641069   chr3:742361-744054 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN A13, ATEXP13, ATHEXP ALPHA 1.22, EXP13, T17B22.9, T17B22_9	6.6	6.6	-0.0	-0.0	100.0%	-5.0
20528	AT2G46870.1   DNA-binding protein, putative, similar to DNA-binding proteins from (Arabidopsis thaliana) RAV1 GI:3868857, RAV2 GI:3868859; contains Pfam profile PF02362: B3 DNA binding domain   chr2:19267987-19269473 FORWARD   Aliases: F19D11.25	3.4	3.4	-0.0	-0.0	100.0%	-5.2

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20529	AT2G18010.1   auxin-responsive family protein, similar to auxin-induced protein TGSAUR22 (GI:10185820) (Tulipa gesneriana) ;similar to indole-3-acetic acid induced protein ARG7 (SP:P32295) (Phaseolus aureus)	2.6	2.6	-0.0	-0.0	100.0%	-5.5
20530	AT5G44770.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.3	3.3	-0.0	-0.0	100.0%	-5.2
20531	AT1G36370.1   glycine hydroxymethyltransferase, putative / serine hydroxymethyltransferase, putative / serine/threonine aldolase, putative, similar to serine hydroxymethyltransferase (Chlamydomonas reinhardtii) GI:17066746; contains Pfam profile PF00464: serine hydroxymethyltransferase	6.5	6.5	0.0	0.0	100.0%	-4.5
20532	AT3G49230.1   expressed protein   chr3:18265414-18266103 FORWARD   Aliases: F2K15.90	3.6	3.6	-0.0	-0.0	100.0%	-5.2
20533	AT5G50910.1   hypothetical protein   chr5:20725635-20726508 REVERSE   Aliases: K3K7.5, K3K7_5	2.1	2.1	0.0	0.0	100.0%	-6.0
20534	AT5G28950.1   hypothetical protein   chr5:10992509-10993439 FORWARD   Aliases: F3F24.50, F3F24_50	3.0	3.0	-0.0	-0.0	100.0%	-5.3
20535	AT1G07160.1   protein phosphatase 2C, putative / PP2C, putative, similar to protein phosphatase 2C GI:2582800 from (Medicago sativa)   chr1:2197907-2199747 REVERSE   Aliases: F10K1.13, F10K1_13	3.7	3.7	-0.0	-0.0	100.0%	-5.1
20536	AT3G10070.1   Symbol: TAFII58   transcription initiation factor IID (TFIID) subunit A family protein, similar to hypothetical protein GB:CAB10099 (Schizosaccharomyces pombe); contains Pfam profile PF03847: Transcription initiation factor TFIID subunit A	4.1	4.2	-0.0	-0.0	100.0%	-5.1
20537	AT3G45610.1   Dof-type zinc finger domain-containing protein, identical to dof6 zinc finger protein GI:5689615 from (Arabidopsis thaliana)   chr3:16750274-16751430 REVERSE   Aliases: F9K21.190	3.4	3.4	-0.0	-0.0	100.0%	-5.1
20538	AT2G18780.1   F-box family protein, contains F-box domain Pfam:PF00646	3.9	3.9	0.0	0.0	100.0%	-4.7
20539	AT1G05720.1   selenoprotein family protein, contains Prosite PS00190: Cytochrome c family heme-binding site signature; similar to 15 kDa selenoprotein (GI:12314088) {Homo sapiens}   chr1:1717461-1718852 REVERSE   Aliases: F3F20.17, F3F20_17	9.0	9.0	0.0	0.0	100.0%	-4.9
20540	AT5G47270.1   disease resistance protein-related, contains weak similarity to Swiss-Prot:P54120 AIG1 protein (Arabidopsis thaliana)   chr5:19209411-19209743 FORWARD   Aliases: MQL5.13, MQL5_13	2.3	2.3	0.0	0.0	100.0%	-6.1
20541	AT1G61240.2   expressed protein, contains Pfam profile PF05212: Protein of unknown function (DUF707)   chr1:22585176-22588868 FORWARD   Aliases: F11P17.21, F11P17_21	3.8	3.8	0.0	0.0	100.0%	-4.9
20542	AT1G13440.1   glyceraldehyde 3-phosphate dehydrogenase, cytosolic, putative / NAD-dependent glyceraldehyde-3-phosphate dehydrogenase, putative, very strong similarity to SP:P25858 Glyceraldehyde 3-phosphate dehydrogenase, cytosolic (EC 1.2.1.12) {Arabidopsis thaliana}; contains Pfam profiles PF02800: Glyceraldehyde 3-phosphate dehydrogenase C-terminal domain, PF00044: Glyceraldehyde 3-phosphate dehydrogenase NAD binding domain	12.4	12.4	-0.0	-0.0	100.0%	-5.5
20543	AT3G28330.1   F-box family protein-related, contains TIGRFAM TIGR01640: F-box protein interaction domain   chr3:10587803-10588949 REVERSE   Aliases: MZF16.14	3.0	3.0	0.0	0.0	100.0%	-5.2
20544	AT5G06810.1   mitochondrial transcription termination factor-related / mTERF-related, contains Pfam profile PF02536: mTERF   chr5:2108494-2112257 FORWARD   Aliases: MPH15.18, MPH15_18	3.9	3.9	-0.0	-0.0	100.0%	-5.1
20545	AT1G56040.1   U-box domain-containing protein, contains Pfam profile PF04564: U-box domain   chr1:20964021-20965535 REVERSE   Aliases: T6H22.23, T6H22_23	2.7	2.7	-0.0	-0.0	100.0%	-5.5
20546	AT2G47410.1   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At5g49430.1); similar to neuronal differentiation-related protein - mouse (GB:JC7538); contains InterPro domain Bromodomain (InterPro:IPR001487); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr2:19455377-19464322 FORWARD   Aliases: T30B22.2	6.6	6.6	-0.0	-0.0	100.0%	-4.8
20547	AT5G50250.1   31 kDa ribonucleoprotein, chloroplast, putative / RNA-binding protein RNP-T, putative / RNA-binding protein 1/2/3, putative / RNA-binding protein cp31, putative, similar to SP:Q04836 31 kDa ribonucleoprotein, chloroplast precursor (RNA-binding protein RNP-T) (1/2/3) (AtRBP33) (cp31) {Arabidopsis thaliana}; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr5:20469713-20471202 REVERSE   Aliases: K6A12.11, K6A12_11	7.0	7.1	-0.0	-0.0	100.0%	-5.1
20548	AT5G56720.1   malate dehydrogenase, cytosolic, putative, similar to cytosolic malate dehydrogenase from Mesembryanthemum crystallinum (SP:O24047), Medicago sativa (SP:O48905), Prunus persica (GI:15982948); contains InterPro entry IPR001236: Lactate/malate dehydrogenase   chr5:22962763-22963944 FORWARD   Aliases: MIK19.17, MIK19_17	3.7	3.7	-0.0	-0.0	100.0%	-4.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20549	AT2G07440.1   two-component responsive regulator-related / response regulator protein-related, similar to response regulator 5 GI:3953599 from (Arabidopsis thaliana); non-consensus (GC) donor site at intron 1   chr2:3093818-3094747 REVERSE   Aliases: T13E11.21, T13E11_21	3.0	3.0	0.0	0.0	100.0%	-5.8
20550	AT5G14980.1   esterase/lipase/thioesterase family protein, low similarity to monoglyceride lipase from (Homo sapiens) GI:14594904, (Mus musculus) GI:2632162; contains Interpro entry IPR000379   chr5:4849603-4850586 FORWARD   Aliases: F2G14.100, F2G14_100	2.4	2.4	0.0	0.0	100.0%	-5.6
20551	AT5G39700.1   Symbol: MYB89   myb family transcription factor (MYB89), identical to transcription factor (MYB89) GI:5823322 from (Arabidopsis thaliana)   chr5:15910989-15911652 REVERSE   Aliases: MIJ24.170, MIJ24_170	3.7	3.7	0.0	0.0	100.0%	-5.3
20552	AT5G58100.1   expressed protein   chr5:23524928-23532246 FORWARD   Aliases: K21L19.10, K21L19_10	5.8	5.8	-0.0	-0.0	100.0%	-4.9
20553	AT1G54880.1   hypothetical protein   chr1:20464705-20465225 REVERSE   Aliases: F14C21.36, F14C21_36	3.1	3.1	-0.0	-0.0	100.0%	-5.5
20554	AT4G23290.2   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr4:12177748-12180836 REVERSE   Aliases: F21P8.180, F21P8_180	2.6	2.6	-0.0	-0.0	100.0%	-5.6
20555	AT1G23680.1   hypothetical protein, contains Pfam profile PF02713: Domain of unknown function DUF220   chr1:8376676-8377145 REVERSE   Aliases: F5O8.23, F5O8_23	3.3	3.3	-0.0	-0.0	100.0%	-5.0
20556	AT1G15800.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At1g80610.1)   chr1:5441077-5443653 REVERSE   Aliases: F7H2.14, F7H2_14	4.8	4.8	-0.0	-0.0	100.0%	-4.4
20557	AT5G46115.1   expressed protein   chr5:18718547-18718967 FORWARD   Aliases: None	3.0	3.0	0.0	0.0	100.0%	-5.4
20558	AT5G39370.1   S-locus glycoprotein, putative, similar to S glycoprotein (Raphanus sativus) (SLG(S8)) GI:3327852; contains Pfam profile PF01453: Lectin (probable mannose binding)   chr5:15774945-15775337 FORWARD   Aliases: MUL8.5, MUL8_5	2.3	2.3	-0.0	-0.0	100.0%	-5.4
20559	AT3G18260.1   reticulon family protein (RTNLB9), weak similarity to RTN2-C (Homo sapiens) GI:3435090; contains Pfam profile PF02453: Reticulon	2.8	2.9	-0.0	-0.0	100.0%	-5.3
20560	AT2G03780.1   translin family protein, similar to SP:Q99598 Translin-associated protein X (Translin-associated factor X) {Homo sapiens}; contains Pfam profile PF01997: Translin family   chr2:1152507-1154284 REVERSE   Aliases: F19B11.23, F19B11_23	4.1	4.0	0.0	0.0	100.0%	-5.3
20561	AT3G07930.3   HhH-GPD base excision DNA repair family protein   chr3:2526636-2528639 FORWARD   Aliases: F17A17.27	3.8	3.8	0.0	0.0	100.0%	-5.4
20562	AT4G26790.2   GDSL-motif lipase/hydrolase family protein, similar to family II lipase EXL3 (GI:15054386), EXL1 (GI:15054382), EXL2 (GI:15054384) (Arabidopsis thaliana); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr4:13487712-13489382 FORWARD   Aliases: F10M23.130, F10M23_130	2.7	2.6	0.0	0.0	100.0%	-4.8
20563	AT2G20070.1   expressed protein, weak similarity to SP:O61705 Neurotoxin BmK-X precursor (BmK10) (Alpha-neurotoxin TX9) {Mesobuthus martensii}	3.2	3.2	-0.0	-0.0	100.0%	-5.2
20564	AT5G47080.3   Symbol: CKB1   similar to casein kinase II beta chain, putative [Arabidopsis thaliana] (TAIR:At4g17640.1); similar to protein kinase 2 beta chain [Nicotiana tabacum] (GB:CAD27343.1); contains InterPro domain Casein kinase II, regulatory subunit (InterPro:IPR000704)   chr5:19141839-19143838 REVERSE   Aliases: CASEIN KINASE II BETA SUBUNIT CKB1, K14A3.3, K14A3_3	6.2	6.1	0.0	0.0	100.0%	-5.2
20565	AT4G31630.1   transcriptional factor B3 family protein, similar to reproductive meristem gene 1 from (Brassica oleracea var. botrytis) GI:3170424, (Arabidopsis thaliana) GI:13604227; contains Pfam profile PF02362: B3 DNA binding domain   chr4:15325349-15327226 REVERSE   Aliases: F28M20.180, F28M20_180	2.7	2.7	-0.0	-0.0	100.0%	-5.4
20566	AT3G51840.1   Symbol: ACX4   short-chain acyl-CoA oxidase, identical to Short-chain acyl CoA oxidase (Arabidopsis thaliana) GI:5478795; contains InterPro entry IPR006089: Acyl-CoA dehydrogenase   chr3:19236337-19240140 REVERSE   Aliases: ACYL COA OXIDASE 4, ATEM1.9, ATG6, ATSCX, SHORT CHAIN ACYL COA OXIDASE	7.8	7.8	0.0	0.0	100.0%	-4.5
20567	AT4G20510.1   expressed protein   chr4:11041668-11044810 FORWARD   Aliases: F9F13.160, F9F13_160	1.9	1.9	0.0	0.0	100.0%	-5.2
20568	AT1G17730.1   SNF7 family protein, contains Pfam domain, PF03357: SNF7 family   chr1:6099097-6100308 FORWARD   Aliases: F11A6.7, F11A6_7	5.8	5.8	0.0	0.0	100.0%	-4.6
20569	AT2G16005.1   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain   chr2:6966234-6967279 REVERSE   Aliases: None	3.1	3.1	-0.0	-0.0	100.0%	-4.8
20570	AT3G45700.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr3:16789698-16792183 FORWARD   Aliases: T6D9.30	4.0	4.0	-0.0	-0.0	100.0%	-4.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20571	AT2G01060.2   myb family transcription factor, contains Pfam profile: PF00249 myb-like DNA-binding domain   chr2:73258-75341 REVERSE   Aliases: F23H14.3, F23H14_3	9.2	9.2	-0.0	-0.0	100.0%	-5.2
20572	AT3G12470.1   expressed protein   chr3:3956064-3956834 REVERSE   Aliases: T2E22.21	2.8	2.8	-0.0	-0.0	100.0%	-5.5
20573	AT2G25590.1   agenet domain-containing protein, contains Pfam PF05641: Agenet domain   chr2:10898373-10900850 FORWARD   Aliases: F3N11.4, F3N11_4	6.6	6.6	0.0	0.0	100.0%	-4.7
20574	AT1G02130.1   Symbol: ATRAB1B   Ras-related protein (ARA-5) / small GTP-binding protein, putative, identical to Ras-related protein ARA-5 SP:P28188 from (Arabidopsis thaliana)   chr1:400045-401854 REVERSE   Aliases: ARA5, ARABIDOPSIS RAS 5, T7I23.6, T7I23_6	6.4	6.4	-0.0	-0.0	100.0%	-4.8
20575	AT1G65360.1   MADS-box protein (AGL23), similar to MADS-box protein GI:2505875 from (Arabidopsis thaliana); contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)	3.3	3.3	0.0	0.0	100.0%	-4.9
20576	AT1G13800.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:4731053-4733704 REVERSE   Aliases: F16A14.3, F16A14_3	3.3	3.3	-0.0	-0.0	100.0%	-5.7
20577	AT3G45280.1   Symbol: SYP72   syntaxin 72 (SYP72), identical to syntaxin of plants 72 (SYP72) (GI:13811650)(Arabidopsis thaliana); identified as SYP72 in Sanderfoot, A.A., et al, Plant Physiology 124:1558-69(2000); syntaxin 8 - Homo sapiens, EMBL:AF115323   chr3:16622398-16624325 REVERSE   Aliases: ATSYP72, F18N11.40, SYNTAXIN OF PLANTS 72	3.6	3.6	0.0	0.0	100.0%	-5.0
20578	AT5G66850.1   Symbol: MAPKKK5   protein kinase family protein, contains Pfam domain, PF00069: Protein kinase domain; identical to cDNA MAP3K gamma protein kinase GI:2315152   chr5:26712833-26716550 REVERSE   Aliases: MUD21.11, MUD21_11	3.2	3.2	0.0	0.0	100.0%	-5.1
20579	AT3G12955.1   auxin-responsive protein-related, similar to indole-3-acetic acid induced protein arg7 (SP:P32295) (Vigna radiata)   chr3:4135507-4136150 REVERSE   Aliases: None	3.1	3.1	-0.0	-0.0	100.0%	-5.0
20580	AT1G77440.2   Symbol: PBC2   similar to 20S proteasome beta subunit C1 (PBC1) (PRCT) [Arabidopsis thaliana] (TAIR:At1g21720.1); similar to 20S proteasome subunit beta type 3 [Oryza sativa (japonica cultivar-group)] (GB:BAD37365.1); contains InterPro domain Multispecific proteasome protease (InterPro:IPR001353)   chr1:29100914-29103344 FORWARD   Aliases: 20S PROTEASOME BETA SUBUNIT PBC2, T5M16.3, T5M16_3	6.3	6.3	0.0	0.0	100.0%	-4.6
20581	AT2G35230.2   VQ motif-containing protein, contains PF05678: VQ motif   chr2:14849397-14851510 FORWARD   Aliases: T4C15.10, T4C15_10	2.5	2.5	-0.0	-0.0	100.0%	-5.5
20582	AT2G19860.1   Symbol: ATHXK2	5.6	5.6	0.0	0.0	100.0%	-5.1
20583	AT5G40410.1   similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:At1g08070.1); similar to putative pentatricopeptide (PPR) repeat-containing protein [Oryza sativa (japonica cultivar-group)] (GB:XP_450548.1); contains InterPro domain PPR repeat (InterPro:IPR002885)   chr5:16188613-16190439 FORWARD   Aliases: MPO12.120, MPO12_120	4.1	4.1	-0.0	-0.0	100.0%	-5.2
20584	AT4G35210.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr4:16751433-16752185 FORWARD   Aliases: T12J5.80, T12J5_80	3.4	3.4	0.0	0.0	100.0%	-5.4
20585	AT3G15790.1   Symbol: MBD11   methyl-CpG-binding domain-containing protein, contains Pfam profile PF01429: Methyl-CpG binding domain   chr3:5343216-5344707 FORWARD   Aliases: MSJ11.19	6.9	6.9	-0.0	-0.0	100.0%	-4.5
20586	AT3G24250.1   glycine-rich protein   chr3:8786771-8787188 FORWARD   Aliases: K13K6.2	5.7	5.7	-0.0	-0.0	100.0%	-5.0
20587	AT1G59660.1   nucleoporin family protein, contains Pfam profiles: PF04096 nucleoporin autopeptidase, PF03093 nucleoporin FG repeat family   chr1:21928358-21933089 FORWARD   Aliases: T30E16.24, T30E16_24	5.8	5.9	-0.0	-0.0	100.0%	-4.4
20588	AT4G08560.1   pumilio/Puf RNA-binding domain-containing protein, low similarity to RNA binding protein PufA (Dictyostelium discoideum) GI:5106561; contains Pfam profile PF00806: Pumilio-family RNA binding repeat   chr4:5450431-5453180 FORWARD   Aliases: T15F16.9, T15F16_9	2.8	2.8	-0.0	-0.0	100.0%	-5.4
20589	AT4G00490.1   beta-amylase, putative / 1,4-alpha-D-glucan maltohydrolase, putative, similar to beta-amylase from SP:O64407 (Vigna unguiculata); contains Pfam profile PF01373: Glycosyl hydrolase family 14   chr4:222348-2225457 FORWARD   Aliases: F6N23.1, F6N23_1	7.3	7.3	-0.0	-0.0	100.0%	-4.4
20590	AT1G44830.1   encodes a member of the DREB subfamily A-5 of ERF/AP2 transcription factor family. The protein contains one AP2 domain. There are 15 members in this subfamily including RAP2.1, RAP2.9 and RAP2.10.   chr1:16936232-16936867 FORWARD   Aliases: T12C22.10, T12C22_10	3.2	3.1	0.0	0.0	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20591	AT1G71930.1   Symbol: ANAC030   no apical meristem (NAM) family protein, similar to NAM GB:CAA63101 from (Petunia x hybrida)   chr1:27079802-27081619 FORWARD   Aliases: ANAC030, F17M19.8, F17M19_8	2.4	2.4	-0.0	-0.0	100.0%	-5.3
20592	AT3G25655.1   expressed protein   chr3:9338769-9339302 REVERSE   Aliases: None	3.0	3.0	0.0	0.0	100.0%	-4.8
20593	AT3G29060.1   similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03260.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At2g03240.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g35350.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g14040.1); similar to EXS family protein / ERD1/XPR1/SYG1 family protein [Arabidopsis thaliana] (TAIR:At1g26730.1); similar to putative xenotropic and polytropic murine retrovirus receptor [Oryza sativa (japonica cultivar-group)] (GB:BAD46522.1); contains InterPro domain SPX, N-terminal (InterPro:IPR004331); contains InterPro domain EXS, C-terminal (InterPro:IPR004342)   chr3:11046227-11049702 REVERSE   Aliases: MRI12.4	3.1	3.1	0.0	0.0	100.0%	-5.1
20594	AT3G19220.1   expressed protein   chr3:6659170-6660858 FORWARD   Aliases: MVI11.22	3.9	3.9	-0.0	-0.0	100.0%	-5.3
20595	AT2G43180.4   expressed protein   chr2:17960020-17962875 REVERSE   Aliases: F14B2.12	3.5	3.5	0.0	0.0	100.0%	-4.8
20596	AT5G02350.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.7	2.7	-0.0	-0.0	100.0%	-4.7
20597	AT1G66120.1   acyl-activating enzyme 11 (AAE11), similar to AMP-binding protein Gl:1903034 from (Brassica napus); contains Pfam AMP-binding domain PF00501; identical to cDNA acyl-activating enzyme 11 (At1g66120) Gl:29893230, acyl-activating enzyme 11 (Arabidopsis thaliana) Gl:29893231   chr1:24616284-24618468 FORWARD   Aliases: F15E12.22, F15E12_22	3.6	3.6	0.0	0.0	100.0%	-4.9
20598	AT1G22760.1   Symbol: PAB3   polyadenylate-binding protein 3 (PABP3)   chr1:8055315-8059004 FORWARD   Aliases: POLY(A) BINDING PROTEIN 3, T22J18.7, T22I18_7	3.2	3.2	-0.0	-0.0	100.0%	-5.4
20599	AT5G03510.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:880224-881252 FORWARD   Aliases: F12E4.290, F12E4_290	3.2	3.2	0.0	0.0	100.0%	-5.2
20600	AT3G07230.1   wound-responsive protein-related, similar to wound-induced basic protein SP:Q09020 (Phaseolus vulgaris) (Plant Physiol. 101 (4), 1409 (1993))   chr3:2299780-2300273 FORWARD   Aliases: T1B9.10	11.1	11.1	0.0	0.0	100.0%	-5.5
20601	AT2G44640.1   expressed protein   chr2:18424319-18426472 FORWARD   Aliases: F16B22.13	7.6	7.6	0.0	0.0	100.0%	-4.4
20602	AT1G34270.1   exostosin family protein, contains Pfam profile: PF03016 Exostosin family   chr1:12492389-12494522 REVERSE   Aliases: F23M19.7, F23M19_7	4.4	4.4	-0.0	-0.0	100.0%	-4.9
20603	AT5G47980.1   transferase family protein, similar to alcohol acyltransferase (Fragaria x ananassa)(Gl:10121328)(PMID:10810141), deacetylvinoline 4-O-acetyltransferase (Catharanthus roseus)(Gl:4091808)(PMID:9681034)   chr5:19446114-19447702 FORWARD   Aliases: MDN11.1	3.3	3.3	0.0	0.0	100.0%	-4.8
20604	AT1G55760.1   BTB/POZ domain-containing protein, Interpro IPR000210/ PS50097: BTBB/POZ domain; similar to POZ 56 protein (Gl:17483747) (Mus musculus)   chr1:20850592-20852720 REVERSE   Aliases: F20N2.15	2.8	2.8	0.0	0.0	100.0%	-5.4
20605	AT1G59710.1   expressed protein, contains Pfam profile: PF04601 protein of unknown function (DUF569)   chr1:21942032-21943849 FORWARD   Aliases: F23H11.2, F23H11_2	4.4	4.4	-0.0	-0.0	100.0%	-5.2
20606	AT1G15750.4   similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g15880.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g80490.1); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g80490.2); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g15880.2); similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At3g16830.1); similar to putative beta transducin-like protein [Solanum bulbocastanum] (GB:AAP45184.1); similar to putative CTV.2 [Oryza sativa (japonica cultivar-group)] (GB:BAD81067.1); similar to WD-40 repeat protein-like [Oryza sativa (japonica cultivar-group)] (GB:XP_480212.1); similar to unnamed protein product [Oryza sativa (japonica cultivar-group)] (GB:NP_912774.1); contains InterPro domain Lissencephaly type-1-like homology motif (InterPro:IPR006594); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680); contains InterPro domain CTLH, C-terminal to LisH motif (InterPro:IPR006595)   chr1:5414360-5420908 REVERSE   Aliases: F7H2.9, F7H2_9	5.8	5.8	-0.0	-0.0	100.0%	-4.8
20607	AT2G23090.1   expressed protein   chr2:9836530-9837490 REVERSE   Aliases: F21P24.15	12.0	12.0	0.0	0.0	100.0%	-5.5
20608	AT3G57330.1   calcium-transporting ATPase, plasma membrane-type, putative / Ca2+-ATPase, putative (ACA11), identical to SP:Q9M2L4:ACAB_ARATH Potential calcium-transporting ATPase 11, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 11) {Arabidopsis thaliana}; strong similarity to calmodulin-stimulated calcium-ATPase (Brassica oleracea) Gl:1805654 Belongs to plant 2B ATPase??s with an N-terminal autoinhibitor.   chr3:21222455-21227353 REVERSE   Aliases: F28O9.180	6.4	6.4	-0.0	-0.0	100.0%	-5.2
20609	AT1G14660.1   Symbol: ATNHX8	2.7	2.7	-0.0	-0.0	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20610	AT3G26150.1   Symbol: CYP71B16   cytochrome P450 71B16, putative (CYP71B16), identical to cytochrome P450 71B16 (SP:Q9LTM7) (Arabidopsis thaliana); similar to cytochrome P450 GB:O65784 (Arabidopsis thaliana)   chr3:9566864-9568463 REVERSE   Aliases: MTC11.6	2.7	2.7	-0.0	-0.0	100.0%	-5.7
20611	AT5G63740.1   zinc finger protein-related   chr5:25528002-25528682 REVERSE   Aliases: MBK5.22, MBK5_22	2.6	2.6	0.0	0.0	100.0%	-5.7
20612	AT5G51460.3   Symbol: ATTPPA	3.6	3.6	0.0	0.0	100.0%	-5.2
20613	AT3G51390.1   zinc finger (DHHC type) family protein, contains Pfam profile PF01529: DHHC zinc finger domain   chr3:19086555-19089096 FORWARD   Aliases: F26O13.30	7.7	7.7	-0.0	-0.0	100.0%	-5.1
20614	AT1G79410.1   transporter-related, low similarity to organic anion transporter 3 (Rattus norvegicus) GI:5545293; contains Pfam profile PF00083: major facilitator superfamily protein   chr1:29872773-29874526 REVERSE   Aliases: T8K14.17, T8K14_17	3.8	3.8	-0.0	-0.0	100.0%	-4.5
20615	AT2G18850.1   similar to SET domain-containing protein [Arabidopsis thaliana] (TAIR:At3g07670.1); similar to hypothetical protein DDB0218318 [Dictyostelium discoideum] (GB:EAL66753.1); contains InterPro domain Nuclear protein SET (InterPro:IPR001214)   chr2:8167816-8170771 FORWARD   Aliases: MSF3.23, MSF3_23	4.0	4.0	0.0	0.0	100.0%	-5.3
20616	AT2G20880.1   AP2 domain-containing transcription factor, putative, similar to AP2 domain containing protein RAP2.4 (Arabidopsis thaliana) GI:2281633   chr2:8993054-8994344 FORWARD   Aliases: F5H14.15, F5H14_15	2.7	2.7	0.0	0.0	100.0%	-4.2
20617	AT1G26660.1   c-myc binding protein, putative / prefoldin, putative, similar to Swiss-Prot:Q99471 prefoldin subunit 5 (C-myc binding protein Mm-1) (Myc modulator 1) (Homo sapiens)   chr1:9211727-9213961 FORWARD   Aliases: T24P13.26	7.7	7.7	0.0	0.0	100.0%	-4.9
20618	AT4G16370.1   Symbol: ATOPT3	9.4	9.4	-0.0	-0.0	100.0%	-4.7
20619	AT4G39450.1   expressed protein   chr4:18347587-18355050 FORWARD   Aliases: F23K16.80, F23K16_80	5.6	5.6	0.0	0.0	100.0%	-5.0
20620	AT3G05780.1   Lon protease, putative, similar to Lon protease homolog 2 SP:P93655   chr3:1714947-1719614 REVERSE   Aliases: F10A16.7, F10A16_7	2.6	2.6	0.0	0.0	100.0%	-5.5
20621	AT1G68200.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:25565781-25567611 FORWARD   Aliases: T22E19.17, T22E19_17	3.6	3.6	0.0	0.0	100.0%	-5.1
20622	AT5G55610.2   expressed protein   chr5:22543043-22545274 FORWARD   Aliases: MDF20.5, MDF20_5	7.1	7.0	0.0	0.0	100.0%	-5.0
20623	AT4G01930.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.8	3.8	0.0	0.0	100.0%	-5.1
20624	AT3G19750.1   hypothetical protein   chr3:6861152-6862936 REVERSE   Aliases: MMB12.24	2.4	2.4	0.0	0.0	100.0%	-5.8
20625	AT4G27930.1   expressed protein   chr4:13902641-13902984 REVERSE   Aliases: T13J8.40, T13J8_40	2.4	2.4	0.0	0.0	100.0%	-5.6
20626	AT4G38410.1   dehydrin, putative, similar to dehydrin ERD10 (Low-temperature-induced protein LTI45) (Arabidopsis thaliana) SWISS-PROT:P42759   chr4:17980934-17981713 FORWARD   Aliases: F22I13.180, F22I13_180	3.2	3.1	0.0	0.0	100.0%	-4.4
20627	AT5G48180.1   kelch repeat-containing protein, contains Pfam PF01344: Kelch motif (5 repeats) ;similar to Tip elongation aberrant protein 1 (Cell polarity protein tea1) (SP:P87061) (Schizosaccharomyces pombe)   chr5:19558163-19559649 REVERSE   Aliases: MIF21.7, MIF21_7	8.3	8.3	0.0	0.0	100.0%	-4.6
20628	AT1G69295.1   beta-1,3-glucanase-related, low similarity to elicitor inducible beta-1,3-glucanase NtEIG-E76 (Nicotiana tabacum) GI:11071974   chr1:26053860-26056230 REVERSE   Aliases: None	3.2	3.3	-0.0	-0.0	100.0%	-5.3
20629	AT1G64260.1   zinc finger protein-related, contains Pfam profiles PF03108: MuDR family transposase, PF04434: SWIM zinc finger   chr1:23851419-23853578 FORWARD   Aliases: F22C12.28, F22C12_28	3.0	3.0	0.0	0.0	100.0%	-5.3
20630	AT5G14090.1   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At3g27025.1)   chr5:4547214-4549419 FORWARD   Aliases: MUA22.9, MUA22_9	2.6	2.6	0.0	0.0	100.0%	-5.5
20631	AT1G30790.1   F-box family protein, contains Pfam PF00646: F-box domain; contains TIGRFAM TIGR01640 : F-box protein interaction domain	3.1	3.1	0.0	0.0	100.0%	-5.5
20632	AT3G58470.1   expressed protein, several hypothetical proteins - Saccharomyces cerevisiae   chr3:21637648-21639546 REVERSE   Aliases: F14P22.60	6.2	6.2	-0.0	-0.0	100.0%	-4.8
20633	AT2G29780.1   kelch repeat-containing F-box family protein, similar to SKP1 interacting partner 6 (Arabidopsis thaliana) GI:10716957; contains Pfam profiles PF01344: Kelch motif, PF00646: F-box domain   chr2:12725209-12726405 REVERSE   Aliases: T27A16.12, T27A16_12	3.6	3.6	0.0	0.0	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20634	AT3G55390.1   integral membrane family protein, MtN24, Medicago truncatula, EMBL:MTY15290; contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)	5.8	5.8	-0.0	-0.0	100.0%	-5.0
20635	AT1G59970.1   matrixin family protein, similar to SP:P29136 Metalloendoproteinase 1 precursor (EC 3.4.24.-) (SMEP1) {Glycine max}; contains InterPro accession IPR001818: Matrixin   chr1:22077199-22078514 FORWARD   Aliases: F23H11.28	5.7	5.7	0.0	0.0	100.0%	-5.2
20636	AT2G17090.1   protein kinase family protein, similar to Arabidopsis thaliana APK1A (SP:Q06548), APK1B (SP:P46573); contains Pfam profile: PF00069 Protein kinase domain   chr2:7442170-7444380 REVERSE   Aliases: F6P23.23, F6P23_23	2.4	2.4	-0.0	-0.0	100.0%	-5.6
20637	AT1G54970.1   Symbol: ATPRP1	3.0	3.0	-0.0	-0.0	100.0%	-4.4
20638	AT3G43970.1   expressed protein, predicted protein, Arabidopsis thaliana   chr3:15788395-15788935 REVERSE   Aliases: T15B3.110	4.2	4.2	-0.0	-0.0	100.0%	-5.4
20639	AT5G65820.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:26357102-26359015 REVERSE   Aliases: K22J17.3, K22J17_3	2.8	2.8	0.0	0.0	100.0%	-5.7
20640	AT1G04940.1   expressed protein, similar to PREDICTED: similar to hypothetical protein FLJ20729 [Canis familiaris] (GB:XP_537090.1)   chr1:1400907-1403111 FORWARD   Aliases: F13M7.7, F13M7_7	3.5	3.5	-0.0	-0.0	100.0%	-5.0
20641	AT2G04600.1   expressed protein   chr2:1608073-1609755 REVERSE   Aliases: F7D11.4, F7D11_4	3.1	3.1	-0.0	-0.0	100.0%	-5.6
20642	AT3G26490.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr3:9705379-9707398 FORWARD   Aliases: F20C19.23	3.2	3.2	0.0	0.0	100.0%	-5.4
20643	AT3G47400.1   pectinesterase family protein, similar to pectinesterase (EC 3.1.1.11) from Vitis vinifera GI:15081598, Lycopersicon esculentum SP:Q43143 SP:P14280; contains Pfam profile PF01095 pectinesterase   chr3:17476575-17479103 FORWARD   Aliases: T21L8.150	3.0	3.0	-0.0	-0.0	100.0%	-5.0
20644	AT2G32350.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr2:13742056-13742865 FORWARD   Aliases: T32F6.13, T32F6_13	2.8	2.8	-0.0	-0.0	100.0%	-5.8
20645	AT2G39705.1   expressed protein   chr2:16563934-16564655 FORWARD   Aliases: None	6.1	6.1	0.0	0.0	100.0%	-4.8
20646	AT1G08780.1   prefoldin, putative, similar to Swiss-Prot:Q9NQP4 prefoldin subunit 4 (Protein C-1) (Homo sapiens)   chr1:2809783-2811194 REVERSE   Aliases: F22O13.27, F22O13_27	9.1	9.1	-0.0	-0.0	100.0%	-4.7
20647	AT1G27220.1   paired amphipathic helix repeat-containing protein, similar to transcriptional repressor SIN3B (Mus musculus) GI:2921547; contains Pfam profile PF02671: Paired amphipathic helix repeat	2.8	2.8	0.0	0.0	100.0%	-5.4
20648	AT4G24390.2   F-box family protein (FBX14), similar to transport inhibitor response 1 protein GI:8777429 from (Arabidopsis thaliana)   chr4:12613388-12616127 REVERSE   Aliases: T22A6.220, T22A6_220	5.4	5.4	0.0	0.0	100.0%	-5.2
20649	AT3G22700.1   F-box family protein, contains Pfam:PF00646 F-box domain	2.8	2.8	-0.0	-0.0	100.0%	-5.8
20650	AT3G56930.1   zinc finger (DHHC type) family protein, low similarity to Golgi-specific DHHC zinc finger protein (Mus musculus) GI:21728103; contains Pfam profile PF01529: DHHC zinc finger domain   chr3:21084474-21087293 FORWARD   Aliases: T8M16.5	3.2	3.2	-0.0	-0.0	100.0%	-4.6
20651	AT4G09500.2   glycosyltransferase family protein, contains Pfam profile: PF00201 UDP-glucuronosyl and UDP-glucosyl transferase	4.1	4.1	-0.0	-0.0	100.0%	-5.0
20652	AT5G67390.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g57340.2); similar to expressed protein [Arabidopsis thaliana] (TAIR:At5g57340.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:XP_469866.1)   chr5:26904911-26905860 REVERSE   Aliases: K8K14.12, K8K14_12	3.0	3.0	-0.0	-0.0	100.0%	-4.9
20653	AT5G51410.2   LUC7 N_terminus domain-containing protein, similar to cisplatin resistance-associated overexpressed protein (Homo sapiens) GI:6899846; contains Pfam profile PF03194: LUC7 N_terminus   chr5:20897967-20900930 REVERSE   Aliases: MFG13.12, MFG13_12	9.2	9.2	-0.0	-0.0	100.0%	-5.3
20654	AT1G51480.1   disease resistance protein (CC-NBS-LRR class), putative, domain signature CC-NBS-LRR exists, suggestive of a disease resistance protein.	2.5	2.5	0.0	0.0	100.0%	-5.6
20655	AT1G23630.1   expressed protein, contains Pfam profile PF02713: Domain of unknown function DUF220; expression supported by MPSS   chr1:8367159-8368327 REVERSE   Aliases: F28C11.22	2.8	2.8	-0.0	-0.0	100.0%	-5.3
20656	AT2G01960.1   expressed protein   chr2:450378-452416 FORWARD   Aliases: F14H20.3, F14H20_3	2.4	2.4	-0.0	-0.0	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20657	AT3G04620.1   expressed protein   chr3:1255532-1256857 REVERSE   Aliases: F7O18.10, F7O18_10	5.8	5.8	0.0	0.0	100.0%	-4.3
20658	AT4G25880.3   similar to pumilio/Puf RNA-binding domain-containing protein [Arabidopsis thaliana] (TAIR:At3g20250.1); similar to pumilio domain-containing protein PPD1 [Populus tremula x Populus tremuloides] (GB:AAF71823.1); contains InterPro domain Pumilio/Puf RNA-binding (InterPro:IPR001313)	5.3	5.3	0.0	0.0	100.0%	-4.9
20659	AT1G22960.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:8128075-8130231 REVERSE   Aliases: F19G10.9, F19G10_9	3.0	3.0	0.0	0.0	100.0%	-5.6
20660	AT4G25510.1   hypothetical protein   chr4:13027453-13028046 REVERSE   Aliases: T30C3.8	2.5	2.5	-0.0	-0.0	100.0%	-5.9
20661	AT1G17610.1   disease resistance protein-related, contains Pfam domain, PF00931: NB-ARC domain, a novel signalling motif found in plant resistance gene products   chr1:6056888-6058350 FORWARD   Aliases: F11A6.20, F11A6_20	2.4	2.4	0.0	0.0	100.0%	-5.7
20662	AT3G05310.1   GTP-binding protein-related, low similarity to rac 1 protein (Physcomitrella patens) GI:7243743; contains Pfam profile PF00036: EF hand (domain)	3.0	3.0	0.0	0.0	100.0%	-5.4
20663	AT1G73590.1   Symbol: PIN1   auxin efflux carrier protein, putative (PIN1), identical to putative auxin efflux carrier protein; AtPIN1 (Arabidopsis thaliana) GI:4151319; contains Pfam profile PF03547: Auxin Efflux Carrier	3.0	3.0	0.0	0.0	100.0%	-5.0
20664	AT5G25490.1   zinc finger (Ran-binding) family protein, contains Pfam domain, PF00641: Zn-finger in Ran binding protein and others   chr5:8876489-8877816 FORWARD   Aliases: T14C9.30, T14C9_30	3.6	3.6	0.0	0.0	100.0%	-5.1
20665	AT5G03190.1   expressed protein   chr5:757845-760381 FORWARD   Aliases: F15A17.220, F15A17_220	4.9	4.9	-0.0	-0.0	100.0%	-5.2
20666	AT3G22360.1   Symbol: AOX1B   alternative oxidase 1b, mitochondrial (AOX1B), identical to GB:O23913 (SP:O23913) from (Arabidopsis thaliana)   chr3:7904163-7905391 FORWARD   Aliases: MCB17.22	3.9	3.9	0.0	0.0	100.0%	-4.7
20667	AT4G08140.1   expressed protein, weak similarity to SP:Q13200 26S proteasome non-ATPase regulatory subunit 2 (26S proteasome regulatory subunit S2) (26S proteasome subunit p97) (Tumor necrosis factor type 1 receptor associated protein 2) {Homo sapiens}   chr4:5135670-5136137 FORWARD   Aliases: F9M13.6, F9M13_6	3.4	3.4	0.0	0.0	100.0%	-5.1
20668	AT4G33580.2   similar to carbonic anhydrase family protein / carbonate dehydratase family protein [Arabidopsis thaliana] (TAIR:At1g58180.2); similar to carbonate dehydratase (EC 4.2.1.1) precursor, chloroplast - Flaveria linearis (GB:S61883); similar to chloroplast carbonic anhydrase precursor [Thlaspi caerulescens] (GB:AAS65454.1); contains InterPro domain Carbonic anhydrase, prokaryotic (InterPro:IPR001765)   chr4:16138362-16141626 FORWARD   Aliases: T16L1.70, T16L1_70	4.3	4.3	-0.0	-0.0	100.0%	-5.0
20669	AT2G13350.1   C2 domain-containing protein, very low similarity to cold-regulated gene SRC2 (Glycine max) GI:2055230; contains Pfam profile PF00168: C2 domain	3.9	3.9	0.0	0.0	100.0%	-5.0
20670	AT3G63380.1   calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPase, putative (ACA12), identical to SP:Q9LY77 Potential calcium-transporting ATPase 12, plasma membrane-type (EC 3.6.3.8) (Ca(2+)-ATPase isoform 12) {Arabidopsis thaliana}; similar to SP:Q9LF79 Calcium-transporting ATPase 8, plasma membrane-type (EC 3.6.3.8) (Ca2+-ATPase, isoform 8) {Arabidopsis thaliana}; contains InterPro Accession IPR006069: Cation transporting ATPase Belongs to plant 2B ATPase??s with an N-terminal autoinhibitor.   chr3:23417586-23421335 REVERSE   Aliases: MAA21.10	2.4	2.4	0.0	0.0	100.0%	-5.2
20671	AT5G25270.1   expressed protein   chr5:8757786-8762005 REVERSE   Aliases: F21J6.3	4.3	4.3	-0.0	-0.0	100.0%	-4.5
20672	AT3G06390.1   integral membrane family protein, similar to hypothetical protein GB:CAB10339 (Arabidopsis thaliana); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr3:1938738-1939785 REVERSE   Aliases: F24P17.14, F24P17_14	3.8	3.8	0.0	0.0	100.0%	-4.2
20673	AT1G77840.1   eukaryotic translation initiation factor 5, putative / eIF-5, putative, similar to SP:P55876 Eukaryotic translation initiation factor 5 (eIF-5) {Zea mays}; contains Pfam profiles PF02020: eIF4-gamma/eIF5/eIF2-epsilon, PF01873: Domain found in IF2B/IF5   chr1:29273381-29275480 FORWARD   Aliases: T32E8.15	9.4	9.4	0.0	0.0	100.0%	-5.1
20674	AT2G03980.1   GDSL-motif lipase/hydrolase family protein, similar to Anther-specific proline-rich protein APG from Brassica napus (SP:P40603 ), Arabidopsis thaliana (GI:22599); contains Pfam profile PF00657: Lipase/Acylhydrolase with GDSL-like motif   chr2:1259196-1262549 FORWARD   Aliases: F3C11.9, F3C11_9	2.7	2.7	-0.0	-0.0	100.0%	-5.5
20675	AT4G16080.1   expressed protein, similar to hypothetical protein [Arabidopsis thaliana] (TAIR:At2g45940.1); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR005174)   chr4:9101360-9102899 REVERSE   Aliases: DL4080C, FCAALL.273	2.7	2.7	-0.0	-0.0	100.0%	-5.1

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20676	AT2G10380.1   hypothetical protein   chr2:4005622-4006571 FORWARD   Aliases: F12P23.11, F12P23_11	3.0	3.0	0.0	0.0	100.0%	-5.4
20677	AT2G17570.1   undecaprenyl pyrophosphate synthetase family protein / UPP synthetase family protein, contains putative undecaprenyl diphosphate synthase domain (PF01255); similar to dehydrodolichyl diphosphate synthetase (DEDOL-PP synthase) (GI:796076) and <i>S. cerevisiae</i> Rer2 (SP:P35196)	5.6	5.6	0.0	0.0	100.0%	-5.1
20678	AT4G14840.1   expressed protein   chr4:8511492-8513722 REVERSE   Aliases: DL3460C, FCAALL.333	2.6	2.6	0.0	0.0	100.0%	-5.6
20679	AT4G00231.1   ataxin-related, contains weak similarity to Ataxin-10 (Spinocerebellar ataxia type 10 protein) (Brain protein E46 homolog) (Swiss-Prot:Q9UBB4) ( <i>Homo sapiens</i> )   chr4:97499-99353 FORWARD   Aliases: None	4.6	4.6	0.0	0.0	100.0%	-5.0
20680	AT1G66930.1   serine/threonine protein kinase family protein, contains Pfam PF00069: Protein kinase domain   chr1:24974186-24976732 FORWARD   Aliases: T4O24.2	2.8	2.8	-0.0	-0.0	100.0%	-4.5
20681	AT5G05010.2   similar to coatmer delta subunit [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:NP_915354.1); contains InterPro domain Clathrin adaptor complex, medium chain (InterPro:IPR001392)   chr5:1476677-1480198 FORWARD   Aliases: MUG13.13, MUG13_13	7.7	7.7	-0.0	-0.0	100.0%	-5.1
20682	AT5G12000.1   similar to protein kinase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g31230.1); similar to protein kinase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g16760.1); similar to protein kinase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At1g78940.1); similar to protein kinase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g24370.1); similar to protein kinase family protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At5g26150.1); similar to putative serine threonine kinase [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_468172.1); similar to serine threonine kinase [ <i>Zea mays</i> ] (GB:AAL59227.1); similar to serine threonine kinase 1 [ <i>Zea mays</i> ] (GB:AAK73111.1); similar to serine threonine kinase 1-like [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:BAD53152.1); similar to putative serine threonine kinase [ <i>Oryza sativa</i> ( <i>japonica</i> cultivar-group)] (GB:XP_463352.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:3873907-3876781 REVERSE   Aliases: F14F18.170, F14F18_170	2.6	2.6	-0.0	-0.0	100.0%	-5.7
20683	AT2G40930.1   Symbol: UBP5   ubiquitin-specific protease 5, putative (UBP5), similar to GI:6648604   chr2:17083406-17089511 REVERSE   Aliases: ATUBP5, PDE323, PIGMENT DEFECTIVE EMBRYO 323, T20B5.13, T20B5_13, UBIQUITIN SPECIFIC PROTEASE 5	4.9	4.9	0.0	0.0	100.0%	-5.2
20684	AT1G78260.2   RNA recognition motif (RRM)-containing protein, similar to RNA recognition motif-containing protein SEB-4 GI:8895698 from ( <i>Xenopus laevis</i> ); contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:29451878-29455297 FORWARD   Aliases: F3F9.20, F3F9_20	3.7	3.7	-0.0	-0.0	100.0%	-4.6
20685	AT1G54120.1   expressed protein   chr1:20210688-20211208 FORWARD   Aliases: F15I1.22, F15I1_22	4.2	4.1	0.0	0.0	100.0%	-4.3
20686	AT1G01530.1   MADS-box protein (AGL28), similar to MADS-box transcription factor GI:6580943 from ( <i>Picea abies</i> ); contains Pfam profile PF00319: SRF-type transcription factor (DNA-binding and dimerisation domain)   chr1:192640-193662 REVERSE   Aliases: F22L4.7, F22L4_7	2.1	2.1	0.0	0.0	100.0%	-6.0
20687	AT1G49100.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase ( <i>Arabidopsis thaliana</i> ) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr1:18169815-18173773 REVERSE   Aliases: F27J15.13, F27J15_13	3.1	3.1	0.0	0.0	100.0%	-4.4
20688	AT5G10860.1   CBS domain-containing protein, contains Pfam profile PF00571: CBS domain	9.2	9.2	0.0	0.0	100.0%	-4.5
20689	AT2G44040.1   dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) { <i>Pseudomonas syringae</i> }; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus   chr2:18228845-18231107 REVERSE   Aliases: F6E13.17	3.7	3.7	-0.0	-0.0	100.0%	-4.2
20690	AT3G59890.2   dihydrodipicolinate reductase family protein, weak similarity to SP:Q52419 Dihydrodipicolinate reductase (EC 1.3.1.26) (DHPR) { <i>Pseudomonas syringae</i> }; contains Pfam profiles PF01113: Dihydrodipicolinate reductase N-terminus, PF05173: Dihydrodipicolinate reductase C-terminus   chr3:22135175-22137461 REVERSE   Aliases: F24G16.160	3.7	3.7	-0.0	-0.0	100.0%	-4.2
20691	AT2G44710.1   RNA recognition motif (RRM)-containing protein   chr2:18439794-18444207 FORWARD   Aliases: F16B22.20	3.3	3.3	0.0	0.0	100.0%	-5.5
20692	AT1G27340.1   F-box family protein, contains Pfam PF00646: F-box domain; similar to fim protein; similar to ESTs gb:T42445, gb:T76780, gb:AA650733, and emb:Z17748   chr1:9495507-9498072 FORWARD   Aliases: F17L21.13, F17L21_13	5.4	5.4	-0.0	-0.0	100.0%	-5.0
20693	AT4G24000.1   Symbol: ATCSLG2   cellulose synthase family protein, similar to cellulose synthase from <i>Gossypium hirsutum</i> (gi:1706956), cellulose synthase-5 from <i>Zea mays</i> (gi:9622882)   chr4:12462040-12465634 FORWARD   Aliases: CSLG2, T32A16.170, T32A16_170	2.4	2.4	-0.0	-0.0	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20694	AT3G04460.1   Pex2/Pex12 N-terminal domain-containing protein, similar to SP:O00623 Peroxisome assembly protein 12 (Peroxin-12) (Peroxisome assembly factor-3) (PAF-3) {Homo sapiens}; contains Pfam profile PF04757: Pex2 / Pex12 amino terminal region   chr3:1186500-1189484 FORWARD   Aliases: T27C4.11, T27C4_11	3.3	3.3	0.0	0.0	100.0%	-5.5
20695	AT5G10250.1   phototropic-responsive protein, putative, similar to root phototropism RPT2 (Arabidopsis thaliana) gi:6959488:gb:AAF33112, a signal transducer of phototropic response PMID:10662859   chr5:3217029-3219369 REVERSE   Aliases: F18D22.20, F18D22_20	2.7	2.7	-0.0	-0.0	100.0%	-5.5
20696	AT5G07900.1   mitochondrial transcription termination factor family protein / mTERF family protein, low similarity to SP:Q99551 Transcription termination factor, mitochondrial precursor (mTERF) {Homo sapiens}; contains Pfam profile PF02536: mTERF	6.5	6.5	-0.0	-0.0	100.0%	-4.7
20697	AT5G26030.2   similar to ferrochelatase II [Arabidopsis thaliana] (TAIR:At2g30390.1); similar to putative ferrochelatase [Oryza sativa (japonica cultivar-group)] (GB:BAD33213.1); similar to probable ferrochelatase (EC 4.99.1.1) - barley (GB:T05736); contains InterPro domain Ferrochelatase (InterPro:IPR001015)	7.1	7.1	0.0	0.0	100.0%	-4.9
20698	AT3G46510.1   armadillo/beta-catenin repeat family protein / U-box domain-containing family protein, contains Pfam domain, PF00514: Armadillo/beta-catenin-like repeats and Pfam, PF04564: U-box domain   chr3:17134724-17137663 REVERSE   Aliases: F12A12.30	3.6	3.6	0.0	0.0	100.0%	-4.8
20699	AT3G61240.2   DEAD/DEAH box helicase, putative (RH12), identical to cDNA DEAD box RNA helicase, RH12 GI:3776000   chr3:22677158-22680471 FORWARD   Aliases: T20K12.140	5.0	5.0	-0.0	-0.0	100.0%	-4.8
20700	AT4G31875.1   expressed protein   chr4:15411707-15412295 REVERSE   Aliases: None	3.3	3.3	0.0	0.0	100.0%	-4.5
20701	AT2G19150.1   pectinesterase family protein, contains Pfam profile: PF01095 pectinesterase   chr2:8312182-8314526 FORWARD   Aliases: T20K24.17, T20K24_17	3.3	3.3	0.0	0.0	100.0%	-4.2
20702	AT2G04550.3   Symbol: IBR5   dual specificity protein phosphatase family protein, contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain   chr2:1588401-1590163 FORWARD   Aliases: INDOLE 3 BUTYRIC ACID??RESPONSE 5, T1O3.4, T1O3_4	4.6	4.6	0.0	0.0	100.0%	-5.3
20703	AT4G20110.1   vacuolar sorting receptor, putative, similar to BP-80 vacuolar sorting receptor (Pisum sativum) GI:1737222; identical to vacuolar sorting receptor-like protein (GI:2827665) (Arabidopsis thaliana)   chr4:10875299-10878740 FORWARD   Aliases: F1C12.2	3.5	3.5	0.0	0.0	100.0%	-4.8
20704	AT3G26040.1   transferase family protein, similar to deacetylindoline 4-O-acetyltransferase (Catharanthus roseus)(GI:4091808)(PMID:9681034), alcohol acyltransferase (Fragaria x ananassa)(GI:10121328)(PMID:10810141)   chr3:9520978-9522307 FORWARD   Aliases: MPE11.19	2.6	2.6	0.0	0.0	100.0%	-5.5
20705	AT3G43700.1   Symbol: ATBPM6	3.7	3.7	0.0	0.0	100.0%	-5.2
20706	AT1G23270.1   expressed protein   chr1:8259591-8260133 REVERSE   Aliases: F26F24.11, F26F24_11	2.5	2.5	0.0	0.0	100.0%	-5.4
20707	AT2G40630.1   expressed protein   chr2:16965224-16968222 FORWARD   Aliases: T2P4.2, T2P4_2	3.4	3.4	0.0	0.0	100.0%	-5.3
20708	AT1G03010.1   phototropic-responsive NPH3 family protein, contains NPH3 family domain, Pfam:PF03000   chr1:693480-696382 FORWARD   Aliases: F10O3.17, F10O3_17	2.3	2.3	-0.0	-0.0	100.0%	-5.4
20709	AT1G04360.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr1:1167456-1168877 REVERSE   Aliases: F19P19.21, F19P19_21	2.7	2.7	0.0	0.0	100.0%	-4.9
20710	AT1G19900.1   glyoxal oxidase-related, contains similarity to glyoxal oxidase precursor (Phanerochaete chrysosporium) gi:1050302:gb:AAA87594   chr1:6906890-6908732 REVERSE   Aliases: F6F9.4, F6F9_4	3.0	3.0	-0.0	-0.0	100.0%	-4.8
20711	AT2G42000.1   plant EC metallothionein-like family 15 protein, 84 C-terminal residues identical to EC protein homolog 1 (SP:P93746) {Arabidopsis thaliana}; contains Pfam PF02068: Plant PEC family metallothionein profile;   chr2:17536321-17536906 REVERSE   Aliases: T6D20.11, T6D20_11	2.7	2.7	-0.0	-0.0	100.0%	-5.3
20712	AT1G16900.1   curculin-like (mannose-binding) lectin family protein, very low similarity to Ser Thr protein kinase GI:2598067 from (Zea mays); contains Pfam lectin (probable mannose binding) domain PF01453 but not the protein kinase domain of the Z. mays protein	4.8	4.8	0.0	0.0	100.0%	-4.9
20713	AT1G11070.1   hydroxyproline-rich glycoprotein family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr1:3690212-3692826 REVERSE   Aliases: T19D16.24, T19D16_24	2.9	2.9	0.0	0.0	100.0%	-5.2
20714	AT2G09910.1   expressed protein   chr2:3760479-3764291 FORWARD   Aliases: F7B19.5, F7B19_5	3.4	3.4	-0.0	-0.0	100.0%	-5.0
20715	AT2G44680.2   casein kinase II beta chain, putative, similar to casein kinase II beta-3 chain (CK II) (Arabidopsis thaliana) SWISS-PROT:O81275	5.1	5.1	-0.0	-0.0	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20716	AT1G67000.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069; contains serine/threonine protein kinase domain, INTERPRO:IPR002290	3.1	3.1	0.0	0.0	100.0%	-5.3
20717	AT1G36240.1   60S ribosomal protein L30 (RPL30A), similar to GI:6984132 from (Euphorbia esula)	2.9	2.9	0.0	0.0	100.0%	-5.2
20718	AT3G59370.1   expressed protein, hypothetical protein F12F1.4 - Arabidopsis thaliana, EMBL:AC002131   chr3:21952849-21953509 REVERSE   Aliases: F25L23.230	2.3	2.3	-0.0	-0.0	100.0%	-4.8
20719	AT3G46340.1   leucine-rich repeat protein kinase, putative, similar to light repressible receptor protein kinase (Arabidopsis thaliana) gi:1321686:emb:CAA66376; contains leucine rich repeat (LRR) domains, Pfam:PF00560; contains protein kinase domain, Pfam:PF00069   chr3:17037643-17042827 FORWARD   Aliases: F18L15.60	2.7	2.7	0.0	0.0	100.0%	-4.6
20720	AT5G02610.1   60S ribosomal protein L35 (RPL35D), ribosomal protein L35- cytosolic, Arabidopsis thaliana, PIR:T00549   chr5:587528-588731 FORWARD   Aliases: T22P11.200, T22P11_200	10.2	10.2	-0.0	-0.0	100.0%	-5.0
20721	AT2G22890.1   expressed protein, ; expression supported by MPSS   chr2:9749580-9750419 REVERSE   Aliases: T20K9.10, T20K9_10	3.5	3.5	0.0	0.0	100.0%	-5.1
20722	AT3G57785.1   expressed protein   chr3:21415551-21416194 REVERSE   Aliases: None	6.5	6.4	0.0	0.0	100.0%	-4.6
20723	AT5G66940.1   Dof-type zinc finger domain-containing protein   chr5:26745215-26745892 REVERSE   Aliases: K8A10.1, K8A10_1	3.6	3.6	0.0	0.0	100.0%	-5.3
20724	AT1G68780.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to disease resistance protein (Lycopersicon esculentum) gi:3894383:gb:AAK78591   chr1:25835466-25837507 REVERSE   Aliases: F14K14.11, F14K14_11	2.4	2.4	0.0	0.0	100.0%	-5.6
20725	AT4G02900.1   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr4:1284066-1287747 FORWARD   Aliases: T5J8.22, T5J8_22	3.1	3.1	0.0	0.0	100.0%	-5.4
20726	AT5G62160.1   Symbol: ZIP12   metal transporter, putative (ZIP12), identical to putative metal transporter ZIP12 (Arabidopsis thaliana) gi:17385794:gb:AAL38437; similar to zinc transporter protein ZIP1 (Glycine max) gi:15418778:gb:AAK37761; member of the Zinc (Zn <sup>2+</sup> )-Iron (Fe <sup>2+</sup> ) permease (ZIP) family, PMID:11500563   chr5:24977333-24978489 FORWARD   Aliases: MTG10.20, MTG10_20	4.8	4.8	-0.0	-0.0	100.0%	-5.3
20727	AT2G22530.1   phosphatidylinositolglycan-related, similar to Pig-o (Mus musculus) GI:8099973   chr2:9580309-9584521 REVERSE   Aliases: F14M13.7, F14M13_7	4.1	4.1	-0.0	-0.0	100.0%	-5.1
20728	AT1G13450.2   similar to DNA-binding protein GT-1-related [Arabidopsis thaliana] (TAIR:At3g25990.1); similar to DNA-binding protein [Nicotiana tabacum] (GB:AAA34085.1); similar to DNA-binding protein B2F - common tobacco (fragment) (GB:PQ0446); contains InterPro domain Myb DNA-binding domain (InterPro:IPR001005)   chr1:4612728-4615350 REVERSE   Aliases: T6J4.18, T6J4_18	6.2	6.2	0.0	0.0	100.0%	-4.8
20729	AT1G72120.1   proton-dependent oligopeptide transport (POT) family protein, contains Pfam profile: PF00854 POT family   chr1:27135795-27140051 FORWARD   Aliases: F28P5.2, F28P5_2	2.5	2.5	-0.0	-0.0	100.0%	-4.7
20730	AT4G04450.1   Symbol: WRKY42	2.8	2.8	-0.0	-0.0	100.0%	-5.4
20731	AT4G04890.1   Symbol: PDF2   homeobox-leucine zipper protein protodermal factor 2 (PDF2), identical to GP:14276060: protodermal factor2 (GI:14276060)	4.3	4.3	-0.0	-0.0	100.0%	-5.0
20732	AT5G25430.1   anion exchange protein family, contains similarity to SWISS-PROT:P02730 anion transport protein (Anion exchange protein 1) (Human){Homo sapiens}	2.6	2.6	0.0	0.0	100.0%	-5.3
20733	AT3G51400.1   expressed protein, contains Pfam profile PF03087: Arabidopsis protein of unknown function   chr3:19088829-19089934 REVERSE   Aliases: F26O13.40	2.5	2.5	-0.0	-0.0	100.0%	-5.5
20734	AT3G19640.1   magnesium transporter CorA-like family protein (MRS2-3), low similarity to SP:Q01926 RNA splicing protein MRS2, mitochondrial precursor {Saccharomyces cerevisiae}; contains Pfam profile PF01544: CorA-like Mg <sup>2+</sup> transporter protein   chr3:6820936-6823312 FORWARD   Aliases: MMB12.11	9.9	9.9	0.0	0.0	100.0%	-5.0
20735	AT3G24550.1   protein kinase family protein, contains Pfam domain PF00069: Protein kinase domain   chr3:8960265-8963575 FORWARD   Aliases: MOB24.11	7.4	7.4	-0.0	-0.0	100.0%	-5.0
20736	AT5G50440.1   Symbol: MEMB12	5.9	5.9	-0.0	-0.0	100.0%	-5.3



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20737	AT1G78630.1   Symbol: EMB1473   ribosomal protein L13 family protein, similar to ribosomal protein L13 GI:170132 from ( <i>Spinacia oleracea</i> )   chr1:29580849-29582551 FORWARD   Aliases: EMB1473, EMBRYO DEFECTIVE 1473, T30F21.4, T30F21_4	8.9	8.9	0.0	0.0	100.0%	-4.4
20738	AT1G70470.1   expressed protein   chr1:26563022-26563697 REVERSE   Aliases: F24J13.4, F24J13_4	2.8	2.8	-0.0	-0.0	100.0%	-4.6
20739	AT1G68320.1   Symbol: MYB62   myb family transcription factor (MYB62), similar to myb-related transcription factor (cpm7) GI:1002799 from ( <i>Craterostigma plantagineum</i> ); contains Pfam profile: myb DNA binding domain PF00249	3.3	3.3	-0.0	-0.0	100.0%	-5.3
20740	AT1G76630.1   tetratricopeptide repeat (TPR)-containing protein, contains Pfam profile: PF00515 TPR Domain (5 copies)   chr1:28764593-28769680 FORWARD   Aliases: F14G6.23	2.8	2.8	-0.0	-0.0	100.0%	-5.4
20741	AT3G25880.1   auxin-resistance protein, putative, similar to Swiss-Prot:P42744 auxin-resistance protein AXR1 ( <i>Arabidopsis thaliana</i> )   chr3:9470950-9471270 REVERSE   Aliases: MPE11.3	2.7	2.7	-0.0	-0.0	100.0%	-5.6
20742	AT5G63690.1   expressed protein   chr5:25510090-25510509 REVERSE   Aliases: MBK5.17, MBK5_17	5.2	5.2	0.0	0.0	100.0%	-4.7
20743	AT5G50830.2   similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g22795.1); similar to Hypothetical protein C33G8.2 [ <i>Caenorhabditis elegans</i> ] (GB:AAC25848.1)	3.4	3.4	-0.0	-0.0	100.0%	-5.1
20744	AT1G55220.1   expressed protein   chr1:20604550-20605103 REVERSE   Aliases: F7A10.6, F7A10_6	2.3	2.3	-0.0	-0.0	100.0%	-5.7
20745	AT1G22480.1   plastocyanin-like domain-containing protein   chr1:7934158-7935371 REVERSE   Aliases: F12K8.17, F12K8_17	2.7	2.7	-0.0	-0.0	100.0%	-5.1
20746	AT1G12740.1   Symbol: CYP87A2   cytochrome P450 family protein, similar to Cytochrome P450 90A1 (SP:Q42569) ( <i>Arabidopsis thaliana</i> )   chr1:4342460-4344615 FORWARD   Aliases: T12C24.27, T12C24_27	1.9	1.9	0.0	0.0	100.0%	-4.3
20747	AT3G27890.1   Symbol: NQR   NADPH-dependent FMN reductase family protein, contains Pfam profile: PF03358 NADPH-dependent FMN reductase   chr3:10351893-10353206 REVERSE   Aliases: K16N12.13, NADPH:QUINONE OXIDOREDUCTASE	8.0	8.0	0.0	0.0	100.0%	-4.9
20748	AT1G32120.1   expressed protein, contains Pfam profile PF04819: Family of unknown function (DUF716) (Plant viral-response family)   chr1:11552906-11558757 FORWARD   Aliases: F3C3.9, F3C3_9	3.4	3.4	0.0	0.0	100.0%	-4.8
20749	AT5G01660.1   kelch repeat-containing protein, similar to SP:P57790 Kelch-like ECH-associated protein 1 (Cytosolic inhibitor of Nrf2) ( <i>Rattus norvegicus</i> ); contains Pfam profile PF01344: Kelch motif   chr5:244501-248142 REVERSE   Aliases: F7A7.180, F7A7_180	5.2	5.2	0.0	0.0	100.0%	-4.9
20750	AT3G61490.2   glycoside hydrolase family 28 protein / polygalacturonase (pectinase) family protein, weak similarity to SP:P27644 Polygalacturonase (EC 3.2.1.15) (Pectinase) ( <i>Agrobacterium tumefaciens</i> ); contains PF00295: Glycosyl hydrolases family 28   chr3:22769363-22771167 FORWARD   Aliases: F2A19.90	5.7	5.6	0.0	0.0	100.0%	-5.3
20751	AT5G35300.1   expressed protein   chr5:13535547-13536179 FORWARD   Aliases: T26D22.30, T26D22_30	3.5	3.5	-0.0	-0.0	100.0%	-5.1
20752	AT5G48940.1   leucine-rich repeat transmembrane protein kinase, putative   chr5:19856936-19861033 FORWARD   Aliases: K19E20.5, K19E20_5	3.4	3.4	-0.0	-0.0	100.0%	-5.3
20753	AT2G34100.1   expressed protein, similar to the Asp-rich region of GP:1633572:U52064   chr2:14406616-14409000 REVERSE   Aliases: T14G11.22, T14G11_22	2.9	2.9	-0.0	-0.0	100.0%	-5.4
20754	AT1G48130.1   Symbol: ATPER1	2.4	2.4	-0.0	-0.0	100.0%	-5.4
20755	AT5G18060.1   auxin-responsive protein, putative, similar to auxin-inducible SAUR (Small Auxin Up RNAs) GI:3043536 from radish ( <i>Raphanus sativus</i> )   chr5:5975964-5976498 FORWARD   Aliases: MCM23.16, MCM23_16	2.8	2.8	-0.0	-0.0	100.0%	-5.1
20756	AT3G56740.1   ubiquitin-associated (UBA)/TS-N domain-containing protein, contains Pfam profile PF00627: UBA/TS-N domain   chr3:21026350-21029521 FORWARD   Aliases: T8M16.70	4.0	4.0	-0.0	-0.0	100.0%	-5.5
20757	AT2G22430.1   Symbol: ATHB6   homeobox-leucine zipper protein 6 (HB-6) / HD-ZIP transcription factor 6, identical to homeobox-leucine zipper protein ATHB-6 (HD-ZIP protein ATHB-6) (SP:P46668) ( <i>Arabidopsis thaliana</i> )   chr2:9533175-9534910 REVERSE   Aliases: F14M13.17, F14M13_17	6.0	6.0	0.0	0.0	100.0%	-4.6
20758	AT4G13210.1   pectate lyase family protein, similar to pectate lyase GP:14531296 from ( <i>Fragaria x ananassa</i> )   chr4:7670036-7673131 FORWARD   Aliases: F17N18.100, F17N18_100	2.5	2.5	-0.0	-0.0	100.0%	-5.6
20759	AT1G35890.1   expressed protein   chr1:13342512-13343165 FORWARD   Aliases: F10O5.6, F10O5_6	2.8	2.8	0.0	0.0	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20760	AT5G39610.1   Symbol: ANAC092   no apical meristem (NAM) family protein, contains Pfam PF02365 : No apical meristem (NAM) protein; similar to cup-shaped cotyledon CUC2 (GI:1944132) (Arabidopsis thaliana)   chr5:15875628-15877011 REVERSE   Aliases: ANAC092, MIJ24.11, MIJ24_11	2.1	2.1	-0.0	-0.0	100.0%	-4.3
20761	AT3G31410.1   expressed protein, similar to hypothetical protein GB:CAB77996 GI:7267513 from (Arabidopsis thaliana)   chr3:12782958-12786060 REVERSE   Aliases: T22B15.43	2.6	2.6	0.0	0.0	100.0%	-6.1
20762	AT2G03180.1   hypothetical protein   chr2:962761-963123 FORWARD   Aliases: T18E12.15, T18E12_15	2.4	2.4	0.0	0.0	100.0%	-5.8
20763	AT3G44720.1   prephenate dehydratase family protein, similar to bacterial PheA gene products   chr3:16282639-16284331 FORWARD   Aliases: T32N15.11	7.2	7.2	-0.0	-0.0	100.0%	-4.7
20764	AT3G17700.1   Symbol: CNBT1   cyclic nucleotide-binding transporter 1 / CNBT1 (CNGC20), identical to cyclic nucleotide-binding transporter 1 (CNBT1) GI:8131898 from (Arabidopsis thaliana); member of the cyclic nucleotide-gated channel (CNGC) family- see PMID:11500563   chr3:6048922-6052556 FORWARD   Aliases: ATCNGC20, CNGC20, CYCLIC NUCLEOTIDE BINDING TRANSPORTER 1, MKP6.28	5.5	5.5	0.0	0.0	100.0%	-4.7
20765	AT2G44370.1   DC1 domain-containing protein, highly similar to GP:2435515:AF024504   chr2:18329070-18330197 REVERSE   Aliases: F4I1.18	2.7	2.7	-0.0	-0.0	100.0%	-4.5
20766	AT5G24910.1   Symbol: CYP714A1   cytochrome P450 family protein, similar to Cytochrome P450 72A1 (SP:Q05047) (Catharanthus roseus); similar to fatty acid omega-hydroxylase cytochrome P450 4A11 - Homo sapiens, PIR:I53015; supported by cDNA: gi_16604323_gb_AY058060.1_   chr5:8567584-8570361 REVERSE   Aliases: F6A4.120, F6A4_120	3.2	3.2	-0.0	-0.0	100.0%	-4.8
20767	AT5G03430.1   phosphoadenosine phosphosulfate (PAPS) reductase family protein, low similarity to SP:P38913 FAD synthetase (EC 2.7.7.2) {Saccharomyces cerevisiae}; contains Pfam profiles PF01507: Phosphoadenosine phosphosulfate reductase family, PF00994: Probable molybdopterin binding domain   chr5:848863-853094 REVERSE   Aliases: F12E4.190, F12E4_190	6.7	6.7	0.0	0.0	100.0%	-5.1
20768	AT4G27300.1   S-locus protein kinase, putative, similar to receptor protein kinase (Ipomoea trifida) gi:836954:gb:AAC23542; contains S-locus glycoprotein family domain, Pfam:PF00954   chr4:13669314-13672354 REVERSE   Aliases: M4I22.110, M4I22_110	3.1	3.1	-0.0	-0.0	100.0%	-5.4
20769	AT2G30970.1   Symbol: ASP1   aspartate aminotransferase, mitochondrial / transaminase A (ASP1), identical to SP:P46643 Aspartate aminotransferase, mitochondrial precursor (EC 2.6.1.1) (Transaminase A) {Arabidopsis thaliana}   chr2:13185926-13188984 FORWARD   Aliases: ASPARTATE AMINOTRANSFERASE 1, F7F1.18, F7F1_18	10.6	10.7	-0.0	-0.0	100.0%	-4.7
20770	AT5G47020.1   glycine-rich protein, strong similarity to unknown protein (emb:CAB87688.1)   chr5:19099232-19107244 FORWARD   Aliases: MQD22.16, MQD22_16	8.0	8.0	-0.0	-0.0	100.0%	-5.1
20771	AT4G27720.1   expressed protein, contains Pfam PF05631: Protein of unknown function (DUF791)   chr4:13831126-13833820 FORWARD   Aliases: T29A15.210, T29A15_210	6.2	6.2	0.0	0.0	100.0%	-4.6
20772	AT4G28550.1   RabGAP/TBC domain-containing protein, similar to SP:P09379 GTPase-activating protein GYP7 (Fragment) {Yarrowia lipolytica}; contains Pfam profile PF00566: TBC domain   chr4:14110890-14113754 FORWARD   Aliases: F20O9.250, F20O9_250	3.8	3.8	-0.0	-0.0	100.0%	-5.2
20773	AT5G43060.1   cysteine proteinase, putative / thiol protease, putative, similar to cysteine proteinase RD21A precursor (thiol protease) GI:435619, SP:P43297 from (Arabidopsis thaliana)   chr5:17286772-17289388 REVERSE   Aliases: MMG4.7, MMG4_7	10.5	10.5	0.0	0.0	100.0%	-5.1
20774	AT5G41520.1   40S ribosomal protein S10 (RPS10B), contains similarity to 40S ribosomal protein S10   chr5:16626419-16627889 REVERSE   Aliases: MBK23.4, MBK23_4	10.0	10.0	0.0	0.0	100.0%	-4.8
20775	AT1G55440.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.5	2.5	-0.0	-0.0	100.0%	-5.4
20776	AT4G25260.1   invertase/pectin methylesterase inhibitor family protein, low similarity to pectinesterase from Phaseolus vulgaris SP:Q43111, Lycopersicon esculentum SP:Q43143, Arabidopsis thaliana SP:Q42534; contains Pfam profile PF04043: Plant invertase/pectin methylesterase inhibitor   chr4:12935720-12936668 REVERSE   Aliases: F24A6.100, F24A6_100	3.0	3.0	-0.0	-0.0	100.0%	-5.0
20777	AT1G68520.1   zinc finger (B-box type) family protein, contains Pfam profile: PF00643 B-box zinc finger   chr1:25712777-25714570 REVERSE   Aliases: T26J14.9, T26J14_9	3.0	3.0	0.0	0.0	100.0%	-5.5
20778	AT3G52080.1   similar to cation/hydrogen exchanger, putative (CHX15) [Arabidopsis thaliana] (TAIR:At2g13620.1); similar to Na <sup>+</sup> /H <sup>+</sup> antiporter-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD82290.1); contains InterPro domain Sodium/hydrogen exchanger (InterPro:IPR006153)   chr3:19326021-19328821 FORWARD   Aliases: F4F15.190	2.7	2.7	-0.0	-0.0	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20779	AT2G26780.1   expressed protein, contains Pfam profile TBP (TATA-binding protein) -interacting protein 120 (TIP120); contains TIGRFAM profile TIGR01612: reticulocyte binding protein	6.6	6.6	-0.0	-0.0	100.0%	-4.9
20780	AT4G19985.1   GCN5-related N-acetyltransferase (GNAT) family protein, contains Pfam profile PF00583: acetyltransferase, GNAT family   chr4:10830318-10832104 REVERSE   Aliases: None	5.0	5.0	-0.0	-0.0	100.0%	-4.6
20781	AT1G04180.1   flavin-containing monooxygenase family protein / FMO family protein, similar to flavin-containing monooxygenases YUCCA (gi:16555352), YUCCA2 (gi:16555354), and YUCCA3 (gi:16555356) from Arabidopsis thaliana; contains Pfam profile PF00743   chr1:1104622-1105987 FORWARD   Aliases: F20D22.5, F20D22_5	2.9	2.9	-0.0	-0.0	100.0%	-5.2
20782	AT1G55310.2   Symbol: SR33   similar to SC35-like splicing factor, 30a kD (SCL30a) [Arabidopsis thaliana] (TAIR:At3g13570.1); similar to PREDICTED P0519E12.127 gene product [Oryza sativa (japonica cultivar-group)] (GB:XP_506493.1); contains InterPro domain RNA-binding region RNP-1 (RNA recognition motif) (InterPro:IPR000504)   chr1:20633732-20636551 FORWARD   Aliases: ATSC33, F7A10.26, F7A10.27, F7A10_26, SCL33	5.6	5.5	0.0	0.0	100.0%	-4.7
20783	AT3G11390.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.2	2.2	0.0	0.0	100.0%	-5.7
20784	AT1G75870.1   expressed protein   chr1:28490193-28490775 FORWARD   Aliases: T4O12.11, T4O12_11	2.7	2.7	0.0	0.0	100.0%	-5.7
20785	AT3G58810.2   Symbol: MTPA2   zinc transporter, putative, similar to zinc transporter 4; ZnT4 (Mus musculus) gi:2582990:gb:AAB82593; similar to zinc transporter ZAT (Arabidopsis thaliana) gi:4206640:gb:AAD11757; member of the cation diffusion facilitator (CDF) family, or cation efflux (CE) family, PMID:11500563   chr3:21760943-21762983 FORWARD   Aliases: ATMTPA2, T20N10.160	4.4	4.4	-0.0	-0.0	100.0%	-4.5
20786	AT3G21410.1   F-box family protein (FBW1), contains similarity to F-box domain IPR:001810;   chr3:7536725-7537957 REVERSE   Aliases: MHC9.9	3.1	3.1	-0.0	-0.0	100.0%	-5.3
20787	AT3G43390.1   expressed protein, similar to At3g24380, At5g36840, At5g35010, At3g42740, At4g05290, At2g14770, At2g05560, At4g08880, At1g34730, At1g27790, At1g34740, At1g27780, At5g36850, At3g42730, At1g52020, At3g24390, At4g05280, At1g25886, At4g03300   chr3:15337252-15341934 REVERSE   Aliases: T5C2.90	2.8	2.8	-0.0	-0.0	100.0%	-5.5
20788	AT3G46730.1   disease resistance protein (CC-NBS class), putative, domain signature CC-NBS exists, suggestive of a disease resistance protein.	2.3	2.3	-0.0	-0.0	100.0%	-5.0
20789	AT5G07560.1   Symbol: GRP20   glycine-rich protein (GRP20), oleosin; glycine-rich protein 20 (GRP20); similar to - Brassica napus, PIR:S50195	2.2	2.2	0.0	0.0	100.0%	-5.5
20790	AT1G63540.1   hydroxyproline-rich glycoprotein family protein   chr1:23571158-23573158 FORWARD   Aliases: F2K11.10, F2K11_10	2.6	2.6	0.0	0.0	100.0%	-5.4
20791	AT5G13480.1   Symbol: FY   similar to WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At5g67320.1); similar to putative FY protein [Oryza sativa (japonica cultivar-group)] (GB:BAD87887.1); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr5:4326587-4331641 REVERSE   Aliases: FY, T6I14.10, T6I14_10	6.2	6.2	-0.0	-0.0	100.0%	-4.8
20792	AT3G05070.1   expressed protein   chr3:1416165-1417743 FORWARD   Aliases: T12H1.3, T12H1_3	8.5	8.5	-0.0	-0.0	100.0%	-4.5
20793	AT5G04050.1   maturase-related, contains similarity to maturase proteins from several species   chr5:1096015-1098920 FORWARD   Aliases: F8F6.260, F8F6_260	3.3	3.3	0.0	0.0	100.0%	-5.5
20794	AT3G29300.1   expressed protein   chr3:11248248-11248889 FORWARD   Aliases: MMF24.5	2.2	2.2	-0.0	-0.0	100.0%	-6.0
20795	AT3G55260.1   glycosyl hydrolase family 20 protein, similar to beta-hexosaminidase A SP:P13723 from (Dictyostelium discoideum)	7.1	7.1	0.0	0.0	100.0%	-4.8
20796	AT2G37590.1   Dof-type zinc finger domain-containing protein   chr2:15776222-15777697 FORWARD   Aliases: F13M22.9, F13M22_9	3.5	3.5	-0.0	-0.0	100.0%	-5.1
20797	AT2G22060.1   expressed protein   chr2:9388072-9389225 FORWARD   Aliases: T16B14.9, T16B14_9	4.3	4.3	-0.0	-0.0	100.0%	-5.1
20798	AT3G62760.1   Symbol: ATGSTF13   glutathione S-transferase, putative, Glutathione transferase III(b) - Zea mays, EMBL:AJ010296   chr3:23228401-23229222 REVERSE   Aliases: F26K9.190	2.5	2.5	-0.0	-0.0	100.0%	-5.5
20799	AT1G76230.1   expressed protein   chr1:28604701-28605274 REVERSE   Aliases: T23E18.16, T23E18_16	3.1	3.1	0.0	0.0	100.0%	-5.4
20800	AT3G10710.1   pectinesterase family protein, contains similarity to pectinesterase GB:AAB57671 (Citrus sinensis); contains Pfam profile: PF01095 pectinesterase   chr3:3352294-3354242 FORWARD   Aliases: T7M13.21	4.0	4.0	0.0	0.0	100.0%	-4.2
20801	AT1G22330.1   RNA recognition motif (RRM)-containing protein, similar to UBP1 interacting protein 1a (Arabidopsis thaliana) GI:19574236; contains InterPro entry IPR000504: RNA-binding region RNP-1 (RNA recognition motif) (RRM)   chr1:7886531-7887703 FORWARD   Aliases: T16E15.6, T16E15_6	2.7	2.7	-0.0	-0.0	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20802	AT2G33340.3   similar to transducin family protein / WD-40 repeat family protein [Arabidopsis thaliana] (TAIR:At1g04510.1); similar to ENSANGP00000016070 [Anopheles gambiae str. PEST] (GB:XP_308568.2); contains InterPro domain Zn-finger, modified RING (InterPro:IPR003613); contains InterPro domain G-protein beta WD-40 repeat (InterPro:IPR001680)   chr2:14133294-14138219 REVERSE   Aliases: F4P9.11, F4P9_11	8.6	8.6	-0.0	-0.0	100.0%	-5.2
20803	AT1G21450.1   Symbol: SCL1   scarecrow-like transcription factor 1 (SCL1), identical to scarecrow-like 1 GB:AAF21043 GI:6644390 from (Arabidopsis thaliana)   chr1:7508960-7511790 FORWARD   Aliases: F24J8.8, F24J8_8, SCARECROW LIKE 1, SCL1	4.7	4.7	-0.0	-0.0	100.0%	-5.1
20804	AT5G17180.1   expressed protein   chr5:5651438-5651809 FORWARD   Aliases: MKP11.3, MKP11_3	3.3	3.3	0.0	0.0	100.0%	-5.4
20805	AT1G66550.1   Symbol: WRKY67	2.3	2.3	-0.0	-0.0	100.0%	-6.1
20806	AT2G04460.1   expressed protein   chr2:1547685-1548254 REVERSE   Aliases: T1O3.13, T1O3_13	2.7	2.7	0.0	0.0	100.0%	-5.6
20807	AT5G65880.1   expressed protein   chr5:26370262-26370900 FORWARD   Aliases: K14B20.5, K14B20_5	8.0	8.0	0.0	0.0	100.0%	-4.7
20808	AT1G75790.1   Symbol: SKS18   multi-copper oxidase type I family protein, contains Pfam profile: PF00394 Multicopper oxidase   chr1:28458442-28461167 REVERSE   Aliases: F10A5.2, F10A5_2, SKS18	2.3	2.3	0.0	0.0	100.0%	-6.0
20809	AT5G25130.1   Symbol: CYP71B12   cytochrome P450 family protein, CYTOCHROME P450 71B1 - Thlaspi arvense, EMBL:L24438   chr5:8668302-8670107 FORWARD   Aliases: F21J6.2	3.2	3.2	-0.0	-0.0	100.0%	-5.0
20810	AT4G04010.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g32840, At2g06430, At2g15140, At2g04980, At2g14130, At3g44500, At2g15190, At3g47260, At5g34900, At3g29210, At2g02210, At3g32900   chr4:1925650-1930394 REVERSE   Aliases: T24H24.3, T24H24_3	2.3	2.3	-0.0	-0.0	100.0%	-5.9
20811	AT4G39490.1   Symbol: CYP96A10   similar to cytochrome P450, putative [Arabidopsis thaliana] (TAIR:At4g32170.1); similar to cytochrome P450, putative [Arabidopsis thaliana] (TAIR:At2g23180.1); similar to putative phytochrome P450 [Oryza sativa (japonica cultivar-group)] (GB:NP_914475.1); contains InterPro domain E-class P450, group I (InterPro:IPR002401); contains InterPro domain Cytochrome P450 (InterPro:IPR001128)   chr4:18365043-18366882 FORWARD   Aliases: F23K16.120, F23K16_120	2.5	2.5	-0.0	-0.0	100.0%	-5.5
20812	AT5G06650.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr5:2043487-2044062 FORWARD   Aliases: F15M7.18, F15M7_18	2.4	2.4	-0.0	-0.0	100.0%	-5.6
20813	AT3G23540.2   expressed protein, similar to expressed protein [Arabidopsis thaliana] (TAIR:At4g14290.1); similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:XP_464484.1)   chr3:8444945-8448077 FORWARD   Aliases: MDB19.2	4.8	4.8	0.0	0.0	100.0%	-4.8
20814	AT3G12030.1   expressed protein, similar to membrane protein GB:BAA86974 GI:6467175 from (Homo sapiens)   chr3:3834367-3835081 REVERSE   Aliases: MEC18.16	4.3	4.3	-0.0	-0.0	100.0%	-5.1
20815	AT1G55350.4   Symbol: DEK1   calpain-type cysteine protease family, identical to calpain-like protein GI:20268660 from (Arabidopsis thaliana); contains Pfam profiles: PF00648 Calpain family cysteine protease, PF01067 Calpain large subunit, domain III; identical to cDNA calpain-like protein GI:20268659	3.5	3.5	-0.0	-0.0	100.0%	-5.1
20816	AT4G23590.1   aminotransferase class I and II family protein, similar to nicotianamine aminotransferase from Hordeum vulgare (GI:6498122, GI:6469087); contains Pfam profile PF00155 aminotransferase, classes I and II   chr4:12307136-12309657 FORWARD   Aliases: F9D16.60, F9D16_60	2.4	2.4	0.0	0.0	100.0%	-5.6
20817	AT5G25340.1   expressed protein   chr5:8793021-8794787 FORWARD   Aliases: F18G18.80, F18G18_80	3.6	3.6	0.0	0.0	100.0%	-5.2
20818	AT5G10760.1   aspartyl protease family protein, contains Pfam domain, PF00026: eukaryotic aspartyl protease   chr5:3400343-3402204 REVERSE   Aliases: MAJ23.1	2.2	2.2	0.0	0.0	100.0%	-5.9
20819	AT4G00740.1   dehydration-responsive protein-related, similar to early-responsive to dehydration stress ERD3 protein (Arabidopsis thaliana) GI:15320410; contains Pfam profile PF03141: Putative methyltransferase   chr4:307431-310482 REVERSE   Aliases: F15P23.2, F15P23_2	5.2	5.2	0.0	0.0	100.0%	-5.0
20820	AT4G34330.1   expressed protein, similar to At14a, GI:11994571 and GI:11994573 (Arabidopsis thaliana); expression supported by MPSS   chr4:16424717-16425894 FORWARD   Aliases: F10M10.100, F10M10_100	2.6	2.6	-0.0	-0.0	100.0%	-5.6
20821	AT5G55980.1   serine-rich protein-related, contains some similarity to serine-rich proteins   chr5:22687527-22687868 FORWARD   Aliases: MDA7.2, MDA7_2	2.6	2.6	0.0	0.0	100.0%	-5.6



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20822	AT4G15620.1   integral membrane family protein, contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr4:8913840-8915658 FORWARD   Aliases: DL3850W, FCAALL.348	3.0	3.0	-0.0	-0.0	100.0%	-5.7
20823	AT1G10990.2   expressed protein, and gencode   chr1:3670278-3671187 REVERSE   Aliases: T19D16.27, T19D16_27	4.4	4.4	0.0	0.0	100.0%	-5.2
20824	AT1G32970.1   subtilase family protein, similar to subtilase GI:9957714 from (Oryza sativa)   chr1:11948701-11951962 REVERSE   Aliases: F9L11.14, F9L11_14	2.8	2.8	-0.0	-0.0	100.0%	-5.4
20825	AT5G52290.1   expressed protein   chr5:21247579-21253780 REVERSE   Aliases: K24M7.2, K24M7_2	2.2	2.2	0.0	0.0	100.0%	-6.1
20826	AT4G27650.1   Symbol: PEL1   pelota (PEL1), identical to pelota (Arabidopsis thaliana) GI:3941543; contains InterPro accession IPR004403: Peptide chain release factor eRF/aRF subunit 1   chr4:13803303-13807941 REVERSE   Aliases: PELOTA, T29A15.140, T29A15_140	7.3	7.3	-0.0	-0.0	100.0%	-4.8
20827	AT2G24255.1   expressed protein   chr2:10323133-10324143 REVERSE   Aliases: None	3.3	3.3	0.0	0.0	100.0%	-5.6
20828	AT3G12540.1   similar to expressed protein [Arabidopsis thaliana] (TAIR:At2g39690.1); similar to putative ternary complex factor [Oryza sativa (japonica cultivar-group)] (GB:XP_550141.1); contains InterPro domain Protein of unknown function DUF547 (InterPro:IPR006869)   chr3:3975253-3977319 FORWARD   Aliases: T2E22.15	2.8	2.8	0.0	0.0	100.0%	-4.7
20829	AT2G47130.1   short-chain dehydrogenase/reductase (SDR) family protein, similar to 3-beta-hydroxysteroiddehydrogenase GI:15983819 from (Digitalis lanata)   chr2:19356606-19357591 REVERSE   Aliases: F14M4.4	4.4	4.4	0.0	0.0	100.0%	-4.8
20830	AT4G26660.1   expressed protein, weak similarity to phragmoplast-associated kinesin-related protein 1 (Arabidopsis thaliana) GI:8745333   chr4:13448690-13452013 FORWARD   Aliases: T15N24.110, T15N24_110	2.3	2.3	0.0	0.0	100.0%	-5.5
20831	AT1G78090.1   Symbol: ATTPPB	4.3	4.3	-0.0	-0.0	100.0%	-4.5
20832	AT2G06140.1   expressed protein   chr2:2392857-2394901 FORWARD   Aliases: F5K7.10, F5K7_10	2.7	2.7	-0.0	-0.0	100.0%	-5.7
20833	AT1G16570.1   glycosyl transferase family 1 protein, contains similarity to mannosyltransferase GI:1800223 from Dictyostelium discoideum; contains Pfam glycosyl transferase, group 1 family protein domain PF00534   chr1:5670258-5673593 REVERSE   Aliases: F19K19.11, F19K19_11	7.8	7.8	-0.0	-0.0	100.0%	-4.8
20834	AT4G17300.1   Symbol: NS1   asparaginyl-tRNA synthetase, chloroplast, mitochondrial / asparagine-tRNA ligase / AsnRS (SYNO), nearly identical to SP:O48593   chr4:9681551-9684984 FORWARD   Aliases: ATNS1, DL4685W, FCAALL.396	7.1	7.1	0.0	0.0	100.0%	-5.1
20835	AT2G12480.2   Symbol: SCPL43	3.6	3.6	0.0	0.0	100.0%	-5.3
20836	AT2G32270.1   Symbol: ZIP3   zinc transporter (ZIP3), identical to zinc transporter (Arabidopsis thaliana) gi:3252870:gb:AAC24199; member of the Zinc (Zn2+)-Iron (Fe2+) permease (ZIP) family, PMID:11500563	3.4	3.4	-0.0	-0.0	100.0%	-4.7
20837	AT3G03150.1   expressed protein   chr3:727561-729467 REVERSE   Aliases: T17B22.16, T17B22_16	9.6	9.6	0.0	0.0	100.0%	-4.6
20838	AT3G52130.1   protease inhibitor/seed storage/lipid transfer protein (LTP) family protein, similar to cysteine-rich 5B protein - Lycopersicon esculentum, PIR2:S39552 (GI:415833); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr3:19343059-19343436 REVERSE   Aliases: F4F15.240	2.8	2.8	0.0	0.0	100.0%	-5.4
20839	AT3G30320.1   hypothetical protein   chr3:11933766-11937173 FORWARD   Aliases: T6J22.7	3.3	3.3	-0.0	-0.0	100.0%	-5.5
20840	AT5G60790.1   Symbol: ATGCN1	6.1	6.0	0.0	0.0	100.0%	-4.9
20841	AT1G21950.1   expressed protein   chr1:7723428-7723852 REVERSE   Aliases: T26F17.18, T26F17_18	3.0	3.0	-0.0	-0.0	100.0%	-5.5
20842	AT3G46500.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, similar to gibberellin 20-oxidase from A. thaliana (gi:1109699), N. tabacum (GI:3402332); contains Pfam profile: PF03171 oxidoreductase, 2OG-Fe(II) oxygenase family   chr3:17131465-17133730 FORWARD   Aliases: F12A12.20	2.2	2.2	0.0	0.0	100.0%	-4.6
20843	AT3G23630.1   Symbol: ATIPT7	3.4	3.4	0.0	0.0	100.0%	-5.4
20844	AT5G17960.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.9	2.9	-0.0	-0.0	100.0%	-5.2
20845	AT3G26230.1   Symbol: CYP71B24   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr3:9599437-9601140 REVERSE   Aliases: MTC11.22	2.9	2.9	0.0	0.0	100.0%	-5.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20846	AT1G03760.1   prefoldin subunit family protein, contains similarity to Swiss-Prot:O94763 RNA polymerase II subunit 5-mediating protein (RPB5-mediating protein) (Homo sapiens); contains Pfam profile PF02996: Prefoldin subunit   chr1:941061-943376 REVERSE   Aliases: F21M11.33, F21M11_33	4.4	4.4	0.0	0.0	100.0%	-5.1
20847	AT3G16090.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr3:5456150-5458972 FORWARD   Aliases: MSL1.13	3.5	3.5	0.0	0.0	100.0%	-5.3
20848	AT2G15260.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain PF00097: Zinc finger, C3HC4 type (RING finger)	2.9	2.9	-0.0	-0.0	100.0%	-5.5
20849	AT2G32510.1   Symbol: MAPKKK17   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:13805898-13807016 REVERSE   Aliases: T26B15.7, T26B15_7	4.8	4.8	-0.0	-0.0	100.0%	-5.1
20850	AT1G62170.1   serpin family protein / serine protease inhibitor family protein, similar to phloem serpin-1 GI:9937311 from (Cucurbita maxima); contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr1:22977541-22979128 FORWARD   Aliases: F19K23.10, F19K23_10	2.5	2.5	-0.0	-0.0	100.0%	-5.7
20851	AT1G67635.1   expressed protein   chr1:25353483-25353815 FORWARD   Aliases: F12A21.23, F12A21_23	2.5	2.5	-0.0	-0.0	100.0%	-5.5
20852	AT4G05240.1   ubiquitin family protein, contains INTERPRO:IPR000626 ubiquitin domain   chr4:2688198-2689016 FORWARD   Aliases: C17L7.160, C17L7_160	2.2	2.2	-0.0	-0.0	100.0%	-6.1
20853	AT5G56300.1   S-adenosyl-L-methionine:carboxyl methyltransferase family protein, similar to SAM:jasmonic acid carboxyl methyltransferase (JMT)(GI:13676829) and to SAM:salicylic acid carboxyl methyltransferase (SAMT) (GI:6002712)(Clarkia breweri)	2.9	2.9	-0.0	-0.0	100.0%	-5.3
20854	AT2G23096.1   oxidoreductase, 2OG-Fe(II) oxygenase family protein, contains Pfam profile: PF03171 oxidoreductase, 2OG-Fe(II) oxygenase family   chr2:9841370-9843315 REVERSE   Aliases: None	3.1	3.1	-0.0	-0.0	100.0%	-4.9
20855	AT3G44380.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr3:16047170-16047867 REVERSE   Aliases: T22K7.60	4.5	4.5	-0.0	-0.0	100.0%	-4.7
20856	AT5G06560.1   expressed protein, contains Pfam profile PF04576: Protein of unknown function, DUF593   chr5:2003305-2006189 REVERSE   Aliases: F15M7.9, F15M7_9	6.3	6.3	0.0	0.0	100.0%	-5.0
20857	AT4G30670.1   expressed protein   chr4:14957371-14957968 REVERSE   Aliases: T10C21.20, T10C21_20	2.9	3.0	-0.0	-0.0	100.0%	-4.4
20858	AT4G00710.1   protein kinase family protein, low similarity to protein kinase (Arabidopsis thaliana) GI:2852449; contains Pfam profile: PF00069 Protein kinase domain   chr4:290048-293453 FORWARD   Aliases: F6N23.9, F6N23_9	5.2	5.2	0.0	0.0	100.0%	-5.0
20859	AT3G28270.2   expressed protein, similar to At14a protein (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	2.7	2.7	-0.0	-0.0	100.0%	-5.6
20860	AT1G54250.1   Symbol: ATRPABC16.5   DNA-directed RNA polymerase I, II, and III, putative, similar to SP:P52434 DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide (EC 2.7.7.6) (RPB17) (RPB8) {Homo sapiens}; contains Pfam profile PF03870: RNA polymerase Rpb8   chr1:20258605-20260220 FORWARD   Aliases: F20D21.7, F20D21_7, RNA POLYMERASE I, II AND III 16.5 KDA SUBUNIT	7.1	7.1	0.0	0.0	100.0%	-4.5
20861	AT3G59600.1   DNA-directed RNA polymerase I, II, and III, putative, similar to SP:P52434 DNA-directed RNA polymerases I, II, and III 17.1 kDa polypeptide (EC 2.7.7.6) (RPB17) (RPB8) {Homo sapiens}; contains Pfam profile PF03870: RNA polymerase Rpb8   chr3:22027362-22029073 FORWARD   Aliases: T16L24.150	7.1	7.1	0.0	0.0	100.0%	-4.5
20862	AT5G32600.1   expressed protein   chr5:12266929-12268873 REVERSE   Aliases: F3D18.1	2.8	2.8	0.0	0.0	100.0%	-5.1
20863	AT4G04650.1   expressed protein   chr4:2353987-2355211 REVERSE   Aliases: T19J18.5, T19J18_5	3.3	3.3	0.0	0.0	100.0%	-5.1
20864	AT3G03190.1   Symbol: ATGSTF11   glutathione S-transferase, putative, identical to glutathione S-transferase GB:AAB09584 from (Arabidopsis thaliana)   chr3:735035-735994 FORWARD   Aliases: ATGSTF6, GLUTATHIONE S TRANSFERASE, GLUTATHIONE S TRANSFERASE F11, T17B22.12, T17B22_12	3.3	3.3	0.0	0.0	100.0%	-4.6
20865	AT2G16410.1   hypothetical protein, similar to zinc finger protein (Arabidopsis thaliana) GI:976277   chr2:7120727-7121341 FORWARD   Aliases: F16F14.9, F16F14_9	3.6	3.6	0.0	0.0	100.0%	-4.8
20866	AT4G10770.1   Symbol: ATOPT7	3.0	3.0	-0.0	-0.0	100.0%	-4.8
20867	AT2G35580.1   serpin family protein / serine protease inhibitor family protein, similar to protein zx (Hordeum vulgare subsp. vulgare) GI:19071, serpin (Triticum aestivum) GI:1885350; contains Pfam profile PF00079: Serpin (serine protease inhibitor)   chr2:14940907-14942561 REVERSE   Aliases: T32F12.4, T32F12_4	3.1	3.0	0.0	0.0	100.0%	-5.0
20868	AT3G50500.1   Symbol: SPK 2 2   protein kinase, putative, similar to abscisic acid-activated protein kinase (Vicia faba) gi:6739629:gb:AAF27340   chr3:18752571-18755054 REVERSE   Aliases: PROTEIN KINASE, T20E23.100	6.2	6.2	0.0	0.0	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20869	AT5G14510.1   armadillo/beta-catenin repeat family protein, contains Pfam profile: PF00514 armadillo/beta-catenin-like repeat   chr5:4677976-4679197 REVERSE   Aliases: T15N1.2	3.3	3.3	-0.0	-0.0	100.0%	-4.4
20870	AT3G42240.1   expressed protein   chr3:14408316-14409279 REVERSE   Aliases: F26B15.40	3.3	3.3	0.0	0.0	100.0%	-5.0
20871	AT3G57080.1   eukaryotic rpb5 RNA polymerase subunit family protein, similar to SP:P19388 DNA-directed RNA polymerase II 23 kDa polypeptide (EC 2.7.7.6) {Homo sapiens}; contains Pfam profiles PF03871: RNA polymerase Rpb5 N-terminal domain, PF01191: RNA polymerase Rpb5 C-terminal domain	6.9	6.9	0.0	0.0	100.0%	-4.9
20872	ATMG00050.1   Symbol: ORF131	3.2	3.2	0.0	0.0	100.0%	-4.7
20873	AT4G11420.1   Symbol: EIF3A   eukaryotic translation initiation factor 3 subunit 10 / eIF-3 theta / eIF3a (TIF3A1), identical to eukaryotic translation initiation factor 3 subunit 10 (eIF-3 theta) (Eukaryotic translation initiation factor 3 large subunit) (eIF3a) (p114). (Arabidopsis thaliana) SWISS-PROT:Q9LD55   chr4:6947471-6952438 REVERSE   Aliases: ATEIF3A 1, ATTIF3A1, EIF3A 1, F25E4.40, F25E4_40, TIF3A1	7.3	7.3	0.0	0.0	100.0%	-4.6
20874	AT1G38950.1   hypothetical protein   chr1:14590293-14590860 FORWARD   Aliases: F12G6.9	3.0	3.0	-0.0	-0.0	100.0%	-5.2
20875	AT3G55690.1   expressed protein, predicted proteins, Arabidopsis thaliana   chr3:20677951-20679484 FORWARD   Aliases: F1I16.100	2.7	2.7	0.0	0.0	100.0%	-5.2
20876	AT3G29410.1   terpene synthase/cyclase family protein, similar to terpene synthase GB:CAA72074 from (Arabidopsis thaliana), contains Pfam profile: PF01397 terpene synthase family   chr3:11303672-11306361 REVERSE   Aliases: MUO10.2	2.8	2.8	-0.0	-0.0	100.0%	-4.3
20877	AT5G50400.1   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	9.1	9.1	-0.0	-0.0	100.0%	-5.2
20878	AT5G24540.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to amygdalin hydrolase isoform AH I precursor (GI:16757966) (Prunus serotina)   chr5:8384879-8388030 REVERSE   Aliases: K18P6.7, K18P6_7	2.7	2.7	-0.0	-0.0	100.0%	-5.6
20879	AT4G17600.1   Symbol: LIL3:1	9.8	9.8	0.0	0.0	100.0%	-4.3
20880	AT3G04740.1   Symbol: SWP   expressed protein (SWP1)   chr3:1293813-1300720 FORWARD   Aliases: F7O18.23, F7O18_23, STRUWWELPETER	5.1	5.1	0.0	0.0	100.0%	-5.0
20881	AT4G07960.1   Symbol: ATCSLC12   glycosyl transferase family 2 protein, similar to cellulose synthase from Agrobacterium tumeficiens (gi:710492) and Agrobacterium radiobacter (gi:710493); contains Pfam glycosyl transferase, group 2 family protein domain PF00535	3.1	3.1	-0.0	-0.0	100.0%	-4.9
20882	AT5G44340.1   Symbol: TUB4   tubulin beta-4 chain (TUB4), nearly identical to SP:P24636 Tubulin beta-4 chain {Arabidopsis thaliana}   chr5:17876422-17878328 REVERSE   Aliases: K9L2.12, K9L2_12	8.9	8.9	-0.0	-0.0	100.0%	-4.8
20883	AT3G24440.1   fibronectin type III domain-containing protein, contains Pfam profile PF00041: Fibronectin type III domain   chr3:8876034-8878178 REVERSE   Aliases: MXP5.1	5.6	5.6	-0.0	-0.0	100.0%	-4.9
20884	AT5G08490.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr5:2745209-2747758 REVERSE   Aliases: F8L15.18	2.9	2.9	-0.0	-0.0	100.0%	-5.3
20885	AT5G64490.1   expressed protein   chr5:25796536-25797534 REVERSE   Aliases: T12B11.8, T12B11_8	2.3	2.3	0.0	0.0	100.0%	-5.6
20886	AT3G52700.1   expressed protein, teichoic acid biosynthesis gene TagB, Staphylococcus aureus, EMBL:SAU91741   chr3:19543394-19544071 REVERSE   Aliases: F3C22.100	2.4	2.4	-0.0	-0.0	100.0%	-5.7
20887	AT1G56210.1   copper chaperone (CCH)-related, low similarity to copper homeostasis factor (GI:3168840)(PMID:9701579) and farnesylated proteins ATPF3 (GI:4097547) and GMFP7 (Glycine max)(GI:4097573); contains PF00403 Heavy-metal-associated domain   chr1:21039283-21040876 FORWARD   Aliases: F14G9.18, F14G9_18	4.1	4.1	-0.0	-0.0	100.0%	-4.8
20888	AT3G06400.1   DNA-dependent ATPase, putative, similar to DNA-dependent ATPase SNF2H (Mus musculus) GI:14028669; contains Pfam profiles PF00271: Helicase conserved C-terminal domain, PF00176: SNF2 family N-terminal domain, PF00249: Myb-like DNA-binding domain   chr3:1941007-1946930 FORWARD   Aliases: F24P17.13, F24P17_13	10.7	10.7	0.0	0.0	100.0%	-5.6
20889	AT5G58840.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from (Cucumis melo); non-consensus acceptor site TT at exon 6   chr5:23776229-23779285 FORWARD   Aliases: K19M22.3, K19M22_3	3.2	3.2	-0.0	-0.0	100.0%	-5.3
20890	AT2G02580.1   Symbol: CYP71B9   cytochrome P450 family protein   chr2:701945-703769 FORWARD   Aliases: T8K22.12, T8K22_12	2.8	2.8	0.0	0.0	100.0%	-5.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20891	AT2G03850.1   late embryogenesis abundant domain-containing protein / LEA domain-containing protein, low similarity to low-temperature-regulated 14.8 kda protein (Brassica napus) GI:544698, cold-regulated gene cor15b (Arabidopsis thaliana) GI:456016; contains Pfam profile PF02987: Late embryogenesis abundant protein   chr2:1175581-1176699 FORWARD   Aliases: T18C20.5, T18C20_5	3.3	3.3	0.0	0.0	100.0%	-5.3
20892	AT1G16090.1   Symbol: WAKL7   wall-associated kinase-related, contains similarity to wall-associated kinase 2 GI:4826399 from (Arabidopsis thaliana); similar to wall-associated kinase 1 (GI:3549626) (Arabidopsis thaliana); contains one transmembrane domain   chr1:5516253-5517816 FORWARD   Aliases: T24D18.19, T24D18_19, WALL ASSOCIATED KINASE LIKE 7	3.4	3.4	0.0	0.0	100.0%	-5.3
20893	AT2G33800.1   ribosomal protein S5 family protein, contains Pfam profiles PF03719: Ribosomal protein S5, C-terminal domain, PF00333: Ribosomal protein S5, N-terminal domain   chr2:14307848-14309506 REVERSE   Aliases: T1B8.10, T1B8_10	9.9	9.9	-0.0	-0.0	100.0%	-4.7
20894	AT5G08120.1   myosin heavy chain-related, identical to myosin heavy chain-like protein GI:1732515 from (Arabidopsis thaliana)   chr5:2600492-2602804 REVERSE   Aliases: T22D6.60, T22D6_60	7.7	7.7	0.0	0.0	100.0%	-4.8
20895	AT4G04750.1   similar to sugar transporter family protein [Arabidopsis thaliana] (TAIR:At4g04760.1); similar to integral membrane protein [Beta vulgaris] (GB:AAB53155.1); contains InterPro domain Sugar transporter superfamily (InterPro:IPR005829); contains InterPro domain Major facilitator superfamily (MFS) (InterPro:IPR007114); contains InterPro domain General substrate transporter (InterPro:IPR005828); contains InterPro domain Sugar transporter (InterPro:IPR003663)   chr4:2417886-2422622 FORWARD   Aliases: T4B21.10, T4B21_10	2.6	2.6	0.0	0.0	100.0%	-4.9
20896	AT5G18370.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:6085038-6088928 REVERSE   Aliases: F20L16.90, F20L16_90	2.7	2.7	-0.0	-0.0	100.0%	-5.4
20897	AT4G15020.1   expressed protein, contains Pfam profile PF04937: Protein of unknown function (DUF 659)   chr4:8575647-8578682 FORWARD   Aliases: DL3551W, FCAALL.174	3.0	3.0	-0.0	-0.0	100.0%	-5.3
20898	AT2G47240.2   similar to long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase, putative [Arabidopsis thaliana] (TAIR:At1g64400.1); similar to long-chain-fatty-acid--CoA ligase / long-chain acyl-CoA synthetase [Arabidopsis thaliana] (TAIR:At4g23850.1); similar to long-chain-fatty-acid--CoA ligase, putative / long-chain acyl-CoA synthetase, putative [Arabidopsis thaliana] (TAIR:At4g11030.1); similar to putative acyl-CoA synthetase [Oryza sativa (japonica cultivar-group)] (GB:BAD73757.1); contains InterPro domain AMP-dependent synthetase and ligase (InterPro:IPR000873)   chr2:19400654-19404901 FORWARD   Aliases: T8I13.8	2.9	2.9	0.0	0.0	100.0%	-5.5
20899	AT4G29130.1   Symbol: ATHXK1	7.9	7.9	0.0	0.0	100.0%	-4.7
20900	AT3G32180.1   expressed protein   chr3:13166126-13166495 REVERSE   Aliases: F6H5.2	2.8	2.8	0.0	0.0	100.0%	-5.5
20901	AT1G71970.1   expressed protein   chr1:27096690-27097689 FORWARD   Aliases: F17M19.12, F17M19_12	4.6	4.6	-0.0	-0.0	100.0%	-4.7
20902	AT3G22460.1   cysteine synthase, putative / O-acetylserine (thiol)-lyase, putative / O-acetylserine sulfhydrylase, putative, nearly identical over 185 amino acids to SP:P47998 Cysteine synthase (EC 4.2.99.8) (O-acetylserine sulfhydrylase) (O-acetylserine (Thiol)-lyase) {Arabidopsis thaliana}   chr3:7963544-7965914 FORWARD   Aliases: F16J14.18	5.6	5.6	-0.0	-0.0	100.0%	-4.6
20903	AT4G01080.1   expressed protein   chr4:466391-468293 REVERSE   Aliases: F2N1.14, F2N1_14	3.8	3.8	0.0	0.0	100.0%	-4.8
20904	AT4G17570.1   zinc finger (GATA type) family protein   chr4:9783897-9787433 REVERSE   Aliases: DL4820C, FCAALL.45	4.6	4.6	-0.0	-0.0	100.0%	-5.3
20905	AT3G26160.1   Symbol: CYP71B17   cytochrome P450 family protein, similar to cytochrome P450 GB:O65784 (Arabidopsis thaliana)   chr3:9569517-9571123 REVERSE   Aliases: MTC11.7	3.2	3.2	-0.0	-0.0	100.0%	-5.2
20906	AT4G13320.1   expressed protein   chr4:7753307-7754082 FORWARD   Aliases: T9E8.60, T9E8_60	2.7	2.7	-0.0	-0.0	100.0%	-5.5
20907	AT3G01490.1   protein kinase, putative, similar to ATMRK1 (Arabidopsis thaliana) gi:2351097:dbj:BAA22079   chr3:190879-193544 REVERSE   Aliases: F4P13.4, F4P13_4	2.8	2.8	0.0	0.0	100.0%	-5.3
20908	AT2G36440.1   expressed protein   chr2:15299727-15299951 FORWARD   Aliases: F1O11.7, F1O11_7	2.8	2.8	-0.0	-0.0	100.0%	-5.6
20909	AT2G22370.1   expressed protein   chr2:9507895-9509269 REVERSE   Aliases: F14M13.23, F14M13_23	6.8	6.8	-0.0	-0.0	100.0%	-5.0
20910	AT3G13510.1   expressed protein, Pfam profile PF03080: Arabidopsis proteins of unknown function   chr3:4403516-4406098 FORWARD   Aliases: MRP15.17	3.6	3.6	0.0	0.0	100.0%	-5.2
20911	AT2G16820.1   hypothetical protein   chr2:7297186-7298034 REVERSE   Aliases: T24I21.23, T24I21_23	2.9	2.9	0.0	0.0	100.0%	-5.8



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20912	AT3G23610.1   dual specificity protein phosphatase (DsPTP1), identical to DsPTP1 protein GI:4150963 from (Arabidopsis thaliana); contains Pfam profile: PF00782 dual specificity phosphatase, catalytic domain	5.9	5.9	-0.0	-0.0	100.0%	-4.9
20913	AT5G64440.1   amidase family protein, low similarity to enantiomerase-selective amidase (Rhodococcus sp.) GI:152052; contains Pfam profile PF01425: Amidase   chr5:25782985-25787673 FORWARD   Aliases: T12B11.3, T12B11_3	6.5	6.5	-0.0	-0.0	100.0%	-4.8
20914	AT5G36650.1   hypothetical protein   chr5:14397498-14397974 REVERSE   Aliases: F24C7.1, F24C7_1	3.3	3.3	-0.0	-0.0	100.0%	-4.2
20915	AT2G11490.1   hypothetical protein   chr2:4611375-4612042 FORWARD   Aliases: F14P14.18, F14P14_18	2.3	2.3	0.0	0.0	100.0%	-5.2
20916	AT4G24730.2   calcineurin-like phosphoesterase family protein, contains Pfam profile: PF00149 calcineurin-like phosphoesterase	6.1	6.1	0.0	0.0	100.0%	-5.0
20917	AT3G11550.1   integral membrane family protein, similar to unknown protein GB:AAD26967 (Arabidopsis thaliana); contains TIGRFAM TIGR01569 : plant integral membrane protein TIGR01569; contains Pfam PF04535 : Domain of unknown function (DUF588)   chr3:3638201-3639203 FORWARD   Aliases: F24K9.22	3.2	3.2	0.0	0.0	100.0%	-4.2
20918	AT5G46020.1   expressed protein   chr5:18680104-18682054 REVERSE   Aliases: MCL19.6, MCL19_6	10.6	10.6	0.0	0.0	100.0%	-5.0
20919	AT3G54580.1   proline-rich extensin-like family protein, contains proline-rich extensin domains, INTERPRO:IPR002965   chr3:20211666-20214760 REVERSE   Aliases: T14E10.150	3.0	3.0	0.0	0.0	100.0%	-4.9
20920	AT5G08080.2   Symbol: SYP132	8.5	8.5	-0.0	-0.0	100.0%	-5.2
20921	AT4G37060.1   patatin, putative, similar to patatin-like latex allergen (Hevea brasiliensis)(PMID:10589016); contains patatin domain PF01734   chr4:17461567-17463728 REVERSE   Aliases: AP22.93, AP22_93	2.9	2.9	-0.0	-0.0	100.0%	-4.9
20922	AT4G37070.3   similar to patatin, putative [Arabidopsis thaliana] (TAIR:At4g37060.1); similar to putative patatin homolog [Oryza sativa (japonica cultivar-group)] (GB:BAD38550.1); contains InterPro domain Patatin (InterPro:IPR002641)   chr4:17464797-17467103 REVERSE   Aliases: AP22.83, AP22_83	2.9	2.9	-0.0	-0.0	100.0%	-4.9
20923	AT5G04710.1   aspartyl aminopeptidase, putative, similar to SP:Q9ULA0 Aspartyl aminopeptidase (EC 3.4.11.21) {Homo sapiens}; contains Pfam profile PF02127: Aminopeptidase I zinc metalloprotease (M18)   chr5:1356991-1360248 REVERSE   Aliases: MUK11.9	5.6	5.6	0.0	0.0	100.0%	-5.0
20924	AT4G23030.1   MATE efflux protein-related, contains Pfam profile PF01554: Uncharacterized membrane protein family   chr4:12072868-12074376 FORWARD   Aliases: F7H19.220, F7H19_220	3.2	3.2	-0.0	-0.0	100.0%	-5.4
20925	AT1G66150.1   Symbol: TMK1   leucine-rich repeat protein kinase, putative (TMK1), identical to protein kinase TMK1 gi:166888:gb:AAA32876, SP:P43298 Putative receptor protein kinase TMK1 precursor (EC 2.7.1.-) {Arabidopsis thaliana}   chr1:24635072-24638412 FORWARD   Aliases: F15E12.4, F15E12_4, TRANSMEMBRANE KINASE 1	3.0	3.0	0.0	0.0	100.0%	-4.6
20926	AT5G60090.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:24213308-24214951 REVERSE   Aliases: MGO3.7, MGO3_7	3.1	3.1	0.0	0.0	100.0%	-5.2
20927	AT4G10840.2   kinesin light chain-related, low similarity to kinesin light chain (Plectonema boryanum) GI:2645229; contains Pfam profile PF00515 TPR Domain   chr4:6656512-6659252 FORWARD   Aliases: F25I24.50, F25I24_50	10.0	10.0	0.0	0.0	100.0%	-5.3
20928	AT5G61580.2   similar to phosphofructokinase family protein [Arabidopsis thaliana] (TAIR:At5g56630.1); similar to phosphofructokinase family protein [Arabidopsis thaliana] (TAIR:At4g26270.1); similar to phosphofructokinase family protein [Arabidopsis thaliana] (TAIR:At4g32840.1); similar to putative pyrophosphate--fructose-6-phosphate1 phosphotransferase [Oryza sativa (japonica cultivar-group)] (GB:NP_916022.1); similar to putative pyrophosphate-dependent phosphofructo-1-kinase [Oryza sativa (japonica cultivar-group)] (GB:NP_914558.1); similar to putative pyrophosphate-dependent phosphofructo-1-kinase [Oryza sativa (japonica cultivar-group)] (GB:BAD87031.1); similar to putative pyrophosphate-fructose-6-phosphate-1-phosphotransferase [Oryza sativa (japonica cultivar-group)] (GB:AAU10835.1); similar to putative diphosphate-fructose-6-phosphate 1-phosphotransferase [Oryza sativa (japonica cultivar-group)] (GB:AAV44044.1); contains InterPro domain Phosphofructokinase (InterPro:IPR000023)   chr5:24778317-24781240 FORWARD   Aliases: K11J9.3, K11J9_3	6.9	6.9	0.0	0.0	100.0%	-5.1
20929	AT3G21280.1   Symbol: UBP7   ubiquitin-specific protease 7, putative (UBP7), similar to GI:11993467   chr3:7477993-7482076 REVERSE   Aliases: MXL8.15, UBIQUITIN SPECIFIC PROTEASE 7	6.0	6.0	-0.0	-0.0	100.0%	-5.1
20930	AT2G30900.1   expressed protein   chr2:13157561-13159494 FORWARD   Aliases: F7F1.11, F7F1_11	3.6	3.6	-0.0	-0.0	100.0%	-4.7
20931	AT3G14240.1   subtilase family protein, contains similarity to SBT1 GI:1771160 from (Lycopersicon esculentum)   chr3:4741480-4744124 REVERSE   Aliases: MLN21.2	6.8	6.8	0.0	0.0	100.0%	-4.9

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20932	AT1G75550.1   glycine-rich protein   chr1:28373098-28373601 REVERSE   Aliases: F10A5.23, F10A5_23	3.6	3.6	-0.0	-0.0	100.0%	-5.1
20933	AT4G05170.1   similar to ethylene-responsive protein-related [Arabidopsis thaliana] (TAIR:At4g21340.1); similar to bHLH transcription factor-like protein [Oryza sativa (japonica cultivar-group)] (GB:BAD53363.1); contains InterPro domain Basic helix-loop-helix dimerization domain bHLH (InterPro:IPR001092)   chr4:2667988-2669362 REVERSE   Aliases: C17L7.90, C17L7_90	2.3	2.3	0.0	0.0	100.0%	-4.2
20934	AT5G47880.2   Symbol: ERF1 1	6.8	6.8	0.0	0.0	100.0%	-5.0
20935	AT4G27585.1   band 7 family protein, similar to stomatin-like protein (Zea mays) GI:7716464; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr4:13766769-13769967 REVERSE   Aliases: None	4.8	4.8	0.0	0.0	100.0%	-4.2
20936	AT5G54100.1   band 7 family protein, similar to stomatin-like protein (Zea mays) GI:7716464; contains Pfam profile PF01145: SPFH domain / Band 7 family   chr5:21971013-21973768 REVERSE   Aliases: MJP23.8, MJP23_8	4.8	4.8	0.0	0.0	100.0%	-4.2
20937	AT5G06480.1   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain   chr5:1976087-1977291 REVERSE   Aliases: F15M7.1, F15M7_1	3.5	3.5	-0.0	-0.0	100.0%	-5.1
20938	AT3G20090.1   Symbol: CYP705A18   cytochrome P450 family protein, similar to Cytochrome P450 93A3 (P450 CP5) (SP:O81973) {Glycine max}; contains Pfam profile: PF00067 cytochrome P450   chr3:7015803-7018366 FORWARD   Aliases: MAL21.13	3.2	3.2	0.0	0.0	100.0%	-5.2
20939	AT4G20790.1   leucine-rich repeat family protein, contains leucine rich repeat (LRR) domains, Pfam:PF00560;   chr4:11134786-11136434 REVERSE   Aliases: F21C20.140, F21C20_140	2.3	2.3	0.0	0.0	100.0%	-6.0
20940	AT1G61710.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.6	2.6	0.0	0.0	100.0%	-5.7
20941	AT4G29540.2   similar to bacterial transferase hexapeptide repeat-containing protein [Arabidopsis thaliana] (TAIR:At4g05210.1); similar to UDP-acetylglucosamine acyltransferase [Acinetobacter sp. ADP1] (GB:YP_046070.1); contains InterPro domain Bacterial transferase hexapeptide repeat (InterPro:IPR001451)   chr4:14497735-14499939 FORWARD   Aliases: T16L4.50, T16L4_50	3.8	3.8	-0.0	-0.0	100.0%	-5.0
20942	AT5G58620.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar) and Pfam domain, PF00023: Ankyrin repeat   chr5:23710566-23713448 FORWARD   Aliases: MZN1.16, MZN1_16	3.7	3.7	0.0	0.0	100.0%	-4.8
20943	AT1G80810.1   expressed protein, similar to androgen-induced prostate proliferative shutoff associated protein (GI:4559410) (Homo sapiens); similar to bimD (GI:168025) (Emericella nidulans)   chr1:30370074-30373790 FORWARD   Aliases: F23A5.16, F23A5_16	5.9	5.9	-0.0	-0.0	100.0%	-4.8
20944	AT4G09100.1   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr4:5811253-5811651 FORWARD   Aliases: T8A17.4	3.3	3.3	0.0	0.0	100.0%	-4.4
20945	AT5G60010.1   ferric reductase-like transmembrane component family protein, similar to respiratory burst oxidase protein D RbohD from Arabidopsis thaliana, EMBL:AF055357 (gi:3242789), respiratory burst oxidase homolog from Solanum tuberosum (GI:16549089); contains Pfam profile PF01794 Ferric reductase like transmembrane component   chr5:24177682-24181631 FORWARD   Aliases: MMN10.18, MMN10_18	2.7	2.7	0.0	0.0	100.0%	-5.5
20946	AT3G43290.1   hypothetical protein, glyceraldehyde-3-phosphate dehydrogenase, Equus caballus, EMBL:AF097179   chr3:15241556-15242103 FORWARD   Aliases: F7K15.140	3.3	3.3	-0.0	-0.0	100.0%	-5.0
20947	AT5G58940.1   Symbol: CRCK1   similar to protein kinase family protein [Arabidopsis thaliana] (TAIR:At4g00330.1); similar to P0529H11.30 [Oryza sativa (japonica cultivar-group)] (GB:NP_915524.1); contains InterPro domain Serine/threonine protein kinase, active site (InterPro:IPR008271); contains InterPro domain Tyrosine protein kinase (InterPro:IPR001245); contains InterPro domain Serine/threonine protein kinase (InterPro:IPR002290); contains InterPro domain Protein kinase (InterPro:IPR000719)   chr5:23815812-23818049 FORWARD   Aliases: CALMODULIN BINDING RECEPTOR LIKE CYTOPLASMIC KINASE 1, K19M22.13, K19M22_13	3.5	3.5	-0.0	-0.0	100.0%	-4.6
20948	AT5G61050.1   histone deacetylase-related / HD-related	2.6	2.6	0.0	0.0	100.0%	-5.4
20949	AT5G55350.1   membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related, contains similarity to wax synthase wax synthase - Simmondsia chinensis, PID:g5020219 similar to wax synthase (gi:5020219) from Simmondsia chinensis   chr5:22459582-22460619 REVERSE   Aliases: MTE17.6, MTE17_6	3.1	3.1	-0.0	-0.0	100.0%	-5.8
20950	AT2G36850.1   Symbol: ATGSL08   glycosyl transferase family 48 protein, contains Pfam profile: PF02364 1,3-beta-glucan synthase   chr2:15461776-15476446 REVERSE   Aliases: ATGSL8, GLUCAN SYNTHASE LIKE 8, GSL08, T1J8.3, T1J8_3	8.2	8.2	-0.0	-0.0	100.0%	-5.0
20951	AT4G23090.1   expressed protein   chr4:12100566-12101491 REVERSE   Aliases: F7H19.280, F7H19_280	3.1	3.1	-0.0	-0.0	100.0%	-5.0

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20952	AT3G56550.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr3:20963875-20965620 REVERSE   Aliases: T5P19.200	2.7	2.7	-0.0	-0.0	100.0%	-5.7
20953	AT1G75670.2   expressed protein, similar to DNA-dependent RNA polymerase 19 kDa polypeptide (EC 2.7.7.6) (A43) (Swiss-Prot:O43036) (Schizosaccharomyces pombe)	6.3	6.3	-0.0	-0.0	100.0%	-4.5
20954	AT4G04340.3   early-responsive to dehydration protein-related / ERD protein-related, similar to ERD4 protein (early-responsive to dehydration stress) (Arabidopsis thaliana) GI:15375406; contains Pfam profile PF02714: Domain of unknown function DUF221   chr4:2122686-2126842 FORWARD   Aliases: T19B17.6, T19B17_6	4.8	4.8	-0.0	-0.0	100.0%	-4.9
20955	AT5G45420.1   myb family transcription factor, contains Pfam profile: PF00249 Myb DNA binding domain   chr5:18421296-18423833 REVERSE   Aliases: MFC19.9, MFC19_9	5.4	5.4	-0.0	-0.0	100.0%	-4.6
20956	AT2G28110.1   Encodes a protein with similarity to glycosyl transferase family 47 proteins that is involved in secondary cell wall biosynthesis. Mutants have irregular xylem formation, reduced cellulose levels and plants are smaller than normal siblings.	3.1	3.1	0.0	0.0	100.0%	-4.4
20957	AT3G15410.1   leucine-rich repeat family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; contains similarity to Hcr2-5D (Lycopersicon esculentum) gi:3894393:gb:AAC78596; identical to leucine-rich repeat protein (Arabidopsis thaliana) gi:2760084:emb:CAA76000   chr3:5203300-5207519 FORWARD   Aliases: MJK13.7	4.7	4.7	0.0	0.0	100.0%	-4.9
20958	AT1G10420.1   expressed protein   chr1:3426978-3427458 REVERSE   Aliases: T10O24.3, T10O24_3	3.0	3.0	-0.0	-0.0	100.0%	-5.4
20959	AT5G35760.1   expressed protein, ; expression supported by MPSS   chr5:13951338-13952012 FORWARD   Aliases: MXH1.19, MXH1_19	2.2	2.2	-0.0	-0.0	100.0%	-5.9
20960	AT2G45430.1   DNA-binding protein-related, contains Pfam domain PF03479: Domain of unknown function (DUF296), found in AT-hook motifs Pfam:PF02178   chr2:18734635-18736009 FORWARD   Aliases: F4L23.6	5.3	5.3	-0.0	-0.0	100.0%	-4.7
20961	AT1G24650.1   leucine-rich repeat family protein / protein kinase family protein, contains Pfam domains PF00560: Leucine Rich Repeat and PF00069: Protein kinase domain   chr1:8734556-8737301 FORWARD   Aliases: F5A9.23	2.8	2.8	-0.0	-0.0	100.0%	-5.5
20962	AT5G14930.2   Symbol: SAG101	3.9	3.9	0.0	0.0	100.0%	-4.7
20963	AT4G33900.1   kelch repeat-containing F-box family protein, contains F-box domain Pfam:PF00646 and Kelch motif Pfam:PF01344   chr4:16251577-16252716 REVERSE   Aliases: F17I5.90, F17I5_90	3.0	3.0	0.0	0.0	100.0%	-5.6
20964	AT1G73190.1   tonoplast intrinsic protein, alpha / alpha-TIP (TIP3.1), identical to SP:P26587 Tonoplast intrinsic protein, alpha (Alpha TIP) (Arabidopsis thaliana) (Plant Physiol. 99, 561-570 (1992))   chr1:27525607-27527428 FORWARD   Aliases: T18K17.14, T18K17_14	2.5	2.5	0.0	0.0	100.0%	-5.3
20965	AT4G27620.2   expressed protein   chr4:13788827-13790964 REVERSE   Aliases: T29A15.110, T29A15_110	3.4	3.5	-0.0	-0.0	100.0%	-5.4
20966	AT1G59520.3   Symbol: CW7   expressed protein (CW7)   chr1:21865049-21869855 FORWARD   Aliases: CW7, T30E16.4, T30E16_4	5.5	5.5	0.0	0.0	100.0%	-4.9
20967	AT1G08740.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g21020, At3g26530, At1g08760, At2g29240, At1g35650, At1g21030   chr1:2795646-2800084 REVERSE   Aliases: F22O13.23, F22O13_23	2.5	2.5	-0.0	-0.0	100.0%	-5.4
20968	AT1G21020.1   expressed protein, similar to At3g26530, At1g08760, At1g08740, At2g29240, At1g35650   chr1:7353529-7356589 FORWARD   Aliases: T22I11.15, T22I11_15	2.5	2.5	-0.0	-0.0	100.0%	-5.4
20969	AT2G29240.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g21020, At3g26530, At1g08760, At1g08740, At1g35650, At1g21030   chr2:12580448-12584889 REVERSE   Aliases: F16P2.38, F16P2_38	2.5	2.5	-0.0	-0.0	100.0%	-5.4
20970	AT3G26530.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g21020, At1g08760, At1g08740, At2g29240, At1g35650	2.5	2.5	-0.0	-0.0	100.0%	-5.4
20971	AT5G44890.1   Ulp1 protease family protein, contains Pfam profile PF02902: Ulp1 protease family, C-terminal catalytic domain; similar to At1g21030, At2g29240, At1g08740, At1g08760   chr5:18143911-18148352 REVERSE   Aliases: K21C13.7	2.5	2.5	-0.0	-0.0	100.0%	-5.4
20972	AT1G32180.1   Symbol: ATCSLD6   cellulose synthase family protein, similar to cellulose synthase catalytic subunit gi:2827143 from (Arabidopsis thaliana), cellulose synthase-9 (gi:9622890) from Zea mays   chr1:11586496-11589631 REVERSE   Aliases: CSLD6, F3C3.4, F3C3_4	2.8	2.8	-0.0	-0.0	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20973	AT3G57920.1   squamosa promoter-binding protein, putative, similar to squamosa promoter binding protein-like 9 (Arabidopsis thaliana) GI:5931677; contains Pfam profile PF03110: SBP domain   chr3:21455298-21456952 REVERSE   Aliases: T10K17.130	3.0	3.0	0.0	0.0	100.0%	-5.6
20974	AT1G14140.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr1:4837924-4839630 REVERSE   Aliases: F7A19.22, F7A19_22	6.0	6.0	0.0	0.0	100.0%	-4.8
20975	AT2G02340.1   Symbol: ATPP2 B8   F-box family protein / SKP1 interacting partner 3-related, contains similarity to SKP1 interacting partner 3 GI:10716951 from (Arabidopsis thaliana)	3.1	3.1	-0.0	-0.0	100.0%	-5.4
20976	AT4G10670.1   Symbol: GTC2   transcription elongation factor-related, low similarity to chromatin-specific transcription elongation factor FACT 140 kDa subunit (Homo sapiens) GI:5499741   chr4:6584723-6586258 FORWARD   Aliases: GLOBAL TRANSCRIPTION FACTOR GROUP C, T4F9.130, T4F9_130	3.6	3.6	0.0	0.0	100.0%	-4.9
20977	AT4G15350.1   Symbol: CYP705A2   cytochrome P450 family protein, contains Pfam profile: PF00067 cytochrome P450   chr4:8762953-8764594 FORWARD   Aliases: DL3720W, FCAALL.274	2.7	2.7	-0.0	-0.0	100.0%	-5.7
20978	AT4G15870.1   Symbol: ATTS1   terpene synthase/cyclase family protein	2.8	2.8	-0.0	-0.0	100.0%	-5.3
20979	AT3G18650.1   MADS-box family protein, contains similarity to hypothetical proteins of (Arabidopsis thaliana)   chr3:6417350-6418510 REVERSE   Aliases: MVE11.1	2.6	2.6	-0.0	-0.0	100.0%	-5.4
20980	AT1G30650.1   Symbol: WRKY14	2.4	2.4	-0.0	-0.0	100.0%	-4.4
20981	AT3G21860.1   Symbol: ASK10   E3 ubiquitin ligase SCF complex subunit SKP1/ASK1 (At10), putative, E3 ubiquitin ligase; similar to Skp1 homolog Skp1b GI:3068809, UIP2 GI:3719211 from (Arabidopsis thaliana)   chr3:7699784-7700242 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 10, ASK10, MSD21.23	2.4	2.4	0.0	0.0	100.0%	-6.0
20982	AT3G57390.2   Symbol: AGL18   MADS-box protein (AGL18), agamous-like protein 15 - Arabidopsis thaliana, PIR:S71200   chr3:21244693-21246884 FORWARD   Aliases: F28O9.240	5.6	5.6	0.0	0.0	100.0%	-5.1
20983	AT5G63010.1   WD-40 repeat family protein, contains 4 WD-40 repeats (PF00400);low similarity to photomorphogenesis repressor (COP1) GI:2702280 (Arabidopsis thaliana) and COP1 GI:11127996 (Ipomoea nil)   chr5:25298940-25300402 FORWARD   Aliases: MJH22.7, MJH22_7	5.5	5.5	-0.0	-0.0	100.0%	-5.3
20984	AT3G10670.1   Symbol: ATNAP7	9.3	9.3	-0.0	-0.0	100.0%	-4.7
20985	AT3G07480.1   expressed protein   chr3:2388958-2389817 FORWARD   Aliases: F21O3.19	8.7	8.7	0.0	0.0	100.0%	-4.7
20986	AT3G46810.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	2.8	2.8	0.0	0.0	100.0%	-5.2
20987	AT5G48770.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:19790503-19794468 REVERSE   Aliases: K24G6.10, K24G6_10	2.2	2.2	-0.0	-0.0	100.0%	-5.6
20988	AT1G65130.1   ubiquitin carboxyl-terminal hydrolase-related, contains Pfam profiles PF00443: Ubiquitin carboxyl-terminal hydrolase, PF04780: Protein of unknown function (DUF629), PF04781: Protein of unknown function (DUF627)   chr1:24200135-24204685 REVERSE   Aliases: T23K8.4, T23K8_4	3.2	3.2	0.0	0.0	100.0%	-5.4
20989	AT5G18940.2   Mo25 family protein, similar to SP:Q06138 MO25 protein {Mus musculus}; contains Pfam profile PF03204: Mo25 protein family   chr5:6325788-6328354 FORWARD   Aliases: F17K4.190, F17K4_190	5.4	5.4	0.0	0.0	100.0%	-4.9
20990	AT1G73120.1   expressed protein   chr1:27500847-27501611 REVERSE   Aliases: T18K17.22, T18K17_22	3.8	3.9	-0.0	-0.0	100.0%	-4.4
20991	AT2G37150.2   zinc finger (C3HC4-type RING finger) family protein, contains Pfam profile: PF00097 zinc finger, C3HC4 type (RING finger)   chr2:15610663-15615497 REVERSE   Aliases: T2N18.9, T2N18_9	3.1	3.1	-0.0	-0.0	100.0%	-5.2
20992	AT5G07630.1   nuclear division RFT family protein, low similarity to SP:P38206 Nuclear division RFT1 protein {Saccharomyces cerevisiae}; contains Pfam profile PF04506: Rft protein   chr5:2412033-2414524 FORWARD   Aliases: MBK20.7, MBK20_7	2.4	2.4	0.0	0.0	100.0%	-5.6
20993	AT4G11000.1   ankyrin repeat family protein, contains ankyrin repeats, Pfam:PF00023   chr4:6731016-6732460 FORWARD   Aliases: T22B4.2	2.9	2.9	-0.0	-0.0	100.0%	-5.1
20994	AT2G14680.1   myosin heavy chain-related, contains weak similarity to Swiss-Prot:P35579 myosin heavy chain, nonmuscle type A (Cellular myosin heavy chain, type A, Nonmuscle myosin heavy chain-A, NMMHC-A) (Homo sapiens)   chr2:6285338-6290998 FORWARD   Aliases: T6B13.8, T6B13_8	5.8	5.8	0.0	0.0	100.0%	-4.9
20995	AT2G20370.1   Symbol: MUR3   exostosin family protein, contains Pfam profile: PF03016	5.6	5.6	-0.0	-0.0	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
20996	AT5G40580.2   Symbol: PBB2   20S proteasome beta subunit B (PBB2) (PRCFC), identical to 20S proteasome beta subunit PBB2 (Arabidopsis thaliana) GI:3421104, cDNA proteasome subunit prcfc GI:2511575   chr5:16265537-16268093 REVERSE   Aliases: 20S PROTEASOME BETA SUBUNIT PBB2, MNF13.100, MNF13_100	8.3	8.3	0.0	0.0	100.0%	-4.7
20997	AT4G35590.1   RWP-RK domain-containing protein, low similarity to minus dominance protein (Chlamydomonas reinhardtii) GI:1928929; contains Pfam profile: PF02042 RWP-RK domain	3.0	3.0	-0.0	-0.0	100.0%	-5.7
20998	AT5G47340.1   palmitoyl protein thioesterase family protein   chr5:19226734-19228361 FORWARD   Aliases: MQL5.20, MQL5_20	2.6	2.6	-0.0	-0.0	100.0%	-5.5
20999	AT3G23310.1   protein kinase, putative, contains protein kinase domain, Pfam:PF00069   chr3:8339044-8343639 FORWARD   Aliases: MLM24.2	4.6	4.6	0.0	0.0	100.0%	-5.0
21000	AT3G25650.1   Symbol: ASK15   Skp1 family protein, similar to Skp1 (Medicago sativa) GI:4959710, fimbriata-associated protein (Antirrhinum majus) GI:2673870, UIP2 (Arabidopsis thaliana) GI:3719211; contains Pfam profile PF01466: Skp1 family, dimerisation domain   chr3:9337113-9337696 REVERSE   Aliases: ARABIDOPSIS SKP1 LIKE 15, ASK15, T5M7.16	2.7	2.7	-0.0	-0.0	100.0%	-5.4
21001	AT1G29500.1   auxin-responsive protein, putative, similar to auxin-induced protein 6B (SP:P33083) (Glycine max)   chr1:10321196-10321850 FORWARD   Aliases: F15D2.8, F15D2_8	2.8	2.8	0.0	0.0	100.0%	-5.5
21002	AT5G13160.1   Symbol: PBS1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:4176584-4179888 FORWARD   Aliases: AVRPPHB SUSCEPTIBLE 1, T19L5.120, T19L5_120	6.6	6.6	-0.0	-0.0	100.0%	-4.9
21003	AT3G10720.2   pectinesterase, putative, contains similarity to pectinesterase from Vitis vinifera GI:15081598, Prunus persica SP:Q43062; contains Pfam profile PF01095 pectinesterase   chr3:3354487-3357619 REVERSE   Aliases: T7M13.20	2.5	2.5	0.0	0.0	100.0%	-5.5
21004	AT1G21312.1   RNA recognition motif (RRM)-containing protein, contains Pfam profile PF00076: RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain   chr1:7462822-7463926 REVERSE   Aliases: None	2.9	2.9	0.0	0.0	100.0%	-5.1
21005	AT1G30350.1   pectate lyase family protein, similar to pectate lyase GP:14289169 from (Salix gilgiana); contains Pfam profile: PF00544: Pectate lyase   chr1:10710176-10711646 REVERSE   Aliases: T4K22.5, T4K22_5	2.5	2.5	-0.0	-0.0	100.0%	-5.8
21006	AT1G76500.1   DNA-binding family protein, contains Pfam domain, PF02178: AT hook motif	4.9	4.9	0.0	0.0	100.0%	-5.3
21007	AT5G41260.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr5:16521140-16524703 FORWARD   Aliases: K1O13.5, K1O13_5	3.2	3.2	-0.0	-0.0	100.0%	-5.0
21008	AT1G24180.1   Symbol: IAR4   pyruvate dehydrogenase E1 component alpha subunit, mitochondrial, putative, similar to SP:P52901 Pyruvate dehydrogenase E1 component alpha subunit, mitochondrial precursor (EC 1.2.4.1) (PDHE1-A) {Arabidopsis thaliana}; contains Pfam profile PF00676: Dehydrogenase E1 component   chr1:8560519-8563484 REVERSE   Aliases: F3I6.11, F3I6_11	10.4	10.4	-0.0	-0.0	100.0%	-5.1
21009	AT1G34500.1   membrane bound O-acyl transferase (MBOAT) family protein / wax synthase-related, similar to wax synthase (Simmondsia chinensis) GI:5020219; contains Pfam profile PF03062: MBOAT family   chr1:12611616-12612641 FORWARD   Aliases: F12K21.19, F12K21_19	3.3	3.3	-0.0	-0.0	100.0%	-5.1
21010	AT5G40170.1   disease resistance family protein, contains leucine rich-repeat (LRR) domains Pfam:PF00560, INTERPRO:IPR001611; similar to Cf-4 (Lycopersicon hirsutum) gi:2808683:emb:CAA05268   chr5:16082319-16084802 REVERSE   Aliases: MSN9.70, MSN9_70	4.7	4.7	0.0	0.0	100.0%	-4.6
21011	AT1G03790.1   zinc finger (CCCH-type) family protein, contains Pfam domain, PF00642: Zinc finger C-x8-C-x5-C-x3-H type (and similar)   chr1:954524-956096 FORWARD   Aliases: F21M11.30, F21M11_30	2.9	2.9	-0.0	-0.0	100.0%	-5.3
21012	AT1G16160.1   Symbol: WAKL5   protein kinase family protein, contains similarity to wall-associated kinase 4 GI:3355308 from (Arabidopsis thaliana)   chr1:5535967-5538263 FORWARD   Aliases: T24D18.24, T24D18_24, WALL ASSOCIATED KINASE LIKE 5	2.8	2.8	0.0	0.0	100.0%	-5.3
21013	AT1G22670.1   protease-associated zinc finger (C3HC4-type RING finger) family protein, contains Pfam domain, PF02225: protease-associated (PA) domain and Pfam domain, PF00097: Zinc finger, C3HC4 type (RING finger); similar to ReMembr-H2 protein JR702 (Arabidopsis thaliana) gi:6942149:gb:AAF32326   chr1:8021843-8023505 REVERSE   Aliases: T22J18.16, T22J18_16	2.2	2.2	-0.0	-0.0	100.0%	-6.1
21014	AT3G58890.1   syntaxin-related family protein, contains a novel domain similar to F-box that is shared among other proteins in Arabidopsis; similar to proteins At3g59270, At1g56610, At3g54160, At1g47920 (syntaxin SYP81),, At5g41830, At3g44180, At1g48390 (Arabidopsis thaliana)   chr3:21782023-21783554 FORWARD   Aliases: T20N10.240	3.2	3.2	0.0	0.0	100.0%	-5.3

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
21015	AT5G65780.1   branched-chain amino acid aminotransferase 5 / branched-chain amino acid transaminase 5 (BCAT5), nearly identical to SP:Q9FYA6 Branched-chain amino acid aminotransferase 5, chloroplast precursor (EC 2.6.1.42) (Atbcat-5) {Arabidopsis thaliana}; contains Pfam profile: PF01063 aminotransferase class IV   chr5:26332616-26335980 FORWARD   Aliases: MPA24.13, MPA24_13	9.5	9.5	-0.0	-0.0	100.0%	-4.7
21016	AT3G10650.1   expressed protein   chr3:3325175-3330897 REVERSE   Aliases: F13M14.6	3.4	3.4	0.0	0.0	100.0%	-5.0
21017	AT4G28250.1   Symbol: ATEXPB3   beta-expansin, putative (EXPB3), similar to soybean pollen allergen (cim1) protein - soybean, PIR2:S48032; beta-expansin gene family, PMID:11641069   chr4:14000044-14002047 REVERSE   Aliases: ARABIDOPSIS THALIANA EXPANSIN B3, ATHEXP BETA 1.6, EXPB3, F26K10.130, F26K10_130	6.4	6.4	-0.0	-0.0	100.0%	-4.5
21018	AT3G59990.3   Symbol: MAP2B   similar to methionyl aminopeptidase, putative / methionine aminopeptidase, putative / peptidase M, putative [Arabidopsis thaliana] (TAIR:At2g44180.1); similar to Metap2-prov protein [Xenopus laevis] (GB:AAH43889.1); contains InterPro domain Methionine aminopeptidase, subfamily 2 (InterPro:IPR002468); contains InterPro domain Metallopeptidase family M24 (InterPro:IPR000994); contains InterPro domain Methionine aminopeptidase (InterPro:IPR001714)   chr3:22166696-22169702 REVERSE   Aliases: F24G16.260, METHIONINE AMINOPEPTIDASE 2B	7.9	7.9	0.0	0.0	100.0%	-4.8
21019	AT5G22700.1   F-box family protein, contains F-box domain Pfam:PF00646	3.5	3.5	-0.0	-0.0	100.0%	-5.3
21020	AT4G17510.1   ubiquitin carboxyl-terminal hydrolase, putative / ubiquitin thiolesterase, putative, similar to SP:Q9JKB1 Ubiquitin carboxyl-terminal hydrolase isozyme L3 (EC 3.4.19.12) (UCH- L3) (Ubiquitin thiolesterase L3) {Mus musculus}; contains Pfam profile PF01088: Ubiquitin carboxyl-terminal hydrolase, family 1   chr4:9766984-9768783 REVERSE   Aliases: DL4790C, FCAALL.31	7.9	7.9	-0.0	-0.0	100.0%	-4.7
21021	AT1G24210.1   paired amphipathic helix repeat-containing protein, similar to transcriptional repressor SIN3B (Mus musculus) GI:2921547; contains Pfam profile PF02671: Paired amphipathic helix repeat	3.8	3.8	0.0	0.0	100.0%	-4.8
21022	AT4G02220.1   zinc finger (MYND type) family protein / programmed cell death 2 C-terminal domain-containing protein, similar to SP:Q16342 Programmed cell death protein 2 (Zinc finger protein Rp-8) {Homo sapiens}; contains Pfam profiles PF01753: MYND finger, PF04194: Programmed cell death protein 2, C-terminal putative domain	5.8	5.8	0.0	0.0	100.0%	-4.8
21023	AT4G27790.1   calcium-binding EF hand family protein, contains INTERPRO:IPR002048 calcium-binding EF-hand domain   chr4:13850052-13851539 FORWARD   Aliases: T27E11.30, T27E11_30	2.3	2.3	0.0	0.0	100.0%	-5.4
21024	AT2G02870.3   similar to kelch repeat-containing F-box family protein [Arabidopsis thaliana] (TAIR:At1g14330.1); similar to kelch repeat-containing F-box-like [Oryza sativa (japonica cultivar-group)] (GB:XP_467797.1); contains InterPro domain Kelch motif (InterPro:IPR006651); contains InterPro domain Cyclin-like F-box (InterPro:IPR001810); contains InterPro domain Kelch repeat (InterPro:IPR006652)   chr2:838035-840152 FORWARD   Aliases: T17M13.4, T17M13_4	6.4	6.5	-0.0	-0.0	100.0%	-5.0
21025	AT1G49350.1   pfkB-type carbohydrate kinase family protein, contains Pfam profile: PF00294 pfkB family carbohydrate kinase   chr1:18268651-18271330 FORWARD   Aliases: F13F21.22, F13F21_22	4.7	4.7	0.0	0.0	100.0%	-5.3
21026	AT4G21760.1   glycosyl hydrolase family 1 protein, contains Pfam PF00232 : Glycosyl hydrolase family 1 domain; TIGRFAM TIGR01233: 6-phospho-beta-galactosidase; similar to dalcochinin 8'-O-beta-glucoside beta-glucosidase precursor (GI:6118076) (Dalbergia cochinchinensis)	2.8	2.8	0.0	0.0	100.0%	-5.5
21027	AT1G33950.1   avirulence-responsive family protein / avirulence induced gene (AIG1) family protein, similar to AIG1 protein SP:P54120 (Arabidopsis thaliana), NTGP4 GB:AAD09518 (Nicotiana tabacum); contains Pfam profile: PF00735 cell division protein (members of this family bind GTP)   chr1:12333026-12339162 REVERSE   Aliases: T3M13.3	2.8	2.8	0.0	0.0	100.0%	-5.8
21028	AT4G33925.1   expressed protein   chr4:16263242-16264229 FORWARD   Aliases: None	5.4	5.4	-0.0	-0.0	100.0%	-4.6
21029	AT5G59320.1   Symbol: LTP3   lipid transfer protein 3 (LTP3), identical to lipid transfer protein 3 from Arabidopsis thaliana (gi:8571921); contains Pfam protease inhibitor/seed storage/LTP family domain PF00234   chr5:23946197-23946965 FORWARD   Aliases: LIPID TRANSFER PROTEIN 3, MNC17.10, MNC17_10	2.8	2.8	0.0	0.0	100.0%	-5.4
21030	AT1G30825.1   Symbol: ARPC2A/DIS2   actin-related protein 2/3 complex 34kDa subunit family / arp2/3 complex 34kDa subunit family, contains Pfam PF04045: Arp2/3 complex, 34kD subunit p34-Arc; similar to ARP2/3 complex 34 kDa subunit (P34-ARC) (Swiss-Prot:O96623) (Dictyostelium discoideum); similar to ARP2/3 complex 34 kDa subunit (P34-ARC) (Actin-related protein 2/3 complex subunit 2) (Swiss-Prot:O15144) (Homo sapiens)	6.1	6.1	0.0	0.0	100.0%	-4.8
21031	AT3G04310.1   expressed protein   chr3:1141588-1142535 REVERSE   Aliases: T6K12.7, T6K12_7	4.9	4.9	-0.0	-0.0	100.0%	-5.0
21032	AT5G03050.1   expressed protein   chr5:715028-716320 REVERSE   Aliases: F15A17.80, F15A17_80	6.4	6.4	-0.0	-0.0	100.0%	-4.6
21033	AT1G58330.1   Symbol: ZW2   transcription factor-related, low similarity to tumor-related protein (Nicotiana glauca x Nicotiana langsdorffii) GI:688423, ocs-element binding factor 4 (Arabidopsis thaliana) GI:414613, mas-binding factor MBF3 (Solanum tuberosum) GI:13195751; supporting cDNA gi:6520153:dbj:AB028196.1:   chr1:21644795-21645699 FORWARD   Aliases: F19C14.6, F19C14_6, ZW2	2.6	2.5	0.0	0.0	100.0%	-5.4

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
21034	AT5G61450.1   2-phosphoglycerate kinase-related, contains weak similarity to 2-phosphoglycerate kinase (GI:467751) (Methanothermobacter ferredoxin)   chr5:24727259-24730171 REVERSE   Aliases: MCI2.1	6.1	6.1	-0.0	-0.0	100.0%	-4.8
21035	AT5G43040.1   DC1 domain-containing protein, contains Pfam profile PF03107: DC1 domain	3.1	3.1	0.0	0.0	100.0%	-5.4
21036	AT1G71420.1   pentatricopeptide (PPR) repeat-containing protein, contains Pfam profile PF01535: PPR repeat   chr1:26921484-26923721 REVERSE   Aliases: F3I17.26, F3I17_26	3.9	3.9	-0.0	-0.0	100.0%	-4.8
21037	AT2G29100.1   Symbol: ATGLR2.9   glutamate receptor family protein (GLR2.9), plant glutamate receptor family, PMID:11379626   chr2:12508169-12511989 REVERSE   Aliases: GLR2.9, T9I4.18, T9I4_18	2.2	2.2	0.0	0.0	100.0%	-5.9
21038	AT3G53590.1   leucine-rich repeat transmembrane protein kinase, putative, CLV1 receptor kinase, Arabidopsis thaliana, EMBL:ATU96879   chr3:19878357-19882629 REVERSE   Aliases: F4P12.290	3.1	3.1	-0.0	-0.0	100.0%	-4.9
21039	AT1G70110.1   lectin protein kinase family protein, contains Pfam domains, PF00138: Legume lectins alpha domain, PF00139: Legume lectins beta domain and PF00069: Protein kinase domain   chr1:26409901-26411986 REVERSE   Aliases: F20P5.16, F20P5_16	2.5	2.5	0.0	0.0	100.0%	-5.7
21040	AT5G50760.1   auxin-responsive family protein, similar to auxin-induced protein TGSUR22 (GI:10185820) (Tulipa gesneriana)   chr5:20661887-20662695 FORWARD   Aliases: MFB16.16, MFB16_16	2.7	2.7	0.0	0.0	100.0%	-4.1
21041	AT1G11410.1   S-locus protein kinase, putative, similar to receptor-like protein kinase (Arabidopsis thaliana) gi:4008008:gb:AAC95352; contains S-locus glycoprotein family domain, Pfam:PF00954   chr1:3841286-3844432 FORWARD   Aliases: T23J18.8, T23J18_8	3.2	3.2	0.0	0.0	100.0%	-5.3
21042	AT4G26430.1   Symbol: CSN6B   COP9 signalosome subunit 6 / CSN subunit 6 (CSN6B), identical to COP9 signalosome subunit 6 (Arabidopsis thaliana) GI:17940314, CSN complex subunit 6B (Arabidopsis thaliana) GI:18056667; contains Pfam profile PF01398: Mov34/MPN/PAD-1 family; supporting cDNA gi:17940313:gb:AF434762.1:AF434762; identical to cDNA CSN complex subunit 6B (CSN6B) GI:18056666   chr4:13355000-13357610 FORWARD   Aliases: M3E9.140, M3E9_140	5.5	5.5	0.0	0.0	100.0%	-4.8
21043	AT4G34090.2   expressed protein   chr4:16326861-16330183 REVERSE   Aliases: F28A23.150, F28A23_150	7.5	7.5	-0.0	-0.0	100.0%	-4.5
21044	AT1G72290.1   trypsin and protease inhibitor family protein / Kunitz family protein, similar to water-soluble chlorophyll protein (Raphanus sativus var. niger) GI:16945735, BnD22 drought induced protein (Brassica napus) GI:17813; contains Pfam profile PF00197: Trypsin and protease inhibitor   chr1:27219451-27220453 FORWARD   Aliases: T9N14.19, T9N14_19	2.1	2.1	-0.0	-0.0	100.0%	-6.0
21045	AT1G10720.1   BSD domain-containing protein, contains Pfam profile PF03909: BSD domain	3.3	3.3	0.0	0.0	100.0%	-5.1
21046	AT3G15390.1   expressed protein, low similarity to PRLI-interacting factor N (Arabidopsis thaliana) GI:11139276   chr3:5196696-5199538 REVERSE   Aliases: MJK13.5	3.0	3.0	-0.0	-0.0	100.0%	-5.7
21047	AT5G66550.1   Maf family protein, contains Pfam domain PF02545: Maf-like protein   chr5:26576856-26578404 REVERSE   Aliases: K1F13.22, K1F13_22	5.4	5.4	-0.0	-0.0	100.0%	-4.7
21048	AT5G39760.1   zinc finger homeobox protein-related / ZF-HD homeobox protein-related, predicted proteins, Arabidopsis thaliana   chr5:15928644-15930058 FORWARD   Aliases: MKM21.8, MKM21_8	3.9	3.9	-0.0	-0.0	100.0%	-5.4
21049	AT1G35617.1   expressed protein   chr1:13153561-13153926 FORWARD   Aliases: F15O4.21	4.0	4.0	0.0	0.0	100.0%	-5.0
21050	AT2G21920.1   expressed protein   chr2:9350490-9354239 REVERSE   Aliases: F7D8.24, F7D8_24	3.2	3.2	0.0	0.0	100.0%	-5.5
21051	AT1G49030.1   expressed protein, similar to PGPS/D12 (Petunia x hybrida) GI:4105794; contains Pfam profile PF04749: Protein of unknown function, DUF614   chr1:18140373-18141514 FORWARD   Aliases: F27J15.18, F27J15_18	2.9	2.9	-0.0	-0.0	100.0%	-5.3
21052	AT4G34660.1   SH3 domain-containing protein 2 (SH3P2), nearly identical to SH3 domain-containing protein 2 (Arabidopsis thaliana) GI:16974678; contains Pfam profile PF00018: SH3 domain   chr4:16545253-16548455 REVERSE   Aliases: T4L20.240, T4L20_240	4.5	4.5	0.0	0.0	100.0%	-5.1
21053	AT2G19630.1   F-box family protein, contains F-box domain Pfam:PF00646	2.7	2.7	-0.0	-0.0	100.0%	-5.7
21054	AT5G03230.1   expressed protein, contains Pfam profile PF04520: Protein of unknown function, DUF584   chr5:769513-770384 FORWARD   Aliases: F15A17.260, F15A17_260	2.7	2.7	0.0	0.0	100.0%	-4.9
21055	AT5G46750.1   human Rev interacting-like family protein / hRIP family protein, contains Pfam profile PF01412: Putative GTP-ase activating protein for Arf   chr5:18987005-18989136 REVERSE   Aliases: MZA15.17, MZA15_17	7.6	7.6	0.0	0.0	100.0%	-4.8

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
21056	AT1G56680.1   glycoside hydrolase family 19 protein, similar to basic endochitinase CHB4 precursor SP:Q06209 from (Brassica napus)   chr1:21254093-21255082 REVERSE   Aliases: F25P12.88, F25P12_88	3.3	3.3	0.0	0.0	100.0%	-5.3
21057	AT1G01700.1   member of KPP-like gene family, homolog of KPP (kinase partner protein) gene in tomato; expressed protein, contains Pfam profile PF03759: Domain of unknown function (DUF315)   chr1:259495-261474 REVERSE   Aliases: KINASE PARTNER PROTEIN LIKE, KPP LIKE, T1N6.8, T1N6_8	2.8	2.8	-0.0	-0.0	100.0%	-5.6
21058	AT5G43670.1   transport protein, putative, similar to Swiss-Prot:Q15436 protein transport protein Sec23A (Homo sapiens)   chr5:17555988-17559161 REVERSE   Aliases: MQO24.2, MQO24_2	3.3	3.3	-0.0	-0.0	100.0%	-5.3
21059	AT1G28430.1   Symbol: CYP705A24   cytochrome P450, putative, similar to cytochrome P450 (CYP93A1) GI:1435059 from (Glycine max)   chr1:9992972-9994628 REVERSE   Aliases: F3M18.13, F3M18_13	2.7	2.7	-0.0	-0.0	100.0%	-5.2
21060	AT1G28390.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr1:9966614-9968272 REVERSE   Aliases: F3M18.17, F3M18_17	5.6	5.6	0.0	0.0	100.0%	-4.8
21061	AT3G60740.1   Symbol: TTN1   tubulin folding cofactor D, identical to tubulin folding cofactor D GI:20514263 from (Arabidopsis thaliana)   chr3:22458244-22464339 REVERSE   Aliases: CHAMPIGNON, CHO, EMB133, EMBRYO DEFECTIVE 133, T4C21.150, TFC D, TITAN 1, TTN1, TUBULIN FOLDING COFACTOR D	4.2	4.2	0.0	0.0	100.0%	-5.5
21062	AT1G04070.1   Symbol: TOM22 I   expressed protein, Contains similarity to hypothetical mitochondrial import receptor subunit gb Z98597 from S. pombe. ESTs gb:T45575 and gb:Z26435 and gb:AA394576 come from this gene   chr1:1050552-1051185 REVERSE   Aliases: ATTOM22 I, F20D22.15, TOM22	6.2	6.2	0.0	0.0	100.0%	-4.8
21063	AT4G36220.1   Symbol: FAH1   cytochrome P450 84A1 (CYP84A1) / ferulate-5-hydroxylase (FAH1), identical to Cytochrome P450 84A1 (Ferulate-5-hydroxylase) (SP:Q42600) (Arabidopsis thaliana)   chr4:17137347-17139638 REVERSE   Aliases: CYP84A1, F23E13.110, F23E13_110, FERULATE 5 HYDROXYLASE, FERULATE 5 HYDROXYLASE 1, SINAPOYL ESTER ACCUMULATION 1	2.8	2.8	-0.0	-0.0	100.0%	-5.1
21064	AT5G58850.1   Symbol: MYB119	2.9	2.9	-0.0	-0.0	100.0%	-5.4
21065	AT5G17470.1   calmodulin-related protein, putative, similar to calmodulin-related protein 2, touch-induced SP:P25070 from (Arabidopsis thaliana)   chr5:5760968-5761408 REVERSE   Aliases: K3M16.40, K3M16_40	4.2	4.2	-0.0	-0.0	100.0%	-5.1
21066	AT5G66800.1   expressed protein   chr5:26688649-26689740 FORWARD   Aliases: MUD21.4, MUD21_4	3.8	3.8	0.0	0.0	100.0%	-4.9
21067	AT4G24860.1   AAA-type ATPase family protein, contains Pfam profile PF00004: ATPase, AAA family   chr4:12801559-12808200 REVERSE   Aliases: F6I7.70, F6I7_70	2.8	2.8	-0.0	-0.0	100.0%	-5.7
21068	AT3G13870.2   Symbol: RHD3   root hair defective 3 (RHD3), identical to root hair defective 3 (RHD3) GI:1839188 from (Arabidopsis thaliana) (Genes Dev (1997) 11(6), 799-811)	7.4	7.4	-0.0	-0.0	100.0%	-4.8
21069	AT2G47290.1   hypothetical protein   chr2:19425803-19426470 FORWARD   Aliases: T8I13.13	3.1	3.1	0.0	0.0	100.0%	-5.3
21070	AT4G30970.1   expressed protein   chr4:15069272-15074594 REVERSE   Aliases: F6I18.120, F6I18_120	3.8	3.8	0.0	0.0	100.0%	-5.5
21071	AT1G30560.1   transporter, putative, similar to glycerol-3-phosphate transporter (glycerol 3-phosphate permease) (Homo sapiens) GI:7543982   chr1:10824743-10826275 FORWARD   Aliases: T5I8.1, T5I8_1	2.2	2.2	0.0	0.0	100.0%	-6.0
21072	AT4G03690.1   expressed protein, very low similarity to SP:Q9UUA2 DNA repair and recombination protein pif1, mitochondrial precursor {Schizosaccharomyces pombe}   chr4:1631725-1634898 FORWARD   Aliases: T5L23.19, T5L23_19	2.3	2.3	0.0	0.0	100.0%	-6.1
21073	AT5G11110.1   similar to sucrose-phosphate synthase, putative [Arabidopsis thaliana] (TAIR:At1g04920.1); similar to sucrose-phosphate synthase, putative [Arabidopsis thaliana] (TAIR:At5g20280.1); similar to sucrose-phosphate synthase, putative [Arabidopsis thaliana] (TAIR:At4g10120.1); similar to sucrose phosphate synthase [Lycopersicon esculentum] (GB:AAU29197.1); similar to sucrose-6-phosphate synthase [Nicotiana tabacum] (GB:AAF06792.1); similar to sucrose-phosphate synthase (EC 2.4.1.14) - spinach (GB:JQ2277); similar to sucrose-phosphate synthase [Solanum tuberosum] (GB:CAA51872.1); similar to sucrose phosphate synthase [Actinidia chinensis] (GB:AAL86360.1); contains InterPro domain Glycosyl transferase, group 1 (InterPro:IPR001296)   chr5:3536227-3541134 FORWARD   Aliases: T5K6.100, T5K6_100	9.0	9.0	0.0	0.0	100.0%	-4.6
21074	AT1G09370.1   similar to invertase/pectin methylesterase inhibitor family protein [Arabidopsis thaliana] (TAIR:At1g09360.1); contains InterPro domain Plant invertase/pectin methylesterase inhibitor (InterPro:IPR007186); contains InterPro domain Pectinesterase inhibitor (InterPro:IPR006501)   chr1:3024898-3025437 FORWARD   Aliases: F14J9.3, F14J9_3	2.2	2.2	0.0	0.0	100.0%	-6.1
21075	AT4G00150.1   scarecrow-like transcription factor 6 (SCL6)   chr4:57199-59286 REVERSE   Aliases: F6N15.20, F6N15_20	4.6	4.6	-0.0	-0.0	100.0%	-5.2



Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
21076	AT5G44050.1   MATE efflux family protein, similar to ripening regulated protein DDTFR18 ( <i>Lycopersicon esculentum</i> ) GI:12231296; contains Pfam profile PF01554: Uncharacterized membrane protein family   chr5:17739711-17743606 FORWARD   Aliases: MRH10.16, MRH10_16	3.4	3.4	-0.0	-0.0	100.0%	-5.2
21077	AT3G01860.2   expressed protein   chr3:303725-304473 FORWARD   Aliases: F28J7.19, F28J7_19	5.5	5.5	-0.0	-0.0	100.0%	-4.4
21078	AT1G74250.1   DNAJ heat shock N-terminal domain-containing protein, contains Pfam domains PF00226: DnaJ domain and PF00096: Zinc finger, C2H2 type   chr1:27923989-27926075 FORWARD   Aliases: F1O17.8, F1O17_8	8.1	8.1	-0.0	-0.0	100.0%	-4.6
21079	AT5G18760.1   zinc finger (C3HC4-type RING finger) family protein, predicted proteins, <i>Arabidopsis thaliana</i> ; contains Pfam profile PF00097: Zinc finger, C3HC4 type (RING finger)   chr5:6258300-6260882 REVERSE   Aliases: F17K4.10, F17K4_10	3.8	3.8	0.0	0.0	100.0%	-5.3
21080	AT5G41950.1   expressed protein   chr5:16802942-16806741 FORWARD   Aliases: MJC20.5, MJC20_5	5.4	5.4	-0.0	-0.0	100.0%	-5.0
21081	AT3G13020.1   hAT dimerisation domain-containing protein, contains Pfam profile: PF04937 domain of unknown function (DUF659), weak hit to PF05699: hAT family dimerisation domain   chr3:4167002-4168924 REVERSE   Aliases: MGH6.14	3.2	3.2	0.0	0.0	100.0%	-5.3
21082	AT3G48770.1   expressed protein   chr3:18090246-18097802 REVERSE   Aliases: T21J18.40	2.9	2.9	-0.0	-0.0	100.0%	-5.4
21083	AT3G50190.1   expressed protein, similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g50130.1); similar to expressed protein [ <i>Arabidopsis thaliana</i> ] (TAIR:At3g50140.1); similar to hypothetical protein [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_481746.1); contains InterPro domain Plant protein of unknown function (InterPro:IPR004158); contains InterPro domain Proline-rich region (InterPro:IPR000694)	2.8	2.8	-0.0	-0.0	100.0%	-4.8
21084	AT2G01140.1   fructose-bisphosphate aldolase, putative, similar to plastidic aldolase NPALDP1 from <i>Nicotiana paniculata</i> (GI:4827251); contains Pfam profile PF00274 Fructose-bisphosphate aldolase class-I   chr2:94810-96634 REVERSE   Aliases: F10A8.2, F10A8_2	11.3	11.3	0.0	0.0	100.0%	-5.4
21085	AT4G19680.2   Symbol: IRT2   similar to iron-responsive transporter (IRT1) [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g19690.2); similar to iron-regulated transporter 1 [ <i>Lycopersicon esculentum</i> ] (GB:AAD30548.1); contains InterPro domain ZIP zinc/iron transport (InterPro:IPR004698); contains InterPro domain Zinc transporter ZIP (InterPro:IPR003689)   chr4:10703386-10704811 FORWARD   Aliases: T16H5.40, T16H5_40	3.1	3.1	0.0	0.0	100.0%	-4.1
21086	AT1G27060.1   regulator of chromosome condensation (RCC1) family protein, low similarity to UVB-resistance protein UVR8 ( <i>Arabidopsis thaliana</i> ) GI:5478530; contains Pfam profile PF00415: Regulator of chromosome condensation (RCC1)	4.2	4.2	0.0	0.0	100.0%	-4.8
21087	AT4G19960.1   potassium transporter family protein, similar to potassium transporter ( <i>Arabidopsis thaliana</i> ) gi:2654088:gb:AAB87687; KUP/HAK/KT Transporter family member, PMID:11500563; contains Pfam profile PF02705: K+ potassium transporter   chr4:10813817-10817060 FORWARD   Aliases: F18F4.60, F18F4_60	4.7	4.7	0.0	0.0	100.0%	-4.9
21088	AT5G23220.1   isochorismatase hydrolase family protein, low similarity to SP:P45743Isochorismatase (EC 3.3.2.1) (2,3 dihydro-2,3 dihydroxybenzoate synthase) (Superoxide-inducible protein) (SOI1) { <i>Bacillus subtilis</i> }; contains Pfam profile PF00857: isochorismatase family protein   chr5:7819819-7820679 REVERSE   Aliases: MKD15.8, MKD15_8	2.7	2.7	0.0	0.0	100.0%	-4.1
21089	AT5G41540.1   disease resistance protein (TIR-NBS-LRR class), putative, domain signature TIR-NBS-LRR exists, suggestive of a disease resistance protein.   chr5:16629887-16633291 REVERSE   Aliases: MBK23.6, MBK23_6	2.8	2.8	0.0	0.0	100.0%	-5.4
21090	AT4G12300.1   Symbol: CYP706A4   cytochrome P450 family protein, flavonoid 3',5'-hydroxylase - <i>Campanula medium</i> , PID:d1003951	5.2	5.2	-0.0	-0.0	100.0%	-4.8
21091	AT4G10410.1   expressed protein   chr4:6448979-6449994 REVERSE   Aliases: F7L13.2	2.8	2.8	-0.0	-0.0	100.0%	-5.2
21092	AT2G27420.1   cysteine proteinase, putative, contains similarity to cysteine protease SPCP1 GI:13491750 from ( <i>Ipomoea batatas</i> )	2.9	2.9	-0.0	-0.0	100.0%	-5.4
21093	AT4G29640.1   cytidine deaminase, putative / cytidine aminohydrolase, putative, identical to cytidine deaminase 5 (CDA5) ( <i>Arabidopsis thaliana</i> ) GI:3818578, cytidine deaminase homolog DesG ( <i>Arabidopsis thaliana</i> ) GI:4836449; similar to cytidine deaminase (CDD) ( <i>Arabidopsis thaliana</i> ) GI:3046700; contains Pfam profile PF00383: Cytidine and deoxycytidylate deaminase zinc-binding   chr4:14525836-14526876 FORWARD   Aliases: T16L4.150, T16L4_150	3.4	3.4	0.0	0.0	100.0%	-4.9
21094	AT2G17510.1   ribonuclease II family protein, similar to SP:P37202 Mitotic control protein dis3 { <i>Schizosaccharomyces pombe</i> }; contains Pfam profile PF00773: RNB-like protein   chr2:7616352-7623049 REVERSE   Aliases: MJB20.7, MJB20_7	4.8	4.8	0.0	0.0	100.0%	-4.7
21095	AT4G18970.1   GDSL-motif lipase/hydrolase family protein, similar to family II lipases EXL3 GI:15054386, EXL1 GI:15054382, EXL2 GI:15054384 from ( <i>Arabidopsis thaliana</i> ); contains Pfam profile PF00657: GDSL-like Lipase/Acylhydrolase	3.2	3.2	-0.0	-0.0	100.0%	-5.6

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
21096	AT2G01240.1   reticulon family protein (RTNLB15), contains Pfam profile PF02453: Reticulon   chr2:128439-129255 REVERSE   Aliases: F10A8.12, F10A8_12	2.7	2.7	-0.0	-0.0	100.0%	-5.2
21097	AT4G00400.1   phospholipid/glycerol acyltransferase family protein   chr4:174072-176837 REVERSE   Aliases: A_IG005I10.4, A_IG005I10_4, F5I10.4, F5I10_4	2.9	2.9	0.0	0.0	100.0%	-5.4
21098	AT2G47300.1   expressed protein   chr2:19427076-19428593 FORWARD   Aliases: T8I13.14	2.1	2.1	0.0	0.0	100.0%	-6.0
21099	AT2G10460.1   expressed protein, includes At2g05890, At4g07450, At3g30630, At3g43100, At2g09960, At3g30550, At1g39430, At2g10460, At4g03640, At5g35250	2.7	2.7	0.0	0.0	100.0%	-5.1
21100	AT1G09380.1   integral membrane family protein / nodulin MtN21-related, similar to MtN21 GI:2598575 (root nodule development) from (Medicago truncatula)   chr1:3026137-3029551 REVERSE   Aliases: F14J9.4, F14J9_4	3.3	3.3	-0.0	-0.0	100.0%	-5.3
21101	AT5G23820.1   MD-2-related lipid recognition domain-containing protein / ML domain-containing protein, contains Pfam profile PF02221: ML domain   chr5:8031271-8033018 FORWARD   Aliases: MRO11.14, MRO11_14	3.5	3.5	0.0	0.0	100.0%	-5.0
21102	AT5G18250.1   expressed protein, similar to unknown protein (dbj:BAA90342.1)   chr5:6033706-6035382 FORWARD   Aliases: MRG7.21, MRG7_21	5.1	5.1	-0.0	-0.0	100.0%	-4.8
21103	AT3G22650.1   F-box family protein, contains F-box domain Pfam:PF00646	2.6	2.6	0.0	0.0	100.0%	-5.5
21104	AT1G31160.1   zinc-binding protein, putative / protein kinase C inhibitor, putative, similar to 14 kDa zinc-binding protein (Protein kinase C inhibitor, PKCI) (Zea mays) Swiss-Prot:P42856   chr1:11122640-11124133 REVERSE   Aliases: F28K20.9, F28K20_9	6.7	6.7	0.0	0.0	100.0%	-4.5
21105	AT5G42920.2   expressed protein   chr5:17223379-17226751 REVERSE   Aliases: MBD2.12, MBD2_12	7.6	7.6	0.0	0.0	100.0%	-5.0
21106	AT5G19630.1   expressed protein   chr5:6627978-6629997 REVERSE   Aliases: T29J13.50, T29J13_50	7.1	7.1	-0.0	-0.0	100.0%	-4.5
21107	AT5G43110.1   pumilio/Puf RNA-binding domain-containing protein, contains similarity to RNA-binding protein   chr5:17327070-17329165 FORWARD   Aliases: MMG4.14, MMG4_14	3.7	3.7	-0.0	-0.0	100.0%	-4.9
21108	AT3G58070.1   zinc finger (C2H2 type) family protein, contains Pfam domain, PF00096: Zinc finger, C2H2 type   chr3:21517590-21518631 REVERSE   Aliases: F9D24.2	3.6	3.6	0.0	0.0	100.0%	-5.2
21109	AT2G26450.1   pectinesterase family protein, contains Pfam profiles: PF01095 pectinesterase, PF04043 plant invertase/pectin methylesterase inhibitor   chr2:11258198-11260690 FORWARD   Aliases: T9J22.12, T9J22_12	2.9	2.9	-0.0	-0.0	100.0%	-5.3
21110	AT3G52310.1   ABC transporter family protein, contains Pfam profile: PF00005 ABC transporter   chr3:19410356-19413931 FORWARD   Aliases: T25B15.80	2.9	2.9	-0.0	-0.0	100.0%	-5.1
21111	AT1G51910.1   protein kinase family protein, contains Serine/Threonine protein kinases active-site signature, PROSITE:PS00108   chr1:19287946-19292054 REVERSE   Aliases: T14L22.12, T14L22_12	3.5	3.5	0.0	0.0	100.0%	-5.3
21112	AT3G03740.1   Symbol: ATBPM4	4.3	4.3	-0.0	-0.0	100.0%	-5.0
21113	AT5G57290.1   60S acidic ribosomal protein P3 (RPP3B)   chr5:23224055-23225121 REVERSE   Aliases: MJB24.10, MJB24_10	9.4	9.4	0.0	0.0	100.0%	-4.5
21114	AT5G27730.1   expressed protein   chr5:9820253-9823090 FORWARD   Aliases: T1G16.60, T1G16_60	4.3	4.3	-0.0	-0.0	100.0%	-5.3
21115	AT4G22430.1   hypothetical protein   chr4:11827786-11828917 FORWARD   Aliases: F7K2.10, F7K2_10	2.7	2.7	-0.0	-0.0	100.0%	-5.5
21116	AT5G48310.1   expressed protein   chr5:19592187-19597588 REVERSE   Aliases: K23F3.3, K23F3_3	5.8	5.8	0.0	0.0	100.0%	-4.9
21117	AT3G18160.2   peroxin-3 family protein, contains Pfam domain, PF04882: Peroxin-3   chr3:6220632-6223079 FORWARD   Aliases: MRC8.15	5.4	5.4	-0.0	-0.0	100.0%	-5.3
21118	AT3G22860.1   Symbol: TIF3C2	2.9	2.9	0.0	0.0	100.0%	-5.5
21119	AT3G17790.1   Symbol: ATACP5	3.6	3.6	-0.0	-0.0	100.0%	-4.5

Rank	Description	15.dpi	5.dpi	M	t	adj.q	B
21120	AT1G33670.1   leucine-rich repeat family protein, contains leucine rich-repeat domains Pfam:PF00560, INTERPRO:IPR001611; similar to receptor kinase-like protein GB:AAB82755 GI:2586083 from ( <i>Oryza longistaminata</i> ) (Science 270 (5243), 1804-1806 (1995))   chr1:12201943-12203388 FORWARD   Aliases: F14M2.19, F14M2_19	2.6	2.6	0.0	0.0	100.0%	-5.6
21121	AT3G11060.1   expressed protein   chr3:3466309-3466950 REVERSE   Aliases: F11B9.2	3.2	3.2	-0.0	-0.0	100.0%	-5.4
21122	AT1G06800.2   lipase class 3 family protein, similar to DEFECTIVE IN ANOTHER DEHISCENCE1 ( <i>Arabidopsis thaliana</i> ) GI:16215706; contains Pfam profile PF01764: Lipase   chr1:2090040-2091685 REVERSE   Aliases: F4H5.11, F4H5_11	3.6	3.6	-0.0	-0.0	100.0%	-5.2
21123	AT4G01420.1   Symbol: CBL5   calcineurin B-like protein 5 (CBL5), identical to calcineurin B-like protein 5 (GI:9965366) ( <i>Arabidopsis thaliana</i> ); similar to <i>N. crassa</i> calcineurin calcium-regulated protein phosphatase, GenBank accession number P87072   chr4:580038-581518 REVERSE   Aliases: CALCINEURIN B LIKE PROTEIN 5, F3D13.2, F3D13_2	2.0	2.0	-0.0	-0.0	100.0%	-6.0
21124	AT2G21480.1   protein kinase family protein, contains protein kinase domain, Pfam:PF00069   chr2:9209833-9212448 REVERSE   Aliases: F3K23.24, F3K23_24	3.2	3.2	-0.0	-0.0	100.0%	-5.5
21125	AT4G38240.2   Symbol: CGL1   alpha-1,3-mannosyl-glycoprotein beta-1,2-N-acetylglucosaminyltransferase, putative, similar to N-acetylglucosaminyltransferase I from <i>Arabidopsis thaliana</i> (gi:5139335); contains AT-AC non-consensus splice sites at intron 13   chr4:17931564-17935319 REVERSE   Aliases: CGL, COMPLEX GLYCAN LESS, F20D10.360, F20D10_360	4.0	4.0	0.0	0.0	100.0%	-5.1
21126	AT5G15640.1   mitochondrial substrate carrier family protein, contains Pfam profile: PF00153 mitochondrial carrier protein   chr5:5087374-5090043 FORWARD   Aliases: F14F8.20, F14F8_20	5.4	5.4	-0.0	-0.0	100.0%	-5.2
21127	AT1G77710.1   expressed protein, similar to hypothetical protein GB:P34661 ( <i>Caenorhabditis elegans</i> )   chr1:29211577-29212943 FORWARD   Aliases: T32E8.4, T32E8_4	11.5	11.5	0.0	0.0	100.0%	-5.0
21128	AT1G53120.1   RNA-binding S4 domain-containing protein	6.6	6.6	-0.0	-0.0	100.0%	-4.7
21129	AT3G23100.1   Symbol: XRCC4   double strand break repair protein, putative (XRCC4), identical to cDNA putative double strand break repair protein (XRCC4) GI:9800642   chr3:8220689-8222155 FORWARD   Aliases: MXC7.14	5.2	5.2	0.0	0.0	100.0%	-5.0
21130	AT1G55830.1   expressed protein, similar to M-type 9 protein (GI:507127) ( <i>Streptococcus pyogenes</i> )   chr1:20871584-20873871 REVERSE   Aliases: F20N2.20	5.4	5.4	-0.0	-0.0	100.0%	-4.6
21131	AT3G28500.1   60S acidic ribosomal protein P2 (RPP2C), similar to acidic ribosomal protein P2b (rpp2b) GB:U62753 GI:2431770 from ( <i>Zea mays</i> )   chr3:10683334-10683968 FORWARD   Aliases: T20D4.1	6.1	6.1	0.0	0.0	100.0%	-4.5
21132	AT1G06080.1   Symbol: ADS1   delta 9 desaturase (ADS1), identical to delta 9 acyl-lipid desaturase (ADS1) GB:BAA25180 GI:2970034 from ( <i>Arabidopsis thaliana</i> )   chr1:1843569-1846299 FORWARD   Aliases: DELTA 9 DESATURASE, DELTA 9 DESATURASE 1, T21E18.13, T21E18_13	2.8	2.8	0.0	0.0	100.0%	-5.3
21133	AT1G66020.1   terpene synthase/cyclase family protein, contains Pfam profile: PF01397: Terpene synthase family	3.4	3.4	0.0	0.0	100.0%	-4.5
21134	AT5G58820.1   subtilase family protein, contains similarity to prepro-cucumisin GI:807698 from ( <i>Cucumis melo</i> )   chr5:23769182-23771999 FORWARD   Aliases: K19M22.2, K19M22_2	2.6	2.6	-0.0	-0.0	100.0%	-6.1
21135	AT1G27310.1   nuclear transport factor 2 (NTF2), putative, similar to Swiss-Prot:P33331 nuclear transport factor 2 (NTF-2) (Nuclear transport factor P10) ( <i>Saccharomyces cerevisiae</i> )   chr1:9484338-9485883 REVERSE   Aliases: F17L21.10, F17L21_10	7.0	7.0	0.0	0.0	100.0%	-4.6
21136	AT3G05760.1   expressed protein   chr3:1707909-1710529 FORWARD   Aliases: F10A16.5, F10A16_5	9.5	9.5	0.0	0.0	100.0%	-5.2
21137	AT2G21540.2   similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g34580.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g39180.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At4g36490.1); similar to SEC14 cytosolic factor, putative / phosphoglyceride transfer protein, putative [ <i>Arabidopsis thaliana</i> ] (TAIR:At2g18180.1); similar to putative SEC14 cytosolic factor [ <i>Oryza sativa</i> (japonica cultivar-group)] (GB:XP_465384.1); contains InterPro domain Cellular retinaldehyde-binding/triple function, C-terminal (InterPro:IPR001251); contains InterPro domain Cellular retinaldehyde binding/alpha-tocopherol transport (InterPro:IPR001071); contains InterPro domain Cellular retinaldehyde-binding/triple function, N-terminal (InterPro:IPR008273)   chr2:9227629-9231359 REVERSE   Aliases: F3K23.30	3.2	3.2	-0.0	-0.0	100.0%	-4.5
21138	AT1G16910.1   expressed protein, contains Pfam profile PF04852: Protein of unknown function (DUF640)   chr1:5785366-5785860 FORWARD   Aliases: F17F16.11	2.8	2.8	0.0	0.0	100.0%	-5.3